Abstract Book

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Symposia Presentation Abstracts

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INLA: A way for ecologists to overcome their worst impulses

Evan M. Adams

Presenting author: **Evan Adams**, Biodiversity Research Institute, evan.adams@briloon.org

INLA—or Integrated Nested Laplace Approximation—is a horrifying name for an R package, but it gives ecologists access to fast and powerful spatial modeling tools. This package was developed by Thiago Martins, Daniel Simpson, Finn Lindgren and Havard Rue (www.r-inla.org) and is handy because you can account for spatial bias in sampling effort when estimating a spatial pattern. Scientists love collecting data, but that desire does not always lead to a data set appropriate for spatial inference. Quantitative ecologists are often cobbling together imperfect data sets from multiple projects or dealing with semi-structured data that lack formalized sampling designs. In this talk, I'll show how INLA can account for preferential spatial sampling and how you can significantly improve your spatial modeling analyses without having model runs take days to finish. As an example, I'll be talking about estimating spatial patterns in mercury exposure across biota in New York State and the factors that influence these patterns. I'll show you what unbalanced sampling looks like, how to account for its effect, and how to interpret the results. Finally, I'll wrap things up with the other kinds of spatial models you can implement in INLA so you can decide if this is something worth exploring for your research.

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dplyr: A useful toolbox for manipulating data

Stepfanie M. Aguillon

Presenting author: **Stepfanie Aguillon**, Cornell University, stepfanie.aguillon@gmail.com

Using the free, open-source program R is becoming increasingly common in the sciences, and particularly so in ornithological research. With the wide array of available "packages" that extend the capabilities of R, it can be difficult for ornithologists to identify useful packages for their own research. In this lightning talk, I will discuss 'dplyr' a data manipulation package that is part of the tidyverse. dplyr makes manipulating data a breeze! From filtering and summarizing single datasets to joining multiple datasets together, dplyr can do it all! This package is useful both for small and large datasets and represents an easy introduction into coding for new users. Additionally, packages within the tidyverse share an underlying coding grammar, so learning to manipulate data with dplyr allows for an easy transition into many other R packages. I will include example code to jumpstart new R users into manipulating data with dplyr and show how easy it can be to make reproducible code in the tidyverse.

Amazonian biogeography from a historical perspective

Alexandre Aleixo

Presenting author: **Alexandre Aleixo**, Finnish Museum of Natural History, University of Helsinki, alexandre.aleixo@helsinki.fi

The mega-diverse Amazonian lowlands are a central area for discussions on processes that drive biotic diversification as well as those on the modern climate-crisis era given its paramount role as a carbon storage and sink ecosystem. Historically, the study of Amazonian biogeography evolved from documenting the ranges of closely related taxa based on specimens collected throughout the basin, to estimating phylogeographies and phylogenies based on molecular data (mainly DNA sequencing) obtained from tissue samples. While over time, vicariant scenarios of diversification driven by either climate change or river-dynamics have dominated the field as competing alternative hypotheses, more recent analyses have supported them as not mutually exclusive. In fact, a synergistic interaction between climate change and an active geological setting might together account for biotic diversification over Amazonian landscapes, with recent analyses also supporting an important role for dispersal over broad time scales. While these drivers of biotic change seem to have affected consistently all Amazonian environments, the responses of avifaunas associated with distinct habitats such as upland terra-firme, seasonally-flooded, and white-sand forests, as well as savannahs, varied significantly, and are explored in more detail. Despite all conceptual advances experienced by Amazonian biogeography during the past decades, the temporal and spatial contexts of the diversification scenarios favored over time have yet to be tested with more robust (mainly genomic) datasets.

The Partners in Flight Focal Species Approach: Using multispecies indicators to inform oak woodland conservation planning and implementation in the Klamath Siskiyou Bioregion of southern Oregon and northern California

John D. Alexander, Caitlyn R. Gillespie, Katherine E. Halstead, Jaime L. Stephens, and Sara Evans-Peters
Presenting author: **John Alexander**, Klamath Bird Observatory, jda@KlamathBird.org

Partners in Flight (PIF) bird conservation plans set conservation objectives for bird populations and their habitats across North America. Many regional PIF plans also identify suites of focal species that are associated with key habitat features; these birds serve as indicators of biodiversity and ecosystem function. We will demonstrate how PIF focal species can be used to drive conservation planning, implementation, and evaluation by describing how PIF's focal species approach was used to develop the Klamath Siskiyou Oak Network Strategic Conservation Action Plan (SAP) and how focal species monitoring is being used to ensure SAP implementation progresses within an adaptive management framework. We used a novel species-centered habitat modeling approach to map the predicted distribution of oak focal species in the SAP's four oak ecosystem targets – oak savanna, oak chaparral, oak woodland, and oak conifer. Specific suites of PIF focal species were identified as key ecological attributes for each target and multi-species occurrence metrics were identified for assessing the current and desired status of each ecosystem target at both local and landscape scales. PIF species prioritizations and conservation objectives were then used to help rank the threats that stress and degrade aspects of the four oak ecosystem targets. Habitat objectives identified for PIF focal species were then used to help develop and prioritize strategies that will be implemented to reduce top ranked threats and improve the status of the ecosystem targets. Now, as the SAP is being implemented within an adaptive management framework, focal species monitoring is being used to measure short- and long-term outcomes to ensure conservation effectiveness.

The neural encoding of optic flow differs among bird species with distinct flight modes

Andrea H. Gaede, Graham Smyth, Vikram B. Baliga, Cristian Gutierrez-Ibañez, Douglas R. Wylie, and Douglas L. Altshuler
Presenting author: **Doug Altshuler**, University of British Columbia, doug@zoology.ubc.ca

Optic flow is processed in evolutionarily conserved midbrain pathways containing retinal recipient nuclei. In birds, these nuclei are called the lentiformis mesencephali (LM) and the nucleus of the Basal Optic Root (nBOR). A key question is, to what extent are optic flow neurons specialized to species-specific behaviors? Hummingbirds use vision to guide hovering flight and their LM is specialized in two respects: 1) in other tetrapods there is a strong bias for forward visual motion, whereas hummingbirds exhibit no direction bias; 2) hummingbird LM neurons are tightly tuned to faster velocities. We first ask if the hummingbird nBOR has shifted concomitantly in direction and velocity preference. Extracellular recordings from nBOR in hummingbirds, zebra finches, and pigeons revealed no differences in either direction or velocity preferences. However, as with the LM, nBOR neurons in hummingbirds are more tightly tuned to stimulus velocity. We next ask if the difference in velocity tuning was due to preference for lower spatial frequencies, higher temporal frequencies, or both. Hummingbird LM neurons were tuned to much lower spatial frequencies moving at much faster velocities. In contrast, differences among species in the spatiotemporal tuning preference of nBOR neurons were modest. However, in both LM and nBOR, hummingbird optic flow neurons were more tightly tuned in the spatiotemporal domain. These surprising changes to optic flow encoding are consistent with the behavior of hover-feeding in dense foliage, in which self-motion would result in fast movements of large images on the retina.

Monitoring disturbance and fragmentation of the endemic Caribbean pine forests of Andros, home of the critically endangered Bahama Oriole

Janine M. Antalffy, Michael G. Rowley, Scott B. Johnson, Shelley Cant-Woodside, Ethan H. Freid, Kevin E. Omland, and Matthew E. Fagan
Presenting author: **Janine Antalffy**, University of Maryland, Baltimore County, jana3@umbc.edu

The islands of Andros in The Bahamas, like other small islands of the Caribbean region, are key to sustaining global biodiversity. With six Important Bird Areas, Andros provides both year-round and wintering habitat for a diverse array of avian species, most notably the critically endangered and endemic resident songbird, the Bahama Oriole. Recent work has demonstrated that, of the many unique habitats on Andros, the Caribbean pine rockland forests provide crucial nesting habitat for the Bahama Oriole. The availability of suitable habitat is central to conservation, and the extent of this unique pine ecosystem on Andris is unknown, as is the response of this habitat to factors associated with climate change in The Caribbean. Monitoring the habitats of Andros, particularly Caribbean pine, is necessary to understand this response to climate change and inform conservation planning for the Bahama Oriole. Here, we developed a 2019 land classification map to assess the status of nine terrestrial habitats on Andros. Our Random Forest land cover classification model predicted habitat classes with high overall accuracy. We found that Caribbean pine was the dominant land class making up roughly a third of the total terrestrial area. Our findings highlight the extensiveness of Bahama Oriole habitat, having important implications for the conservation status of this species. This study presents a baseline tool with which researchers can track changes in habitat extent on Andros over time and better understand the impacts of climate change in this globally important region.

The role of cacao agroforests and secondary forests as reservoirs of bird diversity in Trinidad

Haley Arnold, Amy E. Deacon, Mark F. Hulme, Alex Sansom, Dan Jaggernauth and Anne E. Magurran

Presenting author: **Haley Arnold**, University of St Andrews, ha33@st-andrews.ac.uk

As the amount of pristine habitat on Earth declines, understanding how human-altered habitats can act as biodiversity reservoirs is a key challenge. We compare tree and bird biodiversity in actively cultivated and abandoned cacao agroforests, and primary forests in the Northern Range of Trinidad. We use a space-for-time approach to assess changes over c. 100 years of succession. We found that temporal alpha-diversity was taxon dependent; tree alpha-diversity increased with forest age, but there was no change in bird alpha-diversity. Tree and bird composition varied with forest age. A greater proportion of native trees, and forest-dependent and insectivorous birds were found in older forests. These findings highlight the value of actively-cultivated cacao agroforests and secondary forests, alongside primary forests, as biodiversity reservoirs. They also demonstrate how compositional change between forests at different successional stages can contribute to regional gamma-diversity. Cacao farming thus falls within a 'people and nature' framework supporting both biodiversity and livelihoods.

Unveiling the costs of bearing a novel trait: Experiments on male-male competition in Neotropical brushfinches

Jorge E. Avendaño and Carlos D. Cadena

Presenting author: **Jorge Avendaño**, Universidad de los Andes, jorgeavec@gmail.com

An important step towards understanding the role of social selection driving signal evolution is to assess how individuals perceive and respond to individuals exhibiting novel signals. Further, responses to conspecifics exhibiting novel ornaments may carry some physiological and social costs to senders and receivers, which ultimately may influence their odds of fixation. We assessed the role of a black pectoral band during territorial contests in two allopatric species of Neotropical passerine birds in the genus *Arremon* either having or lacking this plumage trait. Field experiments using taxidermic mounts and playback of conspecific songs revealed that males of both species were equally aggressive towards phenotypes bearing or lacking a pectoral band. We also simulated the presence of a pectoral band (i.e. artificially painted) in a population that lacks this trait, and compared changes in a social-mediated trait (i.e. home-range size) and physiology (i.e. body condition, corticosterone levels) between territorial males with and without pectoral bands. Baseline corticosterone levels increased in males with band after plumage manipulation, although this was not associated with changes in home-range size or body condition. However, some males with band divorced and lost their territories compared to males with no band after manipulation. Our results suggest that the presence or absence of a pectoral band in *Arremon* brushfinches has not likely evolved under via social selection in contexts of male-male competition; however, bearing a pectoral band triggered some costs in the physiology and pair bond stability of males, which may prevent the fixation of this trait.

Host phylogeny influences gut microbiome structure in breeding wood-warblers

Marcella D. Baiz, Elliot T. Miller, Andrew W. Wood, and David P. L. Toews

Presenting author: **Marcella Baiz**, Penn State University, marcelladbaiz@gmail.com

The gut microbiome (GM) can have important consequences for host physiology, health, and behavior. Further, host-specific associations may facilitate reproductive isolation between species upon secondary contact if host GMs are incompatible. Yet, how the environment, host diet and genetics shape the GM is poorly understood for natural populations, particularly for birds. To address this, we collected fecal samples from wood-warblers breeding in sympatry from two localities in Eastern North America across three years. We performed 16S metabarcoding of these samples to characterize the GM of these birds. Our analysis of >200 samples from 14 species shows unique GM structuring by species within this recent and rapidly diverging radiation. Relative to sampling year and geographic locality, host species explains ~4-8-fold more variation in GM between individuals. Further, we detected a positive

relationship in congruence between the host phylogeny and GM dissimilarity that was stronger than that between diet dissimilarity and GM dissimilarity, suggesting host genetics is a better predictor than diet of GM structure. Our results are consistent with other studies suggesting host species identity is an important influence on the avian gut microbiome.

Migration and winter ecology of Eastern Whip-poor-will

Marja H. Bakermans and Andrew C. Vitz

Presenting author: **Marja Bakermans**, Worcester Polytechnic Institute, mbakermans@wpi.edu

Full life-cycle conservation is critical for the Eastern Whip-poor-will (*Antrostomus vociferous*), an aerial insectivore in steep decline (4.4% annual decline in New England since 1966). Since 2018, we focused efforts on whip-poor-will movements and habitat selection during migration and on the wintering grounds. We fitted whip-poor-wills breeding in Massachusetts with Pinpoint GPS loggers (Lotek) programmed to collect location data during the migratory and over-wintering periods and retrieved and downloaded data from 30 units. We quantified land cover data using the North American Land Change Monitoring System and aerial imagery at both migratory stopover sites and overwinter locations. Preliminary results indicate that for migration and wintering locations, birds selected areas with significantly more forest cover (and less agricultural cover) compared to random locations, and this pattern held at multiple spatial scales. During migration, whip-poor-wills made both brief stops and extended stops. We were able to collect 249 location data points on migration, with approximately one-third of those points spent at extended stopovers. Across three spatial scales (i.e., 500m, 2km, and 5km) forest cover was greater at extended stopover locations compared to brief stops (all $P < 0.039$). These data suggest that habitat loss and fragmentation on the wintering grounds and migration routes may contribute to population declines.

Functional evolution of avian taste receptors

Maude W. Baldwin and Yasuka Toda

Presenting author: **Maude Baldwin**, Max Planck Institute for Ornithology, mbaldwin@orn.mpg.de

Taste is an important sense enabling animals to differentiate nutritious from toxic food items. Diversity in taste receptor repertoires across species suggests that the five basic tastes known from mice and humans—sweet , salty, sour, bitter, and savory (umami)—may not exist across all vertebrate clades. For example, birds lack T1R2, a necessary subunit of the sweet receptor in mammals, and although hummingbirds evolved a novel mechanism for sensing nectar sugars, it is not known whether carbohydrate detection has evolved in other bird species. Here we investigate the evolution of taste receptors involved in sweet and umami perception across passerines. Through a combined approach incorporating behavioral assays, ancestral state reconstruction, and functional testing of taste receptors from species with diverse diets and ancestrally reconstructed receptors, we infer the timing of sensory shifts and discuss the ecological implications for the passerine radiation.

Supporting durable grassland habitat conservation through farm bill programs using social-ecological systems science

Jessica C. Barnes, Ashley A. Dayer, Rich Iovanna, and Sarah Cline

Presenting author: **Jessica Barnes**, Virginia Tech, jcbarnes@vt.edu

Across North America, grassland bird populations have experienced dramatic declines over the past 50 years, largely due to habitat loss. Because 85% of grasslands in the U.S. are privately owned, voluntary financial incentive programs, such as the federal Conservation Reserve Program (CRP), are key tools for conserving grassland birds and their habitats. Grasslands established on retired agricultural lands through CRP provide food resources and nesting cover for grassland bird species, but these benefits are temporary if CRP fields are reverted to agriculture when their 10- to 15-year CRP contracts expire. Previous work by our research group found continued grassland conservation, or persistence, on almost 62% of former CRP fields in the southern Great Plains, but very few fields enrolled in other conservation programs after CRP, in spite of landowner interest. Other recent studies have demonstrated strong regional variation in rates of reversion to crops after CRP, but it is unclear what explains these patterns. Through in-depth interviews with landowners whose CRP contracts expired without renewal between 2014 and 2020, we explored landowners' post-CRP decisions and actions in detail. This presentation draws on theoretical frameworks for actor decision-making in complex social-ecological systems to describe the ecological, socioeconomic, and institutional factors that intersect to shape post-CRP land use in this region. We suggest ways to support the transition of expiring CRP grasslands to sustainable grazing operations, other conservation programs, and alternative post-CRP land uses that make financial sense for producers and provide enduring benefits for grassland bird conservation.

Thermal niche breadth and diet explain variation in elevational migration in Himalayan birds

Sahas Barve, Tarun Menon, and Vijay Ramesh

Presenting author: **Sahas Barve**, Smithsonian National Museum of Natural History, sahasbarve@gmail.com

Elevational migration is a globally ubiquitous avian behavior and is seen in over 12% of all species. Understanding the mechanisms that drive variation in elevational movement across an avifaunal assemblage can help explain the evolution of this widespread animal behavior and its role in shaping a montane life history in birds. We used the citizen-science dataset eBird to acquire checklist-based observation data of Himalayan birds. We used comprehensive data cleaning procedures and randomization tests to produce robust estimates of the extent of elevational migration for 239 species of terrestrial birds. We then examined the role of thermal niche breadth, body size, dispersal ability and diet in explaining the extent of elevational migration in Himalayan birds using a multi-model information theoretic framework, separately for the eastern and western Himalayan regions. The extent of elevational movement was best supported by the thermal niche breadth and diet of a species in both regions. High-elevation species had broad thermal niches and showed greater elevational migration, exploiting wintering elevations that were warmer in the winter than their summer elevations in the summer. The effect of thermal niche breadth was however also influenced by the species' diet. Seed-eating birds migrated downslope less than other diet categories. A broad thermal niche may have been key in facilitating some species to colonize the high Himalayas seasonally, during the breeding season.

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track2KBA: An R package for identifying important sites for biodiversity from tracking data

Martin Beal, Steffen Oppel, Jonathan Handley, Elizabeth J. Pearmain, Virginia Morera-Pujol, Ana P. B. Carneiro, Tammy E. Davies, Richard A. Phillips, Philip R. Taylor, Mark G. R. Miller, Aldina M. A. Franco, Inês Catry, Ana R. Patrício, Aissa Regalla, Iain Staniland, Charlotte Boyd, Paulo Catry, and Maria P. Dias

Presenting author: **Martin Beal**, MARE - Marine and Environmental Sciences Centre, ISPA - Instituto Universitário, martinbeal88@gmail.com

Identifying important sites for biodiversity is vital for conservation and management. However, there is a lack of accessible, easily-applied tools that enable practitioners to delineate important sites for highly mobile species using established criteria. We developed the R package 'track2KBA' as a tool to identify important sites using tracking data from individual animals. The method is based on three key steps: (1) identifying individual core areas, (2) assessing population-level representativeness of the sample, and (3) quantifying spatial overlap among individuals and scaling up to the population. We show examples of how the package can be useful for diverse taxa, from both marine and terrestrial systems.

Putting it all together: Ornithometrics — a task view for ornithology

Marc-Olivier Beausoleil

Presenting author: **Marc-Olivier Beausoleil**, McGill University, marc-olivier.beausoleil@mail.mcgill.ca

With the increase in utilization of R in ornithological research and an ever-increasing list of R packages to choose from, challenges are growing to find the package related to a specific field of study and verify which package might be more appropriate to conduct a research. Therefore, to facilitate package discovery, I share a task view or package collection in an "annotated bibliography" format which describes, by topic, the various packages that can be used to analyze ornithological data. Not only are the packages listed in a structured manner, they are also described including key functions. As a bonus, I included websites where ornithological data and data aggregators (such as weather data or bioclimatic variables) could be downloaded by researchers. For some of these websites, data-gathering R packages are added. I will show how to get started with the collection in order to download and install the packages listed.

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warbler and Rraven: Bioacoustics in R

María J. Benítez Saldívar

Presenting author: **María Juliana Benítez Saldívar**, Instituto Multidisciplinario de Biología Vegetal (IMBIV-CONICET), Argentina, julianabenitezsaldivar@gmail.com

The R package warbleR aims to simplify the analysis of the structure of acoustic signals in R, and Rraven connects R and the commonly used Raven Sound Analysis software. warbleR was developed by Marcelo Araya-Salas and Grace Smith-Vidaurre; and Rraven was written by Marcelo Araya-Salas. warbleR includes a wide range of functions for acoustic structure analysis. This package has a clear workflow that streamlines visualization of spectrograms and measurement of acoustic parameters. The Rraven package eases the exchange of data between R and Raven, and includes functions to effortlessly import and relabel Raven selection tables that can be input into multiple warbleR functions for analysis. In addition, selection tables can be exported from R to Raven. This talk will provide examples of warbleR specific tools such as downloading avian vocalizations from the online repository Xeno-Canto, and creating maps of recording locations. Other useful functions for exploring and comparing spectrograms will also be included.

Experimental exposure to noise alters gut microbiota in a songbird

Mae Berlow, Haruka Wada, and Elizabeth P. Derryberry

Presenting author: **Mae Berlow**, University of Tennessee, Knoxville, mae@utk.edu

Noise pollution is an unprecedented evolutionary pressure on wild animals that can lead to alteration of stress hormone levels and changes in foraging behavior. Both corticosterone and feeding behavior can have direct effects on gut bacteria, as well as indirect effects through changes in gut physiology. Therefore, we hypothesized that exposure to noise will alter gut microbial communities via indirect effects on stress hormones and foraging behaviors. We exposed captive White-crowned Sparrows to city-like noise and measured each individual's corticosterone level, food intake and gut microbial diversity at the end of four treatments (acclimation, noise, recovery, and control) using a balanced repeated-measures design. We found evidence to support our prediction for a causal, positive relationship between noise exposure and gut microbiota. We also found evidence that noise acts to increase corticosterone and decrease food intake. However, noise appeared to act directly on the gut microbiome or, more likely, through an unmeasured variable, rather than through indirect effects via corticosterone and food intake. Our results help to explain previous findings that urban, free-living White-crowned Sparrows have higher bacterial richness than rural sparrows. Our findings also add to a growing body of research indicating noise exposure affects stress hormone levels and foraging behaviors. Altogether, our study indicates that noise affects plasma corticosterone, feeding behavior, and the gut microbiome in a songbird and raises new questions as to the mechanism linking noise exposure to gut microbial diversity.

Prairie ponds fuel aerial insectivores: Tales of Tree Swallows in agro-ecosystems

Lisha L. Berzins, Christy A. Morrissey, Andie K. Mazer, David W. Howerter, and Robert G. Clark

Presenting author: **Lisha Berzins**, University of Guelph, lisha.berzins@usask.ca

In the Canadian prairies, agricultural practises have intensified to increase crop production which has led to the loss and degradation of ponds (i.e., flooded wetland basins). Losses of ponds in the prairies may negatively affect aerial insectivores, such as Tree Swallows (*Tachycineta bicolor*), by reducing the quantity or quality of their aquatic food supply during breeding. Analyses of long-term data (28 years) show that pond abundance affects nearly every aspect of reproduction: female swallows lay more eggs, and produce more fledglings and recruits in their lifetime when they experience abundant ponds when breeding. Additionally, nestlings were heavier prior to fledging and were more likely to recruit when raised in years with abundant ponds. A field study conducted in intensively cropped agricultural areas with varying pond abundance (low to high density) further showed that nest box occupancy was lower, and more variable, at sites with low pond abundance. Additionally, adult swallows breeding at sites with low pond abundance produced smaller, lighter nestlings. Nestling body mass prior to fledging is strongly related to food supply, suggesting that sites with low pond abundance may lack high-quality aquatic food resources for rapidly growing nestlings. Overall, because Tree Swallows are more likely to breed, have greater reproductive success, and produce higher-quality nestlings in agricultural landscapes with abundant ponds, this highlights the importance of conserving and restoring ponds to support aerial insectivore populations, and biodiversity more generally.

Estimating dietary niche width in a Neotropical highland endemic bird with multi-tissue stable isotope analysis

Elizabeth Besozzi, Holly Garrot, Pablo Elizondo, and Eli Bridge
Presenting author: **Elizabeth Besozzi**, University of Oklahoma, ebesozzi@ou.edu

The dual threat of climate change and anthropogenic disturbance imperils many montane endemic species. Páramo grasslands – the highest vegetation strata in Costa Rica – are vulnerable to climate-mediated upslope vegetation shifts and are prone to related losses of endemic birds. One such endemic is the Volcano Junco (*Junco vulcani*), which is found only in the isthmian páramo of Costa Rica and western Panama. Somewhat counterintuitively deforestation of highland habitats appears to benefit Volcano Juncos over the short term by allowing populations to expand downslope into disturbed sites that mimic the structure of páramo. However, these “pseudo-páramo” habitats have plant assemblages that differ from real páramo. We used stable isotope analysis to characterize the dietary niche of the Volcano Junco at disturbed and undisturbed sites with different vegetation assemblages. Using isotope ratios from different tissues, we sought to parse the effects of disturbance and vegetation richness on dietary niche width and to quantify individual variation in diet. Our data reveal the potential unseen consequences of the birds’ expansion into pseudo-páramo habitats and establish patterns of individual variation that inform the robustness of population-level estimates of dietary niche width. These results will help balance what may become conflicting priorities for protecting existing forest, and maintaining viable Volcano Junco populations.

A habitat and biodiversity assessment tool to prioritize multi-species conservation actions on agricultural lands

François Blouin, John F. Wilmshurst, Jeff Harder, Robin Bloom, David W. Johns, Paul Watson, and Lisa Nadeau
Presenting author: **Francois Blouin**, Francois Blouin Wildlife Consulting, fdblouin@gmail.com

The grasslands have experienced the greatest loss of breeding birds among all biomes of North America. In Canada, grassland birds have decreased by almost 60% since 1970, with grassland specialists being hit the hardest. Habitat loss, agricultural intensification, direct anthropogenic mortality, and the compounding effects of climate change are substantial threats to these species. The involvement of private landholders in this primarily agricultural landscape is critical to ensuring the conservation of birds and other species at risk (SAR). However, their willingness to embark on government-led strategies for SAR recovery is hindered by distrust, fear of policies and regulations, and lack of support or economic incentives. We developed an online tool to assist agricultural producers in identifying multi-species conservation actions relevant to their operation. It was designed to be easy to use and to allay regulatory and policy concerns by focusing on habitat management rather than species outcomes. The tool uses species occurrence databases and models from various sources to determine potential species at risk occurrence at the management unit level. Key habitat requirements and Beneficial Management Practices (BMP) are organized to minimize conflicts between species, and to optimize the anticipated impact on species populations. Producers identify habitats on their land and the tool identifies and ranks BMPs appropriate for their situation. Producers can then prioritize actions based on their priorities and constraints. In Alberta, the tool is integrated into the provincial Environmental Farm Plan, a free whole-farm self-assessment program aimed at improving environmental stewardship on agricultural lands.

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moult and moultmcmc: Inference for moult phenology models

Philipp H. Boersch-Supan
Presenting author: **Philipp Boersch-Supan**, British Trust for Ornithology, pboesu@gmail.com

Observations of moult state are commonly collected during bird ringing. They encapsulate information about a crucial part of the avian lifecycle. In most free-living bird populations moult progression and duration in individuals cannot be observed fully. Typically snapshot measurements of (re)captured individuals are used to infer these parameters on a population level. As an additional complication, recording of moult in the field may take various forms both in terms of the subset of the population that is sampled, and whether moult is recorded as a categorical state or a continuous progression score. Although Underhill & Zucchini (1989; Ibis 130:358) proposed a general modelling framework for moult phenology, ad-hoc inference approaches for moult data remain common. In part this is because easy-to-use software implementations of these models were lacking until recently. I describe the R package "moult" (Erni et al. 2013; J Stat Soft 52:8) for maximum likelihood inference of moult timing and duration, as well as the "moultmcmc" package which implements Bayesian inference for this class of models. Bayesian inference provides less biased estimates of moult timing and duration and more accurate uncertainty quantification than existing maximum likelihood methods, and allows a straightforward inclusion of hierarchical structures to accommodate the integration of moult data sets using different modes of recording, or to model individual heterogeneity in moult timing and progression when multiple recaptures are available for some individuals. This allows a better understanding of moult — a key energetic constraint on avian migration, reproduction, and survival — in the context of the full annual cycle.

Not only pigeons: Avian olfactory navigation studied by satellite telemetry

Francesco Bonadonna and Anna Gagliardo
Presenting author: **Francesco Bonadonna**, CNRS-France, francesco.bonadonna@cefe.cnrs.fr

The olfactory navigation hypothesis proposed to explain homing pigeon navigation predicts that birds learn the association of wind directions and wind-borne odours at home, and once displaced, determine the home direction on the basis of local environmental odours at the release site. Since whatever selection mechanism does not create a trait, but advantages existing traits, it was unlikely that artificial selection of this domestic species created the olfactory-navigation trait in pigeons, and that this mechanism was absent in other species. Actually, development of wildlife telemetry in the two last decades brought strong evidence on olfactory navigation also wild birds such as gulls, petrels, and passerines. Wild individuals artificially displaced both during migration or during incubation showed impaired capacities of compensating displacements only if deprived of their sense of smell. Contrariwise, satellite telemetry failed to find any validation for a magnetic navigation hypothesis. In spite of the fact that the nature of the olfactory map in wild birds is not yet elucidated we are confident that the continuous evolution of satellite technology will allow in a short future to elucidate, as it has been for pigeons, the details of the olfactory navigation mechanism in wild birds.

Addressing barriers to diversity in bird conservation

Susan Bonfield, Dalia Dorta, and Sheylda Díaz-Mendez
Presenting author: **Susan Bonfield**, Environment for the Americas, sbonfield@environmentamericas.org

Environment for the Americas has developed a model internship program that helps to recruit diverse youth for internship positions on federal lands and with non-governmental organizations. To improve the program, we have conducted almost a decade of surveys to examine the barriers diverse youth may face when applying for these positions and working at sites where staff, visitors, and other interns may be predominantly White. Our model has been very successful in addressing barriers and creating pathways to careers in science, natural resources, and bird conservation. Survey responses show that issues of connection, confidence, comfort, and capability can be addressed through considerations of culture, staff awareness of Diversity, Equity, and Inclusion, training, communication, and mentorship. This presentation shares our model and presents some of survey results from participating interns over the past decade.

Minor interspecies differences in breeding phenology and productivity between two co-existing aerial insectivores

Chloe K. Boynton, Olga C. Lansdorp, Nancy A. Mahony, and Tony D. Williams
Presenting author: **Chloe Boynton**, Environment and Climate Change Canada, chloe.boynton@canada.ca

Aerial insectivore populations have declined significantly across Canada for the last fifty years. While there are several suggested drivers of these population declines, including agricultural intensification, not all species are showing similar spatio-temporal population trends. Therefore, comparing interspecies differences in breeding productivity on the breeding grounds is vital to better understanding what is driving population variation among aerial insectivores. We examined breeding productivity and phenology in relation to habitat, weather and insect availability for two co-occurring swallow species, Tree Swallow (*Tachinyeta bicolor*; -3.37 regional annual trend index) and Barn Swallow (*Hirundo rustica*; -4.92 regional annual trend index) over four years on the southern coast of British Columbia, Canada. We found only minor interspecies differences in breeding productivity (clutch size, fledge success, brood size) comparing first broods, although Barn Swallows are double-brooded, suggesting higher potential productivity than Tree Swallows. However, Tree Swallows had larger clutches, earlier lay dates and more rapid cumulative laying than Barn Swallows. There was little effect of habitat on breeding productivity or phenology for either species and we found no significant difference in total insect abundance between crop and pasture habitats. Overall, our study suggests there is little interspecies variation in breeding productivity for first broods between these two co-occurring aerial insectivores in British Columbia. Therefore, it is more likely that interspecies differences in population trends in this region are caused by factors operating outside the breeding grounds, or during post-breeding.

Cognitive adaptation, reduced movement, and female choice along a montane gradient in a food-caching bird

Carrie L. Branch, Benjamin R. Sonnenberg, Angela M. Pitera, and Vladimir V. Pravosudov

Presenting author: **Carrie Branch**, Cornell University, clb345@cornell.edu

Environmental gradients often create different selective pressures among populations and may drive local adaptation. Along mountain slopes, heterogeneity occurs rapidly and predictably, resulting in local adaption on a rather small spatial scale. Mountain Chickadees are nonmigratory, food-caching birds that inhabit continuous montane gradients and use spatial cognition to recover their food stores and survive winter. Previous research shows that individuals inhabiting harsher, high elevations exhibit superior cognitive abilities and associated brain morphology compared to their milder, low-elevation counterparts. Recently, we've shown that natural selection is acting on the spatial cognitive abilities of Mountain Chickadees, resulting in local adaptation despite reduced movement and gene flow. Here I will discuss elevation-related variation in secondary sexual traits and the role females play in maintaining local adaptation via female choice.

When capacity building comes home to roost: How small teams protect the Black-capped Petrel in Haiti

Adam Brown and Anderson Jean

Presenting author: **Adam Brown**, Environmental Protection in the Caribbean (EPIC), abrown@epicislands.org

The Black-capped Petrel is an endangered Caribbean endemic seabird. With only five known nesting colonies, all located on the island of Hispaniola, the species is threatened by habitat loss, introduced predators, and strike risks along its flyways. Since 2012, a small team of conservationists, scientists, humanitarians, educators, and storytellers have worked together to protect the petrel from extinction. Herein, we detail the methods used to protect the species since the inception of the conservation process, the capacity building of young Haitian scientists to participate in petrel conservation, and the critical role capacity building played in protecting the Black-capped Petrel during the COVID-19 global pandemic. The pandemic forced international teams to stay away from Haiti and local Haitian-based conservation teams worked in smaller groups and in areas closer to their homes. In 2020, we recorded the highest number of Black-capped Petrel chicks fledged at both the Morne Vincent (n=15) and Tet Opak (n=38) petrel colonies, since the start of nest monitoring in 2012.

Representative public science: How two black grad students are making science accessible to all

Murry Burgess, Lauren Pharr, and Caren Cooper

Presenting author: **Lauren Pharr**, North Carolina State University, lpharr@ncsu.edu

Representation of Black, Indigenous, and other People of Color (BIPOC) in ornithology research, field work, lab work, and birding, can inspire members of these underrepresented groups to participate in these pursuits. BIPOC Ornithologists can advance broader diversity, equity, and inclusion goals through public science activities that elevate their representation. Their representation is important for both BIPOC and white audiences in academia and beyond and further encourages diversity in the field — people who feel welcome in the environment are more likely to stay there. Representation also breaks down stereotypes as well as bias, and improves the discipline of science (in scope, types of research, etc.) overall. Public science activities enable interactions among scientists and members of the public, and can amplify representation. This presentation features two Black graduate students who study birds and counter underrepresentation by carrying out public science to reach diverse audiences. Their public science activities include participation in social media campaigns such as #BlackBirdersWeek, contributing blog posts, public talks, bird-banding demonstrations, and authoring children's books about nature and science. These students deal with the ongoing challenges unique to Black women in natural sciences, and in response, promote awareness, education, and unique perspectives to create a more inclusive culture in Ornithology. Diversity continues to fuel innovation and performance. Therefore, by continuing to work towards increasing diversity through public science

activities, we will continue to address and break systemic barriers between science, the outdoors, and communities of color.

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bbsAssistant: An R package for downloading and handling data and information from the North American Breeding Bird Survey

Jessica L. Burnett

Presenting author: **Jessica Burnett**, USGS Core Science Systems, jburnett@usgs.gov

The North American Breeding Bird Survey (BBS) is the world's longest-running standardized survey of breeding birds. The BBS observations dataset currently comprises over 6.5 million data points (species count by route by year), and is freely and readily available for public use. The R package `bbsAssistant` contains functions to facilitate the downloading and querying of the BBS observations dataset, associated metadata, and authoritative analyses as published by the US Geological Survey. The package functions default to the most recent versions of the data, metadata, and analytical results but allow users to obtain historical releases of each. The package is published in the public domain (Creative Commons Zero v1.0 Universal).

Shifting From single species to multi-species and ecosystem-based approaches to conservation in Canada

Alaine F. Camfield

Presenting author: **Alaine Camfield**, Canadian Wildlife Service, Environment and Climate Change Canada, alaine.camfield@canada.ca

In June 2018, Canadian federal, provincial and territorial (F/P/T) governments approved the Pan-Canadian Approach to Transforming Species at Risk Conservation in Canada. This new approach represents key strategic shifts in conservation from predominantly single-species to more multi-species and ecosystem-based approaches, and from broad, independent efforts to more targeted and collaborative efforts on shared priority places, species and sectors. The Pan-Canadian Approach also shifts emphasis away from assessment and planning and focuses on increasing effort on implementing actions that achieve meaningful outcomes. The Pan-Canadian approach aims to achieve: better conservation outcomes for more species at risk, improved return on investment, and increased co-benefits for biodiversity and ecosystems. Eleven F/P/T priority places have been identified across the country under the Pan-Canadian Approach. The places selected have significant biodiversity, high concentrations of species at risk, and opportunities to advance conservation efforts. Although the initiatives began through F/P/T governments they are expanding to include collaboration with Indigenous peoples, other partners and stakeholders. In each priority place, collaborative teams use participatory planning tools such as the Open Standards for the Practice of Conservation and other decision support tools to implement conservation under an adaptive management framework. Enabled by the Canada Nature Fund and through matched funding by partners, these foundational activities are allowing partners to work together on-the-ground and co-invest in shared priority actions, such as: habitat stewardship, habitat restoration, education and outreach and other key actions.

Introduction: The relative importance and onset of different mechanisms of reproductive isolation

Leonardo Campagna and J. Albert C. Uy

Presenting author: **Leonardo Campagna**, Cornell Lab of Ornithology, lc736@cornell.edu

Reproductive isolation defines biological species and can be achieved in different ways and at different time scales, yet all of these mechanisms ultimately reduce or prevent gene flow between divergent populations. Traditionally, the different mechanisms that lead to reproductive isolation have been classified as pre or postzygotic, depending on whether they act before or after mating occurs. Prezygotic mechanisms include behavioral changes that affect mating signals, changes in foraging or migration behavior, and reproductive timing. Postzygotic barriers act after mating, such as selection against hybrids displaying intermediate phenotypes or the evolution of genetic incompatibilities, chromosomal rearrangements, changes in proteins that mediate sperm and egg recognition, and neo-sex chromosomes. Various factors can affect the specific mechanisms that can be at play between two diverging populations, including the amount of time they have evolved in allopatry before coming back into contact, specific structural properties of the genome (e.g., the existence of macromutations such as large inversions), and properties of a species mating system (e.g., divergent sexual selection on male mating traits). Some of these mechanisms may be key in causing speciation when gene flow persists, while others are a consequence of divergence in allopatry. The relative strength and stability of different mechanisms of reproductive isolation remains a matter of debate. This symposium aims to explore, through empirical and theoretical examples, when in the speciation process these different barriers may arise, their relative strength and likely prevalence in nature.

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pavo: Color analysis in birds

Luke C. Campillo

Presenting author: **Luke Campillo**, University of Hawaii, campillo@hawaii.edu

Birds see the world differently than humans, so analysis of plumage coloration should therefore be conducted from a “birds eye view.” In this talk, I will introduce the package pavo, which has the ability to take raw spectrophotometric plumage reflectance data (hereafter “spec data”) and turn it into something we humans can interpret (pavo also has the capacity to perform analysis on images, but that is outside the scope of this talk). For ornithological applications, spec data, measured as percentage of light reflected at each wavelength across the avian visual spectrum (300-700nm), often results in a very large data matrix formatted in an unintuitive, instrument-specific fashion. Moreover, even if a savvy R-user could wrangle these data into something operable, there were no built-in functions to calculate trait values that would be useful for analysis (e.g., the Euclidean distance in color space between two plumage patches). Thankfully, the developers of pavo have made it incredibly easy to seamlessly read in raw spec data, filter according to specific project needs, and produce publication-quality figures in an intuitive and comprehensive package. This is a must-learn for any ornithologist serious about working with coloration data.

Patterns of initial microbiome assembly in Neotropical birds

Felipe Campos-Cerda and Brendan J. M. Bohannan

Presenting author: **Felipe Campos-Cerda**, UNAM, camposcf1@gmail.com

Microbiomes (i.e., the community of microbes associated to an animal) deeply change animals' lives, impacting a wide array of developmental and physiological processes. Microbial associations are practically developed anew on each generation making microbiome assembly a very important event on an animal’s life. Following the nidobiome framework, we explored if nest architecture affected the nest’s microclimate and if that in turn influenced microbiome assembly in neotropical birds. The nidobiome framework is an integrative perspective to understand microbiome assembly, where nests have a central role at mediating the order and intensity of microbial exposure of neonates. The nidobiome recognizes nests as environments whose particular conditions result from parental decisions (e.g., structure and placement), and such conditions 1) may act as an environmental filter where only certain microbes can establish, and 2) facilitate microbial transmission from parents to offspring. We found evidence that tropical nests avoid extreme heat by evaporative cooling, a trait not previously reported in nests. We also found that nest architecture influenced microbiome assembly, with community composition following different temporal trajectories depending on nest type (i.e., cup nests, basket nests, cavity nests). We also expect some microbial taxa to show differential abundances as a response to microclimatic differences inside nests of different architectures. Our results show how the nidobiome framework can help discover new traits, such as nests displaying evaporative cooling, and facilitate the integration of information coming from multiple species, such as comparing trajectories of microbiome assembly from various bird species.

Idiosyncratic patterns and recent dynamics revealed by demographic modelling in seven Amazonian white-sand ecosystems birds

João M. G. Capurucho, Mary Ashley, Camila Ribas, and John Bates

Presenting author: **João Marcos Guimarães Capurucho**, Field Museum of Natural History, jcapurucho@fieldmuseum.org

White-sand ecosystems (WSE) have a patchy distribution throughout Amazonia. Larger and more connected patches are found in northern Amazonia while more isolated and smaller patches are found in southern Amazonia. WSE harbor a specialized community of birds that add to overall Amazonian diversity. Previous molecular studies have suggested recent changes in population size for WSE birds. We studied genetic structure, demographic history, and population size changes in seven WSE birds using Ultra-conserved elements (UCEs). Genetic structure was idiosyncratic with the Amazon river representing the only barrier shared among WSE species. Population structure in most cases is very recent, going back no more than 200,000 years. Among the 16 geographically structured populations identified among the study species, eight showed signal of population size changes and seven of these occur north of the Amazon river. Population expansion was identified as happening at two distinct moments: ~100,000 years ago involving six populations, and ~50,000 years ago involving two populations. The grouping of co-expanding populations is consistent with differences in habitat preference, corresponding to species that prefer open vegetation versus those preferring dense scrubby to forested vegetation. Overall, expansions could have been driven by the genesis of new WSE patches as observed in the geological record. The recent population structure and demographic changes suggest that WSE birds likely went through several cycles of connection, fragmentation, local extinction, and expansion of populations during climatic changes in the Pleistocene.

Using wing morphology to determine variation in natal dispersal distances in North American birds

Jonathan J. Chu and Santiago Claramunt

Presenting author: **Jonathan Chu**, University of Toronto, jonathanjojo.chu@mail.utoronto.ca

Dispersal is fundamental to many processes such as community connectivity, gene flow, speciation, and macroevolution. Natal dispersal, defined as the movement of an animal from birth site to first established breeding site, is usually the longest dispersal event among birds and thus the most influential. Empirical evidence has been ambiguous regarding the factors that explain variation in dispersal distances across species. Moreover, the cost of movement or flight efficiency have seldom been considered. Here we use large-scale mark-recovery data to estimate natal dispersal distances in North American birds and incorporate morphologically based flight efficiency proxies, ecological and behavioural factors into models that explain the variation of dispersal distances across species. We show that flight efficiency, as estimated by the hand-wing index, the aspect ratio, or the lift-to-drag ratio, is a significant predictor of natal dispersal distances. The best model consisted of flight efficiency, population size and habitat and could explain 45% of the variation. However, across models, ecological and behavioural variables were less important; only flight efficiency and population size had high variable importance across these models. We suggest that natal dispersal distance is primarily a function of the energetic cost of movement determined by flight morphology.

Lessons from flyway-scale shorebird conservation planning

Rob P. Clay, Scott Johnston, River Gates, Stan Senner, Brad Andres, Kelli Stone, and Isadora Angarita-Martínez

Presenting author: **Rob Clay**, Manomet, rclay@manomet.org

In late 2011, conservationists began conceptualizing a strategy for shorebird conservation within the Americas Atlantic Flyway, building from the success of the business plan for the recovery of the US East coast population of American Oystercatcher. This resulted in the production of a Business Strategy and a Business Plan in 2015. Since then, a Shorebird Conservation Strategy has been developed for the Americas Pacific Flyway (2016), and a strategic framework is currently under development for the Midcontinent Flyway. The Arctic Migratory Bird Initiative has also developed a workplan for the conservation of priority Arctic species throughout the Americas. The sequential development of these planning frameworks has facilitated the sharing of experiences and lessons learned, including: 1. Early engagement with key stakeholders throughout the flyway to shape and guide the planning process; 2. The value of national ornithological meetings as venues for input; 3. Alignment with national planning processes, such as national plans and bird conservation strategies; 4. Framing within the context of national commitments under Multilateral Environment Agreements; 5. Consideration of human wellbeing benefits and promotion of co-benefits; and 6. Government-to-government engagement. The Covid-19 pandemic had an initial major impact on development of the Midcontinent framework, but has since proved invaluable in terms of the opportunity to engage more people and institutions in the planning process through virtual means. Finally, the dashboard and story map approach pioneered by the Atlantic Flyway has demonstrated the importance and feasibility of tracking achievements at the flyway-scale.

Ecology of near-threatened Sickle-winged Nightjar in grasslands of northern Argentina

Kristina L. Cockle, Olga Villalba, Nestor Fariña, Alejandro Pietrek, Alejandro Bodrati, and Luis G. Pagano

Presenting author: **Kristina Cockle**, Instituto de Biología Subtropical (IBS)-CONICET, kristinacockle@gmail.com

Aerial insectivores are likely declining in the Neotropics, but their conservation is complicated by large knowledge gaps regarding their life history and habitat requirements. Using spotlighting, banding and radio-tracking (2012–2021), we examined habitat use, home-range size and age- and sex-specific survivorship of near-threatened Sickle-winged Nightjars (*Eleothreptus anomalus*) in a grassland reserve in northeastern Argentina. Sickle-winged Nightjars (216 banded, 8 radio-tagged) exclusively used native tall grassland for foraging, roosting, and nesting, avoiding exotic pine plantations, but using areas recently cleared of pines in restoration efforts. Males were smaller than females, detected four times more often, displayed at specific points along roads, never had brood patches, and foraged over smaller, overlapping home ranges (50% kernel adult male: 17 ± 7 ha; adult female: 84 ± 44; 1-yr old male: 162 ± 59 [mean ± SE, n = 6]) encompassing display sites, suggesting a lek-like mating system that may require hundreds of hectares of contiguous native grassland to maintain populations. A yearling male was captured 4.3 km from where it hatched. Yearlings developed a brood patch (female) and performed displays (male). According to our best-supported Cormack-Jolly-Seber model, detectability was four times higher for males than females, and annual survival 40% higher for adults than juveniles. Since 1996 the study region saw a doubling in plantation cover and 900% increase in insecticide use, highlighting the urgency for studies of aerial insectivore diets, prey availability, and toxicity, as well as conservation actions to protect South American grasslands from exotic pine plantations and agro-industry.

Understanding attitudes and norms of beach recreationists to reduce disturbances to shorebirds

Carolyn A. Comber and Ashley A. Dayer

Presenting author: **Carolyn Comber**, Virginia Tech, ccomber1@vt.edu

Human disturbance contributes to the decline of shorebirds. Disturbance can result from a variety of human activities, such as beach walking. Research shows that beach walking can negatively affect shorebirds. To minimize the harmful impacts of disturbance, we used a community-based social marketing approach to inform efforts to encourage beach walkers to walk around shorebird flocks rather than through them. Specifically, we sought to understand the benefits and constraints to this behavior. We recruited 27 participants from public Facebook groups associated with coastal areas on the Atlantic Coast. Using insights from the interviews, we created an online survey and administered it to a purchased sample of beach walkers (n = 1046) with experience walking on East Coast beaches in the last 12 months. We found that most beach walkers are not willing to walk the recommended distances needed to minimize disturbances to most shorebird species. We found that the constraints most predictive of people's willingness to walk around shorebird flocks included being unaware of the need to walk around flocks, the disbelief that there is a need to walk around flocks, and not knowing which birds were considered shorebirds. Benefits to walking around flocks related to personal satisfaction and personal enjoyment for people who wanted to view shorebirds in their natural state. People also cited reduced disturbance for shorebirds as a benefit to walking around flocks. We apply our results to suggest strategies for changing people's beach walking behavior and strategies for improving the knowledge gap related to shorebird disturbance and maximizing positive feelings about walking around shorebird flocks.

Automated telemetry reveals evidence of long-distance prospecting in Kirtland's Warblers

Nathan W. Cooper and Peter P. Marra

Presenting author: **Nathan Cooper**, Smithsonian Migratory Bird Center, nathanwands@gmail.com

Technology has revolutionized our ability to track animals across the globe, significantly advancing our understanding of animal movement. Technological and logistical challenges, however, have led to non-migratory movements that fall outside of the territory/home range paradigm receiving less attention. This may have resulted in a widespread underestimation of the frequency and spatial scale at which animals either move outside of their territories and home ranges or adopt altogether different space use strategies. We used a breeding range-wide automated radio-telemetry system to track movements of the Kirtland's Warbler. By attaching radio-tags on the wintering grounds and relocating the same individuals on the breeding grounds, we were able to sample the population without regard to their eventual breeding status or space use strategy. We found that a surprising proportion of breeders and most non-breeders made long-distance movements during the breeding season while conspecifics remained within their small territories. Movement frequency peaked during the nestling and fledgling periods, indicating that both breeders and non-breeders were likely prospecting to inform dispersal. A literature review revealed that Kirtland's Warblers moved farther than most species in absolute distances, and farther than all other species relative to normal daily movements. We argue that similarly long-distance movements likely exist in many other species, but have gone undetected because of technological limitations, research biases, and logistical challenges. Underestimation of the scale of these poorly understood life history behaviors has important implications for the ecology, evolution, and conservation of animals.

Honeycreeper hosts: Testing the effects of diet, environment, and evolutionary history on the gut microbiome using a classic example of adaptive radiation in Hawai'i

Maria S. Costantini, Elin Videvall, Michael G. Campana, Robert C. Fleischer, and Floyd A. Reed

Presenting author: **Maria Costantini**, University of Hawai'i at Manoa, mariacos@hawaii.edu

A component of endangered species management that has historically been overlooked is the relationship between a host and its gut microbiome. In animals, the microbiome has a strong influence on the health, fitness, and behavior of their hosts, and is often considered critically important to the animal's survival. The composition of the microbiome community can be altered by an individual's diet, environment, and evolutionary history. However, the extent to which and precisely how each of these factors influence microbiome composition and structure in wild bird populations has been minimally investigated. This project aimed to explore these three factors across the remaining species of the Hawaiian honeycreeper lineage. Most of the extant honeycreeper species are experiencing severe population declines due to a multitude of threats in the wild. It is likely that many of these threats also alter the composition, and potential functionality, of the host-associated microbiomes. This project used amplicon-based sequencing of the 16S rRNA gene to characterize the gut microbiome of Hawaiian honeycreepers across the remaining lineage in relation to diet, environment, and evolutionary history. Fecal samples, a proxy for the gut, were collected from 14 of the remaining 17 honeycreeper species and sequenced using the Illumina MiSeq platform. Preliminary results from two honeycreeper species suggest that diet and environment influence both the composition and structure of the associated microbial communities. Phylogeny-wide results will provide a baseline for microbiome work in Hawaiian honeycreepers, which will prove essential for conservation planning.

Habitat fragmentation shapes natal dispersal and genetic structure in the Placid Greenbul, an Afrotropical cooperative breeder

Laurence Cousseau, Martijn Hammers, Dries Van de Loock, Beate Apfelbeck, Mwangi Githiru, Erik Matthysen, and Luc Lens

Presenting author: **Laurence Cousseau**, Ghent University, laurence.cousseau@ugent.be

In cooperative breeding species, individuals delay dispersal and independent breeding and opt to help raise offspring that are not their own. The fragmentation of pristine habitats may result in spatial variation in the fitness pay-off of delayed dispersal and in turn affect the expression of cooperative breeding. Increased habitat isolation may increase dispersal costs, promoting delayed dispersal. Alternatively, reduced patch size and quality may decrease benefits of philopatry, promoting dispersal. We studied gene flow and natal dispersal in an Afrotropical cooperatively-breeding songbird (Placid Greenbul, *Phyllastrephus placidus*), in the highly fragmented cloud forests of the Taita Hills (SE Kenya). We found that almost 90% of fledglings settled within their natal subpopulation. Males born in fragmented forest dispersed about 1 year earlier than those born in continuous forest and, contrary to females, mostly settled within their natal patch. Females only rarely delayed their dispersal for more than 1 year, both in fragmented and continuous forests. These patterns of natal dispersal were reflected in the spatial genetic structure as well as in the direction of gene flow. Our results suggest that early male dispersal is jointly driven by a decrease in the value of the natal territory and an increase in local breeding opportunities in fragmented forest. Continued habitat disturbance may further explain the observed recent increase in genetic admixture within the Taita Hills metapopulation.

Sperm as a reproductive barrier between species

Emily R. A. Cramer

Presenting author: **Emily Cramer**, University of Oslo Natural History Museum, becky.cramer@nhm.uio.no

Birds are a model system for studying speciation and reproductive isolation, and particularly for testing if sexual selection drives these processes. Most work on the latter topic focuses on traits such as plumage and song, while sperm and ejaculate characteristics have been relatively neglected. However, these traits can be under strong sexual selection due to sperm competition and/or cryptic female choice, e.g., following extra-pair copulation. Sperm morphology correlates with and evolves more rapidly under higher extra-pair paternity, highlighting the potential for sperm phenotypes to diverge due to sexual selection in isolated populations. Copulations with heterospecifics result

in further selection on and diversification of sperm in hybrid zones . Diverged sperm phenotypes may then result in a fertilization advantage for conspecific sperm via several mechanisms. Most empirical work has focused on sperm swimming performance in female reproductive tract fluid, simulating sperm entering the female reproductive tract after copulation. Here, barriers may arise via prior exposure; females that had likely copulated with heterospecifics caused lower sperm performance, while other females did not. Selection during storage in females' specialized sperm storage tubules or in interactions with the ovum at the point of fertilization could also result in conspecific fertilization advantages. Following fertilization, sperm can represent a postzygotic barrier. That is, hybrid males may produce non-functional sperm or sperm that is inferior in competition/cryptic female choice. Studying sperm as a pre- and post-zygotic barrier is necessary to fully understand speciation in birds and the role of sexual selection in speciation.

The Ridgway's Hawk (*Buteo ridgwayi*): Returning from the brink of extinction

Marta Curti, Thomas I. Hayes, Russell Thorstrom, and Christine Hayes
Presenting author: **Marta Curti**, The Peregrine Fund, mcurti@peregrinefund.org

The Ridgway's Hawk is one of only three island-endemic buteos found worldwide and one of 11 diurnal raptors listed as critically endangered by the IUCN. Endemic to Hispaniola, this hawk was once found throughout the island. However, anthropogenic (i.e. persecution) and natural threats (i.e. infestations by parasitic flies (*Philornis* spp.) caused the species to decline over the past several decades. Despite these threats, a small, isolated stronghold population remained in Los Haitises National Park, Dominican Republic. But by the year 2000, this population was estimated at only 250-350 individuals. The Peregrine Fund has been working with this species for over 2 decades with three goals in mind: 1) increase the species' population, 2) increase the species' distribution, and 3) make the project sustainable in the long-term. Today, conservation efforts have reversed the decline of this species, and the population is growing. Hands-on management has led to significant increases in productivity. In 2011, for example, we knew of only 37 pairs of hawks, which fledged 18 young. In 2019, we monitored 144 pairs which produced 126 fledglings. Reintroduction efforts have resulted in a new breeding population in Punta Cana, DR. This population now includes 19 pairs and more than 50 wild-hatched young have fledged. Environmental education and community development programs wherein we hire and train local community members – 20 of which are currently working directly in conservation efforts – coupled with partnerships with local entities have proven to be successful strategies for bringing this species back from the brink of extinction.

When does the gut microbiota affect bird behaviour?

Gabrielle L. Davidson
Presenting author: **Gabrielle Davidson**, University of Cambridge, gd339@cam.ac.uk

Emerging research on 'wild microbiomes' points to links between diet, habitat, host physiology and phylogeny. Observational and descriptive studies of avian microbiomes provide important groundwork for developing and testing predictions regarding evolutionary and ecological processes associated with microbes and their hosts. However, the directionality of these effects is not always clear. How can we differentiate the causes from the consequences of microbiome variation? Here I will argue that the gut microbiome may be an important trait mediating behavioural plasticity in wild birds via the so-called microbiome-gut-brain axis, but that evidence supporting this theory is lacking. Using Great Tits (*Parus major*) as an example study system, I will highlight the benefits and limitations of manipulative studies for pinpointing causal relationships between behaviour and the gut microbiome. Alongside logistical and methodological challenges, I will discuss laboratory-inspired techniques that may be applied to wild systems while maintaining a balance between ecological validity and robust causal inference.

Advancing scientific knowledge and conservation of birds through inclusion of conservation social sciences

Ashley A. Dayer, Jessica C. Barnes, Alia M. Dietsch, Jacqueline M. Keating, and Liliana C. Naves
Presenting author: **Ashley Dayer**, Virginia Tech, dayer@vt.edu

Conservation social sciences—disciplines that apply social science theories and approaches to conservation challenges—play an essential role in advancing the science and practice of bird conservation. We connect insights about the contributions of the conservation social sciences in biodiversity conservation to the specific context of bird conservation and argue for the importance of inclusion of conservation social science in ornithological societies. In this presentation, we will introduce the conservation social sciences and demonstrate how they can improve the

design and implementation of conservation efforts for birds. Based on a symposium at the 2019 American Ornithological Society (AOS) annual meeting and a subsequent manuscript published in Ornithological Applications, we will present a set of recommendations that could further support the inclusion of conservation social sciences in the AOS. These recommendations build on strategies from other conservation societies, including establishing a social science working group, hosting social science conference plenaries and themes, and publishing high-quality social science articles, along with encouraging ornithologists and bird conservationists to participate in training and collaborate with social scientists. Following these recommendations, in 2020, the American Ornithological Society (AOS) issued an explicit invitation for social science submissions to the Society's journal, Ornithological Applications, but garnering submissions remains a challenge. We end with a call to action for the Society and its members to connect ornithological activities with relevant social scientists to grow the flock of bird conservation scientists.

Life cycle phenology and seasonal diet variation of Grenadian Birds in agroforests, and the contribution of diverse agricultural systems to the ecological resilience of tropical island bird communities

Christopher C. De Ruyck and Nicola Koper

Presenting author: **Chris De Ruyck**, Natural Resources Institute, umderuy2@myumanitoba.ca

Island biogeography, ecological release and taxon cycle theories make broadly supported predictions about species' distributions and the evolution of generalist traits among island colonizing species in the Caribbean. However, it is less clear how release and selection for generalist traits affects the evolution of other life history characteristics such as the moult and breeding phenology of island birds, and how this influences the ecological resilience of island communities. We conducted mist-netting within agroforest habitats on Grenada to characterise the breeding and moult phenology of 9 bird species (3 endemic to the East Caribbean), and used DNA metabarcoding on fecal samples to examine diet composition and diet-niche overlap across seasons. We observed high rates of diet overlap amongst widely distributed species as expected, with less overlap in less widespread species. Wet season diets showed greater plant and invertebrate diversity, with less diet overlap across species than dry season diets. Breeding periods and moult duration varied considerably by species; however, peak moult intensity was typically synchronized across species, coinciding with high invertebrate abundance in the wet season. We also found high rates (25 to 60%) of breeding condition adults simultaneously moulting flight feathers in nearly all species, which also coincided with peak insect abundance. In combination, these patterns suggest that the population density of these species is most likely regulated by dry season food availability, while the wet season provides a surplus of invertebrate food, which enables generalist-released species to exhibit greater flexibility in overlapping moult and breeding periods.

A chromosomic inversion in the hybrid zone between *Rhegmatorhina hoffmannsi* and *berlepschi*

Glaucia Del-Rio, Marco Rego, Brant Faircloth, and Robb Brumfield

Presenting author: **Glaucia Del-Rio**, Louisiana State University, gdelri1@lsu.edu

Rhegmatorhina hoffmannsi and *berlepschi* are sister species that have divergent mitochondrial haplotypes across the Aripuanã River, but the centers of the plumage and nuclear transitions are located ~180 km to the north of the mitochondrial break. Because the mitochondrial haplotypes do not cross the river barrier, we hypothesize that cytonuclear incompatibilities could be responsible. To test this hypothesis, we sequenced a reference genome (N50=73 Mb) for *hoffmannsi*, and resequenced nuclear and mitochondrial genomes (~11X) for 70 individuals spanning the hybrid zone. We compared genomes using Fst outlier analysis, and conducted haplotype analysis for candidate genes. We found evidence for a ~3Mb inversion at chromosome five when comparing birds with different mitochondrial haplotypes. The putative inverted region contains seven genes that code for proteins with mitochondrial functions. PCA results for the inverted region suggest a fitness asymmetry, because individuals with the *berlepschi* mitochondrial haplotype can be homozygous for the inversion, heterozygous for the inverted state, and homozygous for the non-inverted state, but individuals with the *hoffmannsi* mitochondrial haplotype are always homozygous for the non-inverted state. A genetic fitness asymmetry could explain the displaced nuclear and mitochondrial clines. We also found that genes responsible for differences in plumage color between the two species are not physically linked to putative genes responsible for mito-nuclear incompatibilities. The lack of linkage between speciation genes and plumage color genes suggest the *hoffmannsi* plumage color alleles will continue moving northward, and may eventually result in extinction of the *berlepschi* phenotype.

The form and function of avian rictal bristles

Mariane G. Delaunay, Carl Larsen, and Robyn A. Grant

Presenting author: **Robyn Grant**, Manchester Metropolitan University, robyn.grant@mmu.ac.uk

Avian rictal bristles are present in many species of birds and are likely to play a sensory role. However, bristle presence, anatomy and function have not yet been described in many species. We present here the bristle morphology and follicle anatomy of 12 Caprimulgiform species. Overall, we find that species with short, thin, branching bristles that lack mechanoreceptors tend to forage diurnally, whereas species with longer bristles and mechanoreceptors around their bristle follicles tend to forage nocturnally. We went on to compare bristle presence and morphology (length and shape) in 1,022 avian species, representing 418 genera, from 91 families and 29 orders. Our results reveal that rictal bristle presence is the likely ancestral state of the avian phylogeny used here. Rictal bristles are also more likely to be present in nocturnal extant species, and those that forage by sallying, plunge diving and scanning. We suggest that rictal bristles are likely to be tactile in many species and may aid in navigation, foraging and collision avoidance in dark environments.

Integrating migration data to build full annual cycle, single and multi-species conservation prioritizations for boreal birds

William DeLuca, Jill Deppe, Joanna Grand, Tim Meehan, Nichole Michael, Sara Saunders, Nathaniel Seavy, Melanie Smith, and Chad Wilsey

Presenting author: **William DeLuca**, National Audubon Society, william.deluca@audubon.org

Conservation resources are limited, and difficult decisions are often required to allocate resources to maximize conservation impact. The difficulty in effectively allocating limited conservation resources can be exacerbated for migratory species that span hemispheres over the course of a year. We explored two potential strategies for prioritizing locations for the full annual cycle conservation of migratory birds: a single and multi-species approach. For each approach we used eBird Status and Trends occurrence data to estimate stationary season space use. For migratory seasons we used a novel data integration process to combine tracking, banding, connectivity, and eBird data to estimate spatial migratory patterns. We used the program Zonation to optimize across the four seasons of the annual cycle for 26 North American breeding, boreal landbirds. We then conducted a similar process for the boreal, migratory songbird, Blackpoll Warbler (*Setophaga striata*). These results demonstrate the potential to use full annual cycle information for migratory birds to coordinate hemispheric conservation strategies and investments. Single-species prioritizations can also be extremely important to direct and inform species-based conservation efforts, such as those suggested by the Road to Recovery efforts.

Singing in a silent spring: Birds respond to a half-century soundscape reversion during the Anthropause

Elizabeth P. Derryberry, Jennifer N. Phillips, Ruth Simberloff, Graham E. Derryberry, Michael J. Blum, and David Luther

Presenting author: **Elizabeth Derryberry**, University of Tennessee, liz@utk.edu

Actions taken to control the COVID-19 pandemic conspicuously reduced motor vehicle traffic, potentially alleviating auditory pressures on animals that rely on sound for survival and reproduction. Here we evaluate whether a common songbird responsively exploited newly emptied acoustic space by comparing soundscapes and songs across the San Francisco Bay Area prior to, during, and after the statewide shutdown in California, USA. We show that noise levels in urban areas were dramatically lower during the shutdown, characteristic of traffic in the mid-1950s. We also show that birds responded by producing higher-performance songs at lower amplitudes, effectively maximizing communication distance and salience. These findings illustrate that behavioral traits can change rapidly in response to newly favorable conditions, indicating an inherent resilience to long-standing anthropogenic pressures like noise pollution.

Sudden and dramatic decrease of humans in outdoor spaces: Effects on urban Dark-eyed Juncos

Eleanor Diamant, Marlene Walters, Felisha Wong, and Pamela Yeh

Presenting author: **Pamela Yeh**, UCLA, pamelayeh@ucla.edu

Over the last few decades, populations of Dark-eyed Juncos have colonized multiple urban centers throughout coastal California, including at several University of California college campuses. We had been documenting individual reproductive behaviors for years before the COVID-19 pandemic. The "pandemic pause" that occurred on the college campuses represented a significant change in human activity and human-induced disturbances. We present here some of our findings of differences in bird behavior from pre-pandemic and during-pandemic breeding seasons. We discuss these findings in the context of the massive decrease in human activity in college campuses during the pandemic.

Effects of agriculture on nestling diet, quality and post-fledging survival: A comparative study between two sympatric species of aerial insectivores in Saskatchewan

Ana M. Diaz, Christy Morrissey, and Keith A. Hobson

Presenting author: **Ana Maria Diaz**, University of Saksatchewan, ana.diaz@usask.ca

It is still unclear how landscape changes caused by intensification of agriculture have affected population trends of aerial insectivores in North America. Key demographic drivers of population change include the quality and survival of juvenile birds. Tree Swallows (*Tachycineta bicolor*) and Barn Swallows (*Hirundo rustica*) are two sympatric species of aerial insectivores that breed in the Saskatchewan agroecosystems. In 2020 and 2021, we conducted a comparative study to investigate potential responses of Tree and Barn Swallow nestlings to landscape composition (relative coverage of annual row crops and wetlands). We assessed nestling diet and condition along a gradient of agricultural intensity following a scale-of-effect approach. Relative use of terrestrial and aquatic-emergent insects was investigated using stable hydrogen isotope (d2H) measurements of feathers and local insect taxa. We also assessed potential carry-over effects of condition in the nest on early post-fledging survival using nanotags and the novel Motus automated radio telemetry network. Fledglings were tracked for an average of 16.4 ± 11.7 days after tagging. Preliminary analyses suggest that the contribution of aquatic prey to the diet of both species was higher in natal areas with greater abundance of ponds in the vicinity of the nest (<500m). Contrary to our prediction, no effect of landscape composition on chick condition was found in either of the two species. We speculate that differences in parental care, foraging strategies, and prey quality and quantity in prairie agricultural landscapes act to buffer negative effects of agriculture on aerial insectivores.

Summer-winter variation in the gut microbiota composition of homing pigeons

Maurine W. Dietz, Kevin D. Matson, Maaike A. Versteegh, Marco van der Velde, Joana F. Salles, and B. Irene Tieleman

Presenting author: **Maurine Dietz**, Groningen Institute for Evolutionary Life Sciences, University of Groningen, m.w.dietz@rug.nl

Gut microbiotas (GM) play a pivotal role in host physiology and behaviour, and GM may affect seasonal variation in host status. We investigated summer-winter differences in GM in 14 homing pigeons (*Columba livia*) that lived outdoors, by collecting cloacal swabs in both seasons in 2 years. Since diet was constant, seasonal differences in GM may be due to temperature or daylength variation. Since temperature effects may be mediated by host metabolism, we measured basal metabolic rate (BMR). As daylength influences immune function via the circadian clock and may indirectly influence GM via e.g., immune system-GM interaction, we measured 7 immune indices. Richness was higher in winter in females. Bray-Curtis dissimilarities (BC) differed between seasons and sexes. BC ordination matched with that of metabolism (BMR, including body mass and size, as body mass affects BMR), but not with immune function ordination. The most abundant genus (12%) and associated higher taxa were more abundant in winter (though not significantly for its phylum, Firmicutes, the most abundant phylum, 43%). Relative abundance of one of the five most abundant phyla (>5%) differed between seasons (more Bacteroidetes in summer), while four differed between sexes, and three varied with immune function. Thus, immune function correlated with taxa relative abundances and not with other GM aspects, suggesting that this may be an unlikely link between daylength and GM. The alternating peaks in Firmicutes and Bacteroidetes comply with general temperature effects on GM in the literature. Together with the correlation between BC and metabolism, and the constant diet, these results suggest that temperature (partly) drove the summer-winter differences in GM.

Evaluating the umbrella potential of the boreal caribou to achieve multi-species conservation in the Canadian boreal forest

Teegan Docherty, Diana Stralberg, Becky Stewart, Jeff Ball, Anna Calvert, Alaine Camfield, Amanda Dookie, Samuel Haché, Christopher Lauzon, Deepa Pureswaran, Natalie Savoie, Victoria Snable, Cory Toth, Junior Tremblay, Pierre Vernier, Alana Westwood, Ryan Zimmerling, and Fiona Schmiegelow

Presenting author: **Teegan Docherty**, University of Alberta, tdochert@ualberta.ca

Ambitious global targets to increase protected areas and slow biodiversity loss will require more efficient conservation strategies. Here we investigate if delivering conservation for the boreal caribou (*Rangifer tarandus*) has co-benefits for avian conservation as a step towards advancing multi-species conservation planning in the Canadian boreal forest. The aims of this study were to (i) measure the overlap between caribou ranges and bird populations and (ii) evaluate the overlap and gaps between caribou ranges and priority areas for avian conservation across the boreal region. We generated multi-species prioritizations based on density predictions for 138 bird species using the Zonation software. We selected five factors to influence prioritizations: (1) prioritization metric (species diversity vs. representation), (2) habitat association, (3) conservation status, (4) anthropogenic disturbance, and (5) geographic stratification. We found that prioritizations—and their overlap with the caribou ranges—shifted depending on the factors and conservation objectives of a particular scenario, with large differences between prioritization metrics and solutions including disturbance. Areas of high conservation value for birds had lower-than-expected overlap with caribou ranges for most representation-focused scenarios and higher-than-expected overlap for many diversity-focused scenarios. In particular, when solutions included disturbance, the caribou ranges captured higher boreal bird population sizes than would be expected if populations were distributed at random. This approach allows for the selection of high-priority areas for a given conservation objective and identifies opportunities for multi-species conservation.

Spatial-temporally explicit modelling of changes in aerial insectivore abundance and anthropogenic effects in Canada

Courtney Donkersteeg, Adam C. Smith, and Roslyn Dakin

Presenting author: **Courtney Donkersteeg**, Carleton University, courtneydonkersteeg@cmail.carleton.ca

This study used a hierarchical Bayesian population trend model with covariates consisting of ~700 spatial data points from the Breeding Bird Survey, Canada Agricultural Census, and an expert-derived human footprint magnitude scale. We tested 17 aerial insectivore species to determine if this model could accurately reflect the effects already supported by smaller, controlled experiments regarding the relationship between anthropogenic effects and avian abundance. While this model provides an excellent and adaptable framework for the analysis of the drivers of avian population change, more variables including climate patterns need to be incorporated for the model to accurately reflect previously supported relationships.

Listen, Learn, Liaise: Replacing the three S's with the three L's for successful multispecies conservation programs

Brad Downey, Paul Jones, Katheryn Taylor, Brandy Downey, and Craig DeMaere

Presenting author: **Brad Downey**, Alberta Conservation Association, Brad.Downey@ab-conservation.com

Over the past 150 years, cultivation, urbanization, and industrial development have replaced much of North America's native prairie. Native prairie ecosystems are of vital importance to many species at risk (SAR), as well as providing economic and ecological goods and services. If society wants to conserve the North American prairie ecosystem, including the many SAR, then partnerships between public agencies, nongovernmental organizations, and private landholders need to be established and strengthened. To benefit all SAR, this partnership should metamorphose from the typical single-species prescriptive management into one that addresses the needs of multiple species. We present our MULTISAR Program and the framework that is used to achieve voluntary partnerships with the ranching community that alleviates their fear of SAR protection. Enhancing the ability of the ranching community to manage multiple SAR on their properties will ensure SAR have a place to call home. Through listening, learning, and liaising (3 L approach) with those on the ground that manage the habitat on a daily basis we can develop mutual trust and respect that leads to open and honest communication and a greater desire to implement projects that are mutually beneficial. This approach has opened many doors and helps reduce the old verbiage of Shoot, Shovel, and Shut up when it comes to SAR protection. The 3L approach also fosters common ground between landholders and conservation groups.

A private channel of communication: High-frequency vocalizations and hearing in hummingbirds

Fernanda G. Duque

Presenting author: **Fernanda Duque**, Georgia State University, fduque1@gsu.edu

Some species of hummingbirds produce high-frequency (HF) vocalizations (> 8 kHz) beyond the frequency range at which most birds sing. Among hummingbirds producing HF vocalizations, the Ecuadorian Hillstar (*Oreotrochilus chimborazo*) produces the song with the highest fundamental frequency in an avian vocalization. The HF song is produced as part of the male courtship display for females and as a territorial signal for other males suggesting that HF vocalizations mediate complex social interactions in the species. For these vocal signals to be effective, hummingbirds must be able to hear them. However, until recently there had not been evidence that birds could hear HF sounds and use them in communication. We showed behavioral and neural evidence of HF hearing in *O. chimborazo*. In the field, hummingbirds respond more to the playback of HF song than to playback of ambient noise. To determine activation in brain auditory regions, we induced ZENK protein expression, a marker of neural activation, in the auditory areas of the brain after exposure to the HF song (> 10kHz). We found significantly higher ZENK expression in the brain auditory regions of hummingbirds exposed to the HF song compared to controls exposed to a playback of silence. Together, the behavioral and neural responses showed that the Ecuadorian Hillstar can hear its HF song. It is likely that other hummingbirds producing HF vocalizations can also hear these signals. While some owls have evolved specialized ears and hearing for hunting, this is, to our knowledge, the first evidence of HF hearing in a bird that uses this ability for conspecific communication.

sf, raster, and tmap: The spatial data trinity

Matthew E. Dyson

Presenting author: **Matt Dyson**, Wilfrid Laurier University, matt.e.dyson@gmail.com

Spatial analysis and the production of maps is common practice for ornithological research. Here, I will highlight my workflow and the packages that I use, sf, raster, and tmap, for the basic processing of spatial data in R as well as the production of publication-quality maps and interactive maps that you can share with your collaborators. Processing spatial data in R improves the clarity and reproducibility of your results and improves the efficiency of your workflow.

naturecounts: Millions of bird occurrence records at your fingertips

Danielle M. Ethier, Denis Lepage, and Stefanie E. LaZerte

Presenting author: **Danielle Ethier**, Birds Canada, dethier@birdscanada.org

There is no shortage of high-quality citizen science data being collected on birds across North America, and beyond. Many of these datasets are freely available to researchers and are being used to unravel the ecology of species throughout their annual cycle. However, many of these datasets have yet to be fully explored, and there remains a vast amount of untapped potential. The naturecounts R-package will start you down the path to untapping this potential! NatureCounts is a database platform, managed by Birds Canada, which is used to facilitate the collection, management, analysis and sharing of natural inventory and monitoring data, with a focus on birds. Some of the datasets include: eBird Canada, the Canadian Migration Monitoring Network, Project FeederWatch, Canadian Breeding Bird Atlases, and many more. All of these datasets are publicly accessible through an open-source R software package, naturecounts (creators: S. LaZerte and D. Lepage). This presentation will explore the functionalities of the naturecounts R-package, which will put millions of bird occurrence records at your fingertips. Get started here: `remotes::install_github("BirdStudiesCanada/naturecounts")`

Light-mediated flexibility in foraging tactics of a crepuscular insectivore

Ruben Evens, Michiel Lathouwers, Felix Liechti, Jean-Nicolas Pradervand, Eddy Ulenaers, and Bart Kempenaers.

Presenting author: **Ruben Evens**, Hasselt University, ruben.evens@uhasselt.be

Astronomical light pollution is one of the most pervasive, rapidly-expanding pollutants causing a broad-scale illumination of the nocturnal sky. It infiltrates far into natural areas and fundamentally changes the natural night-time environment which has been consistent in evolutionary history and tightly controls animals' circadian rhythms. Artificial skyglow may affect crepuscular and nocturnal light conditions, e.g. mimic a full-moon night in terms of sky brightness, especially during overcast nights, when the sky should be naturally-dark. In this study, we investigated the light-mediated foraging behaviour of European Nightjars (*Caprimulgus europaeus*, hereafter nightjar). Similar to most members of the Caprimulgidae, nightjars are crepuscular insectivores which visually detect the silhouettes of flying insects against the illuminated sky. Assuming that variation in sky brightness affects prey detectability rather than prey availability, we hypothesised that a full moon and artificial skyglow both improve prey detectability and allow individuals to increase nocturnal foraging activity. We quantified individuals' (66 individuals, 258 nights) nocturnal flycatching activity in breeding and foraging habitat using a combination of GPS-loggers and tri-axi accelerometers. Our data show that nightjars' nocturnal foraging activity increases, as expected, when nocturnal moonlight increases, but also when measured sky brightness increased (i.e. accounting for possible artificial skyglow). In sites subjected to higher levels of artificial skyglow, nocturnal foraging activity was increased, with indications that skyglow may weaken lunar-mediated responses in nocturnal foraging activity.

Genetic diversity and the lack of consistency in taxonomy hinder biogeographic interpretation: A case study with Galbuliformes

Mateus Ferreira, Joel Cracraft, Alexandre Aleixo, and Camila Ribas

Presenting author: **Mateus Ferreira**, Universidade Federal de Roraima, mateusf.bio@gmail.com

Galbulidae (jacamars) and Bucconidae (puffbirds) are sister families endemic to the Neotropical region. Together they comprise 57 species and more than a 100 described subspecies. Both families have their highest diversity in Amazonia. Within Galbulidae, most species have restricted and parapatric / allopatric distributions in relation to other closely related species, while within Bucconidae, species are widespread and polytypic. In this study, we obtained mtDNA sequence data for over 400 samples, and used previous published results, of all widespread species to uncover phylogeographic patterns. Then, based on these results, we selected and sequenced thousands of Ultraconserved Elements to reconstruct the phylogenetic relationships among these phylogeographic groups and propose the first phylogenetic hypothesis for these two families with dense taxon sampling. Our phylogeographic results recovered phylogeographic breaks in almost all studied groups, most of them associated with the main tributaries of the Amazon River, and many corresponding to already described subspecies. We then reconstructed phylogenetic relationships based on over 2,000 UCE loci using a concatenated approach in a Bayesian Inference framework. Overall, most nodes had high support, and the relationships among genera, species and intraspecific diversity were discussed. We propose the recognition of all subspecies that received support from the phylogeographic and phylogenomic approaches as distinct species. We found evidence of paraphyly of several species and proposed taxonomic changes to deal with that.

Data-driven, multi-species planning for the conservation of grassland birds in the south-central United States

Jane A. Fitzgerald, Cara J. Joos, Anna Matthews, Thomas W. Bonnot, and Christopher M. Lituma

Presenting author: **Jane Fitzgerald**, Central Hardwoods Joint Venture, jfitzgerald@abcbirds.org

The Central Hardwoods Joint Venture (CHJV) is leading efforts to develop a multi-species and multi-regional full annual cycle research project to evaluate how habitat and landscape variables affect population growth of a suite of grassland species in the south-central USA. The results will give us a better understanding of when, where, and how these populations are limited which will inform and refine grassland bird conservation for a four-Joint Venture geography. Part of our project development involves mapping densities of 3 grassland species for two JVs using point count data, and then using these results to validate the use of eBird and/or BBS data for all four Joint Ventures. If these citizen science data sources are comparable to empirically collected data, then future multi-species conservation planning will be easier and less expensive in coming years.

Chimney Swift use of a large migratory roost in Northern Ontario

Jennifer Foote and Jennie Pearce

Presenting author: **Jennifer Foote**, Algoma University, jennifer.foote@algomau.ca

North American aerial insectivores, including Chimney Swifts (*Chaetura pelagica*), have experienced serious population declines over the last 50 years. Investigating the factors contributing to these declines is important for management and conservation. In Ontario, most research on Chimney Swifts has been concentrated in Southern Ontario and we know very little about northern swift populations. We monitored a large roosting population in Sault Ste Marie at a pair of roosting chimneys (Post Office/Courthouse), using a video dataset that was sporadic between 2006-2013 and daily from 2014- 2020. We found that roost attendance was highly variable during spring migration and peaked at over 2000 roosting birds. Our data shows that SwiftWatch nights capture population trends well but do not always detect peaks in swift numbers. Chimney Swifts originally roosted in the Courthouse chimney but following capping of that chimney switched to the Post Office in 2013. Following un-capping of the Courthouse chimney, swifts roosted in both chimneys in 2016 before switching back to roost primarily the courthouse in 2017. In 2019 few swifts used either roost and swifts were observed congregating around the chimneys but departed without entering. Potential explanations for recent reduction in roosting include harassment and predation by gulls or disturbance by rock doves roosting in chimneys. The Sault Ste Marie roost was perhaps one of the largest in Canada and its reduced roosting population is cause for concern as this site likely connects populations to high quality nesting habitat in the northern part of the province.

Early-life environmental drivers of movement in fledgling pelagic seabirds

Caitlin K. Frankish, Andrea Manica, Thomas A. Clay, Marius Somveille, Cleo Cunningham, Stephanie Prince, Andrew G. Wood, and Richard A. Phillips
Presenting author: **Caitlin Frankish**, British Antarctic Survey, caitlin.frankish@gmail.com

Optimal selection of foraging habitat is key to survival, but it remains unclear how naïve individuals are able to locate and access resource patches in completely new environments. In many animals, dispersing juveniles receive no parental guidance and hence external cues may play an important role in guiding movements. However, it remains challenging to pinpoint when and how individuals learn to exploit their local environment, especially in species with cryptic life-stages. Here, we investigate the movements of juveniles of two wide-ranging and threatened seabird species, the White-chinned Petrel (*Procellaria aequinoctialis*, n=13) and Gray-headed Albatross (*Thalassarche chrysostoma*, n=23), tracked from Bird Island (South Georgia) for up to 10 months in 2015, 2018 and 2019. We use mechanistic frameworks to investigate the extent to which chlorophyll concentrations (representing primary productivity) and ocean surface winds influence juvenile movements over time, and gain crucial insight into the relative roles of learning vs. innate mechanisms in shaping foraging strategies. We also assess the conservation implications of movements by quantifying the overlap of juvenile and adult birds with their greatest threat, incidental mortality in longline fisheries. We demonstrate that fledglings made greater use of regions exposed to fishing activity, suggesting they are likely more susceptible to bycatch.

Anthropogenic light at night influences fledge dates, migration timing, and migratory routes in aerial insectivores

Kevin C. Fraser, Christina M. Davy, Saeedeh Bani Assadi, Alicia M. Korpach, and Reyd A. Smith
Presenting author: **Kevin Fraser**, University of Manitoba, kevin.fraser@umanitoba.ca

Anthropogenic light at night (ALAN) is expected to impact migratory behaviour owing to the critical role that light can play in cueing and shaping avian migration timing and routes. Using two aerial insectivores, we investigated the impact of ALAN on the development of migration timing in nestlings, the cueing of migration in adults, and on migratory routes and stopovers. We found that nestling Purple Martins (*Progne subis*) experimentally exposed to white ALAN had later fledge dates, but green ALAN had less of an effect. Adults that experienced more than 10 nights of ALAN at overwintering sites in Brazil initiated and completed spring migration 8 days earlier on average as compared to birds not exposed to ALAN. Eastern Whip-poor-wills (*Antrostomus vociferous*) selected fall migration routes that maximized the use of darker skies and selected stopover sites in dark areas. We encourage further research on the impact of ALAN on avian aerial insectivores in the context of steep population declines in this group.

What we can learn about evolution, ecology and conservation from studying tropical montane birds

Benjamin G. Freeman

Presenting author: **Benjamin Freeman**, University of British Columbia, benjamingfreeman@gmail.com

For centuries, biologists have been inspired by tropical diversity. Tropical mountains offer an exceptional environment for investigating speciation and community assembly, as they are Earths' hottest biodiversity hotspots. These fundamental ideas have taken on renewed relevance in the climate change era, as warming temperatures are predicted to cause species to shift their elevational distributions upslope, potentially setting in motion an "escalator to extinction" that threatens the persistence of high elevation populations and species. In this symposium, researchers from around the world will examine the evolution, ecology and conservation of the most species-rich avifaunas on Earth, addressing how this diversity – birds of many feathers – originated and how it is faring in the Anthropocene. Here I introduce this symposium, and provide a brief overview of the topics that researchers will shed new light upon in this symposium.

Faster evolution of song discrimination leads to faster diversification in New World passerine birds

Benjamin G Freeman, Jonathan Rolland, Graham Montgomery, and Dolph Schluter

Presenting author: **Benjamin Freeman**, University of British Columbia, benjamingfreeman@gmail.com

Faster evolution of premating reproductive isolation could lead to faster speciation and diversification. Alternatively, longer-term evolutionary dynamics may be disassociated with how fast lineages evolve premating barriers, for example if ecological factors drive longer-term diversification rates. Here we address this question using a comparative dataset of how allopatric pairs of closely related passerine birds perceive each other's songs: in total, we performed 2,250 playback experiments that simulated secondary contact between 176 sister pairs of passerine birds. We find that evolutionary rates of song discrimination are positively associated with diversification rate. This link is most prominent in suboscines (innate song) and weaker in oscine songbirds (learned song).

Patterns and consequences of natal dispersal in a declining population of Canada Jays at the southern edge of their range

Matthew Fuirst, Dan Strickland, and D. Ryan Norris

Presenting author: **Matthew Fuirst**, University of Guelph, mfuirst@gmail.com

Although estimating juvenile dispersal is essential for understanding variation in fitness and long-term population dynamics, it has been challenging to determine when individuals disperse and where they go after they leave their natal territories, particularly for species in which a portion of their offspring delay dispersal until after their first year. The Canada Jay (*Perisoreus canadensis*) is a territorial, food-caching resident songbird of North America's boreal forest. Juveniles either disperse soon after they fledge the nest (ejectees) or after their first year (dominant juveniles). From 2017-2020, we radio tracked 38 dispersing juveniles from a declining population of Canada Jays at the southern edge of their range in Algonquin Provincial Park, Ontario. Dispersal distances ranged from 1.0 – 15.0 km (mean ± SD: 3.9 ± 4.5), with dominant juveniles tending to travel shorter distances (3.0 ± 4.7 km, 1.0 – 15.0, 3.0 ± 4.7, n = 22) than ejectees (6.3 ± 3.6, 4.5 – 11.7, n = 16), the latter of which often travelled through kilometers of vacant habitat before settling. Dominant juveniles were also more likely to survive once they left their natal territories (0.92) compared to ejectees (0.24) and more likely to acquire a higher-quality breeding habitat. Our results suggest that juvenile Canada Jays experience significant fitness benefits from delaying dispersal, despite the fact that they forgo breeding opportunities in their first year.

Audition of Northern Saw-whet Owls (*Aegolius acadicus*)

Megan D. Gall and Glenn A. Proudfoot

Presenting author: **Megan Gall**, Vassar College, megall@vassar.edu

Northern saw-whet owls (*Aegolius acadicus*) are small owls that are capable of extraordinary audition. They can hunt in very low light levels and rely on audition to detect and localize prey. Clearly, their very large ear openings, an almost complete facial ruff, and the bony ear morphology of the squamosal-occipital wings that are thought to amplify and direct sound into the ears influence their auditory sensitivity. In this talk we review our recent work on audition in saw-whet owls. In particular we focus on how these owls respond to stimuli that differ in acoustic frequency, and how differences in the spatial location of the sound source and the level of background noise affect auditory sensitivity.

Interacting effects of poor weather and agricultural landscapes on the fledging success of a declining aerial insectivore

Daniel R. Garrett, Fanie Pelletier, Dany Garant, and Marc Bélisle

Presenting author: **Daniel Garrett**, Université de Sherbrooke, daniel.garrett@usherbrooke.ca

Climate change predicts the increased frequency, duration, and intensity of inclement weather periods such as unseasonably low temperatures and prolonged precipitation. Many migratory species have advanced the phenology of important life history stages, and as a result, are likely exposed to these periods of inclement weather more often, risking reduced fitness and population growth. For declining avian species, including aerial insectivores, anthropogenic landscape changes such as agricultural intensification are another driver of population decline. These landscape changes may affect the foraging ability or costs of food provisioning for parents, as well as reduce nestlings' probability to survive periods of inclement weather, through for example pesticide exposure impairing thermoregulation and causing punctual anorexia. Breeding in agro-intensive landscapes may thus exacerbate the negative effects of inclement weather. We used daily temperatures related to significant reductions of insect prey availability (cold snaps) combined with measures of precipitation and, while accounting for food availability, assessed their impact on Tree Swallow (*Tachycineta bicolor*) fledging success, an aerial insectivore breeding across a gradient of agricultural intensification. Fledging success decreased with the number of cold snap days experienced by a brood, and this relationship was worsened during periods of prolonged precipitation. We further found that the overall negative effect of inclement weather was exacerbated in more agro-intensive landscapes. Our results indicate that two of the primary hypothesized drivers of many avian population declines may interact to further increase the rate of decline in certain landscape contexts.

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motus: Managing motus data in R

Elizabeth A. Gow and Amie MacDonald

Presenting author: **Amie MacDonald**, Birds Canada, amacdonald@birdscanada.org

The R package motus is a valuable tool for ornithologists using The Motus Wildlife Tracking System, an international collaborative research network that uses coordinated automated radio-telemetry to track birds at local to hemispheric scales. The package motus is used to download and manage detections and deployment data from the Motus database, and allows users to create summary plots, and transform and analyze Motus data. The motus package was created by John Brzustowski, Denis LePage, and Steffi LaZerte, and is maintained and updated by Birds Canada. Many tracking technologies rely on specific software to process data from tagged birds, but the motus package allows Motus users (i.e., anyone tracking birds within the Motus network) to download, update and view their data without specialized software. There is also a detailed and regularly updated manual that takes users step-by-step through how to download, organize, filter and view their data. We will share an example of how the motus package has been used to summarize Motus data from Dunlin.

How participation in community science on private lands influences participants' conservation behaviors

Rachael E. Green, Ashley A. Dayer, and Amy E. M. Johnson

Presenting author: **Rachael Green**, Virginia Tech, rg1132@vt.edu

Increased conservation research on private lands is critical for generating knowledge to support biodiversity; this may be accomplished in part by community science (CS) programs. In addition, participation in CS may also positively influence participants' conservation behaviors. Our research sought to elucidate the influence of CS on participants' conservation behaviors as well as the factors that are associated with conservation behavior change. We conducted an online survey of community scientists (n = 104) that had participated in a Smithsonian private lands conservation research program, Virginia Working Landscapes. On average, respondents had volunteered for 3.5 years. They conducted biological monitoring surveys of plants (40%), birds (38%), mammals (30%), and pollinators (30%). Volunteering as community scientists positively impacted respondents to create, manage, or restore wildlife habitat on private (63%) and public lands (40%). Participation also impacted respondents' engagement in local conservation groups (63%), participation in other community science projects (56%), support for conservation issues through civic engagement (44%), and donations to conservation organizations (43%). Factors that influenced respondents' adoption of these conservation behaviors included having adequate amounts of time, having the necessary knowledge and skills, confidence in their ability, and access to money and resources. Some respondents also found inspiration to engage in conservation behaviors while conducting research on landowners' properties. Our findings illustrate that the conservation outcomes of CS can extend beyond community scientists' research duties and lead to far-reaching conservation benefits.

An overview of the Eastern Habitat Joint Venture multi-species conservation planning

Alan Hanson and Tania Morais

Presenting author: **Alan Hanson**, Canadian Wildlife Service, al.hanson@canada.ca

The Eastern Habitat Joint Venture (EHJV) is an all-bird habitat conservation partnership of federal and provincial governments and non-government organizations in Canada's six easternmost provinces. During the last 30 years, conservation planning in the EHJV has evolved from being focused on delivering the North American Waterfowl Management Plan (NAWMP) waterfowl objectives to a focus on all-bird habitat in line with Bird Conservation Region (BCR) plans and using Conservation Standards for the Practice of Conservation to rank pressures and identify strategies for on-the-ground conservation delivery. The challenges of considering all bird species, across such a diverse landscape such as the EHJV, within conservation planning are numerous but the potential rewards in terms of conservation efficiency are great. Linking local information on species and habitats to larger scale habitat and bird monitoring data through GIS allows an inclusive identification of conservation needs and potential solutions. To be effective, multi-species conservation planning products must be usable by policy makers, land managers and the on-the-ground conservation delivery partners. This presentation details the EHJV's experience with multi-species conservation planning and the lessons learned.

Influence of land use, foraging habitat, and diet effects on swallow neonicotinoid exposure in prairie agroecosystems

Mercy E. Harris, Christy A. Morrissey, and Keith A. Hobson

Presenting author: **Mercy Harris**, University of Saskatchewan, mercy.harris@usask.ca

Contaminant exposure is a potentially important contributor to aerial insectivore declines, but exposure to many contaminants, including agrochemicals, remains largely unstudied in the guild. Neonicotinoid insecticides (NNIs) are of particular interest because they are widespread in the environment, can accumulate in insect prey, and cause adverse effects in several other bird species. To investigate aerial insectivore NNI exposure, we are examining whether NNI exposure is affected by foraging location, diet, or local land use in two species with contrasting foraging ecologies, Barn Swallows (*Hirundo rustica*) and Tree Swallows (*Tachycineta bicolor*). In 2020, we worked in landscapes of varying agricultural intensities in Saskatchewan, Canada, and collected foraging movement data from adult swallows (Barn Swallow n=26, Tree Swallow n=33) fitted with GPS tags. We collected plasma samples (Barn Swallow n=101, Tree Swallow n=56) to assess NNI exposure, and fecal samples (Barn Swallow n=83, Tree Swallow n=70) to indicate diet compositions through DNA metabarcoding. Preliminary results indicate that Tree Swallows selected strongly for wetlands, whereas Barn Swallows used wetland and noncrop habitat similarly while avoiding annual cropland. Analyses of diet composition and NNI exposure is pending. Given the declines in this guild and potential threats from agriculture, this project will not only help us understand the importance of insecticide exposure in farmland-breeding aerial insectivores, but also provide a foundation for future study of conservation strategies to reduce these impacts.

Molecular analysis of mechanoreceptors in the domestic duck bill (*Anas platyrhynchos*)

Thomas R. Hart, Jason A. Flynn, and Eve R. Schneider

Presenting author: **Eve Schneider**, University of Kentucky, eves@uky.edu

Many Anseriformes are tactile foragers, using the sense of touch in their bills to find food under conditions where other senses are less informative. Like other vertebrates, all touch information in the head (and bill) is transduced and conveyed to the brain by neurons of the trigeminal ganglia. In the duck's bill these neurons interact with non-neuronal cells called corpuscles. Recently, lamellar cells of corpuscles have been shown to be directly sensitive to force in duck embryos (Nikolaev et al., Sci Adv, 2020). Here, we use in situ hybridization and differential transcriptomics in adult and embryonic duck skin to identify molecules that regulate corpuscle development.

COVID-19 lockdown reveals tourists as seabird guardians

Jonas Hentati-Sundberg, Per-Arvid Berglund, Aron Hejdstrom, and Olof Olsson
Presenting author: **Per-Arvid Berglund**, Baltic Seabird Project, perarvid.berglund@gmail.com

The widespread lockdowns put in place to limit the spread of the new coronavirus disease (COVID-19) offers a rare opportunity in understanding how human presence influences ecosystems. Using data from long-term seabird monitoring, we reveal a previously concealed guarding effect by tourist groups on an iconic seabird colony in the Baltic Sea. The absence of tourists in 2020 lead to a sevenfold increase in presence of White-tailed Eagles (*Haliaeetus albicilla*), a sevenfold increase in their disturbance of breeding Common Murres (*Uria aalge*) and causing 26% lower murre productivity than the long-term average. Eagles did not prey on murres, but their frequent disturbances delayed egg laying and facilitated egg predation from Herring Gulls (*Larus argentatus*) and Hooded Crows (*Corvus cornix*). Based on our findings, we suggest that human presence could be used as a strategic measure in guarding seabird colonies, and that a social-ecological systems perspective is vital for long-term success in protected area management.

Avian infrasonic sensitivity: Is this a niche ability, or pervasive sensory phenomenon?

Evan M. Hill
Presenting author: **Evan Hill**, University of Nebraska-Kearney, hillem@unk.edu

In the 1970's, a group of researchers discovered that the auditory range of the homing pigeon (*Columba livia*) extended well below those frequencies that humans are capable of detecting at normal listening levels. This acoustic space is anthropomorphically defined based on the lower limit of the human auditory range (typically <20 Hz) and is commonly referred to as infrasound. Follow-up work investigating the infrasonic sensitivity of the pigeon led to the hypothesis that these acoustic signals serve as cues that aid in the bird's navigational system. In 2013, a study using different methodology replicated the original pigeon results and a second line of research investigating infrasonic sensitivity in birds was born. In the subsequent years, five additional species have had their hearing ranges assessed, resulting in two more species with infrasound sensitivity: the domestic chicken (*Gallus gallus domesticus*) and the Indian Peafowl (*Pavo cristatus*). These findings are peculiar, as neither species travels long distances where infrasonic navigational cues could be applicable in the same fashion as is hypothesized for the pigeon. We currently know so little about the low frequency hearing of most birds that it is difficult to theorize about what purpose these signals serve for the animals capable of detecting them. However, the increasing number of identified infrasound-sensitive birds suggests that this ability may be pervasive among this class and likely serves multiple different purposes for animals occupying different phylogenic and ecological niches.

Assessing the phylogenetic signal of the avian microbiome

Sarah M. Hird
Presenting author: **Sarah Hird**, University of Connecticut, sarah.hird@uconn.edu

The microbiome can distinguish individuals and taxa and thus, can be considered a trait of the host. However, it is unclear how this trait evolves. Using phylogenetic comparative methods, and various ways of defining the microbiome as a trait of the host, I have found that the avian microbiome contains little phylogenetic signal and that the taxa within the avian microbiome changes rapidly. This finding holds across datasets.

Tracking the importance of aquatic-emergent insects in the diets of aerial insectivores in southern Ontario, Canada: Towards an understanding of nutritional landscapes

Keith A. Hobson, Corrine Genier, Kaelyn Bumelis, Jackson Kusack, Mike Cadman, Greg Mitchell, and Chris Guglielmo
Presenting author: **Keith Hobson**, University of Western Ontario, khobson6@uwo.ca

Attention has been focused on the relative importance of aquatic emergent insects in diets of aerial insectivorous birds, especially during the nestling growth phase. This has led to considerable interest in the importance of long-chain polyunsaturated fatty acids (PUFAs) to this guild during the breeding season and how species may vary in their dependence on aquatic emergent vs. terrestrial insects. We have been engaged in several studies of diets and movements of four species of swallows (Barn: *Hirundo rustica*, Cliff: *Petrochilidon pyrrhonota*, Tree: *Tachycineta bicolor,* Bank: *Riparia riparia*) and Purple Martin (*Progne subis*) breeding sympatrically in southern Ontario, Canada. We evaluated the use of naturally occurring stable isotopes of hydrogen in feathers of nestlings and in insect chitin to evaluate relative dependence of individuals on aquatic emergent insects. This isotope provided a consistent and reliable biomarker of use of insects emanating from Lake Erie and those from terrestrial sources. We found that Barn Swallows had the lowest proportion of aquatic insects in nestling diets followed by Cliff Swallows and then by Tree Swallows, Purple Martin and Bank Swallows. Plasma fatty acid assays revealed expected differential occurrence of EPA and DHA in birds nesting near Lake Erie with lakeside birds having higher omega-3 EPA and lower omega-6 ARA compared to inland birds. Fecal DNA samples were less informative but did reveal an overwhelming dependence of all species on Diptera. We discuss the importance of our results in terms of conservation actions designed to consider nutritional landscapes

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Understanding the observation filter: Impacts on volunteer data collection caused by the COVID-19 pandemic

Wesley M. Hochachka, Hany Alonso, Carlos Gutiérrez-Expósito, Eliot Miller, and Alison Johnston

Presenting author: **Wesley Hochachka**, Cornell University, wmh6@cornell.edu

Decreased human activity associated with the COVID-19 pandemic can be used as a natural experiment with which to better understand the responses of birds to living in human-dominated environments. Making use of this natural experiment requires that comparable data have been collected prior to and during the pandemic. Direct comparability should not be assumed, because the COVID-19 pandemic may have altered not only birds' behaviour but also when, where, and how data were collected. We have explored whether the process of collecting data describing the distribution and abundance of birds has been altered during the COVID-19 pandemic. For this, we have analysed data from eBird, looking for changes in: (1) the types of habitats in which observations were made, and (2) the amount and type of effort expended. In order to examine whether the impacts of the pandemic on human activity have varied around the globe, we have made these comparisons in four different political units (California, New York state, Portugal and Spain) that differed in the severity of curtailment of human activity. The most notable change was in the landscapes in which observations were made. For example, human-dominated landscapes were proportionally more common in the data collected during the pandemic, although only in three of the four regions. We also found subtler changes in observers' effort. Erroneous conclusions about the impacts of the COVID-19 pandemic on birds may result if researchers fail to account for changes in behaviour of the observers through whom information about the natural world is filtered; further, researchers need to be aware of regional differences in how observer behaviour has changed.

Gut microbiota as a potential mediator of phenotypic plasticity in birds

Jennifer L. Houtz, Conor C. Taff, and Maren N. Vitousek

Presenting author: **Jennifer Houtz**, Cornell University, jlh498@cornell.edu

Many temperate breeding birds face variable environmental conditions, and the ability to shift phenotype to match these conditions may impact fitness. Gut microbial composition is both shaped by the environment and has myriad effects on host phenotype. Recent evidence suggests gut microbiota could be involved in facilitating developmental plasticity or reversible phenotypic flexibility. Here, we present results from two studies investigating the potential for gut microbiota to mediate phenotypic plasticity in Tree Swallows (*Tachycineta bicolor*). In captive nestlings, antibiotic treatment shifted gut microbial composition and eliminated thermally-induced plasticity in the glucocorticoid stress response and pectoral muscle mass. In free-living adult females, there was a positive association between adaptive mass loss and loss of microbial diversity from incubation through early provisioning. These results indicate that changes in gut microbiota are tightly linked to plasticity in other phenotypic traits, and may play a role in mediating adaptive phenotypic plasticity.

Experimental manipulation of dietary carotenoids alters the cloacal microbiome in a colorful bird

Pierce Hutton, Mathieu Giraudeau, and Kevin J. McGraw

Presenting author: **Pierce Hutton**, Arizona State University, pierce.hutton@gmail.com

Many animals communicate their underlying quality using colorful visual signals. While some communicative colors are generated by non-dietary pigments, others require pigments that are extracted from the diet (e.g. carotenoid-based colors). Previous studies in numerous taxa show intra- and inter-specific variation in the amount of carotenoid intake in the diet. Variability in carotenoid intake could hypothetically affect digestive physiology, including the gut microbiome, which can cause changes in other important physiological and behavioral axes. To test this hypothesis, during pre-breeding we captured male House Finches from the South Mountain Regional Park near Phoenix, AZ, USA. We specifically targeted pre-breeding birds because mating may affect the pre-treatment baseline microbiome measurements. After transport and acclimation to the captive environment, we fed half of the individuals a diet of sunflower seeds and tap water (the control group, very low carotenoid diet), and the other half the same diet, but with carotenoid beadlets added to their water (lutein and zeaxanthin in amounts found in diets of wild finches). We sampled the cloacal microbiome before and after dietary treatments. Interestingly, we found that bacterial ß-diversity differed between groups after (but not before) the dietary treatment. These results may have important implications for how we understand the co-evolution of diet, gut microbiota, and pigment-based visual signals.

Factors influencing apparent annual survival in two sympatric breeding swallow species

Tara L. Imlay, Hilary Mann, Andrew Ding, Peter Thomas, Becky Whittam, Marty L. Leonard, and Qing Zhao

Presenting author: **Tara Imlay**, Canadian Wildlife Service, Environment and Climate Change Canada, Tara.Imlay@ec.gc.ca

For many species of declining birds, adult survival rates are the demographic process that is most influential on population trends. Using a mark-recapture dataset collected from 2012-2019, we determined apparent annual adult survival rates for Barn Swallow *Hirundo rustica* and female Tree Swallows *Tachycineta bicolor*. We then modelled the relationships between apparent survival and wind, disease risk, and number of active nests during the breeding season; El Niño-Southern Oscillation and Enhanced Vegetation Index (EVI) during the winter; and cold snaps and precipitation during the pre-breeding period. We also accounted for density dependent processes by incorporating Breeding Bird Survey annual population indices in our models. In most cases, the relationships between weather or climate variables and survival of both species indicate that conditions likely to be favourable for high insect availability resulted in high survival. For female Barn Swallows, more nests at a breeding site was related to higher survival, suggesting that the number of nests may be an indication of site quality. At a regional scale, survival was lower when the BBS index was higher, suggesting that density-dependence may affect survival rates. Finally, there was a negative relationship between EVI and survival for female Barn Swallows. Collectively, our results suggest that factors throughout the annual cycle of these species affect survival, but the factors during the migratory period remains an important knowledge gap. Improving adult survival rates, and, ultimately, population growth, will be best achieved by maintaining sites that support large numbers of swallows and promote higher insect availability throughout the year.

How do assortative mating and low hybrid fitness influence "reproductive isolation"?

Darren Irwin

Presenting author: **Darren Irwin**, University of British Columbia, Vancouver, irwin@zoology.ubc.ca

It is often said that distinct species are "reproductive isolated," and that such isolation can be attributed to either prezygotic or postzygotic barriers. I present results of computer models of contact zones between populations that can differ in mate preference and where hybrids can have low fitness. The models can be run in a spatial context with limited dispersal or in a non-spatial context where two populations are fully sympatric. In the spatial model, only a small reduction in fitness can maintain a narrow hybrid zone between two species. Without low hybrid fitness, substantial levels of assortative mating are ineffective in preventing blending of two species into one. In the non-spatial model, the consequences of interbreeding are also dependent on hybrid fitness. When hybrid fitness is high, just a small rate of interbreeding can lead to merging of species. When hybrid fitness is low, hybridization can lead to population declines, causing extinction of one or both species. The intrinsic growth rate of the population influences the likelihood of these outcomes, as high intrinsic growth rate lessens the potential for population decline. In both models, strong assortative mating between two species can cause low fitness of hybrids, because rare mating types are less likely to be selected as mates. Given these results, it is likely that many closely related species fail to coexist in the same region because of a tendency to interbreed. In such cases, if there is limited dispersal then low hybrid fitness can lead to the formation of narrow and stable hybrid zones. These results suggest that examination of the behaviours and fitness of hybrids is key to understanding speciation and species coexistence.

Estimating the sensory abilities of extinct species

Andrew N. Iwaniuk

Presenting author: **Andrew Iwaniuk**, University of Lethbridge, andrew.iwaniuk@uleth.ca

Sensory abilities are due, in part, to the anatomy of the sensory organs and their targets in the brain. This is perhaps best illustrated by the primary visual pathway in birds: the evolution of highly sensitive, low-acuity vision coincides with a small optic nerve and optic tectum whereas the evolution of highly acute, low sensitivity vision coincides with a large optic nerve and optic tectum. This relationship between brain morphology and vision has been used to infer the visual acuity and sensitivity of endangered species and, increasingly, of extinct species. Brains of extinct species are almost entirely lacking, but micro-CT imaging can be used to reconstruct digital endocasts that approximate brain size and shape. By comparing brain histology with endocasts, we showed that the relative surface areas of the optic lobe can be used to estimate the volume of the optic tectum. Using this relationship and data for extant species, it has been suggested that elephant birds (*Aepyornis* sp.) and a moa species (*Dinornis robustus*) had low visual acuity and might have been nocturnal. Preliminary data for the extinct Hawaiian ibises similarly suggests low visual acuity and nocturnal behavior. The strongest case for low acuity and nocturnality, however, is the "mole-duck" (*Talpanas lippa*) based on the extreme reduction of the optic lobe and optic nerve. Although these examples focus on vision, the same principle can potentially be applied to the other senses such that it will be possible to reconstruct the sensory abilities of extinct species. In doing so, we can obtain new insights into sensory system evolution in birds and a more accurate estimate of the niches occupied by extinct species.

Field characteristics affect swallow foraging in the Little Campbell River Watershed, British Columbia

Michelle M. Jackson, Ken R. Summers, and Christy Juteau

Presenting author: **Michelle Jackson**, A Rocha Canada, michelle.jackson@arocha.ca

The loss of open field habitat is a primary driver of population declines for swallows in North America. We assessed the importance of open fields for foraging swallows by conducting swallow foraging surveys in 31 fields (hay, pasture, or old field) in southwestern British Columbia during 2017-2018. We calculated rate-of-use for five swallow species and estimated associations with field- and survey-level characteristics for Barn Swallows (*Hirundo rustica*) and Violet-green Swallows (*Tachycineta thalassina*). Swallow numbers and foraging locations remained relatively constant across the two study years (1.08 +/- 1.40 swallows/survey in 2017 vs. 1.27 +/- 2.12 in 2018). Barn Swallows were detected most frequently (66% of all surveys in 2017 and 72% in 2018), followed by Violet-green (25% of surveys in 2017 and 33% in 2018), Tree (*Tachycineta bicolor*; <25% of surveys), Cliff (*Petrochelidon pyrrhonota*; <10% of surveys), and Northern Rough-Winged Swallows (*Stelgidopteryx serripennis*; <5% of surveys). Zero-inflated Poisson models showed that Barn Swallow rate-of-use was higher in fields surrounded by more farm buildings within 100 m, while Violet-green Swallow presence was best predicted by more non-farm buildings and survey order (earlier in the season). This study highlights the importance of maintaining agricultural landscapes for Barn Swallows, including open fields for foraging in close proximity to farm buildings for nest sites.

Avian foraging and species richness in the Retreat Gardens: A national park in urban Nassau, The Bahamas

Scott Johnson and Janeczka Johnson

Presenting author: **Scott Johnson**, BRON Ltd., cubophisvudii@gmail.com

Urbanization has had a profound effect on natural ecosystems around the world. In The Bahamas, National Parks and protected areas offer birds and other animals a safe refuge from many major threats, including urban development. Unfortunately, our understanding of the foraging behavior of birds in Bahamian national parks has been poorly studied, leaving large gaps in our understanding of avian behavior in national parks in urban areas. From 4th September 2017 to 19th July 2019, we collected foraging data and other observations of birds at the Retreat Gardens National Park by walking along park trails from 7 a.m. to 8:30 a.m, three days a week. A total of 64 species

(35 migrants, 24 residents, five introduced) representing 20 families were observed in the park. A total of 965 foraging observations from 43 species were collected during the study period. Fruit consumption accounted for over 47% of foraging observations, followed by arthropods and flowers (32.1% and 16.2%, respectively). Plants in the families Arecaceae, Moraceae, Anacardiaceae, Polygonaceae made up the majority of foraging observations and add further justification for the importance of planting fruit trees as a food source for resident and migrant birds and the importance of national parks as safe places for wildlife to thrive in an urban environment.

Identifying full-annual-cycle groups of North American landbirds to facilitate multi-species conservation and study design

Cara J. Joos, Alaine Camfield, Judith Toms, Maureen D. Correll, Scott G. Somershoe, Samuel Hache, and Randy Dettmers

Presenting author: **Cara Joos**, Central Hardwoods Joint Venture, cjoos@abcbirds.org

The Full Annual Cycle Working Group of the Partners In Flight Science Committee developed a method to systematically identify groups of species that are representative of particular full-annual-cycle geographies and habitats. These results will facilitate identification of species suitable for multi-species conservation planning and actions. Simultaneously working with representative species within each group will help us to systematically fill in data gaps for full-annual-cycle modeling in ways that maximize our ability to extrapolate findings across species occupying similar geographies and habitats.

Gastrointestinal processes and pathways that mediate interactions between avian hosts and their microbes

William H. Karasov

Presenting author: **William Karasov**, University of Wisconsin-Madison, wkarasov@wisc.edu

Microbes in the gastrointestinal (GI) tract exist in a milieu that includes biochemicals formed, excreted or secreted by the host. Avian hosts receive biochemicals of microbial origin that cross the GI tract and potentially have functional significance (e.g., nutritional, immunological, etc.). Microbes are found in greatest numbers free or attached to particles in the lumen of the cecum (foregut fermentation chambers are rare in birds) or in the intestine of very large birds. Microbes adherent to the tube wall likely occur in all birds including small passerines, which lack cecae and have intestinal transit times probably too fast to sustain luminal microbial populations. Avian host energy gain via short-chain fatty acids from microbial fermentation seems reasonably understood in terms of already described passive and mediated absorption pathways. Microbial breakdown of the host's excreted uric acid may be important to maintenance of the microbiome, but, whether, how, and where quantitatively important recovery of microbially-produced water soluble amino acids and vitamins occurs is a major unknown. The recent finding that intestinal paracellular permeability to hydrophilic compounds is quite high in many birds might be important for host absorption of microbial hydrophilic products. Tight junction passage of larger microbial immunologically-active or toxic compounds might be excluded by the effective pore radius (~4-5 angstroms), but there is also a putative low capacity "leak" pathway, thought to accommodate larger molecules, although it has not been studied in birds. Differences in avian gut structure and function could result in differences from mammals in host-microbe interactions.

When female mating preferences do, and do not, lead to reproductive isolation: Behavioral and genomic insights from Red-backed Fairywrens

Sarah Khalil, Jennifer Walsh, Jordan Karubian, and Michael S. Webster

Presenting author: **Sarah Khalil**, Tulane University, skhalil@tulane.edu

Divergent sexual signals and associated female mating preferences can lead to rapid reproductive isolation between populations, but it remains unclear whether this is a common pattern in evolution. Our studies of the Red-backed Fairywren *(Malurus melanocephalus)* in Australia show divergence in both male plumage color and song across two recognized subspecies. However, although song does appear to reduce gene flow between these subspecies, plumage signals do not. Behavioral experiments suggest that females of one subspecies have mating preferences for males with plumage signals of the other. This could arise if female mating preferences do not strongly coevolve with male signals, but instead predate the origination of male plumage signals. Our genomic analyses combining whole-genome sequencing of both hybrid and allopatric populations, as well as targeted sequencing of hundreds of

individuals of 16 populations across the species range, support this hypothesis. We identify divergent loci that likely underlie plumage differences between subspecies, show strong signals of positive selection, and have introgressed from one subspecies to the other in a direction that matches expectations from behavioral experiments. We discuss these results with respect to other bird taxa, many of which show similar patterns of plumage introgression across subspecies or species boundaries. Pre-existing mating biases for plumage signals might be common in birds, and may complicate the early stages of speciation.

What does an avian host want from its intestinal microbiome and how does it encourage that outcome?

Kirk C. Klasing and Andrea M. DeRogatis
Presenting author: **Kirk Klasing**, University of California, Davis, kcklasing@ucdavis.edu

The gastrointestinal organs of birds are among the most variable and plastic of the organs and range from simple tubes with low retention rates of digesta to systems with large areas for digesta storage and microbial-assisted digestion. The microbiota in the digestive tract has similarly diverse and plastic relationships with the host. Beneficial aspects of the microbiome include development and maturation of the immune system, competitive exclusion of pathogens, unlocking food nutrients especially energy in fiber, and synthesizing essential nutrients (e.g. amino acids and vitamins). Presumably all avian species benefit from microbial relationships important for the development of the immune system and pathogen exclusion. Those species that provide areas in their tract devoted to establishing a large microbiome add on important nutritional functions. Birds encourage the establishment of a predictable and non-pathogenic microflora prior to and during hatching. The embryo and hatchling absorb protective proteins in egg yolk and hatchlings imbibe protective proteins and nutrients present in egg white. Both guide the establishment of the microflora for the early days and weeks of the chick's life. Circumstantial evidence indicates that some of the nutrients in egg white are indigestible by the chick and serve to nourish very specific microbial communities. As these maternal sources wane, chicks begin synthesizing and secreting protective proteins and nutrients that continue to guide the composition of the microbiome to facilitate their useful contributions to intestinal function and health.

Full annual cycle insights on Common Nighthawk population trend

Elly Knight, Autumn-Lynn Harrison, Amy Scarpignato, Erin Bayne, Steven Van Wilgenburg, and Peter Marra
Presenting author: **Elly Knight**, University of Alberta, ecknight@ualberta.ca

Conservation of migratory species is complicated by the varying environmental conditions that populations experience across the annual cycle. Species generally show varying population trends across their ranges, and those differential trends can be used to test alternative hypotheses for factors contributing to observed declines. The Common Nighthawk (*Chordeiles minor*) is a member of the rapidly declining guild of aerial insectivorous birds for which multiple hypotheses have been proposed to explain their declines. We collected high-resolution GPS tracking data during migration and on the nonbreeding grounds from 52 adult Common Nighthawks from 12 breeding locations with population trends varying from -6.27 to 0.74 %/year. We used that tracking data and global remote-sensing data to develop competing count models for Common Nighthawk breeding survey data and evaluate alternative hypotheses for their declines. Potential explanatory variables included pesticide application rate, agricultural landcover, forest cover change, road density, drought index, and weather. We used a continuous evaluation of migratory connectivity to narrow down the times and places within the annual cycle to include in our analysis because differential population trends can only be driven by conditions when migratory connectivity is high. Preliminary analysis suggests the causes of differential population trends likely occur on the breeding grounds, in northern South America during spring migration, or while crossing the Gulf of Mexico, and are unlikely during other times of migration and the nonbreeding period.

Finch in a pinch: Effects of urbanization on the gut microbiota and parasite resistance of Darwin's finches in the Galapagos Islands

Sarah A. Knutie and Grace J. Vaziri
Presenting author: **Sarah Knutie**, University of Connecticut, saknutie@gmail.com

Human population size is increasing exponentially and, in turn, the urban environment is one of the few ecosystems that is rapidly expanding. A recent example of urbanization is in the Galapagos Islands, which is home to the iconic Darwin's finches. The Galapagos currently hosts 225,000 tourists each year and is home to over 21,300 permanent residents. Consequently, humans have altered the food availability for birds and introduced parasites to the Galapagos, such as the avian vampire fly (*Philornis downsi*), which causes up to 100% mortality in nestling finches. However, our recent experimental work shows that Small Ground-Finches (*Geospiza fuliginosa*; a species of Darwin's finch) in urban areas are more resistant to the parasite compared to finches in non-urban areas. Because human activity can influence the diet and gut microbiota of finches and the microbiota can affect host resistance, microbiota could be mediating the observed patterns of the effect of urbanization on parasite resistance in finches. Here, we present results on the effect of urbanization on the gut microbiota of Darwin's finches and whether the microbiota is potentially mediating the effect of urbanization on finch resistance to parasitism.

Impact of artificial rearing on the microbiota and health of endangered Whooping Crane chicks

Kevin D. Kohl, Brian K. Trevelline, Cory Duckworth, and Barry K. Hartup

Presenting author: **Kevin Kohl**, University of Pittsburgh, kkohl@pitt.edu

Many threatened and endangered species undergo captive breeding programs to facilitate species recovery. The eggs of Whooping Cranes (*Grus americana*) are often removed from parents and are artificially raised by costumed humans to increase the number of young that survive each year. However, artificially reared crane chicks exhibit high rates of respiratory infections and other morbidities. Given that host-associated microbes are often transmitted from parents to offspring and impact numerous aspects of host health and physiology, we hypothesized that artificial rearing altered the microbiome of Whooping Crane chicks. Indeed, we found that artificially-reared and parent-reared chicks harbor distinct microbiomes in both their guts and airways, based on 16S rRNA sequencing. Several genera of opportunistic airway pathogens were more prevalent in the tracheas of artificially-reared chicks. Additionally, chicks reared under different conditions host gut microbial communities with different functional representation, as revealed by metagenomic sequencing. Specifically, we have identified several pathways (alanine, aspartate, and glutamate metabolism, betalain biosynthesis, indole alkaloid biosynthesis, and ether lipid metabolism) that are less abundant in artificially-reared birds compared to parent-reared birds. These pathways could underlie the health disparities between artificially-reared and parent-reared chicks.

Foraging range and habitat use of the Purple Martin (*Progne subis*)

Kristen Lalla, Barbara Frei, Kevin C. Fraser, Joe Siegrist, Jason D. Fischer, James D. Ray, Mario Cohn-Haft, and Kyle H. Elliott

Presenting author: **Kristen Lalla**, McGill University, kristen.lalla@mail.mcgill.ca

Purple Martins are long-distance migrants and are exposed to a variety of conditions and habitats throughout their annual cycle. We studied foraging range and habitat selection at two points in the annual cycle: chick-rearing in eastern North America and the non-breeding period in or near the Amazon basin in South America. We expected that chick-rearing breeding individuals would have smaller foraging ranges than non-breeding birds because they must feed their chicks frequently, and that we would observe a latitudinal gradient in foraging range size as individuals at higher latitudes can take advantage of stronger resource pulses and therefore would have smaller foraging ranges. We also predicted that foraging purple martins select for water-based habitats throughout their annual cycle due to their association with water in many parts of their range. We used data from 101 GPS tracks deployed on adult Purple Martins from 2016 to 2020. Breeding status, but not latitude, predicted foraging range size, suggesting that chick-rearing birds are strongly constrained by feeding their offspring. Individuals across regions selected positively for wetland habitat; therefore, wetlands may be critical in producing insects in Purple Martins' diets.

Disentangling water type from geographic region in determining Amazonian floodplain forest avifaunas

Thiago Orsi Laranjeiras, Anaís Rebeca Prestes Rowedder, Benjamin Gilmore, Luciano Nicolás Naka, Torbjorn Haugaasen, and Mario Cohn-Haft

Presenting author: **Thiago Laranjeiras**, Instituto Chico Mendes de Conservação da Biodiversidade,
thiago.laranjeiras@icmbio.gov.br

River or water type is an important determinant of the rich Amazonian floodplain forest avifauna. Yet, how the arrangement of the distinct river types throughout the biome affects the distribution of floodplain birds is poorly known, preventing broader synthesis. Here, we explore geographic variation in Amazonian floodplain forest avifaunas, cross-comparing white- and blackwater floodplains in the Rio Negro basin with isolated counterparts in the Rio Solimões, using rapid standardized sampling at 24 sites (ten 15-min point-counts per site). The main axis of variation (first axis of an ordination) in avian species composition separated the sites from the Negro basin from those in the Solimões, indicating a stronger effect of geographic region. Despite significant differences in the avifaunas between distinct river types in both sub-basins (expressed on the ordination's second axis), more bird species (20, including 10 floodplain specialists) were associated with a single sub-basin, regardless of water type, than the contrary (9, with 5 floodplain specialists). Overall, around one quarter of all floodplain specialists (27 of 108) was significantly associated with only one river type in one of the sub-basins. Although the effects of a variation in water and floodplain attributes within river types or of the geographic distance alone cannot be completely discarded, these findings reinforce the emergent view that the Amazonian floodplains are composed of multiple biogeographic regions. Further directed faunal sampling, considering the discontinuities and isolation of the distinct Amazonian river types, should increase our capacity to depict the intricate biogeographical mosaic of the world's most diverse floodplains.

How can ornithologists find R packages?

Stefanie E. LaZerte

Presenting author: **Stefanie LaZerte**, steffilazerte.ca, sel@steffilazerte.ca

R is powerful free and open-source software (FOSS) for statistical programming. Because R is FOSS it reduces financial barriers to conducting science and is therefore used by ornithologists all over the world with different backgrounds and experiences. R can be extended with "packages" developed by this community, but exploring the thousands of packages available can be overwhelming. In this lighting talk I will share tips, tricks, and resources to help ornithologists find great R packages which can make their work faster, easier, more robust, and reproducible.

Bridging shortfalls in Amazonian avian biogeography

Alexander C. Lees and Alexandre Aleixo

Presenting author: **Alexander Lees**, Manchester Metropolitan University, alexander.lees@mmu.ac.uk

Biodiversity shortfalls represent the gaps between realized knowledge and sufficient knowledge needed to answer theoretical or applied ecological and evolutionary questions. Avian diversity reaches its terrestrial asymptote in the forests of the Amazon basin and we are now increasingly aware of how this diversity has been accrued across time and space. Three principle shortfalls affect our understanding of bird biogeography – the 'Linnaean shortfall' reflected by the ongoing occasional discovery of undescribed species; the 'Wallacean Shortfall' is characterised by a lack of information on species geographic ranges and range filling; and the 'Darwinian Shortfall' – gaps in our comprehension of evolutionary relationships in the avian tree of life. Here, we discuss the importance and magnitude of each of these shortfalls relative to our knowledge of Amazonian birds, highlighting recent advances and proposed research priorities. In particular we argue that more emphasis needs to be placed on investigating geographic variation within species, critical for understanding evolutionary relationships. It has been argued that many avian subspecies are poorly supported and often arbitrarily demarcated subdivisions of geographic gradients in character variation, but many also represent valid species taxa with distributions dictated by as yet poorly understood topoedaphic determinants. This knowledge is essential to secure the long-term resilience of the world's most speciose avifauna, at a time that habitat loss, especially along the Arc of Deforestation threatens to erase unsampled populations and contact zones between taxa and with any hope of us understanding or conserving their evolutionary history.

How phenotypic plasticity and natural selection shape blood-oxygen carrying capacity and elevational ranges in Andean birds

Ethan B. Linck, Jessie L. Williamson, Emil Bautista, Elizabeth J. Beckman, Phred M. Benham, Shane G. DuBay, L. Monica Flores, Chauncey R. Gadek, Andrew B. Johnson, Matthew R. Jones, Jano Nuñez-

Zapata, Alessandra Quiñonez, C. Jonathan Schmitt, Dora Susanibar, Jorge Tiravanti C., Thomas Valqui, Karen Verde-Guerra, Natalie A. Wright, Jay F. Storz, and Christopher C. Witt
Presenting author: **Ethan Linck**, University of New Mexico, ethanblinck@gmail.com

Phenotypic plasticity can facilitate evolution of broad niches, such as when plastic traits improve environment-specific performance. Conversely, phenotypic plasticity may constrain niche amplitude when it is costly to performance. A well-known example of maladaptive plasticity occurs when high-elevation hypoxia triggers erythropoietin-mediated augmentation of blood-oxygen carrying capacity, increasing tissue oxygenation at the cost of heightened blood viscosity. Here, we ask 1) whether elevational plasticity in blood-oxygen carrying capacity constrains or promotes elevational range breadth on evolutionary timescales, and 2) whether the strength of natural selection to optimize blood-oxygen carrying capacity is predictably related to elevation or the position of a local population within its species' elevational range. We measured total and cellular hemoglobin concentration and hematocrit for each of 137 species of Andean birds, estimating plasticity as the rate of change in these traits with elevation, and assuming their coefficient of variation was negatively correlated with the strength of directional selection. Our data rejected the hypothesis that maladaptive plasticity limits range breadth; rather, species with broader ranges tended to have higher plasticity. Local variation was reduced near elevational range limits and at high elevations, suggesting that the strength of natural selection to optimize blood-oxygen carrying capacity varies systematically across elevational ranges. Our findings illustrate how respiratory trait plasticity and local adaptation are mechanistically linked to the biogeography of montane species.

Changing patterns of nest predation and predator communities along a tropical elevation gradient

Gustavo A. Londoño, Manuel A. Sánchez-Martínez, Juan Pablo Gomez, Douglas Levey, and Scott K. Robinson
Presenting author: **Gustavo Londono**, Universidad Icesi, Cali, Colombia, galondono@icesi.edu.co

Nest predation is widely recognized as a strong selective force shaping population dynamics, life history, evolution, behavior and ecology. Predator communities and the relative abundance of each predator likely change along gradients much as other communities change; indeed, changes in predator communities have been documented to vary among regions, latitude, land use and habitat. These changes in community composition and predator abundance could also change the selective pressures underlying such life history traits as nest placement, elevational migration, behavior near the nest, nesting sociality, and the duration of the nesting period (the development of young). Empirical data on changes in nest predation rates and predator communities, however, are essentially lacking for bird communities along elevation gradients, which has prevented us from understanding the extent to which changing patterns of nest predation may be driving community turnover in tropical montane regions. We used 338 nests for which we had predator identification data to evaluate nest predator changes along a tropical elevational gradient. We found that nest predation pressures decreased with elevation and that these changes reflected the loss of lowland predators that do not tolerate colder climates. Also, just a few of the many potential nest predators accounted for very large proportions of the nest predation events, which suggests that only a few nest predators may be acting as environmental filters.

Evaluating evidence of mitonuclear incompatibilities with the sex chromosomes in an avian hybrid zone

Kelsie A. Lopez, Callum S. McDiarmid, Simon C. Griffith, Irby J. Lovette, and Daniel M. Hooper
Presenting author: **Kelsie Lopez**, Cornell University, kal259@cornell.edu

The exploration of hybrid zones and the intergenomic conflicts exposed through hybridization provide windows into the processes of divergence and speciation. Sex chromosomes and mitonuclear incompatibilities have strong associations with the genetics of hybrid dysfunction. In ZW sex-determining systems, maternal co-inheritance of the mitochondrial and W chromosomes immediately exposes incompatibilities between these maternal contributions of one species and the Z chromosome of another. We analyze mitochondrial and Z chromosome admixture in the Long-tailed Finch (*Poephila acuticauda*) of Australia, where hybridizing subspecies differ prominently in Z chromosome genotype and in bill color, yet the respective centers of geographic admixture for these two traits are offset by 350 km. We report two well-defined mitochondrial clades that diverged ~0.5 Mya. Mitochondrial contact is geographically co-located within a hybrid zone of Z chromosome admixture and is displaced from bill color

admixture by nearly 400 km. Consistent with Haldane's rule expectations, hybrid zone females are significantly less likely than males to carry an admixed Z chromosome or have mismatched Z-mitochondrial genotypes. Furthermore, there are significantly fewer than expected mitonuclear mismatches in hybrid zone females and paternal backcross males. Results suggest a potential for mitonuclear/sex chromosome incompatibilities in the emergence of reproductive isolation in this system.

The role of gene flow in reducing biodiversity along elevational gradients

Vanessa E. Luzuriaga-Aveiga, Mauricio Ugarte, and Jason Weir
Presenting author: **Vanessa Luzuriaga**, University of Toronto Scarborough,
vanessa.luzuriagaaveiga@mail.utoronto.ca

Elevational replacement species, connected by hybrid zones, could have formed by either parapatric speciation or secondary contact after a period of geographic separation. In the face of gene flow, recently diverged populations either reinforce their reproductive barriers or widely hybridize in the lack of complete reproductive isolation. Gene flow dynamics in young elevational replacement species with strong phenotypic differentiation, however, remain poorly understood in the Andes. Here, we used coalescent modelling and a genome-wide sample of SNPs to estimate rates of gene flow and discriminate between parapatric speciation and population fusion following secondary contact at the contact zone between two phenotypically distinct but genomically weakly diverged species of *Ramphocelus* tanagers, that replace each other elevationally in the Andean foothills. Our demographic modelling suggests that this species pair differentiated in allopatry but high levels of asymmetric gene flow at secondary contact led to a rapid homogenization of a large portion of the genome. However, a handful of SNPs remain highly differentiated, potentially involved in the maintenance of their distinctive plumage colouration.

Elevational differentiation is associated with rapid trait evolution but not faster speciation of Amazonian birds

Vanessa E. Luzuriaga-Aveiga and Jason Weir.
Presenting author: **Vanessa Luzuriaga**, University of Toronto Scarborough,
vanessa.luzuriagaaveiga@mail.utoronto.ca

The pace at which traits evolve and speciation occurs is often speeded up when ecologically mediated divergent selection is strong. But the role that ecological opportunity might have played in the build-up of species richness and trait diversity remains poorly studied in the continental Neotropics. Here, we estimated rates of trait divergence and diversification across a large dataset of closely related species pairs of Andean and Amazonian passerine birds. We used difference in elevational range occupancy as a proxy for the degree of ecological divergence between sister pairs. Our results show the role of elevational differentiation as a potential accelerator of diversification, song, colour and morphometric evolution.

Pre- and post-hurricane population assessment of Bridled Quail-Dove (*Geotrygon mystacea)* on St. Eustatius, Caribbean Netherlands

Hannah Madden, Frank Rivera-Milán, and Kevin Verdel
Presenting author: **Hannah Madden**, Caribbean Netherlands Science Institute, hannah.madden@cnsi.nl

The Bridled Quail-Dove (*Geotrygon mystacea*) is endemic to the Eastern Caribbean. To date, few studies have been conducted on the species and its population size in the region remains unknown. Nevertheless, it is thought to be declining across its natural range, despite being classified as a species of Least Concern. We quantitatively assessed the population size of Bridled Quail-Dove on St. Eustatius before and after hurricanes Irma and Maria in 2017. Based on calculations of detection probability, pre-hurricane density estimates ranged from 2.48 (SE ± 0.5) individuals/ha in 2016 to 2.36 ± 0.6 individuals/ha in 2017. Post-hurricane density estimates were 0.58 ± 0.2 individuals/ha in 2018 and 0.54 ± 0.2 individuals/ha in 2019. The 2019 population experienced a significant decline of 77.1% and could be at risk of extirpation. Given that the dove exclusively inhabits mid-to upper elevations of a dormant volcano, hurricane impacts, vegetation disturbance, habitat degradation, and predation by invasive Black Rats (*Rattus rattus*) may play a role in the species' decline. Surveys will be repeated in May 2021 to assess recovery of the Bridled Quail-dove population on St. Eustatius, the results of which will be presented at the AOS virtual meeting.

Implications of multiple brooding for Barn Swallow (*Hirundo rustica*) conservation strategies

Hilary A.R. Mann, Tara L. Imlay, and Marty L. Leonard

Presenting author: **Hilary Mann**, Dalhousie University, hilary.mann@dal.ca

The number of broods produced in a breeding season is an important component of reproductive success, but rarely considered in conservation strategies. Understanding how multiple brooding affects population growth rates, and the factors that affect this behaviour can be used to inform interventions for multi-brooded species. Therefore, we assessed if multiple brooding could be an effective target for conservation interventions in a Threatened Species at Risk, the Barn Swallow (*Hirundo rustica*). We quantified demographic rates at 18 breeding sites in New Brunswick and Nova Scotia, Canada from 2012-2019. Using these rates, we applied a Life Stage Simulation Analysis to measure the extent that changes in multiple brooding impacted the population growth rate, relative to changes in other rates like survival. Then, to inform potential interventions, we determined the effect of landscape features (landcover, the presence of livestock and metal roofs) and spring weather at these sites on the incidence of multiple brooding. We found that increases in the incidence of multiple brooding would improve population growth rates, though not as substantially as equivalent increases to survival rates. Further, multiple brooding was more likely at sites with fewer roads and buildings, and in areas with warmer, drier and less windy spring weather. Interventions such as prioritizing the conservation of breeding sites with these characteristics will ensure that sites with higher incidences of multiple brooding are not lost, which in turn may help improve the stability of the population in the future.

Stakeholder perceptions as an essential tool for Golden Eagle conservation in the American West

Lauren M. McGough, Kenneth E. Wallen, and Nate A. Bickford

Presenting author: **Lauren McGough**, Colorado State University Pueblo, Berkutchi@gmail.com

The conservation status of the golden eagle (*Aquila chrysaetos*) is affected by several direct and indirect anthropogenic factors. Data from USFWS suggests an overall population decline in the American West, with additional USFWS data indicating that firearms (n = ~700) lead all significant known causes of golden eagle mortality in the Western United States. Persecution by direct human action, i.e., firearm mortality, is a persistent and complex conservation challenge with broad consequences that range from ecological (e.g., trophic cascades via intraguild predation) to cultural (e.g., the perpetuation of shooting eagles as socially acceptable). Understanding the cognitive and sociocultural factors that contribute to golden eagle persecution and mortality in the American West is essential to its remediation. This study utilizes qualitative interviews and analysis to gather data on the individual and sociocultural dimensions of human-eagle conflict among stakeholders in the mountain-prairie region of Wyoming, Montana, Utah, and Idaho.

Drivers of avian richness and turnover in the Peruvian Andes

Sabrina M. McNew, Lisa N. Barrow, Jessie L. Williamson, Spencer C. Galen, Heather Skeen, Shane G. DuBay, Ariel M. Gaffney, Andrew B. Johnson, Emil Bautista, Paloma Ordoñez, C. Jonathan Schmitt, Ashley Smiley, Thomas Valqui, John M. Bates, Shannon J. Hackett, and Christopher C. Witt

Presenting author: **Sabrina McNew**, Cornell Lab of Ornithology, sm983@cornell.edu

The Andes are a global hotspot for biodiversity, evolutionary distinctness, and small-ranged species. The exceptional diversity in this region is a product of both high species richness (the number of species in individual communities) and high turnover (the change composition among communities). Various eco-evolutionary processes may generate richness and turnover, including adaptive specialization on particular habitats, barriers to dispersal, and interactions among species. Species interactions are thought to be particularly important in shaping avian neotropical diversity; however, parasitism has received less attention compared to competition and bird-plant mutualisms. In this study we identified the factors underlying species richness and turnover in interacting bird and haemosporidian communities of the Peruvian Andes. We found that net primary productivity and elevation were strong drivers of bird species richness, explaining 78% of variation among our 18 study communities. In contrast, turnover was most strongly predicted by temperature and precipitation, with smaller contributions of net primary productivity and elevation. Overall, both species richness and turnover were largely driven by environmental filtering and our results suggest that parasites and barriers to dispersal have had surprisingly minor effects on bird biodiversity. For both richness and turnover, our models of avian diversity explain a high proportion of variance (> 75%), suggesting that ecological explanations for Neotropical diversity have been under-appreciated compared to historical ones. We discuss these results as well as present interactive maps created by our models that can be used to explore patterns of biodiversity.

Aerial insectivores on the brink: Vulnerability to projected climate change

Nicole L. Michel, Brooke L. Bateman, Lotem Taylor, Joanna X. Wu, and Chad B. Wilsey
Presenting author: **Nicole Michel**, National Audubon Society, Nicole.Michel@audubon.org

North America's birds are in crisis, with nearly 3 billion birds lost since 1970. Aerial insectivores have been particularly hard hit, with North American populations declining by 32% and over 156 million of swifts, swallows, martins, and flycatchers lost during the last 50 years. As small-bodied birds reliant on aquatically-sourced insects and favorable weather conditions for foraging, this guild is uniquely susceptible to climatic perturbations. Indeed, population declines in several swift and swallow species have been linked to climate, and ongoing climate change will likely exacerbate these trends. Here, we evaluate the climate change vulnerability of North American aerial insectivorous birds by drawing on a recent large-scale assessment of climate change vulnerability of over 600 North American species. This effort involved building species distribution models based on 140+ million records from point count datasets in Mexico, the United States, and Canada; bird-guild specific habitat and land-use covariates; the latest IPCC climate data; and advanced modeling methods. Our results indicate that 58% of aerial insectivores are vulnerable to climate change, with projected range loss as great as 82% (Gray Flycatcher). Of these climate vulnerable species, 53% would have reduced vulnerability with a 1.5 °C versus a 3.0 °C warming scenario. Under a 3.0 °C warming scenario, 87% of species faced multiple additional climate-related threats in summer, notably extreme heat and fire weather. This work highlights the need to support conservation and advocacy to address climate change, and protect this already declining group of birds from further threat.

Priority areas for conservation in the Northwest Territories: Do we need to choose between boreal birds and caribou?

Tatiane Micheletti, Frances E.C. Stewart, Samuel Haché, Ceres Barros, Erin M. Bayne, Alex M. Chubaty, Steve G. Cumming, Amanda Dookie, Isabelle Duclos, Ian M.S. Eddy, Fawziah Gadallah, James Hodson, Mathieu Leblond, C. Lisa Mahon, Rhiannon Pankratz, Fiona Schmiegelow, Diana Stralberg, Junior A. Tremblay, Steven L. Van Wilgenburg, and Eliot J.B. McIntire
Presenting author: **Samuel Hache**, Canadian Wildlife Service, samuel.hache@canada.ca

Multi-species conservation is based on the premise that spatial allocation of land management can achieve species- or community-based conservation targets and maintain ecological processes of interest in a cost-effective way. In the boreal biome, a region that is considered the nursery of many North American migratory birds and Canadian species at risk, woodland caribou (*Rangifer tarandus caribou*) is a species of great conservation concern. The objective of this study was to use integrated simulation and optimization approaches to 1) assess whether caribou can act as an umbrella species for boreal landbird conservation in the present and in the future, and 2) identify areas where multi-species conservation opportunities currently exist and under projected climate-sensitive forest dynamics in the Northwest Territories, Canada. Our ecological models were implemented within the Spatial Discrete Event Simulation (SpaDES) framework, a suite of R packages for nimble and reproducible spatial simulation. Depending on the conservation target used for caribou (maintaining 30 - 70% of the highest quality selected caribou habitat), there was different overlap with high landbird diversity areas (55 - 89%). Percent overlap of selected caribou habitat and landbird diversity areas was also expected to increase through time, based on the CCSM4 Global Climate Model scenario. The highest overlap occurred in the central portion of the study area and near waterbodies. Our preliminary results suggest that in northern boreal ecosystems woodland caribou could be a good umbrella species. Conservation actions targeted towards this species could benefit a number of landbirds, and potentially a wider range of species.

Genomewide data reveal the role of natural and sexual selection in driving intra-island diversification in a Reunion songbird (*Zosterops borbonicus*)

Borja Milá, Maëva Gabrielli, Yann Bourgeois, and Christophe Thébaud
Presenting author: **Borja Milá**, Spanish National Research Council, b.mila@csic.es

Oceanic islands provide unique scenarios in which to identify the factors involved in population divergence and speciation. The Reunion Gray White-eye (*Zosterops borbonicus*) shows several geographically-structured plumage color forms on the small yet ecologically complex island of Reunion, Indian Ocean. Three lowland forms show narrow contact zones across geographic barriers, and are separated from a polymorphic (gray/brown) form restricted to the highlands. We use genome-wide markers and phenotypic data to understand the relative roles of local adaptation and sexual selection in the evolutionary history of this unique intra-island radiation. A phylogeny based on genomewide SNPs reveals that the gray-headed form is paraphyletic and basal to the others, indicating a lowland origin followed by an expansion into the highlands. Signatures of selection associated with elevation are found mostly on autosomes, whereas most high-Fst variants separating the three lowland forms are located on the Z chromosome. Pedigree analyses revealed that the sympatric gray/brown birds in the highlands represent a true genetic polymorphism, caused by a single locus on chromosome 1. Our genomic and morphometric results show the early role of ecology in dividing populations into highland and lowland forms, whereas the existence of independent lineages in the lowlands suggests the existence of premating isolating barriers to reproduction, likely due to sexual selection on plumage traits. Our results indicate that dispersal in the Reunion Gray White-eye is extremely limited and suggest the role of natural and sexual selection in restricting gene flow between incipient evolutionary lineages.

Post-fledging movement and habitat associations of an at-risk aerial insectivore: A Motus Wildlife Tracking System study

Greg W. Mitchell, Dean R. Evans, Jackson W. Kusack, Mike D. Cadman, C. Myles Falconer, and Keith A. Hobson

Presenting author: **Greg Mitchell**, Environment and Climate Change Canada, gregory.mitchell@canada.ca

Barn Swallow (*Hirundo rustica*) populations have declined steeply in Canada since the 1970s. Critical to their conservation is having an understanding of their habitat requirements throughout their annual cycle. One of the least studied stages of the annual cycle for any bird species is the post-fledging period. We used the Motus Wildlife Tracking System to study the post-fledging movement and habitat associations of 149 juvenile barn swallows over an area spanning 60 000 km2 in Southern Ontario, Canada. We found juveniles from 1st broods that survived until migration migrated at older ages (64 versus 43 days of age) and moved larger minimum cumulative distances relative to birds from 2nd broods (~580 versus ~350 km, respectively). However, birds from 2nd broods had higher overall movement rates by 18 km/day, suggesting they are trying to make up for lost time. Birds from 2nd broods also tended to move to and stay near Motus stations in landscapes with higher amounts of grassland, pasture, and forages relative to nearby stations, whereas birds from 1st broods tended to be less choosy about land cover. Together, increased movement rates, younger ages at migration, and stronger associations with more natural open land covers suggest that birds from 2nd broods might experience stronger temporal and energetic constraints prior to migration relative to birds from 1st broods. Our results also suggest that maintaining more natural open land covers across the region may be beneficial for juvenile Barn Swallows from 2nd broods preparing for their first migration.

Moving beyond barriers to enacting DEI in conservation

Nia Morales

Presenting author: **Nia Morales**, University of Florida, n.morales@ufl.edu

Much of the attention to diversity, equity, and inclusion in conservation has focused on barriers to participation in nature-based recreation (such as birdwatching) and barriers to recruitment and retention in careers. However, to move forward, organizations must critically examine what DEI means to them and thoughtfully enact solutions to support underrepresented or marginalized groups and engage with communities in meaningful ways. This presentation will highlight research illustrating these barriers and share preliminary results from a qualitative study aimed at defining key components of undergraduate field experiences in ecology and geosciences in an effort to redefine these pivotal introductory experiences in science and conservation. Creating positive experiences for underrepresented students will address barriers and build a foundation for a diverse, equitable, and inclusive future of conservation. The results presented will also provide helpful recommendations for organizations to move beyond the focus on barriers and enact DEI in their work.

Forging collaborative networks to address aerial insectivore research priorities across the Americas

Christy Morrissey, Lisha Berzins, and Ryan Norris

Presenting author: **Christy Morrissey**, University of Saskatchewan, christy.morrissey@usask.ca

Aerial insectivores are a diverse avian guild with complex life histories experiencing the steepest population declines of any group in North America. This prompted significant research investment to address hypothesized drivers of declines including loss of insect prey, climate change effects, and land use change. There have been major scientific advancements in our understanding of the factors and mechanisms underpinning changes in key demographic parameters affecting productivity and survival such as the importance of aquatic resources, local climate, and migratory connectivity. However, research has largely focussed on studying a few select species (e.g. Tree Swallows, Barn Swallows) and locations dominantly in eastern Canada and the United States. Collective action is now urgently needed to study those aerial insectivores in greatest decline across diverse geographies and throughout their full annual cycle. Following on a successful workshop in spring 2020, a large group of researchers have launched an Aerial Insectivore Research Network to identify and tackle the challenges through an integrated and coordinated research partnership across the Western Hemisphere. We present a synthesis of the main pressures and knowledge gaps for aerial insectivores, our identified research priorities, and a recent initiative to tackle one of the most pressing threats of how agriculture and exposure to pesticides are influencing breeding and wintering swallows across the migratory range.

Perseverance during a pandemic: Implementation of a mainland non-native predator management program as a conservation tool for the endangered White-breasted Thrasher

Jennifer Mortensen, Jeff Dawson, Izabela Barata, Luke Jones, Saphira Hunt, Pius Haynes, Jeannette Victor, Aloysius Charles, and Stephen Lesmond

Presenting author: **Jennifer Mortensen**, University of Arkansas, mortejen@gmail.com

“One of the rarest of West Indian birds”, is how the White-breasted Thrasher (*Ramphocinclus brachyurus*) was described by the ornithologist James Bond in the mid-20th century. The Martinique subspecies had just been declared extinct and the Saint Lucian subspecies had been extirpated from much of its range. Yet the bird persevered. A pair was rediscovered on the Caravelle Peninsula in Martinique, and by the 2000s, the population decline driven by conversion of dry forest to agriculture and pasture and introduction of the mongoose appeared to have ameliorated, mostly due to the establishment of a nature reserve. In Saint Lucia, a large parcel of land that was under cultivation until the last few decades of the 20th century was left untended, where dry forest then regenerated and is now the stronghold of the species distribution at ~1000 birds (73% of global population). However, recent extensive habitat loss in this range along with increased pressure by non-native mammalian predators motivated the creation of the first conservation plan for the species in 2014. Our work, that brings together Caribbean-, US- and UK-based ecologists and naturalists, is implementing several of the species’ recommended recovery projects, most of which will benefit all dry forest avifauna in the region. This work has been delayed due to the pandemic, but here we present two years of camera trapping data (>30,000 photos across ~5000 trap-days) and the first-year implementation of a mainland invasive species control program across four experimental sites.

Rethinking rivers: Reticulate and micro-endemic histories of diversification in upland forest birds

Lukas J. Musher

Presenting author: **Lukas Musher**, Academy of Natural Sciences of Drexel University, lmusher@amnh.org

Large Amazonian rivers impede gene flow for many organisms but frequently rearrange, thereby weakening their effects as long-term barriers. Alternatively, if rivers are barriers, rearrangements could stimulate diversification by promoting cycles of allopatry and secondary contact. We sequenced tens of thousands of DNA markers to test the drivers of population divergence and introgression in six avian species-complexes in southern Amazonia. We first tested the assumption that rivers are long-term barriers for birds and found that both large and relatively small rivers drove genomic divergence in all species. We then tested if species diverged with or without gene flow, and recovered reticulate histories for all species complexes, including at least one case of probable hybrid speciation. Our results are consistent with the hypothesis that river rearrangements promote differentiation by facilitating population isolation and secondary contact. We propose that Amazonian hyper-diversity originates from fine-scale ‘barrier displacement’ processes – such as river dynamics – which allow populations to differentiate, genomically recombine, and disperse out from centers of origin.

The escalator race: Ecological correlates of elevational range shifts in tropical birds

Monte H. C. Neate-Clegg, Samuel E. I. Jones, Joseph A. Tobias, William D. Newmark, and Çagan H. Sekercioglu

Presenting author: **Monte Neate-Clegg**, University of Utah, monteneateclegg@gmail.com

Globally, birds have been shown to respond to climate change by shifting their elevational distributions, on the so-called "escalator to extinction". This phenomenon is especially prevalent in the tropics, where elevational gradients are hotspots of diversity and endemism. Empirical evidence has suggested that elevational range shifts are far from uniform across species, varying greatly in the direction (upslope vs. downslope) and rate of change (speed of elevational shift). However, little is known about the drivers of these variable responses to climate change, limiting our ability to accurately project changes in the future. Here, we compile empirical estimates of elevational shift rates (m/yr) for 421 bird species from eight study sites across the tropics. On average, species shifted their mean elevations upslope by 1.63 ± 0.30 m/yr, their upper limits by 1.62 m ± 0.38 m/yr, and their lower limits by 2.81 ± 0.42 m/yr. Our results indicate that elevational shift rates are associated with species' traits, particularly body size, dispersal ability, and territoriality. However, these effects vary substantially across sites, suggesting that responses of tropical montane bird communities to climate change are complex and best predicted within the local or regional context.

"Life as a 'blirder" — how the intersectionality of motives, benefits, and values can help BIPOC birders exist in the field

Milton G. Newberry, III

Presenting author: **Milton Newberry**, Bucknell University, mgn003@bucknell.edu

A plethora of past research has explored individuals' motivations for participating in environmental stewardship and nature-based recreation activities (e.g., birding). These motives help explain the factors that recruit people, including BIPOC individuals, into these actions but limited research and evaluations have explored the intrinsic benefits that people receive from their engagement and how that shapes future experiences. This presentation will delve into the concept of psychological benefits for participation in birding and how they aid in participant retention. Furthermore, it is posited that the underlying values that guide individual behavior may be more pertinent variables to measure when assessing why BIPOC individuals engage with nature-based recreation activities such as birding. Finally, this presentation will discuss the novel idea of merging theories (e.g., Value-Belief-Norm & Hope Theory) with several methods of describing motives and intrinsic assets (e.g., Volunteers Function Inventory & Psychological Benefits) into practice to explore why BIPOC individuals endure in birding despite the adversities faced in the field. Organizations should consider what they can do to establish an environment of "true acceptance versus tolerance" for BIPOC individuals to help them exist and persist in birding.

A global screen for magnetic field-driven neuronal activity in the pigeon brain

Gregory C. Nordmann, Spencer D. Balay, Simon Nimpf, Lukas Landler, E. Pascal Malkemper, Lyubov Ushakova, and David A. Keays

Presenting author: **Gregory Nordmann**, IMP Vienna, gregory.nordmann@imp.ac.at

The remarkable navigatory abilities of the Rock Pigeon (*Columba livia*) are facilitated by a sensory system that allows the detection of magnetic fields. While there is compelling behavioral evidence demonstrating the existence of a magnetic sense, the primary sensory cells have yet to be identified, and the neuronal circuits that process magnetic information in the brain are largely unknown. To address these issues, we combine tissue clearing and light sheet microscopy to map magnetically induced C-FOS expression in the pigeon. We adapted existing open source software to register data from individual pigeon brains to custom-built reference templates, allowing us to compare neuronal activity between treatment groups at cellular resolution on a brain wide scale. As a proof-of-principle, we challenged pigeons with high-frequency sounds and show that our analysis pipeline detects activity in major brainstem and forebrain stations of the central auditory pathway. We then stimulated pigeons with rotating magnetic fields and globally screened the pigeon brains for magnetic field-driven neuronal activity. This screen confirmed activation of brain nuclei previously implicated in magnetoreception (e.g. the vestibular nuclei or the hippocampus) and revealed activation in novel circuits. Our experimental platform therefore (i) represents an important tool to globally assess sensory-driven immediate early gene expression in the avian brain, and (ii) contributes to further describing the pigeon's central magnetosensory pathway.

The Bahama Oriole Project — hopeful news from a Caribbean Island endemic

Kevin E. Omland, Shelley Cant, Janine M. Antalffy, Scott B. Johnson, Bradley L. Watson, Michael G. Rowley, Richard C. Stanley, Collin E. Studds, and Michelle J. Moyer

Presenting author: **Kevin Omland**, UMBC, omland@umbc.edu

The Caribbean is home to over twenty songbird species listed by IUCN as threatened, including the critically endangered Bahama Oriole. This species was extirpated from Abaco in the 1990s and is now restricted to Andros. Studies suggested there were fewer than 300 of these orioles, and that they mostly nested in coconut palms in developed areas. Bahamas National Trust together with the Omland Lab UMBC began the Bahama Oriole Project in 2016. Our goals were to: 1) quantify habitat use and current population size, 2) evaluate current threats to the population, and 3) promote awareness of this charismatic songbird. Our team has made many important discoveries showing that the species is not doing as badly as had been feared. We documented that the species breeds in native Caribbean Pine forests, and that the majority of the population likely breeds in pine forest. We estimate that 1200 to 2800 individuals remain on our study site on North Andros, and likely there are at least twice that many across Andros. Thus, the orioles seem to be hanging on in spite of the loss of many of the coconut palms in towns, in spite of cowbirds that parasitize nests in towns, in spite of invasive predators including cats and rats, and in spite of several near misses by recent hurricanes. More information is needed to determine what are the main threats to the population and what habitats the species uses in the non-breeding season. The Bahama Oriole has been resilient so far, but sea level rise and increasing hurricane strength mean that the species is becoming ever more vulnerable to a direct hit. Future possible reintroduction of the oriole to Abaco would make the species more resilient to hurricanes and other future threats.

Increasing temperatures are driving population declines in a biodiversity hotspot indicator species, the Cape Rockjumper (*Chaetops frenatus*)

Krista N. Oswald

Presenting author: **Krista Oswald**, Rhodes University, knoswald@gmail.com

The Fynbos biome is the only biodiversity hotspot that encompasses an entire global floral kingdom, all within 90,000-hectares. Its climate has been historically stable, maintained by a fine balance of low precipitation and regular fire, and is predicted to decrease in size by ~50% in the next few decades due to climate change. Cape Rockjumpers (*Chaetops frenatus*) are only found in Mountain Fynbos habitat, South Africa's sky islands limited to the far southwest corner of the country. Rockjumpers are inextricably linked to their habitat, and so their responses to climate change may predict consequences for the habitat itself. Rockjumper populations are currently at risk from a combination of direct (i.e. behavioural changes) and indirect (i.e. changing ecological landscape) effects of warming temperatures. At higher temperatures, rockjumper adults spent less time foraging, provisioned less leading to smaller nestlings, and faced increasing nest predation (predominantly due to snakes). Predictive modelling shows how these effects individually (but more importantly, combined) are likely to increase in coming decades. Using the rockjumper's responses as an indication, it is likely biodiversity of the entire Fynbos itself will face worrying consequences due to climate change. With no time to adapt, and restricted by oceans at higher latitudes, the highly specialized flora and fauna may find their sky island habitat becoming submerged.

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osmdata: Roadless areas and avian diversity

Mark Padgham

Presenting author: **Mark Padgham**, rOpenSci, mark.padgham@email.com

Roadless areas are of great biological importance. While a great deal of open data enable quantification of the biological diversity of a range of animal groups, data needed to quantify roadless areas is comparatively difficult to obtain in standardised form able to facilitate broad-scale comparisons between disparate geographic regions. This talk will present results drawn from two open data sets: the eBird data set curated by the Cornell Lab of Ornithology, used to quantify avian diversity, and Open Street Map (OSM), the world's most complete open data set of streets, ways, and the spatial structure of the world in general. Avian diversity was quantified by the total numbers of species observed at official eBird "hotspots" over the preceding ten years, obtained via rOpenSci's 'rebird' package. All roadless areas within a fixed radius of each hotspot were extracted from OSM using rOpenSci's 'osmdata' package. Diversity was then related to a range of statistics summarising the amount and form of nearby roadless areas, revealing roadless areas to be very strongly related to avian diversity. While the size of surrounding natural areas alone was very significantly correlated with avian diversity, the median sizes of roadless areas was considerably more strongly and significantly correlated, indicating the abiding importance of roadlessness beyond sizes of natural areas alone. Most importantly, the global coverage of these two data sets means that such analyses can readily extend well beyond the traditionally data-rich global north, to provide equally insightful analysis across much of the world.

Bias in birdwatchers: Does neighborhood incomes affect estimates of bird richness?

Deja J. Perkins, Caren B. Cooper, and Madhusudan Katti

Presenting author: **Deja Perkins**, North Carolina State University, djperkin@ncsu.edu

Birdwatchers make important contributions to ornithology research and conservation through citizen science. Like most citizen science, ornithology projects typically allow volunteers autonomy in selecting where to collect data. Participants in citizen science are overwhelmingly white and affluent. Consequently, volunteer-generated datasets can have significant spatial bias of data obtained around the homes and preferred places of the volunteers. We compared the influence of neighborhood income on estimates of species richness based on volunteer data from two projects with different protocols. We examined data from eBird volunteers in Tucson who submitted checklists following stationary protocols and data from Tucson Bird Count volunteers who collected checklists according to a systematic sampling, “atlas-style” protocol. eBird checklists were disproportionately more common in middle-income census tracts. Tucson Bird Count checklists produced estimates of species richness that exhibited a moderate “luxury effect'', that is, species richness increased with neighborhood income. Paradoxically, despite oversampling middle-income areas, eBird data underestimated species richness overall and did not detect a luxury effect.

Impacts of the early environment on post-fledging movement patterns of Snail Kites

Caroline L. Poli and Robert J. R. Fletcher

Presenting author: **Caroline Poli**, University of Florida, cpoli@ufl.edu

Natal dispersal is an important mechanism that drives population dynamics and gene flow. Conditions during early development may influence behavior of individual organisms, which can affect the outcome of natal dispersal. In particular, exploratory movements, which are often driven by the natal environment, are hypothesized to increase dispersal success. We sought to examine potential links between early conditions, patterns of exploration, and dispersal using GPS-tracking data from 71 fledgling Snail Kites (*Rostrhamus sociabilis*) across 16 wetlands. We summarized movement behavior and tested for an effect of two key environmental drivers of post-fledging movement: natal hydrology and snail density. Tracked birds remained within 3.2 km of the nest site for up to 58 days post-fledging and during that time, birds explored surrounding wetlands using occasional foray flights that began and ended at the natal wetland, and were characterized by rapid, moderate-distance movements. Birds that experienced low water levels at the nest initiated forays and emigrated from the natal site earlier than birds exposed to high water levels, but the time spent in forays and distance traveled did not appear to differ by natal hydrology. We further tested whether movement behavior was related to the success, timing, and distance of dispersal movements. Our results highlight how early-life environments can have long-term effects on an endangered bird, and point to hydrology at fledging as a key determinant of movement behavior.

Prospecting and informed dispersal: Understanding and predicting their joint eco-evolutionary dynamics

Aurore Ponchon, Alice Scarpa, Greta Bocedi, Stephen C.F. Palmer, and Justin M.J. Travis

Presenting author: **Aurore Ponchon**, University of Aberdeen, aurore.ponchon@gmail.com

The ability of individuals to leave a current breeding area and select a future one is important, because such decisions can have multiple consequences on individual fitness, but also on metapopulation dynamics, structure and long-term persistence through non-random dispersal patterns. In the wild, many colonial and territorial bird species display informed dispersal strategies, where individuals use information, such as conspecific breeding success gathered during prospecting, to decide whether and where to disperse. Understanding informed dispersal strategies is essential for relating individual behaviour to subsequent movements and then determining how emigration and settlement decisions affect individual fitness and demography. Although numerous theoretical studies have explored the eco-evolutionary dynamics of dispersal, very few have integrated prospecting and public information use in both emigration and settlement phases. Using an individual-based modelling approach, I detail how prospecting and

emigration rate concomitantly evolve in a heterogeneous but temporally auto-correlated environment and relate those results to empirical observations with implications for natal dispersal.

Evolution of species recognition when ecology and sexual selection favor signal stasis

Trevor D. Price and Pratap Singh

Presenting author: **Trevor Price**, University of Chicago, pricet@uchicago.edu

Many closely related species differ strikingly in colors, vocalizations, and other signals that are the focus of species recognition, thereby resulting in premating reproductive isolation. Yet many examples are known where related coexisting species appear very similar without hybridizing. In this paper we focus on evolution of species recognition in four species of *Stachyridiopsis* babblers, species that occupy similar, thick vegetation between 0m-3m off the ground. They sing extremely similar songs, with a single repeated narrow-bandwidth low-frequency note. We attribute the similarity among species to strong selection pressures to maximize transmission. The similarity conflicts with ease of species recognition. On the basis of playback of manipulated songs, we show song differences together (frequency, associated with differences in body size and syllable structure) are sufficient for species recognition where species coexist. The species that occurs is more variable in its syllable structure than the species present in sympatry, and responds to songs of all the other species. These results suggest both songs and song recognition have evolved in response to species interactions.

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soundecology: Using acoustic indices for landscape assessment and monitoring

John E. Quinn

Presenting author: **John Quinn**, Furman University, john.quinn@furman.edu

The volume and breadth of acoustic data only continues to increase. Processing these data quickly and consistently allows for diverse applications in research and practice. The soundecology package, developed by Luis J. Villanueva-Rivera and Bryan C. Pijanowski, provides a go-to set of code to calculate multiple well-recognized acoustic indices. In this lightning talk, I will highlight how this package can be used to quickly calculate indices for conservation assessment and monitoring. Examples will be drawn from ongoing efforts in different ecosystem types including mixed forest, agriculture, and urban.

Amazonian suture zones

Marco Rego, Glaucia Del-Rio, and Robb Brumfield

Presenting author: **Marco Rego**, Louisiana State University, mrego1@lsu.edu

Suture zones are thought to form from large-scale biogeographic events that affect a phylogenetically diverse group of taxa. In the Amazon basin, wide rivers structure the landscape and shape the distribution of terrestrial vertebrates. Turnovers of terrestrial vertebrates across Amazonian rivers is relatively common making these rivers true suture zones, but not all Amazonian rivers are associated with turnovers, and even those that do, become less effective dispersal barriers towards their narrower headwaters. Although the trend of certain Amazonian rivers to cluster great amounts of turnovers is widely discussed in the literature, there are no studies with detailed mapping of Amazonian suture zones that apply modern GIS and other computational techniques. Here we present a comprehensive assessment of Amazonian suture zones. We assembled a database with nearly 620,000 distributional records of c. 4,100 bird taxa (species and subspecies) found in the Amazon Basin. Most data points represent museum specimen records. Based on point localities for each taxon, we generated polygonal distributions and overlapped the edges of each taxon's polygon (considering a buffer of 50km) with the polygons of its close relatives. Our results confirm that Amazonian rivers differ considerably in their effectiveness in separating sister taxa, and that even the same river has varying levels of isolation potential depending on where the river is examined. We found that taxon turnovers cluster at river headwaters and other interfluve regions where there is no apparent dispersal barrier. We also detected suture zones along the eastern Andean slope and the Tepui regions that correspond to altitudinal gradients and adjacent mountain ranges.

Birds short-circuit the community assembly cycle: Testing Diamond's continuous speciation model

Bouwe R. Reijenga, David J. Murrell, and Alex L. Pigot

Presenting author: **Bouwe Reijenga**, University College London, bouwe.reijenga.18@ucl.ac.uk

Mountain ranges are home to exceptional species rich avian communities. Imperative to the accumulation of diversity is the rate at which sister species transition to sympatry and occur in the same geographical area. J. Diamond suggested a cycle in which sympatry is initially prohibited by competition. Sympatry may be established by diverging in elevational zone, either facilitated by competition at secondary contact or divergence in allopatry irrespective of competition–ecological sorting. Subsequent speciation events result in a repetition of transitions and formation of elevational zonation of closely related species. Elevational zonation may dissolve after sisters have diverged in their ecological niche, boosting local diversity. However, the frequency and accuracy of these pathways remains largely untested. Here, we attempted to fill this gap by analysing a global dataset of avian sister species and develop a series of multistate Markov transition models. We find that sister species primarily transition directly into sympatry without diverging in elevational niche while only a small proportion of pairs become elevational replacements, short-circuiting Diamond's cycle by directly diverging in ecological niche. Second, of the pairs that have attained divergent elevational zones, the majority have done so through ecological sorting rather than divergence at secondary contact. Concomitantly, our study provides a proof-of-concept in which limited geographic and phylogenetic information can be combined to model and dissect transition pathways and investigate how biodiversity accumulates.

Biogeography in a changing Amazonia: The past as a key to a challenging future

Camila C. Ribas

Presenting author: **Camila Ribas**, Instituto Nacional de Pesquisas da Amazônia, camilaribas@gmail.com

These are both exciting and worrying times for Amazonian biogeography. While we have been accumulating biotic and abiotic data on historical and current patterns, opening many possibilities to test hypotheses about the processes involved in assembling the most biodiverse biome on Earth, this same biome faces unprecedented threats, and biogeography has also a role in informing about these threats. Biogeography has been important in evidencing the heterogeneity of Amazonia, both regarding its history and its current organization, which is essential to protect it from spatially heterogeneous and cumulative impacts of deforestation, fire, infrastructure development and climate change. Recent studies have shown the contrasting history of birds associated to different Amazonian habitats in different regions, the differential effect of barriers for birds with varying ecological traits, the different degrees of threat to lineages endemic to specific regions and habitat types, and the underlying problem of incompletely known avian diversity that enhances the challenge of making realistic inferences about current patterns, and mitigating environmental impacts. A breakthrough advance in Amazonian biogeography has been multidisciplinarity. There is increasing integration between Earth scientists and evolutionary biologists interested in Amazonian biogeography, and large ongoing collaborative projects promise a very interesting trans disciplinary future. Another important advance has been the establishment of research partnerships with local traditional populations, who hold invaluable knowledge about this intricate socioecological system, and both preserve and depend on healthy ecosystems, free-flowing rivers, and standing forests.

Multi-species conservation planning for declining grassland bird populations in Prairie Canada

Barry G. Robinson and Jeffrey R. Ball

Presenting author: **Barry Robinson**, Environment and Climate Change Canada, barry.robinson@canada.ca

Grassland bird populations of North America have declined by 53% since 1970. Widespread conversion of native grasslands to cropland have contributed significantly to these declines suggesting that conservation action targeting remaining native grasslands would benefit multiple species. We developed a multi-species conservation plan in the Canadian Prairie Potholes for 4 species of grassland birds of highest conservation priority: Baird's Sparrow, Chestnut-collared Longspur, Thick-billed Longspur, and Sprague's Pipit. Our goals were to identify high-priority habitats for these four species and set spatially explicit habitat conservation objectives to meet existing population objectives. We simulated grassland conversion to cropland across the landscape and used species density models to establish a relationship between grassland loss rates and population declines. We used this relationship to determine the maximum grassland loss rates that would still allow population objectives to be met. By comparing this to estimates of actual grassland loss rates, we determined that 4.4 million acres of grassland needs to be conserved over the next 15 years in order to meet population objectives. To make this objective spatially explicit, we overlaid the high priority habitats for these species with a previously developed model of conversion risk. By targeting grasslands that are a relatively high priority for the focal species and also at high risk of conversion, conservation practitioners can ensure their efforts maximize benefits to grassland birds.

Single versus multi-species planning and management: A false dichotomy in bird conservation

Kenneth V. Rosenberg, Tom C. Will, Wendy E. Easton, and Randy Dettmers

Presenting author: **Kenneth Rosenberg**, Cornell Lab of Ornithology, kvr2@cornell.edu

Over the past three decades, debates have raged as to the efficacy of planning approaches focused on individual species versus those focused on habitats, broad threats, landscapes, or ecosystems. In the U.S. and Canada, agencies and programs have vacillated between single- and multi-species approaches, often asynchronously in the two countries. The loss of 2.9 billion birds across > 300 declining species tells us that addressing a wide range of broad habitat needs and threats without a collective targeted approach has failed in stemming declines of the most vulnerable species. Although general threats to birds are well-known, for most species we do not know the specific limiting factors, or precisely where and when these factors are most limiting. Our Road to Recovery approach promotes continental and co-produced research targeted at causes of decline on a species-by-species basis, because even species in the same habitat can experience different threats throughout their annual cycle. With more precise knowledge of limiting factors for priority species, we can build multi-species conservation strategies that address representative habitat needs, while also aiming to recover populations of the most urgently declining species. Single- versus multi-species approaches therefore represents a false dichotomy—both are needed, in an iterative and adaptive sequence, to effectively reverse avian declines. We propose a complimentary approach where explicit recovery goals and strategies for priority species are embedded within multi-species conservation plans for habitats and landscapes. We present examples of successful multi-species planning, including for a suite of declining grassland birds.

Multi-species conservation in Mesoamerica and Cuba: Lessons from the field

Natalia A. Rossi and Roan McNab

Presenting author: **Natalia Rossi**, Wildlife Conservation Society, nrossi@wcs.org

Mesoamerica's last five great intact forests—spanning from Mexico to Colombia—are biodiversity hotspots and strongholds for globally irreplaceable species, including many migratory birds. Together they cover more than 12 million hectares; hold about half the region's forest carbon stocks; provide water and other life-giving natural resources to 5 million people; and harbor several World Heritage sites, including the ruins of ancient civilizations. Nearly half are managed by Indigenous and local communities. On the other hand, the Cuban archipelago comprises about 50% of the insular Caribbean's landmass, harboring incredible biodiversity and endemism and the most extensive coastal wetlands in the region—including the iconic Zapata Swamp. Mesoamerica and Cuba's unique forest and coastal habitats are vital flyways and wintering grounds for migratory birds arriving from North America. Using an ecosystem-based approach, the Wildlife Conservation Society (WCS) has worked in the region to safeguard these critical habitats and the bird species they help sustain. Working side-by-side with local partners WCS has used a multi-species approach to protect and restore forests in Mesoamerica and coastal wetlands in Cuba. From Scarlet Macaws to over 100 migrant bird species in Mesoamerican forests and coastal wetlands; and from cavity-nesting birds in flooded palm savannas to the endemic Bee Hummingbird to raptors and shorebirds in the Zapata swamp, WCS is securing wintering grounds for an incredible array of North American migrant birds. This presentation will feature WCS multi-species conservation projects in Mesoamerica and Cuba and their outcomes in promoting full-cycle conservation of the birds we share.

Reproductive microbiomes: Intra- and inter-specific variation in avian ejaculate microbiomes

Melissah Rowe

Presenting author: **Melissah Rowe**, Netherlands Institute of Ecology, m.rowe@nioo.knaw.nl

Microbiomes are emerging as fundamental contributors to the biology of their hosts. Studies of animal microbiomes have focused on the oral, skin, and gut microbiome, whereas relatively little is known about the reproductive microbiome (i.e., microbiome of the reproductive tract, genitalia, gametes, and reproductive fluids of males and females). Reproductive microbiomes, however, can have significant impacts on the reproductive function and success of individuals, as well as critical repercussions for evolutionary processes related to sexual selection, sexual conflict, and the evolution of host mating systems. Most notably, little attention has been paid to the reproductive microbiome of males, especially in wild animal species. Using both culture-dependent and culture-independent methods (16S amplicon sequencing), I demonstrate that avian ejaculates harbour highly variable microbial communities at both the intra- and inter-specific levels. I discuss these findings in the context of bacterial-induced sperm dysfunction, and consider the potential repercussions of ejaculate microbiomes for the evolution of male reproductive physiology and the dynamics of fertilisation in birds.

Empirical tests of habitat selection theory reveal that conspecific density and patch quality, but not habitat amount, drive long-distance immigration in a wild bird

Clark S. Rushing, T. Brandt Ryder, Jonathon J. Valente, T. Scott Sillett, and Peter P. Marra

Presenting author: **Clark Rushing**, Utah State University, crushing05@gmail.com

Individuals that disperse long distances from their natal site must select breeding patches with no prior knowledge of patch suitability. Despite decades of theoretical studies examining which cues dispersing individuals should use to select breeding patches, few empirical studies have tested the predictions of these theories at spatial scales relevant to long-distance dispersal in wild animal populations. Here, we use a novel assignment model based on multiple intrinsic markers to quantify natal dispersal distances of Wood Thrush (*Hylocichla mustelina*) breeding in forest fragments. We show that long-distance natal dispersal in this species is more frequent than commonly assumed for songbirds and that habitat selection by these individuals is driven by density-dependence and patch quality but not the amount of habitat surrounding breeding patches. These results represent an important contribution to understanding habitat selection by dispersing individuals, especially with regards to long-distance dispersal.

Ethno-racial and social patterns in birdwatcher specialization

Jonathan D. Rutter, Ashley A. Dayer, Howie W. Harshaw, Nicholas W. Cole, Jennie N. Duberstein, David C. Fulton, Andrew H. Raedeke, and Rudy M. Schuster

Presenting author: **Jonathan Rutter**, Virginia Tech, rutter@vt.edu

Although birdwatchers comprise a large and growing proportion of the American public, there is a lack of racial and ethnic diversity in the birdwatching community. Previous research suggests that this homogeneity is self-perpetuating, as Black, Indigenous, and/or people of color (BIPOC) are less likely to pursue activities in which no one they know participates. However, it is unclear whether this trend in participation also applies to degree of participant involvement, or recreation specialization. Using a national survey of US birdwatchers, we measured recreation specialization among birdwatchers along affective, cognitive, and behavioral dimensions. We also determined whether respondents had social connections (acquaintances, close friends, or relatives) who birdwatch. We constructed linear regression models to investigate how specialization varied by ethno-racial group. As expected, the ethno-racial composition of birdwatchers was significantly less diverse than the American public. Of the 29,380 respondents who reported their ethno-racial group, 5.2% were BIPOC, while 94.8% were non-Hispanic White. However, we observed no statistically significant ethno-racial patterns in overall degree of recreation specialization, even when controlling for social connection and demographics. Considering the component dimensions of specialization individually, we found that some ethno-racial predictors were statistically significant, but not practically significant. We conclude that while some ethno-racial groups are underrepresented among birdwatchers, our results suggest that they are no less specialized. Therefore, efforts to build a more inclusive birdwatching community should focus on increasing participation from BIPOC.

Can kiwi trust their gut? Captive rearing alters the Brown Kiwi (*Apteryx mantelli*) microbiome

Priscilla A. San Juan, Isabel Castro, and Manpreet K. Dhami

Presenting author: **Priscilla San Juan**, Stanford University, psanjuan@stanford.edu

Captive rearing is often critical for animals that are vulnerable to extinction in the wild. However, few studies have investigated the extent at which captivity impacts hosts and their gut microbiota, despite mounting evidence indicating that host health is affected by gut microbes. We assessed the influence of captivity on the gut microbiome of the Brown Kiwi (*Apteryx mantelli*), a flightless bird endemic to New Zealand. We collected wild ($n = 68$) and captive ($n = 38$) kiwi feces at seven sites on the north island of New Zealand. Using bacterial 16S rRNA and fungal ITS gene profiling, we found that captivity was a significant predictor of the kiwi gut bacterial and fungal communities. Captive samples had lower bacterial (ANOVA, $p < 0.001$) and fungal (ANOVA, $p = 0.012$) diversity and different composition when compared to wild samples (PERMANOVA, $r^2 = 0.07$, $p = 0.001$). To further support this difference, ordination (NMDS) showed clustering by captivity status. Firmicutes dominated the gut microbiome

of wild kiwi, while Proteobacteria dominated in captive kiwi. History of coccidiosis, a gut parasite primarily affecting captive kiwi, showed a marginally significant effect on bacteria ($r^2 = 0.048$, $p = 0.095$) and fungi ($r^2 = 0.074$, $p = 0.087$). Our findings demonstrate captivity's potential to shape the Brown Kiwi gut microbiome, but further investigation is needed to elucidate the effects of these differences on welfare.

Effects of COVID-19 lockdowns on migratory and backyard birds: A review of research approaches and comparative results

Olivia V. Sanderfoot, Michael Schrimpf, Nicola Koper, and Beth Gardner

Presenting author: **Olivia Sanderfoot**, University of Washington School of Environmental and Forest Sciences, oliviavs@uw.edu

Travel restrictions during COVID-19 lockdowns in the spring of 2020 resulted in a rapid decline in human mobility in cities around the world. Consequently, light, noise, and air pollution in many major metropolitan areas suddenly decreased, providing a unique opportunity to study how human activity and anthropogenic pollution influence birds and our observations of them in urban settings. By reviewing recent studies on the topic and examining community science data at complementary spatial scales, we illustrate how avian responses to COVID-19 lockdowns vary among species and locations. Our two independent studies highlight the benefits of linking bird observations with data on human mobility during the most far-reaching global experiment in recent memory. We show that decreased human mobility primarily resulted in migratory birds in the United States and Canada making greater use of developed areas. We also demonstrate how smaller-scale shifts in human mobility in the Northwestern United States influenced the detection of birds and the ways people participate in community science. Some unanticipated outcomes of lockdowns on birds challenge our pre-existing assumptions about how human mobility affects avifauna. Studies on the impacts of COVID-19 lockdowns on birds demonstrate the value of community science, as volunteer-collected data can be leveraged to assess rapid changes in bird distributions and community assemblages. Together, this body of research will spark important conversations about how human mobility affects the presence and detection of birds and help us identify practical monitoring and conservation strategies for a post-pandemic world.

Genomic regions underlying divergent plumage and migratory traits relevant to speciation in Barn Swallows

Drew R. Schield, Javan C. Carter, Elizabeth S.C. Scordato, and Rebecca J. Safran

Presenting author: **Drew Schield**, University of Colorado Boulder, drew.schield@colorado.edu

Identifying genomic regions underlying traits involved in reproductive isolation and local adaptation is a central goal in speciation research. We investigated patterns of genetic differentiation using whole genome sequences from parental and admixed populations across two Barn Swallow (*Hirundo rustica*) hybrid zones associated with migratory divides in Asia, regions which represent recent secondary contact zones between subspecies that diverged during the Holocene and that have divergent plumage and migratory traits. We first looked for evidence of 'differentiation islands' between parental populations that may house genes and regulators involved in divergent traits. We then employed an admixture mapping approach focused on hybrid populations to identify associations between genomic regions and phenotypic, plumage coloration, and stable isotope (a proxy for non-breeding location) variables. We identified overlapping regions from both sets of analyses as likely candidates involved in reproductive isolation, and further used a suite of population genetic statistics to infer whether differentiation has evolved due to linked selection, divergence hitchhiking, or a complement of processes. Our results indicate that, even despite low background levels of differentiation between Barn Swallow subspecies, the genomic landscape of differentiation is complex, with multiple regions putatively underlying divergent traits scattered across chromosomes, and concentrated on chromosome 4A and the Z chromosome. Our findings provide a useful contrast to studies that have uncovered comparatively simple genomic divergence architectures during avian speciation.

Multi-species conservation planning in theory and practice – is a bird in hand worth two in the bush?

Fiona K. A. Schmiegelow

Presenting author: **Fiona Schmiegelow**, University of Alberta / Yukon University, fiona.schmiegelow@ualberta.ca

Multi-species conservation planning has emerged as a front-line approach to stemming declines of bird populations across North America. Conceptually, this approach has roots in theories that underlay use of focal and surrogate species, fine and coarse filter planning, and ecosystem-based management. Given the urgent need to identify and address historic drivers of decline, as well as anticipate future challenges associated with climate change, it is imperative that multi-species frameworks employ a multi-faceted approach that builds on these conceptual underpinnings to advance broad-scale conservation actions with measurable outcomes at multiple scales. I explore antecedents to current multi-species approaches from both a theoretical and practical perspective, and identify factors that increase the likelihood of successful outcomes when implementing multi-species conservation plans for North American bird populations.

Using replicate hybrid zone transects to examine the genetic architecture of reproductive barriers

Georgy Semenov, Amber Rice, Mark Robbins, Alana Alexander, Rena Schweizer, Matthew Carling, Zac Cheviron, and Scott Taylor

Presenting author: **Georgy Semenov**, University of Colorado, georgy.semenov@colorado.edu

The degree to which the genetic architecture of reproductive isolation co-varies with environment remains a subject of active debate. While the same phenotypes and underlying genes can repeatedly play a role in maintaining boundaries between lineages across species' ranges, genetic architecture of reproductive barriers may also differ due to geographic variation in selection regimes and targets. We addressed this topic by studying replicate transects across an extensive hybrid zone between Black-capped and Carolina Chickadees. These species have a long and narrow hybrid zone extending from New Jersey to Kansas, that is shaped by reduced fitness of hybrids due to strong intrinsic selection, as well as by differential response of parental species to warming winter temperatures. We sequenced whole genomes of hundreds of individuals sampled across two geographically remote transects to test whether the same or different genomic regions and genes show reduced introgression consistent with reproductive barriers. While previous studies highlighted consistent spatiotemporal dynamics of the Black-capped and Carolina Chickadee hybrid zone in Pennsylvania, our study adds a geographical component to understanding of the dynamics of boundaries between recently diverged species.

Evolution of complex social structure in a cooperative breeder

Shailee S. Shah and Dustin R. Rubenstein

Presenting author: **Shailee Shah**, Columbia University, sss2254@columbia.edu

Many cooperatively breeding species display complex social structure, comprising surprisingly high proportions of non-kin individuals and multiple breeding pairs. Such societies occur in a range of taxa – from birds and mammals, to crustaceans, arachnids, and insects. However, the factors driving the demographic processes leading to their formation and maintenance are poorly understood. We leveraged long-term data spanning 31 breeding seasons from nine social groups to examine immigration of non-kin into social groups of Superb Starlings (*Lamprotornis superbus*), an obligate, plural cooperative breeder forming mixed-kin groups. Using empirical and simulation modelling approaches, we show that immigrants are vital to the stability and productivity of cooperative social groups in a temporally variable and unpredictable environment. Further, dispersing individuals are more likely to join larger groups, which tend to occupy higher quality territories, to maximize individual reproduction and survival. Overall, our results underscore the adaptive nature of plural breeding, mixed-kin cooperative societies in an unpredictable environment and provide insight into how natal dispersal decisions drive cooperative social group dynamics across a spatiotemporally variable landscape.

Patterns of reproductive isolation in recently sympatric *Myzomela* honeyeaters with neo-sex chromosomes

Elsie H. Shogren, Christina Muirhead, Jason M. Sardell, Daven C. Presgraves, and J. Albert C. Uy

Presenting author: **Elsie Shogren**, University of Rochester, elsie.shogren@gmail.com

The *Myzomela* honeyeaters of the Solomon Islands possess neo-sex chromosomes and, due to recent secondary contact between species, present a unique opportunity to study the role of sex chromosomes in reproductive isolation. Within the last 100 years *M. cardinalis*, a species with bright red plumage, has colonized a large island

inhabited by *M. tristrami*, a species with all black plumage. Studies of hybridization across diverse taxa consistently implicate sex chromosomes as hotspots of hybrid incompatibility, through mechanisms including heterogamy (Haldane's rule) and sexual conflict. Rapidly evolving "neo-sex chromosomes," such as those seen in *Myzomela*, can provide direct insights into both sex chromosome evolution and the central role of sex chromosomes in hybrid incompatibilities. We use long-read sequencing and high-throughput population sequencing to develop a detailed view of speciation and hybridization in the Solomon Island honeyeaters. Preliminary assembly of long high-fidelity sequence reads suggests that the neo-sex chromosome was formed through an unusual W-autosome fusion. Ongoing analyses of whole-genome resequence data are exploring the regions of the genome and specific loci resistant to introgression, offering insights into the role of sex chromosomes in speciation.

Spatial variation in aerial insectivore declines

Dave Shutler

Presenting author: **Dave Shutler**, Acadia University, dave.shutler@acadiau.ca

Overwhelming evidence of declines in aerial insectivores has emerged from multiple sources, but quantifying causes has proven more difficult. Perhaps unsurprisingly, (some) evidence also suggests declines in aerial insects. Whether directly or indirectly, insectivore/insect declines point to climate change, habitat loss and degradation, acid precipitation, and pesticides as likely and potential culprits; a less familiar reason for insect declines is non-native plants. Further contributors to insectivore declines include light pollution and attendant collisions with human-made structures, cats and other predators, and diseases. Spatial variation in the magnitude of changes in each of these causal elements should provide clues to reasons for declines, but clues must also explain why declines have hit aerial insectivores more than, for example, granivores. A further challenge is quantifying some suspected causal elements, such as spatial variation in cat density, which will constrain focusing conservation efforts.

Habitat use and stable isotopes inform winter ecology in the Eastern Whip-poor-will

Aaron A. Skinner, Michael P. Ward, Ian Souza-Cole, James R. Wright, Frank R. Thompson III, Thomas J. Benson, Stephen N. Matthews, and Christopher M. Tonra

Presenting author: **Aaron A. Skinner**, The Ohio State University, skinnerayayron93@gmail.com

The Eastern Whip-poor-will (*Antrostomus vociferus*) has declined by 70% in recent decades, yet an understanding of when and where populations are limited throughout the annual cycle remains poorly understood. We deployed 115 archival GPS tags on Whip-poor-wills in the summers of 2017 and 2019 in five breeding areas across four states in the Midwestern US. We extracted data from the wintering grounds from 52 tags, and combined spatial data from the tags with landcover data to examine home range size and habitat use. Preliminary analyses show that home range size varied considerably, from 0.2 – 11.2 ha. Land use also varied greatly in the landscapes surrounding home ranges (500m buffer around the home range). While all birds had some forest in the surrounding landscape, it ranged from 13-100% of the buffer, and agriculture and scrub were the second and third most prominent landcovers, respectively. Additional analyses will focus on, 1) winter home range size using continuous time movement models, 2) winter Carbon and Nitrogen stable isotope ratios (n=40) to see how stable isotope ratios vary with land cover and home range size, and 3) how home range size varies with percent forest, percent agriculture, and total edge (m), both in the home range and surrounding landscape, as well as elevation (m), latitude, and body size. This work fills important knowledge gaps in the whip-poor-will annual cycle, grounding and informing future conservation plans that will assist in the recovery of this once common bird and other similar migratory insectivores.

Exploring the avian microbiota-gut-brain axis in captive and wild songbirds

Morgan C. Slevin, Jennifer L. Houtz, Maren N. Vitousek, and Rindy C. Anderson

Presenting author: **Morgan Slevin**, Florida Atlantic University, mslevin2018@fau.edu

All animals host a gut microbiome, the natural bacterial community in the gastrointestinal tract. Emerging research in mammals shows the gut microbiome is related to host health in general, as well as important facets of health such as cognitive function, behavior, and the stress response. These relationships are collectively known as the gut-brain-HPA axis. Despite a wealth of research detailing these relationships in rodents and humans, relatively very little is known about this system in birds and other taxa. Here I review my preliminary evidence supporting a microbiota-gut-brain axis in a captive Zebra Finch *(Taeniopygia guttata*) population. I then summarize my progress in the remainder of my dissertation where I am studying how the hypothalamic-pituitary-adrenal axis mediates communication within the microbiota-gut-brain axis of wild Northern Cardinals (*Cardinalis cardinalis*). Using repeated song playbacks on subjects' territories, I will experimentally provoke a chronic stress response in territorial males to test for effects of challenges on the gut microbiome, body condition, and beak coloration. Better understanding a wild bird's gut microbiome, and how that community relates to stress, health, and behavior, is a first step to using microbiomes as a tool to index wild animal population health, as well as ameliorate stress and improve the health of animals in captive breeding and rehabilitation and release programs.

Are birds ever *really* limited by temperature?

Jacob B. Socolar

Presenting author: **Jacob Socolar**, Cornell Lab of Ornithology, jacob.socolar@gmail.com

Through the lens of global change biology, the ornithological community often treats temperature as a predominant determinant of species ranges. However, empirical evidence for the primacy of temperature is extremely thin. A synthesis of available data and anecdata suggests that the causal influence of temperature on montane bird distributions is filtered through a tangled web of interacting variables (habitat structure, resource availability, etc.) that exercise direct proximate control over bird distributions. Pinning down species' proximate requirements may point the way towards more nuanced management and conservation planning for tropical montane birds in a warming world.

Resilient Caribbean birds and people: Science, outreach, and conservation in a challenging time

Lisa G. Sorenson

Presenting author: **Lisa Sorenson**, BirdsCaribbean, Lisa.Sorenson@BirdsCaribbean.org

The Caribbean region has been battered in the last few years by a multitude of challenges, including devastating hurricanes and myriad threats to habitats, such as development, pollution, invasive species, and even a volcano. In addition, COVID-19, has devastated Caribbean island economies that are highly dependent on tourism. Nonetheless, our partners and birds have survived, and field studies and conservation projects have made significant progress. I will share a whirlwind tour of recent case studies and projects that highlight the dynamic and dedicated work of our partners and our regional projects, including hurricane recovery, Caribbean Waterbird Census monitoring, and bringing communities together to enjoy, restore, and conserve our endemic and migratory birds and their habitats.

The avian lumbosacral organ and the potential for balance sensation in the spinal cord

Kathryn E. Stanchak, Kimberly E. Miller, Eric W. Lumsden, Maxwell H. Gray, David J. Perkel, and Bingni W. Brunton

Presenting author: **Kathryn Stanchak**, University of Washington, stanchak@uw.edu

Birds have exceptional locomotor abilities, including perching on swaying branches and the precise coordination of head and body motion. These abilities may be enabled by a highly modified synsacral spinal cord and column that has been hypothesized to serve as an additional set of balance sensors--sensors that transduce body motion into neural signals. Within the synsacrum, the spinal cord has a series of lateral accessory lobes that roughly align with recessed bony canals in the synsacrum. The spinal cord also splits dorsally, and within this split rests an egg-shaped feature called the glycogen body. This set of modifications is collectively known as the avian lumbosacral organ (LSO). In this talk, we describe LSO anatomy and hypotheses for how it might function as a balance sensor. Then, we present new immunohistological findings within the neural tissue of the LSO and new comparative data on the shape of the interior of the synsacrum. Specifically, we have found that the LSO spinal cord expresses Myosin 7a, a protein implicated in inner ear sensing, and that perching birds tend to have more exaggerated LSO bony morphology. Finally, we will describe a framework for future studies to test hypotheses of LSO function and its potential role in avian locomotor control.

A habitat-based approach to developing a Conservation Investment Strategy for three migratory birds that depend on Latin America's mid-elevation forests

Rebecca L. M. Stewart, Nicholas J. Bayly, Randy Dettmers, Maria Alejandra Meneses Giorgi, Ana M. González, Rosabel Miró, Estuardo Secaira, and Yenifer Diaz Wong

Presenting author: **Becky Stewart**, Canadian Wildlife Service, Environment and Climate Change Canada, becky.stewart@canada.ca

Conservation Investment Strategies (CISs) are results-driven and enable groups to collaborate across broad landscapes to achieve common goals. Further, CISs attach dollar amounts to outcomes, and thus enable funders to track a return on investment. In 2020, Partners In Flight Eastern Working Group advanced a project to engage Canadian, US, and Latin American partners in the development of a CIS for Central and South America's mid-elevation forests. An Open Standards for the Practice of Conservation (Conservation Standards; CS) process, led by a CS coach and coordinated by Audubon Panama and SELVA, was undertaken to develop the strategy's key elements. Over 2 months, 50 partners, from 10 countries and representing government, ENGOs and private industry, engaged in a virtual workshop series. The non-breeding distributions of three high conservation priority migratory birds: Golden-winged Warbler (*Vermivora chrysoptera*), Cerulean Warbler (*Setophaga cerulea*) and Canada Warbler (*Cardellina canadensis*) define the strategy's focal geography, but its conservation target is these birds shared forest habitat. This broadens the project's scope and its relevance to partners and it is expected that the strategies and actions identified therein will benefit multiple species along with other biodiversity targets. We believe the breadth of partnership, and the plan's potential to address multiple priorities, is essential to conserving migratory species across diverse jurisdictions and landscapes and will enable partners to leverage additional resources to advance conservation at scale. Further, the project, its successes and challenges, should help inform similar efforts moving forward.

Orphaned refugees or opportunistic queuers: Variation in natal dispersal in the cooperatively breeding Florida Scrub-Jay

Young Ha Suh, Reed Bowman, and John W. Fitzpatrick
Presenting author: **Young Ha Suh**, Cornell University, ys757@cornell.edu

Why unrelated members form groups in avian cooperative breeders remains a pertinent topic in evolutionary biology because benefits for non-kin group members are not obvious. We studied dispersal to join unrelated social groups in the Florida Scrub-Jay (*Aphelocoma coerulescens*), a cooperatively breeding species that primarily forms kin-based groups. We evaluated potential adaptive benefits of dispersing to become an unrelated helper (subordinate dispersal) versus dispersing to pair and breed (direct dispersal) by examining proximate and ultimate factors relating to these two strategies. Of birds that reached age one year, 28% were subordinate dispersers, eventually becoming unrelated helpers at non-natal territories before they acquired a breeding territory or disappeared. Subordinate dispersers departed at younger ages and moved greater distances than direct dispersers. For both sexes, subordinate dispersers joined groups with fewer same-sex helpers than in their natal group. Direct and subordinate dispersers showed similar survival and were equally likely to become breeders, but male subordinate dispersers took longer to breed, lived for fewer breeding seasons, and produced fewer total numbers of fledglings than direct dispersers. In Florida Scrub-Jays, subordinate dispersal appears to be an alternative strategy for female helpers but a best-of-a-bad-job for males, with reproductive costs constraining the latter. This research is consistent with the sexual asymmetry in dispersal in Florida Scrub-Jays and highlights the plasticity in dispersal strategies given social and environmental conditions, offering a new perspective in our understanding of non-kin based social groups.

100-year resurvey of Mexico shows differential impact on montane vs. lowland avifaunas to climate change and land use

Ryan S. Terrill, Morgan W. Tingley, Adolfo G. Navarro S., A. Townsend Peterson, Vicente Rodriguez, Humberto Antonio Berlanga García, Whitney L. E. Tsai Nakashima, John Klicka, and John E. McCormack
Presenting author: **Ryan Terrill**, Occidental College, ornithoterrill@gmail.com

The indelible footprint of the Anthropocene interacts with diversity in ways that are often idiosyncratic to individual species and ecosystems. When viewed across ecoregions, separate mechanisms like habitat destruction and climate change may interact as a "double-edged sword" for avian diversity, but these mechanisms likely affect lowland birds and montane birds differentially. Particularly, montane avifaunas have been shown to be driven upslope by a warming climate while lowland birds may suffer substantially from habitat degradation. However, the overall effect may be to homogenize bird communities through promotion of populations of generalist and commensal species, with knock-on extinction and extirpation of specialized birds and regional endemics. In this study, we aim to understand how and why avian communities have changed in Mexico over the past 100 years. Using occupancy models to appropriately compare presence-only specimen data to systematic survey data and community science data, we are beginning to understand how bird species and communities have been affected by human impacts since the 1930s across all of Mexico. Here, we present preliminary results from this Mexican Bird Resurvey Project (MBRP), and discuss implications and future directions.

Riverscape dynamics shape microevolutionary processes across Amazonian floodplains

Gregory Thom, Eduardo Shultz, Alexandre Aleixo, Cristina Miyaki, and Camila C. Ribas
Presenting author: **Gregory Thom**, American Museum of Natural History, gthomesilva@amnh.org

The Amazon Basin harbors the largest and most diverse flooded habitats in the world. Yet, levels of diversity and origination are still poorly known in well-studied groups like birds. Here we present an overview of recently developed comparative phylogenomic studies exploring the effects of historical environmental changes and current connectivity on population differentiation. We show that changes in the fluvial landscape induced by climate variation during the Mid- and Late Pleistocene play a central role in the formation of genetic structure, levels of introgression, and long-term population persistence. Although shared patterns of diversification have been reported for river island specialists, variation in species history is associated with habitat preference. Habitat specialists, restricted to river-created environments, are more prone to be geographically structured and have more dynamic populations over time than more generalist species. We show how historical demography is associated with the sediment load of large Amazonian rivers, and that phylogeographic breaks match major physical features created by past alterations in the sedimentary budget of rivers. We point out that the central portion of the Amazon River basin is a suture zone for taxa isolated across the main Amazonian sub-basins. Lastly, we argue that the high diversity of environments of the Amazonian floodplains offer exciting opportunities to study hybridization events, the role of competition in driving genomic divergence, and the role of habitat preference on species evolutionary trajectories.

Nesting habitat of a northern population of Chimney Swifts (*Chaetura pelagica*) in forested landscape using the Motus arrays

Jérémie Tixier, Junior A. Tremblay, Isabelle Devost, André Desrochers, François Shaffer, Vincent Lamarre, Camille Bégin-Marchand, Pascal Côté, and Patrick Paré
Presenting author: **Jérémie Tixier**, Université Laval, jeremie.tixier.1@ulaval.ca

Chimney Swifts (*Chaetura pelagica*) have seen their population drastically decline in the past decades and own threatened status in Canada since 2007. Reduced availability of aerial insects likely due to pesticides, increased frequency of extreme weather events and the loss of roosting and breeding habitats have been identified as main threats to the species. While little information is available on the species nesting in natural habitats, the potential of breeding in these habitats is largely unknown and could be an important component for long-term viability of the species. In Québec, within the last 55 years, only five nests in hollow trees have been reported. Our study objective is to document nesting of Chimney Swifts in natural habitats. The study is located in a forested landscape at the northern limit of the species' range in Québec (Haute-Mauricie) where Chimney Swifts are captured at a roost chimney at the Sanatorium Historique Lac-Édouard. A pulley system and a mist net allow catching birds in the chimney to equip them with Motus nanotags. In May 2019, 16 swifts were captured at the roosting site and equipped with nanotags. Birds' movements during the nesting season were tracked using a network of five Motus stations as well as mobile telemetry by car, boat, ORV and foot. Amongst marked birds, four were tracked in their natural habitat and two led us to trees used as nesting sites: a 77-cm dbh dead sugar maple (3.8 m height) and a 82-cm dbh live yellow birch (23.7 m height) respectively located 20.5 and 22 km from the roosting site. The project continues in 2021 with 20 nanotags deployed in spring, and enhanced Motus network in the study area.

Genomics of hybridization and isolation in extant and extinct *Vermivora* warblers

David Toews, Marcella Baiz, Andrew Wood, Scott Taylor, and Irby Lovette
Presenting author: **David Toews**, Pennsylvania State University, toews@psu.edu

Understanding the barriers to reproduction in closely related species is a central goal of evolutionary biology. Hybrid zones are particularly important in this vein as, by definition, they only occur between taxa that are not completely reproductively isolated. Determining the extent of isolation can, in part, be measured by evidence of gene flow obtained from genome-wide markers. This is particularly useful for hybridizing species with very little genomic divergence due to extensive hybridization. We have applied such genomic tools over the past several years to study hybridizing Golden-winged and Blue-winged (*Vermivora*) Warblers. Here we discuss recent findings connecting plumage variation in different hybrid classes, the genetic bases for those traits, and their putative role in maintaining isolation in the face of significant gene flow. We also describe, for the first time, a whole-genome analysis with the only other member of the *Vermivora* genus, the extinct Bachman's (*V. bachmanii*) Warbler. Comparing toepad ancient DNA from a specimen collected in 1890, we find novel evidence of admixture between *V. bachmani* and the ancestor of the two extant *Vermivora* species. Together, we highlight the role of genomic data to study reproductive isolation and hybridization in contemporary and ancient lineages.

Fluctuations in bird populations in a coastal forest in Puerto Rico show resiliency after natural events

Adrianne G. Tossas

Presenting author: **Adrianne Tossas**, University of Puerto Rico, Aguadilla, agtossas@gmail.com

From 2009- 2021 I surveyed bird populations in Guajataca State Forest, northwestern Puerto Rico. A total of 1,772 individuals from 23 species was recorded in 150 point counts. No difference was found in the overall abundance of bird species during the first seven years of the study (mean = 0.63 individuals/count). However, a 7- 13% decline in abundance was observed two years after an extreme drought affected the island in 2015. The passage of category 4 Hurricane Maria through the study area in 2017 dramatically altered the habitat and further affected the avian diversity. Tree uprootings, broken branches, and severe defoliation caused the canopy cover to open by 22% compared to the previous year. Two years after the passage of the hurricane, six species showed population declines (e.g., Bananaquit *Coereba flaveola*, Puerto Rican Tody *Todus mexicanus*), while nine species increased (e. g., Puerto Rican Bullfinch *Melopyrrha portoricensis*, Puerto Rican Vireo *Vireo latimeri*), possibly due to improved detectability after the opening of the forest structure. Omnivorous species increased after the hurricane compared to declines in the insectivorous, nectarivorous and frugivorous foraging guilds. In 2021, the mean number of individuals resembles pre-hurricane levels (2017), thus showing resiliency in the avian community. Nonetheless, long-term monitoring is needed because trends differ among species, and to determine if the abundance will reach the values found in years before the drought.

Migratory microbiota: Remodeling of the Blackpoll Warbler gut microbiome over fall migration

Brian K. Trevelline

Presenting author: **Brian Trevelline**, Cornell University, brian.trevelline@gmail.com

A recent surge in research has demonstrated that the gut microbiome—the archaeal, bacterial, fungal, and viral communities in the intestinal tract—strongly influences host physiology and performance. However, the vast majority of microbiome research has been conducted in humans and model organisms, while the potential importance of host-microbe interactions in wild birds remains insufficiently explored. Notably, it is currently unknown how the gut microbiome responds to the energetic and physiological challenges of migration, or whether microbiota can help migrants overcome these challenges. To help fill this knowledge gap, we investigated the gut microbiome of the Neotropical migratory Blackpoll Warbler (*Setophaga striata*) at several locations along its North American fall migration route. Our analysis revealed a significant remodeling of the gut microbiome in migratory and staging blackpolls compared to those in the stationary breeding phase. Specifically, blackpolls harbored a less diverse and less taxonomically-rich microbiome upon arrival to staging sites. Further, changes in the taxonomic composition of the blackpoll gut microbiome were accompanied by concomitant increase in bacterial genes that may aid in fruit digestion and lipogenesis, suggesting that the gut microbiome may play a role in pre-migration fattening. These results will be discussed within the broader context of dietary, environmental, and physiological factors that may initiate changes in the blackpoll gut microbiome, while also highlighting the utility of germ-free birds to further investigate how the gut microbiome may influence the physiology and performance of migratory passerines.

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seewave and tuneR: Sound analysis in ornithology

Yi-Chin (Sunny) Tseng

Presenting author: **Yi-Chin Tseng**, University of Northern British Columbia, sunnyyctseng@gmail.com

Audio recordings of birds are important tools for biologists and ecologists involved in avian bioacoustics, which includes topics such as bird communication and related behaviour, sound production, identification techniques and application, and environmental monitoring. Given the increasing amount of audios that need to be processed, using R as the tool has been becoming more common among researchers as a way to efficiently analyze, manipulate, display, edit and synthesize audios. In this talk, R packages "tuneR", created by Uwe Ligges, and "seewave", created by Jerome Sueur, will be introduced. These two packages enable R to read, edit, and write audios (.wav or .mp3). Basic sound processing such as Fourier transformation, creating spectrograms, and separating sound files will be demonstrated. Further, functions such as high-pass filter, noise reduction, pre-emphasizing will also be introduced. Advanced analyses such as extracting Mel-Frequency Cepstral Coefficients and other sound characteristics will be included as well. Research work related to automatic bird sound detection system, which was done with the packages, will be shared.

Rapid speciation via the evolution of pre-mating isolation in the Iberá Seedeater

Sheela P. Turbek, Melanie Browne, Adrián S. Di Giacomo, Cecilia Kopuchian, Wesley M. Hochachka, Cecilia Estalles, Darío A. Lijtmaer, Pablo L. Tubaro, Luís Fábio Silveira, Irby J. Lovette, Rebecca Safran, Scott Taylor, and Leonardo Campagna

Presenting author: **Sheela Turbek**, University of Colorado Boulder, sheela.turbek@colorado.edu

Post-zygotic isolation often takes longer to evolve than the time to speciation of many taxa, and pre-mating isolation has therefore been proposed as a powerful reproductive barrier maintaining sympatric species early in divergence. However, the ease with which assortative mating can break down has called into question the importance of pre-mating isolation during incipient speciation. We combined whole-genome and double digest restriction-site associated DNA (ddRAD) sequencing data with fine-scale behavioral analyses from several years of detailed field study to quantify assortative mating, the traits used in species recognition, and the origin of the genomic variants involved in pre-mating isolation between two sympatric species of capuchino seedeaters (*Sporophila hypoxantha* and *Sporophila iberaensis*). Capuchino seedeaters comprise a recent, rapid avian radiation characterized by striking differences in male plumage coloration and song despite remarkably little ecological or genomic divergence. Though *S. hypoxantha* and *S. iberaensis* lack temporal or spatial barriers to reproduction, are genetically almost identical, and have a high rate of extra-pair paternity, we documented complete assortative mating with regard to both social and extra-pair mates associated with the genomic regions that underlie differences in male plumage patterning. In addition, males responded more aggressively to conspecific song and plumage than heterospecific traits in simulated territorial interactions. Plumage differentiation likely originated through the reassembly of standing genetic variation, indicating how novel sexual signals may quickly arise and maintain species boundaries early in divergence.

Climate-driven changes in insect phenology shift timing of nutrient availability for declining aerial insectivores

Cornelia W. Twining, J. Ryan Shipley, Margaux Mathieu-Resuge, Tarn Preet Parmar, Martin J. Kainz, Dominik Martin-Creuzburg, Catherine H. Graham, Christine Weber, David W. Winkler, and Blake Matthews

Presenting author: **Cornelia Twining**, Swiss Federal Institute of Aquatic Science and Technology,
cornelia.twining@gmail.com

Birds must synchronize their reproduction with both seasonal changes in environmental conditions and the phenology of resources. While it is well-established that climate change has the potential to decouple resource supply from consumer demand, threatening the persistence of wild bird populations, the underlying ecological mechanisms and fitness consequences of mismatch are poorly understood. Here, we use long term records of aquatic and terrestrial insect availability and egg-hatching times of multiple aerial insectivore species to investigate mismatches between the availability of, and demand for nutrients that are crucial for developing chicks. We show that the phenologies of aquatic and terrestrial insects are asynchronous, and that their relative biomasses drive the seasonal availability of omega-3 long-chain polyunsaturated fatty acids (n-3 LCPUFAs) for aerial insectivores. Aquatic insects, which have high n-3 LCPUFA content, reach peak biomass earlier in the breeding season than terrestrial insects, which are nearly devoid of these physiologically-vital fats. Based on data spanning over thirty years, we also find that aquatic and terrestrial insect phenologies have advanced substantially faster than those of aerial insectivores, shifting the seasonal availability of n-3 LCPUFAs for these rapidly-declining species. Furthermore, due to the fundamental differences in n-3 LCPUFA content between aquatic and terrestrial insects, phenological mismatches between aerial insectivores and aquatic insects cannot simply be offset by seasonal advancements in terrestrial insects.

Using multi-species data to establish indicators for adaptive management in the boreal forest

Steven L. Van Wilgenburg, Leanne Heisler, Ryan Fisher, and Gigi Pittoello

Presenting author: **Steven Van Wilgenburg**, Environment and Climate Change Canada, steven.vanwilgenburg@Canada.ca

Widespread declines in avian populations over recent decades have garnered considerable attention, leading to a re-evaluation of how we manage their populations across large areas. Most jurisdictions do not directly manage bird populations per se; instead, efforts focus on managing human activities that affect the amount, condition, and distribution of bird habitat. These efforts often include adaptive operations emulating natural spatiotemporal patterns in habitat heterogeneity thereby promoting multi-species conservation. In an effort to support planning that accounts for both economic and ecological sustainability, jurisdictions need to develop adaptive management frameworks that include species indicators from many taxa that can effectively and efficiently track habitat management actions through time. Here, we established species indicators of forest condition for the boreal forest in Saskatchewan using a suite of avian species tightly linked to a broad range of upland forest niches and the overall landscape-condition of the forest. In addition, a viability assessment for the indicator was also developed using the Conservation Standards framework to provide information on when important changes in the boreal bird community, and therefore the forest, may be occurring. This indicator alongside GIS-based indicators will track change in composition of Saskatchewan's boreal forest and help guide habitat conservation while supporting responsible economic growth in the province.

Introduction to avian microbiome research

Elin Videvall

Presenting author: **Elin Videvall**, Brown University, elin.videvall@gmail.com

There has been a recent surge of interest in animal-associated microbiomes given their important roles in host health and behavior. However, microbiome research in birds is still lagging behind that of mammals, despite the enormous potential of avian studies to explore outstanding questions in ecology and evolution. In this overview talk, I will start the symposium 'A bird's-eye view of the microbiome' by providing an introduction to avian microbiome research. What is a microbiome? And why is it important? I will provide examples of how we can sample different microbiomes of birds and highlight some of the fascinating research being conducted to explore these microbial communities.

The genomic architecture of reproductive isolation in a hybrid zone between Bullock's and Baltimore Orioles

Jennifer Walsh, Shawn M. Billerman, Bronwyn G. Butcher, Vanya G. Rohwer, David P.L. Toews, and Irby J. Lovette

Presenting author: **Jennifer Walsh**, Cornell University, jlw395@cornell.edu

Hybrid zones are excellent model systems for evolutionary studies as they provide a diversity of recombinant genotypes through generations of mutation, recombination, and gene flow. By documenting the extent of admixture on a genome-wide scale, we gain insight into the underlying genomic architecture of reproductive isolation in natural systems. Here we leverage a historically prominent hybrid zone between two species: the Baltimore (*Icterus galbula*) and the Bullock's (*I. bullockii*) oriole. Based on whole-genome sequences of 60 individuals from both allopatric and admixed individuals, we found that genome-wide divergence was generally high (Fst = 0.19) with several elevated peaks of divergence across the landscape. We further documented evidence of a large, putative inversion on the Z chromosome, which we hypothesize has important implications for hybridization outcomes between the two species. We explored patterns of differential introgression between the orioles by employing a subset of ancestry informative markers designed to target heterogeneous regions across the genome (neutral, fixed, phenotype-linked, and inversion-linked) in an additional 300 individuals sampled across the Platte River transect. Based on this subset of data, we see strong selection in the form of narrow clines for markers linked to plumage as well as those linked to the inversion. Our findings describe a divergent landscape and strong selection for several regions across the genome, conditions which are consistent with the observed narrowing of the hybrid zone over the past 50 years.

Signatures of mitonuclear coevolution shaping cryptic differentiation in a warbler species complex

Silu Wang, Madelyn Ore, Else Mikkelsen, Julie A. Lee-Yaw, David P. L. Toews, Sievert Rohwer, and Darren E. Irwin

Presenting author: **Silu Wang**, University of California, Berkeley, siluwang.evo@gmail.com

Mitochondrial (mtDNA) and nuclear (nDNA) genes interact to govern metabolic pathways of mitochondria. When differentiated populations interbreed at secondary contact, incompatibilities between mtDNA of one population and nDNA of the other could result in low fitness of hybrids. In northwestern North America, two hybridizing species of warblers, *Setophaga occidentalis* and *S. townsendi*, provide an excellent system to investigate the potential co-adaptation of mitochondrial and nuclear DNA. The inland population of *S. townsendi* harbors mtDNA that is half a million years divergent from the mtDNA of *S. occidentalis*. These populations also differ strongly in a few nDNA regions. Coastal populations of *S. townsendi* have mixed ancestry, consistent with an origin of these coastal populations through hybridization between *S. occidentalis* and inland *S. townsendi*. Of the few highly-differentiated nDNA regions between inland *S. townsendi* and *S. occidentalis*, a 1.2Mb gene block on chromosome 5 (chr5) is also differentiated between coastal and inland *S. townsendi*. Genes in this 1.2Mb block are associated with fatty acid oxidation and energy-related signaling transduction, both of which are closely associated with mitochondrial function. Genetic variation within this chr5 gene block covaries with mtDNA within and among coastal *S. townsendi* populations and displays signatures of a selective sweep. We show that such mitonuclear coevolution might be maintained by climate-related selection, because mitonuclear ancestry is correlated with climatic conditions among sampling sites. Together, our observation suggests climatic-associated mitonuclear coadaptation underpins cryptic differentiation in this species complex.

The birds Dorian left behind

Bradley Watson, Scott Johnson, George Wallace, Daniel Lebbin, Christopher Johnson, and David Knowles

Presenting author: **Bradley Watson**, Bahamas National Trust, bwatson@bnt.bs

In September 2019, Hurricane Dorian slammed into the northern Bahamas islands of Abaco and Grand Bahama, causing billions of dollars in damage, dozens of human deaths and destroying much of the pineland ecosystems, with as much as 100% tree mortality in some areas. The pineland and coppice ecosystems are important habitats for many species of native and endemic animals, including five endemic Bahamian birds. Such a catastrophic storm may have caused major declines among these endemics, with two species (the Bahama Warbler and Bahama Swallow) already listed as Near Threatened and Endangered, respectively. The Bahamas National Trust in association with American Bird Conservancy and with support from the National Geographic Society and BirdsCaribbean spent 10 days on each island, conducting bird and vegetation surveys in both damaged and undamaged pineland and coppice habitats. We will discuss the results of those surveys and the steps we have taken and will take to conserve native and migratory birds, and the habitats they rely on.

Near complete postzygotic isolation in three cryptic pairs of Amazonian antbirds

Jason T. Weir

Presenting author: **Jason Weir**, University of Toronto, jason.weir@utoronto.ca

While ornithologists have placed great emphasis on the contribution of song and colour divergence to the development of reproductive isolation, the potential role of postzygotic isolation as a key driver of speciation remains poorly explored. Here I use hybrid-zone dynamics for three cryptic, sibling species pairs of antbirds (belonging to the genera *Hypocnemis*, *Hypocnemoides*, and *Willisornis*) from the Amazon to infer that despite minimal colour and song divergence and frequent interbreeding at hybrid zones, intrinsic postzygotic barriers are substantial and have rendered most of the genome immune to introgression. I present simulations suggesting that premating isolation alone is unlikely to drive these patterns while postzygotic isolation by itself or in combination with premating isolation is generally required to maintain species boundaries at contact zones. These results have implications for our taxonomic understanding of species richness in the Amazon because they suggest that a substantial proportion of the plethora of taxa classified as subspecies due to their limited song and plumage differentiation, many of which are substantially differentiated in mitochondrial DNA, may in fact represent full biological species.

MixSIAR: An R package for avian diet analysis

Elena H. West

Presenting author: **Elena West**, University of Minnesota, elwest@umn.edu

Stable isotope mixing models have become a popular tool for quantifying food webs and thus animal diets, given the isotopic ratios of consumer tissues and food sources. The R statistical package MixSIAR (Stock et al. 2018) is a Bayesian framework that incorporates several advantages over previous mixing model software, including options for fixed and random effects, priors, and error terms. MixSIAR is a powerful tool that allows researchers flexibility in building their models. Dr. Elena West will share examples from her research on diet reconstruction in Steller's Jays and Red-headed Woodpeckers.

Minimizing potential Allee effects in Psittacine reintroductions: An example from Puerto Rico

Thomas H. White, Jr., Wilfredo Abreu, Gabriel Benitez, Arelis Jhonson, Marisel Lopez, Limary Ramirez, Iris Rodriguez, Miguel Toledo, Pablo Torres, and Jafet Velez

Presenting author: **Thomas White**, US Fish and Wildlife Service, thomas_white@fws.gov

The family Psittacidae comprises over 400 species, an ever-increasing number of which are considered threatened with extinction. In recent decades, conservation strategies for these species have increasingly employed reintroduction as a technique for reestablishing populations in areas where previously extirpated. Because most Psittacines are highly social and flocking species, reintroduction efforts may face the numerical and methodological challenge of overcoming initial Allee effects during the critical establishment phase of the reintroduction. These Allee effects can result from failures to achieve adequate site fidelity, survival, and flock cohesion of released individuals, thus jeopardizing success of the reintroduction. Over the past 20 years, efforts to reestablish and augment populations of the critically endangered Puerto Rican parrot (*Amazona vittata*) have periodically faced the challenge of apparent Allee effects. These challenges have been mitigated via a novel release strategy designed to promote site fidelity, flock cohesion and rapid reproduction of released parrots. Efforts to date have resulted in not only the reestablishment of an additional wild population on Puerto Rico, but also the reestablishment of the species in the El Yunque National Forest following its extirpation there by the Category 5 hurricane Maria in 2017. This promising release strategy has potential applicability to reintroductions of other psittacines and highly social species in general.

Evolution of blood-oxygen carrying capacity in hummingbirds

Jessie L. Williamson, Ethan B. Linck, Emil Bautista, Ashley Smiley, Jimmy A. McGuire, Robert Dudley, and Christopher C. Witt

Presenting author: **Jessie Williamson**, University of New Mexico & Museum of Southwestern Biology, jwilliamson0110@gmail.com

Hummingbirds have the highest mass-specific metabolic rates among endotherms, so their blood-O2 carrying capacity should be finely tuned to supply O2 to respiring tissues under a variety of ambient conditions. It is not known whether blood-O2 carrying capacity varies predictably with variation in partial pressure of O2 or other aspects of the environment, nor whether known adaptations in the O2-binding affinity of hemoglobin affect optimal blood-O2 carrying capacity. We sought to identify causes of variation in blood traits that affect O2 carrying capacity, within and among species. We measured total hemoglobin concentration ([Hb]), hematocrit (Hct), erythrocyte count (TRBC), mean cell volume (MCV), mean cellular hemoglobin concentration (MCHC), and mean cellular hemoglobin content (MCH) from >1,200 individuals of 77 species representing all 9 major hummingbird clades, and spanning sea level to >4,500 meters along the Andean elevational gradient. We modeled each of the six blood characteristics using a suite of environmental parameters, individual traits, and species traits. [Hb], Hct, and TRBC increased predictably with elevation, while MCV, MCH, and MCHC decreased with elevation. There was no phylogenetic conservatism in blood traits, but strong effects of species identity suggest that blood-O2 carrying capacity is subject to optimization on rapid timescales. Hummingbirds increased blood-O2 carrying capacity primarily by producing more erythrocytes, and secondarily by producing larger erythrocytes, but species varied in the extent to which they relied on more versus larger cells. Our results illustrate the interplay of physiology and environment across the evolution of hummingbirds.

The Caribbean Motus Collaboration: Informing and promoting conservation of Caribbean birds through monitoring

Maya Wilson, Holly Garrod, Jeff Gerbracht, C. Justin Proctor, Ann Sutton, Adrianne Tossas, and Lisa Sorenson

Presenting author: **Maya Wilson**, BirdsCaribbean, Maya.Wilson@BirdsCaribbean.org

The insular Caribbean is a global biodiversity hotspot that is home to over 700 bird species. Roughly half of these species are residents, including 171 that are endemic to the region. The other half are migratory—some spend the entire winter in the Caribbean, while others use one or more islands as stopover sites to rest and refuel during their long journeys. Bird populations, including many Caribbean species, are declining at alarming rates. We need to identify the most critical sites and habitats and assess the threats they face in order to protect them. BirdsCaribbean and our partners are developing long-term monitoring programs to fill critical information gaps and increase support for bird conservation using several tools, including the Motus Wildlife Tracking System. Motus is a powerful collaborative research network developed by Birds Canada. It uses arrays of automated radio telemetry stations to detect tags deployed on small animals to study their movements. Data from this network have already expanded our understanding of bird movements, including pinpointing migration routes and key stopover sites, as well as habitat use and behavior during breeding and non-breeding seasons. However, there is currently a gap in the network in the Caribbean. The Caribbean Motus Collaboration (CMC) is using a multi-pronged approach to expand Motus in the region by installing receiver stations in strategic locations throughout the islands, deploying tags on priority bird species, and implementing an educational curriculum. The CMC will aim to provide information and engage communities to conserve birds throughout their full life cycles and reverse population declines.

Prioritizing the conservation of migratory birds and resident vertebrates in the Neotropics under alternative planning strategies

Scott Wilson, Hsien-Yung Lin, Richard Schuster, Camila Gómez, Ana M. González, Esteban Botero-Delgadillo, Nicholas J. Bayly, Joseph R. Bennett, Amanda D. Rodewald, and Viviana Ruiz Gutierrez

Presenting author: **Scott Wilson**, Environment and Climate Change Canada, scott.wilson@canada.ca

Neotropical countries are increasingly receiving resources from temperate nations to aid the conservation of migratory birds that move between temperate and tropical regions during the annual cycle. If allocated strategically, these resources could also contribute to other conservation initiatives; here, we show how they could help threatened resident vertebrates. Using eBird distribution models, we delineated the region with the greatest richness of federally listed Nearctic-Neotropical migrants during the stationary nonbreeding period. Within this region, we identified the extent of protection, projected forest loss, and conducted a systematic prioritization for 1,018 Red-listed vertebrates using IUCN range maps. The prioritization examined two scenarios to reach a 30% land area target: maximize areas with the highest species representation (Maximum Utility) or minimize the number of species excluded (Minimum Shortfall). Listed migrant richness was greatest along a corridor from the Yucatan peninsula through the Northern Andes. The western Colombian and Ecuadorian Andes had the greatest richness across resident taxa, whereas taxa-specific hotspots included montane areas of central Guatemala (amphibians and reptiles) and the eastern slope of Colombia's Eastern Andes (mammals). Maximum Utility favored the western Andes where there are few protected areas and projected forest loss throughout. Minimum Shortfall emphasized regions throughout Central America. Our results provide opportunities for decision makers to direct conservation resources for migratory birds in a manner that benefits threatened resident taxa and to consider the risk of habitat loss in deciding the type of conservation strategies needed.

Integrating visual and somatosensory information in the avian brain

Douglas R. Wylie, Cristian Gutierrez-Ibanez, Maximo Fernandez, Madison C. Pilon, Gonzalo J. Marin, and Andrew N. Iwaniuk

Presenting author: **Douglas Wylie**, University of Alberta, dwylie@ualberta.ca

Integration of information from two or more sensory modalities is important for enhancing object salience and critical for many behaviours. Although this occurs in many sites in the brain, in this presentation we will focus on the medial spiriform nucleus in the midbrain. We show, in pigeons, that this is a major site of visual-somatosensory integration. The somatosensory information arises from two forebrain areas, the rostral "wulst" and the arcopallium, likely conveying information from the body and beak, respectively. Similarly, visual information arises from the caudal "wulst" and the arcopallium as well. We infer that this integration supports sophisticated sensori-motor behaviours for two reasons. First, the medial spiriform nucleus receives input from the nidopallium, a forebrain area involved in planning. Second, the medial spiriform nucleus projects heavily to the cerebellum, which is critical for fine motor control. Finally, we show that the medial spiriform nucleus is enlarged 2 to 5X in parrots compared to other birds. We believe that this reflects a sophisticated object representation in birds and supports fine motor control for behaviours requiring visual-somatosensory integration. For example, seed-husking observed in parrots involves visual identification, visuo-motor grasping with the feet, and sophisticated manipulation with the tongue.

Pine forest nesting in the critically endangered Bahama Oriole: New habitat recommendations to ensure population resilience

Briana M. Yancy, Janine M. Antalffy, Michael G. Rowley, Lehron E. Rolle, Scott B. Johnson, Shelley Cant-Woodside, and Kevin E. Omland

Presenting author: **Briana Yancy**, UMBC, ag56811@umbc.edu

Habitat loss is a major threat to island species throughout the Caribbean, so having reliable data on habitat usage is crucial to conserving key habitats. The Bahama Oriole is a critically endangered species endemic to Andros in The Bahamas. Previous research suggested that the Bahama Oriole nested almost exclusively in coconut palms (*Cocos nucifera*) in developed habitats. However, our team has now documented many nests in remote pine forests, and we began characterizing these nest sites. Our goals were to document where orioles nest in pine forests and to quantify nest site vegetation at multiple scales to determine if orioles show a preference for specific habitat characteristics. We recorded characteristics of 12 nests trees, including tree height, tree diameter, and nest height. We also took measurements of vegetation in 10-m and 100-m radius plots around the nest and compared these measurements to control plots. We documented six nests in Caribbean pine and six nests in Key thatch palms. Orioles nested in a range of pine forest habitats. However, on average, Bahama Orioles nested in pine forests with more tall thatch palms (> 2 m tall) in the understory compared to control plots. They also tended to nest in the tallest thatch palms in the understory. Habitat loss and strengthening hurricanes are major concerns for this oriole, but the findings from this study indicate the Bahama Oriole likely has greater resilience than feared given it is not confined to developed habitat along the coast. Our results indicate the importance of conserving pine forests on Andros, especially those with tall thatch palms in the understory. Conserving pine forests throughout the Caribbean is crucial to many endemic and migratory birds.

Post-hurricane mangrove restoration in the British Virgin Islands: Practical lessons in building coastal resilience

Susan Zaluski

Presenting author: **Susan Zaluski**, H. Lavity Stoutt Community College, susanjvdps@gmail.com

After landfall of Hurricanes Irma and Maria in 2017, the mangrove ecosystems of the British Virgin Islands (BVI) were left devastated with an estimated 90% of coastal red mangroves destroyed (Moore 2018) and varying forms of damage exhibited in other mangrove areas. With the immense loss of mature mangroves and existing propagules washed away from the understory during the storms, natural regeneration and recolonization were significantly impeded. Residual hurricane debris, increased herbivore pressure on remaining mangroves and other factors have posed further challenges to natural regeneration. In the 3+ years since the 2017 devastation, BVI mangrove restoration initiatives have coalesced into a Territory-wide movement being led by a handful of key environmental organizations and agencies using a community-based restoration framework involving hundreds of volunteers representing at least fifteen CBOs and youth groups. International, regional and local partners supporting this work include University of New Hampshire, The Caribbean Development Bank, BirdsCaribbean, The International Union for the Conservation of Nature (IUCN), Darwin Plus Initiative, Roehampton University, UniteBVI, WellBeing Foundation, Jost Van Dykes BVI Preservation Society, The National Parks Trust of the Virgin Islands, The Ministry of Natural Resources Labour and Immigration and the H. Lavity Stoutt Community College. This presentation will give an overview on post hurricane restoration initiatives and lessons learnt for restoring coastal ecosystems and building small island resilience to the impacts of climate change.

Contributed Oral Presentation Abstracts

BIRDS OF MANY
FEATHERS
FLOCK TOGETHER
9-13 AUGUST 2021
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Listed alphabetically by last name of first author

Empirical evidence of different egg morphs that match host eggs in the Brush Cuckoo (*Cacomantis variolosus*)

Virginia E. Abernathy and Wei Liang

Presenting author: **Virginia Abernathy**, Clemson University, vaberna@clemson.edu

One of the most efficient defenses against obligate brood parasitism in birds is egg ejection, where a host recognizes and removes the parasitic egg from the nest. This defense often selects for egg mimicry in parasitic species to reduce the likelihood of egg ejection. If a parasite uses multiple host species with distinctive egg types, this could lead to the evolution of egg gentes (host-specific egg types) in the parasite. There is observational evidence that the brood parasitic Brush Cuckoo (*Cacomantis variolosus*) might exhibit egg gentes, but there has been no objective study conducted to determine how closely eggs of this cuckoo species resemble those of its hosts from a bird's visual perspective. Using objective measurements to quantify egg appearance, we found that Brush Cuckoos exhibit at least two egg morphs that closely match the eggs of two of its primary hosts in color, luminance and volume. While the determination of actual egg gentes in the Brush Cuckoo was beyond the scope of our study, our results are a first and necessary step in determining whether egg gentes might exist in this species. We suggest at least a third egg morph matching another primary host (or at least the genus of that host) might exist, but more data would be necessary to confirm this. Additionally, we provide a mechanism researchers can use to help distinguish between Brush Cuckoo eggs that are closely matched to their host eggs for future studies in this system.

Patterns of genetic variation in the endangered yellow-nosed albatrosses revealed by high-throughput sequencing data

Dilini K. Abeyrama, Peter G. Ryan, and Theresa M. Burg

Presenting author: **Dilini Abeyrama**, University of Lethbridge, dilini.abeyrama@uleth.ca

The two species of yellow-nosed albatrosses, Atlantic (*Thalassarche chlororhynchos*) and Indian (*Thalassarche carteri*), are morphologically similar, however, they show some differences in behaviour and breeding range. A previous study with mitochondrial and nuclear markers, including microsatellite markers Occa9 and Pema7, revealed that the two species are genetically distinct and that, within each of the species, different populations are undergoing differentiation. We sequenced 96 yellow-nosed albatross samples from four breeding islands (Atlantic: Nightingale, Inaccessible, and Gough; Indian: Amsterdam) and bycatch samples from South Africa and New Zealand using Illumina sequencing. The sequences were analysed using the Stacks pipeline and aligned to a reference genome. Following filtering, 373,960 SNPs and 69 individuals were included in the downstream analyses. Our results confirmed that the two species are genetically distinct. SNP data separated the Atlantic Yellow-nosed Albatross breeding on Nightingale Island from two other breeding populations. Indian Yellow-nosed Albatross bycatch samples caught around South Africa are genetically different than birds breeding on Amsterdam Island and caught around New Zealand.

A review of wood-warbler (Parulidae) predation of vertebrates and accounts of two new observations

Michael E. Akresh, Steven Lamonde, Lillian Stokes, Frank Kahoun, and Janet M. Clarke Storr

Presenting author: **Michael Akresh**, Antioch University New England, makresh@antioch.edu

Wood-warblers (Parulidae) eat insects, spiders, fruit, and nectar, but preying on vertebrates is rarely recorded. We conducted a literature review to determine which species of Parulidae have been observed to capture or consume vertebrate species such as small lizards, amphibians, and fish. We also provide information on two previously unpublished observations; 1) a Black-and-white Warbler (*Mniotilta varia*) photographed with a bark anole (*Anolis distichus*) in its mouth on San Salvador Island, The Bahamas, and 2) a Yellow-throated Warbler (*Setophaga dominica*) photographed preying on a brown anole (*Anolis sagrei*) in Florida, USA. The latter observation was particularly interesting as the brown anole shed its tail (exhibiting caudal autotomy) and briefly escaped, but was then recaptured by the warbler. Including these two unpublished events, our literature review found records of 20 separate observations of 12 Parulidae species preying on vertebrates. The majority of predation records were of lizards (65%), with an additional 25% of amphibians, and 10% of fish. We hypothesize that vertebrate predation by wood-warblers is opportunistic and potentially limited by the difficulty in capturing, handling, and consuming vertebrate prey. However, there is also non-mutually exclusive evidence to suggest birds exhibit plasticity in prey items, and switch to preying on vertebrates during stressful environmental conditions or taxing periods during the avian life cycle. Our study synthesizes previous findings and can assist future research in better understanding trophic interactions, evolution, and the natural history of both the warblers and their vertebrate prey.

Balancing conservation priorities for grassland and forest specialist bird communities in an agriculture-dominated landscape

Niloofar Alavi, Devin R. de Zwaan, Gregory Mitchell, David Lapen, Jason Duffe, and Scott Wilson
Presenting author: **Niloofar Alavi**, Environment and Climate Change Canada, niloofar.alavi@canada.ca

Effective conservation planning requires allocating limited resources to maximize success, requiring difficult decisions when habitat needs of multiple threatened species do not align. In the agricultural-dominated landscape of eastern Ontario and southwestern Quebec, conflicting goals exist between threatened grassland birds that benefit from some agriculture practices and those of a diverse woodland bird community that requires forest recovery. Using multi-scale species distribution models and a prioritization analysis with Breeding Bird Survey data, we identified regions that maximize habitat suitability for 8 threatened grassland and forest species as well as overall species diversity. We also used time-removal abundance models to assess the importance of fine-scale habitat traits such as linear woody features (LWF) for 38 species. We identified regions that maximize species-at-risk diversity in the southwest near Lake Huron, as well as along the shore and southeast of the St. Lawrence River. These areas represent complex landscape structures with a balance among forest patches, wetland/grassland habitat, and agricultural crops like corn, soy, and cereals. Abundance models indicated that LWFs positively affect 12/38 species, including the Chestnut-sided Warbler (*Setophaga pensylvanica*) and Least Flycatcher (*Empidonax minimus*). Despite drastic landscape changes associated with agroecosystems, we show that targeted habitat protection and enhancement prioritizing structural diversity can maximize protection of bird communities with directly contrasting needs. We also highlight multiple pathways to achieve this balance, such as retaining forest patches or dividing crop fields with hedgerows, improving flexibility in conservation approaches.

Brood engineering through a Goldilocks principle maximizes fitness for a nest-sharing brood parasite

Nicholas D. Antonson, Wendy M. Schelsky, Deryk Tolman, Rebecca M. Kilner, and Mark E. Hauber
Presenting author: **Nicholas Antonson**, University of Illinois at Urbana-Champaign, nda4@illinois.edu

The grand challenge for nest-sharing generalist brood parasites is to successfully compete with host young of many different species to maximize resource acquisition from foster parents. To do so, parasitic nestlings raised in suboptimal conditions may employ brood reduction as a mechanism to engineer their adoptive niche and improve their probability of survival. Here, we investigated the survival of and brood reduction by parasitic Brown-headed Cowbird (*Molothrus ater*) nestlings through manipulating brood sizes at hatching in nests of Prothonotary Warbler (*Protonotaria citrea*) hosts. Consistent with a Goldilocks principle from comparative data, cowbird survival in manipulated warbler broods was highest in intermediate brood sizes of two host chicks compared to too few (zero) or too many (four) host chicks. Experimentally, greater cowbird mortality was associated with reduced parental provisioning to the parasite in both the small and the large brood sizes and occurred mostly at the early nestling stage. In turn, cowbirds optimized nestmate numbers for their own development by reducing host broods significantly more in large, relative to intermediate, brood sizes. Such patterns of brood reduction toward the cowbird's optimal brood size suggest that brood parasitic young employ a niche construction strategy to buffer the effects of variable rearing environments.

Does the abundance of ectoparasites in the nest affect nestling condition and fledging success?

Tracy Alice O. Apienti and Colleen T. Barber
Presenting author: **Tracy Alice Apienti**, Saint Mary's University, citashay1@gmail.com

Nestlings of most passerine species face many stressors including early exposure to ectoparasites. Ectoparasites negatively impact the health of nestlings by feeding on their blood and feathers, leaving the nestlings in poor condition, and reducing their chances to fledge. European Starlings (*Sturnus vulgaris*) are cavity-nesting passerines; they nest in the holes of trees and artificial nest boxes that accumulate ectoparasites. Parents are known to line their nest with feathers to serve as a barrier to ectoparasites. Only one study on the ectoparasite community of European Starlings exists and it was done in Halifax, Nova Scotia (Fairn et al. 2014). My objectives were to 1) identify the

abundance and types of ectoparasite in starling nests, 2) determine whether ectoparasite abundance reduces nestling condition and fledging success, and 3) determine whether the mass of feathers in the nest reduces ectoparasite abundance and quantify the number of cigarette butts present in nests. This study was conducted in June 2020 on nine nests from the late broods of European Starlings. The number of ectoparasites per nest ranged from 8-31. The only ectoparasites found were adult hen fleas (Ceratophyllus gallinae). I found no relationship between ectoparasite abundance and a) mean nestling condition in the brood, b) proportion of nestlings that fledged and c) mass of feathers. These results suggest that nestlings were not affected by this particular prevalence of ectoparasites. It also suggests that feathers do not serve as a barrier and may instead be present in the nest to attract the opposite sex. Future studies should examine the effects of different ectoparasite prevalences on nestlings.

Introgression and cryptic speciation in a North American passerine

Kenneth K. Askelson, Garth M. Spellman, and Darren E. Irwin

Presenting author: **Kenneth Askelson**, University of British Columbia, askelson@zoology.ubc.ca

Designating species is not always obvious. Geographic variation in organisms may be subtle or lacking altogether. In these situations, genomics has a strong role to play in assessing divergence within the genome and assisting in designating species. In North America, White-breasted Nuthatches (*Sitta carolinensis*; WBNU) are considered a single species but recent genetic work has suggested they might comprise three or four distinct species. To assess speciation in WBNU, we used genomics to characterize population structure across the genome. We constructed a chromosome-level genome assembly for WBNU and sequenced over 300 WBNU samples across North America using a reduced representation method, Genotyping by Sequencing. Genomic variation revealed four discrete and highly differentiated populations corresponding to those previously described: Pacific, Rocky Mountain South, Rocky Mountain North, and Eastern populations. Our sampling includes places where populations come into close geographic contact, and we have detected a small number of hybrids. This result suggests a high level of reproductive isolation between populations. However, we also find a strong signal of introgression between groups, with some areas appearing to be introgressive sweeps. It is likely that gene flow occurred between populations when reproductive isolation was less complete, allowing genomic regions to cross species boundaries. Altogether, we find that WBNU appears to comprise four species despite similar morphological appearances, with complex patterns of introgression and heterogeneous differentiation across the genome.

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eBird status and trends update: Distributions, abundances, and habitat associations for 800+ species

Tom Auer, Daniel Fink, Alison Johnston, Matt Strimas-Mackey, Orin Robinson, Shawn Ligocki, Wesley Hochachka, Chris Wood, Ian Davies, Marshall Iliff, and Luke Seitz

Presenting author: **Tom Auer**, Cornell Lab of Ornithology, mta45@cornell.edu

As of December 2021, eBird Status and Trend products provide ecological information for 807 bird species, including over 170 species outside of the Western Hemisphere, describing their range boundaries and relative abundances at high spatiotemporal resolution and their habitat associations regionally. To generate these products, we use statistical and machine learning analyses combining eBird data with environmental data from NASA and other sources. These analyses are used to estimate the occurrence and abundance of species at weekly intervals and 2.9km resolution, also yielding information about positive and negative habitat associations at the landscape scale. These estimates are summarized to produce a suite of visualizations and data products available at https://ebird.org/science/status-and-trends. In this presentation we will provide an update about the 2020 version of eBird Status and Trends products and what has changed since the 2019 version, including: new environmental covariates, improved range boundaries, updates to visualizations, a few examples from species outside of the western hemisphere, and information about new terms of use for the data products.

Demography and destination: Modeling summer survival and winter migration of Canada Warblers in the central Appalachian Mountains

Stephanie H. Augustine and Christopher T. Rota

Presenting author: **Stephanie Augustine**, West Virginia University, sha0016@mix.wvu.edu

Canada Warblers (*Cardellina canadensis*) are a Nearctic-Neotropical migratory songbird that has exhibited apparent declines in abundance over recent decades. This species occupies a wide range of environmental conditions throughout its range but lacks substantial data regarding elements driving variation in demography and the strength of population migratory connectivity. The aims of this research are to (1) determine the relationship between demography and environmental conditions, including shrub cover and riparian areas, along an elevation gradient and (2) ascertain migratory route and wintering locations of a population of Canada Warblers breeding in the central Appalachian Mountains. Our research takes place at six study sites ranging in elevation from 526 – 1282m spanning an approximately 130km north-south gradient within the Monongahela National Forest in West Virginia. We will estimate apparent survival with a three-year mark recapture study; in 2019 and 2020 a total of 211 birds were uniquely color-banded. To determine migration strategies, in 2020 we also deployed 32 of the adult males with light-level geolocator tags. During the 2020 field season, we observed a 32% return rate of banded birds, with 73% of birds re-sighted within 100 m of their 2019 locations. Re-sight data collected in the 2021 field season will be used to account for interannual local movements and correct for detection probability to model true survival. We will also retrieve geolocators, which will elucidate patterns of population connectivity and establish a baseline for full annual cycle modeling of this species for the future.

Translocated Lesser Prairie-Chicken lek dynamics and female space use

Carly Aulicky, David Haukos, Kent Fricke, Liza Rossi, Jonathan Reitz, and Kraig Schultz

Presenting author: **Carly Aulicky**, Kansas Cooperative Fish and Wildlife Research Unit, caulicky@gmail.com

Translocation of lek-breeding prairie grouse offers unique challenges and considerations. Translocation efforts are considered successful with lek persistence, but the focus on translocating males first to bolster or form leks is based on untested assumptions about how lek breeding species disperse and navigate new landscapes. This approach assumes males are the dispersing sex, despite increasing evidence of long-distance movement by females. Female-driven dispersal implies that males form leks following female space use and habitat constraints in accordance with the hotspot hypothesis. We tested the hotspot hypothesis in shaping lek formation and stability of translocated Lesser Prairie-Chickens (*Tympanuchus pallidicinctus*) in the Sand Sagebrush Prairie Ecoregion using the spatial movements of 32 GPS- and 24 VHF-equipped females. We used ArcGIS optimized hotspot analysis to identify significant clusters of female locations and evaluated where translocated males formed leks and the persistence of those leks. We found the spatial use of female lesser prairie-chickens drove the dynamics of leks as expected under the hotspot hypothesis and leks formed in location clusters. We found the number of nesting attempts by females within a 5 to 2 km distance had the greatest influence on the persistence of formed leks into a subsequent year. Based on our findings, future translocation efforts should focus on creating nesting habitat to sustain long-term nest site selection prior to releasing birds, rather than methodology focused on creating or bolstering leks without accounting for female behavior.

Expansion and contraction of ecological niche space drives the disassembly of cloud forest bird communities in tropical montane countrysides

Ian J. Ausprey, Felicity L. Newell, and Scott K. Robinson

Presenting author: **Ian Ausprey**, University of Florida, iausprey@ufl.edu

Community disassembly caused by anthropogenic disturbance is hypothesized to be driven by changes in ecological niche space as quantified by functional traits related to morphology, behavior, diet, and habitat. Using intensive field surveys of cloud forest bird communities across seven replicate landscapes in the Peruvian Andes, together with community hierarchical distance sampling models and n-dimensional hypervolumes, we demonstrate that a suite of 15 morphological and life history traits related to diet, foraging behavior, habitat, and light micro-environments strongly predicts species-specific abundance changes in countryside habitats compared to forest. Species adapted to structurally dense understory habitats and plant-based diets increased in abundance in early successional and mixed-intensity agricultural habitats. We observed similar patterns for species with broad elevational range limits, suggesting that increased environmental niche breadth ameliorates disturbance sensitivity. Collectively, functional trait space contracted within agricultural habitats for movement and dispersal traits while expanding for traits related to diet and elevation, demonstrating the dynamic changes to the ecological niche that drive community disassembly in disturbed landscapes.

Does living in the city make Northern Cardinals change color?

Daniel T. Baldassarre and Kristie M. Drzewiecki

Presenting author: **Daniel Baldassarre**, SUNY Oswego, daniel.baldassarre@oswego.edu

Urbanization is rapidly increasing, and it is critical that we understand how wildlife responds to such anthropogenic change. The Northern Cardinal (*Cardinalis cardinalis*) is a widespread songbird that readily breeds in urban areas. One way urbanization may affect Northern Cardinals is by altering their plumage and bill color, which are used as social signals. Such a color change can happen if urban birds have a different diet than rural birds, since dietary carotenoids contribute to color variation. To test this idea, we captured Northern Cardinals at a rural and an urban site in upstate New York and compared the color of multiple patches using reflectance spectrometry, image analyses, and avian visual modeling. Our preliminary results indicated little to no difference in male plumage color. However, urban males had redder bills than rural males, and urban females had pinker, more saturated underwings than rural females. These results suggest that urbanization may affect Northern Cardinal color, and thus their social signals and mating interactions. Further data collection and analyses are ongoing, as are efforts to directly quantify carotenoids and diet. Together, these results can give us a more complete understanding of how human activity affects Northern Cardinal communication.

How the timing of long-distance migration in songbirds responds to an experimental manipulation of photoperiod in the wild

Saeedeh Bani Assadi and Kevin C. Fraser

Presenting author: **Saeedeh Bani Assadi**, University of Manitoba, s.baniassadi@gmail.com

Previous laboratory studies have shown the major role of photoperiod in the timing of avian life-cycle events, such as migration. Advancement in the timing of breeding can expose nestlings to new photoperiod regimes, which may influence their subsequent migration timing. To explore this potential ontogenetic effect, we investigated how the timing of post-breeding movements of a long-distance migratory songbird (Purple Martin, *Progne subis*) responded to experimental manipulation of photoperiod during nestling development in the wild. We installed programmable lights in nest boxes at two breeding colonies in Manitoba, Canada, and exposed nestlings to an extended photoperiod that simulated an earlier calendar date from hatch to fledge date. We then tracked their fledge and departure dates using automated radio-telemetry and compared timing to controls. Our results showed that young in the extended day length group had delayed timing as predicted by the simulated, earlier calendar date. They stayed in the nest longer, fledged later, and departed for their fall migration later than birds that experienced natural daylength. This study demonstrates how photoperiod during nesting (ontogenetic effect) influences the fledge and first post-breeding movement timing (phenotypic plasticity) of juvenile songbirds in the wild.

Making bird specimen data more consistent, accessible, and informative

John M. Bates, Carla Cicero, A. Townsend Peterson, John Wieczorek, and Paula F. Zermoglio

Presenting author: **A. Townsend Peterson**, University of Kansas, town@ku.edu

Major strides have been made toward broad, open sharing of biodiversity data, and bird data have figured prominently in building global biodiversity information resources. These data, however, have been of limited utility because of inconsistent, non-controlled content in data fields; for example, a query of over 181M records, including 8M birds, from museum collections revealed >22K (467 for birds alone) distinct values entered for sex. As a consequence, queries depending on such fields, such as locating all skeletons of a particular age and sex of a particular species have not been fruitful. This limitation led to an initiative focused on transforming current data resources into consistent and controlled content, to make such queries feasible. To this end, we convened curators and collection managers of 34 bird specimen collections of different sizes that contribute data to global biodiversity information networks. For each of four data realms (sex, life stage, body part, and preservation method), we discussed and debated the concepts as a group, and created 'translation tables' that link the full diversity of content in collection databases to a much-reduced set of actual concepts in each field. This effort resulted in a much clearer view of the holdings of our collective specimen resources, in which 92% of specimens that have a value in the sex field have an interpretable and biologically meaningful value for sex (i.e., not 'unknown'). For the other fields, percentages are 57% for life stage, 97% for body part, and 95% for preservation method. Such community-driven data-improvement efforts have significant potential to improve and augment biodiversity information resources for research and education.

Northern Bobwhite breeding movements, survival, and the cost of reproduction

Adam C. Behney

Presenting author: **Adam Behney**, Colorado Parks and Wildlife, adam.behney@state.co.us

The tradeoff between current and future reproduction is a fundamental component of species' life history strategies. An individual's current reproductive effort may reduce its future reproductive potential, through various costs associated with reproduction. These costs may be realized in numerous ways and manifest prior to, during, or after breeding. I studied the relationships between prebreeding movements, survival, and breeding stage in Northern Bobwhites in Colorado over 4 years to test hypotheses related to the cost of reproduction. First, I tested whether bobwhites that ultimately initiated a nest had different prebreeding movements or home ranges than those that did not initiate a nest, and whether increased movements as bobwhites searched for food or nesting sites resulted in lower survival. Second, I tested for differences in survival among nonbreeding bobwhites and those in various stages of breeding (laying, incubating, brood-rearing). I found that bobwhites that initiated a nest had larger prebreeding home ranges (29.2 vs. 18.7 ha). However, even though breeders covered more area than nonbreeders, there were no survival consequences of these movements and, interestingly, survival was actually greater for bobwhites that had longer recent daily movement distances. Daily survival rate was lowest for bobwhites during brood-rearing and greatest during laying, with nonbreeding and incubating survival rates similar and in between. For this population of bobwhites, greater mortality during brood-rearing may represent a cost of reproduction. However, there does not seem to be a survival cost of reproduction associated with greater movements prior to nesting.

Speciation and color evolution in hummingbirds

Diego F. Beltrán, Allison J. Shultz, and Juan L. Parra

Presenting author: **Diego Beltrán**, Universidad de Antioquia, diego.beltran@udea.edu.co

A fascinating pattern in nature is the uneven distribution of biodiversity among clades, some with low species richness and phenotypic variation in contrast to others with remarkable species richness and phenotypic diversity. In animals, communication signals are crucial for intra- and interspecific interactions, and are likely an important factor in speciation. However, evidence for the association between the evolution of such signals and speciation is mixed. In hummingbirds, plumage coloration is an important communication signal, particularly for mate selection. Here, using reflectance data for 237 hummingbird species (~66% of total diversity), we demonstrate that color evolution rates are associated with speciation rates, and that differences among feather patches are consistent with an interplay between natural and sexual selection. We found that female color evolution rates of multiple plumage elements, including the gorget, were similar to those of males. While male color evolution in this patch was associated with speciation, female gorget color evolution was not. In other patches, the relationship between speciation and color evolution rates was pervasive between sexes. We anticipate that future studies on animal communication will likely find that evolution of signaling traits of both sexes has played a vital role in generating signal and species diversity.

Do form and function predict the acoustic transmission properties of male and female bird songs?

Lauryn Benedict, Braelei Hardt, and Lorraine Dargis

Presenting author: **Lauryn Benedict**, University of Northern Colorado, lauryn.benedict@unco.edu

Signal evolution has been well studied in birds, with extensive research examining how multiple factors impact the form and function of male broadcast songs. Much less work has examined the properties of female songs. Males and females, even when occupying the same territories, often exhibit differentiated sex roles and may experience varied selective pressures on their communication signals, particularly in temperate latitudes. Evaluating the transmission properties of both male and female songs can therefore illuminate how evolution shapes signal form, and will help to explain the vast diversity of avian vocalizations. In this study, we investigated the transmission properties of Canyon Wren (*Catherpes mexicanus*) male and female songs. The songs of this species have highly sex-specific structures and different contextual use patterns. Male songs are pure-toned, or whistle-like in quality, and most frequently used in long-distance broadcast communication. Female songs, in contrast, are 'buzzy' sounding, and are most often used in short-distance aggressive signaling. We examined four measures of acoustic degradation, hypothesizing that male songs would transmit farther than female songs. Results supported our prediction that the 'buzzy' sounding female songs would degrade rapidly with distance. The pure-toned notes of male Canyon Wren songs, in contrast, showed good acoustic fidelity over relatively long distances. These outcomes support a match between song form and function, and highlight sex differences in communication. Canyon Wrens provide a unique study system where male and female signals have apparently evolved under different selective pressures and have strikingly different transmission properties.

Spatial variation in population genomic responses to anthropogenic change within tidal marsh populations of the Savannah Sparrow

Phred M. Benham, Jennifer Walsh, and Rauri C. K. Bowie

Presenting author: **Phred Benham**, Museum of Vertebrate Zoology, UC Berkeley, phbenham@gmail.com

Tidal marshes have been dramatically impacted by human activities with many of the specialized bird species occupying these habitats now classified as threatened or endangered. One of these species is the Savannah Sparrow (*Passerculus sandwichensis)*, which includes several tidal marsh populations in California and Mexico that are of conservation concern. To evaluate population genomic responses of Savannah Sparrows to anthropogenic change, we sequenced 296 sparrows from California and Mexico collected between 1889 and 2017. Sparrows were sequenced using a custom-designed capture array targeting exons from ~14,000 genes and ~3,500 non-genic regions. Our sampling includes paired modern (post-2000) and historic (pre-1970) specimens from 10 tidal marsh locations and two interior populations. We compared patterns of population structure change between modern and historical datasets. This showed overall similar patterns of structure among populations, but evidence for temporal divergence within populations due to changing allele frequencies from drift, gene flow, and/or selection. Metrics of genetic diversity provide evidence for population contraction in the most endangered tidal marsh population (Belding's Savannah Sparrow, *P. s. beldingi*) and little evidence for temporal change in interior populations. However, we observed variable changes across other tidal marsh populations with some showing dramatic elimination of genetic diversity towards the present time while others actually show evidence for greater diversity despite reductions in habitat. Our results highlight the immense potential of museum collections for documenting population genetic responses to specific human activities.

Is a river barrier hindering introgression of a sexually selected trait?

Kevin F. P. Bennett, Robb T. Brumfield, Gerald S. Wilkinson, and Michael J. Braun

Presenting author: **Kevin Bennett**, University of Maryland, College Park, kbennett@umd.edu

In northwest Panama, Golden-collared and White-collared Manakins (*Manacus vitellinus* and *M. candei*, respectively) interbreed in a narrow hybrid zone, across which the yellow collar of male vitellinus has introgressed into candei populations via positive sexual selection through male-male competition and/or female choice. Introgression appears to have stalled at the Río Changuinola: nearly all males have yellow collars east of the river and nearly all have white collars to the west, and similar conditions have existed for at least 25 years. Rivers in tropical forests can serve as major dispersal barriers and isolate populations on either bank. On the other hand, traits under positive selection should sweep to fixation, and this may be especially true for sexual traits where conditions favor strong sexual selection, as in *Manacus* where mating success among males is highly uneven. Therefore, one of two conditions is likely to be true: the Río Changuinola is a strong barrier to gene flow preventing the spread of an advantageous trait, or some form of selection is preventing introgression of yellow collars west of the river. Using restriction site-associated DNA sequencing (RAD-seq) data from eight populations on either side of the upper, middle, and lower reaches of the river, we quantify cross-river gene flow and assess the strength of the barrier presented by the river. This talk will present the results of this study and discuss its implications for the *Manacus* system and the paradigm of tropical riverine barriers.

Metabarcoding of Eastern Whip-poor-will fecal samples suggests strong reliance on moths: Implications for conservation

Thomas J. Benson, Ian F. Souza-Cole, Aaron A. Skinner, James R. Wright, Christopher M. Tonra, Frank R. Thompson, III, Stephen N. Matthews, Jeffrey T. Foster, Rebecca L. Mau, and Michael P. Ward

Presenting author: **Thomas Benson**, Illinois Natural History Survey, University of Illinois at Urbana-Champaign, tjbenson@illinois.edu

Declines in aerial insectivore populations have been well documented, although causes of these declines remain poorly understood. Documentation of widespread declines in insect populations has led to speculation about the potential role of food limitation in avian population decreases. To better understand this potential link, however, requires improved knowledge of bird diets, including spatiotemporal variation in consumed taxa. Using metabarcoding, we set out to examine arthropod taxa consumed by breeding Eastern Whip-poor-wills (*Antrostomus vociferus*) using fecal samples (n = 141) collected from nine different sites in Illinois, Missouri, Ohio, and Wisconsin in May and June of 2019 and 2020. Moths comprised the vast majority of identified sequences (=80%) across years, with flies, cockroaches, and beetles making up a minor proportion. Although the minor components of diet appeared to vary among sites and years, moths often comprised >90% of identified sequences and multivariate analyses of diet suggest broad taxonomic similarity even among sites as far as 1,000 km apart. Moreover, estimates of whip-poor-will abundance from a concurrent study in Illinois demonstrate a strong positive relationship between abundance of moths and whip-poor-wills. Overall, these results suggest conservation efforts for this species, and perhaps other nightjars, would benefit from increased focus on the factors affecting moth populations.

An update on the use of drones to study and conserve birds

David M. Bird

Presenting author: **David Bird**, McGill University, david.bird@mcgill.ca

Over the past 13 years, the use of unmanned aerial vehicles, or drones, continues to be popular with ornithologists. Drones have many advantages over traditional survey and research techniques, as they may minimize human mortality due to plane crashes, reduce cost and disturbance, increase accuracy, and allow the collection of high-resolution data over large and/or otherwise inaccessible areas. Despite the current pandemic, their use is now becoming commonplace among researchers, especially those involved with photographic population surveys of both breeding (e.g. penguin colonies) and non-breeding birds (e.g. crow roosts) using different types of camera sensors (e.g. visible, thermal-IR); individual nest inspections, most often involving raptors (e.g. hole-nesting species); and bird dispersal, either for nuisance birds or to deter birds from hazards. The goal of this presentation is to provide an update on the latest progress on the use of this technology.

Arrival time and habitat use of migratory birds wintering in northern Ghana, West Africa

Samuel Boakye Yiadom, Sandra Goded, Nathaniel N. D. Annorbah, and Nico Arcilla

Presenting author: **Samuel Boakye Yiadom**, International Bird Conservation Partnership, nico.arcilla@aya.yale.edu

Many migratory bird species are declining, including species that nest in Europe and winter in Africa (Afro-Palearctic migrants). In many cases, the drivers of these declines remain poorly understood. Most research on these species has focused on their breeding grounds, while their ecology and threats associated with stopover and wintering grounds remain poorly known, particularly in Africa. Here, we documented arrival time, abundance, and distribution of bird species wintering at an urban university campus in northern Ghana. We conducted surveys on four 1-km line transects from August 2018 to March 2019 and identified a total of 92 bird species, of which 28% (26 species) were migrants. Of the migratory species we documented, 46% were Afro-Palearctic migrants, and 54% were Intra-African migrants. Most migrants arrived in the months of September and November, but nine species arrived in late December. Afro-Palearctic migrants were most abundant on fallow cultivated land in this area, where rice is planted in the wet season but which is open with scattered trees in the dry season that coincides with the northern winter. By contrast, Intra-African migrant and resident species were most abundant in exotic neem (*Azadirachta indica*) tree plantations. These findings contribute to our knowledge of the winter ecology of Afro-Palearctic migratory birds, which is important knowledge for their conservation. They also represent a step towards understanding the effects of land use on birds in woodland-savannas of West Africa, where resident and wintering birds face multiple novel threats to their continued survival.

Using genomic data to model migratory timing: A Common Yellowthroat case study

Taylor Bobowski, Christen Bossu, Teia Schweizer, Emily Cohen, and Kristen Ruegg

Presenting author: **Taylor Bobowski**, Colorado State University, taylorbobowski@gmail.com

Migration, the seasonal movement of animals, allows organisms to exploit seasonally favorable conditions across a large geographic area. In avian species, the timing of spring migration is key for maximizing resources, such as food or territory, on the breeding grounds while minimizing risk exposure to winter conditions. A large body of research has shown that for many species, factors such as sex, condition, and spring phenology of food can be key predictors of migratory timing. However, the methods for studying timing have historically been limited by relatively small sample sizes at high effort (such as banding-recapture or radio tagging). Here, we utilize genomic data to define genetically distinct populations across the full breeding range of the Common Yellowthroat (*Geothlypis trichas*). We then use genetic assignment methods to identify the breeding ground of origin for 1,051 migrant samples collected at key migratory stopover points across 15 years. We conclude that sex, estimated migration distance, genetic population, and breeding ground phenology are all highly significant predictors of migratory timing.

The mobbing behavior of the Brown-crested Flycatcher against a common bird of prey in a tropical dry forest

Katherine Bonilla-Badilla

Presenting author: **Katherine Bonilla-Badilla**, Universidad de Costa Rica, kia.2604@gmail.com

In the Neotropics, the Ferruginous Pygmy-Owl (*Glaucidium brasilianum*) is one of the most commonly mobbed birds. Its vocalizations are recognized by several mobbing species. However, for many of them, their responses towards the presence of the predator and their roles as intra- or heterospecific mobbing birds have not been described. My objective was to determine the behavior of the Brown-crested Flycatcher (*Myiarchus tyrannulus*) towards the vocalizations of the Ferruginous Pygmy-Owl, in order to evaluate if this flycatcher is acting as a mobbing bird, in a seasonal dry forest of Costa Rica. Using playback experiments, I broadcast three stimuli in front of the Brown-crested Flycatcher as follows: a) Ferruginous Pygmy-Owl, b) its own species (Brown-crested Flycatcher) and c. a control. The Brown-crested Flycatcher vocalized more under the stimuli of Ferruginous Pygmy-Owl (mean=27, SD=±32) and their own species (mean=24, SD=±30) than the control (mean=12, SD=±11). In addition, they approached faster (less latency, s) to the loudspeaker under the stimulus of Ferruginous Pygmy-Owl (mean=142, SD=±115) than to the stimulus of their own species (mean=172, SD=±123). However, they remained for less time (s) in the study radius (25 m) under the stimulus of Ferruginous Pygmy-Owl (mean=50, SD=±71) than under the stimulus of their own species (mean= 82, SD=±106). In conclusion, Brown-crested Flycatcher is a mobbing bird that may be acting as a messenger in the presence of predators such as this pygmy-owl, given the active vocal and behavioral response it presented to the playback experiments. This is the first study testing this mobbing behavior in Brown-crested Flycatcher using playback experiments.

Metal contaminant quantification of tissues from Red-shouldered Hawks (*Buteo lineatus*) reveals the blood feather for non-lethal sampling

Jennifer T. Bouchenot, Melanie J. Beazley, Chase M. Mason, and Eric W. Goolsby

Presenting author: **Jennifer Bouchenot**, University of Central Florida, jennifer.bouchenot@ucf.edu

Birds of prey are popular biomonitoring agents for environmental metal pollutants and can provide a variety of sample types for contaminant quantification. Feathers accumulate contaminants by external deposition and assimilation into the keratin structure during development as a blood feather. This study investigates the use of blood feathers as a non-lethal sample type for metal contaminant monitoring. We salvaged feather, kidney, and blood feather samples from 50 previously deceased Red-shouldered Hawks (*Buteo lineatus*) and livers from 42 of these individuals spanning four distinct age groups at a rehabilitation center near Orlando, Fl. Samples were digested and analyzed for Al, Cr, Mn, Fe, Co, Ni, Cu, Zn, As, Cd, Gd, and Pb with an Inductively Coupled Plasma Mass Spectrometer. For mature birds, significant ($p<.05$) differences in Zn concentration were observed between sexes in blood feather and liver samples, but insignificant among younger age groups. Feathers, nor blood feathers, had a significant correlation compared to internal organs for Zn across all age groups ($p<.05$). The average liver values for toxic metals were below sublethal thresholds, such as Cd (0.43 ug/g) and Pb (0.36 ug/g). Sampled birds were admitted between March to June encompassing a portion of the breeding season, which may explain the sex differences. This study unveils the blood feather as a viable nonlethal sampling method with uses spanning multiple age groups.

Prey DNA on talons and beaks reveals what a migrating raptor eats

Ryan P. Bourbour, Cody M. Aylward, Chris W. Tyson, Breanna L. Martinico, Alisha M. Goodbla, Teresa E. Ely, Allen M. Fish, Angus C. Hull, and Joshua M. Hull

Presenting author: **Ryan Bourbour**, University of California, Davis, rpbourbour@ucdavis.edu

Migration is a significant portion of a bird's annual cycle, yet the foraging ecology of migrating raptors that hunt regularly en route remains largely unexplored. During fall migration, bird-eating raptors, e.g. falcons and accipiters, are thought to rely on flocks of migrant songbirds as a critical resource to fuel the energetic demands of long-distance migration. This hypothesis has been difficult to investigate due to the logistical challenges of documenting prey selection of these highly mobile and inconspicuous predators during this difficult-to-study life history stage. To address these knowledge gaps, our objective was to describe the dietary trends of bird-eating raptors across the migration season using a novel beak and talon swab method to collect prey DNA. In fall of 2015 and 2016, we swabbed visible and trace prey remains from the exterior surfaces of beaks and talons of migrating Merlins (n=72; *Falco columbarius*) and Sharp-shinned Hawks (n=565; *Accipiter striatus*) that were banded at a long-term raptor migration monitoring station on the Pacific Coast of California, USA. We used a DNA metabarcoding approach to target avian prey DNA collected on swabs. We detected avian prey DNA on 80% of the raptors sampled with an average of 3 prey items per individual raptor. We documented prey DNA from >1500 prey items comprising 81 prey species. This method overcomes challenges associated with prey DNA sample collection for birds that do not readily defecate in hand and is a quick and non-invasive method to implement at the end of the standard banding process. By revealing what fuels raptor migration, we can begin to investigate predator-prey interactions and coevolutionary relationships within migration corridors.

A test of the acoustic adaptation hypothesis explaining range expansion in songbirds with large vocal repertoires: Enhancing our understanding of the Great-tailed Grackle (*Quiscalus mexicanus*) alarm call

Samantha Bowser and Maggie MacPherson

Presenting author: **Samantha Bowser**, Arizona State University, slbowser@asu.edu

Bird species with large vocal repertoires and geographic ranges may have high plasticity in acoustic qualities to match tone, range, and pitch in heterogeneous soundscapes. We test the acoustic adaptation hypothesis in the Great-tailed Grackle (*Quiscalus mexicanus*), a species with a large vocal repertoire that is extending its northern range into the US. We used a reciprocal playback experiment to test whether variation in alarm calls explains differences in the northern extent of year round invasion fronts among three subspecies. The alarm call signals low intensity excitement and research in other species shows that differences in acoustic qualities of alarm calls reflect the urgency of threats tailored to the receiving audience. As alarm calls are expected to signal habitat and receiver-dependent information, we tested whether they differed among subspecies that occupy different geographic areas. We found differences between introductory notes of alarm calls among subspecies that were recorded during the nonbreeding season of 2020/2021. We found the COVID-19 pandemic to significantly impact ease of locating *Q. mexicanus* individuals, potentially due to lowered availability of human food waste in this urban-adapted species. Preliminary findings of differences in responses to conspecific playback may support the acoustic adaptation hypothesis and explain differences in northward range expansion among *Q. mexicanus* subspecies in the US. Ongoing research will test these differences within a phylogenetic comparative framework and include habitat modeling to improve our understanding of differential rates of range expansion among *Q. mexicanus* subspecies.

Bison restoration to mixed-grass prairie is associated with increases in avian diversity and mammal occupancy in riparian areas via effects on vegetation

Andy J. Boyce, Hila Shamon, and William J McShea

Presenting author: **Andy Boyce**, Smithsonian Conservation Biology Institute, boycea@si.edu

Rewilding seeks to achieve conservation outcomes through the restoration of natural processes. In grassland ecosystems, grazing by large herbivores is a highly influential process that affects biodiversity by modifying the vegetative environment through selective consumption. Here, we test whether rewilding efforts (reintroduction of bison) are associated with positive biodiversity outcomes in networks of riparian habitat within a temperate grassland ecosystem in northcentral Montana. We used a long time-series of remote sensing imagery to examine changes in riparian vegetation structure in streams within bison and cattle pastures. We then assessed how vegetation structure influenced and diversity of bird communities and detection rates of mammals in these same riparian networks in a mixed-grass prairie in northcentral Montana. We found that percent cover of woody vegetation and native grasses and forbs increased more rapidly over time in bison pastures, and that these changes in vegetation structure were associated with increased bird diversity and cervid occupancy. In conclusion, bison reintroduction appears to function as a passive riparian restoration strategy with positive diversity outcomes for birds and mammals.

Social network structure in winter flocks involving chickadees and titmice in New York

Margaret N. Boyle, David N. Bonter, and Robert L. Curry

Presenting author: **Margaret Boyle**, Villanova University, mboyle13@villanova.edu

Because interspecies interactions shape the behavior of species on both population and individual levels, it is important to study mixed-species social systems in the wild. In the northeastern United States, *Poecile atricapillus* (Black-capped Chickadee, BCCH) and *Baeolophus bicolor* (Tufted Titmouse, TUTI) are two dominant nuclear species found in mixed species flocks during the winter season. No previous study has investigated the interactions between TUTI and BCCH to infer dominance behavior using social network analysis. The recent northward expansion of the TUTI's range resulted in an increased geographical overlap with BCCH; understanding these assemblages is necessary to predict the effect of TUTI on naïve BCCH populations. We analyzed a feeder visitation dataset that used radio-frequency identification (RFID) methods at Ithaca, NY (2009-2010); we constructed social networks to investigate flock composition and infer dominance interactions between BCCH and TUTI. Total flock numbers at feeders ranged from five to 33 individuals. Although both species co-occur in geographically similar networks, community analysis suggests that TUTI have more network associates, regardless of species, than BCCH— even though BCCH outnumbered TUTI 129:35. Both species on the periphery of the network have stronger associations with conspecifics than heterospecifics. Therefore, we can infer that BCCH may be actively avoiding TUTI's aggression during these interactions. These findings could suggest possible energy-loss effects on BCCH fitness when avoiding TUTI confrontation. Additionally, this study could predict dominance interactions between TUTI and TUTI-naïve BCCH in the future, as TUTI expands northward.

Examining avian species richness, diversity, and turnover in a private working forest

Rebecca D. Bracken, Daniel U. Greene, Darren A. Miller, and Scott A. Rush

Presenting author: **Rebecca Bracken**, Mississippi State University, r_bracken1@hotmail.com

In the southeastern U.S., changes in ecosystem properties have been implicated in recent avian population declines. However, active forest management maintains landscape heterogeneity, leading to increased benefits for avian communities. Yet, in managed forests, local avian population trajectories can be difficult to evaluate. Therefore, using a private working forest as a model, we examined species richness, diversity, and turnover over a 21-year time period, using the same set of replicated stands from stand establishment to harvest. We conducted avian point counts within five experimental blocks of loblolly pine (Pinus taeda) stands in Mississippi during the breeding season from 1999-2020. We determined species richness, diversity, and turnover for each year based on number of species detected by total survey area and by treatment type. We grouped values based on stand age class (young open canopy, mid-unthinned, mid-thinned, late-thinned; 1-5, 6-10, 16-20, and 21+ years old, respectively). We fit multiple generalized linear models and ANOVAs to compare between stand stage and treatment types and modeled total species turnover. Preliminary results indicate that species richness was significantly influenced by stand stage, with young open canopy stands being significantly different from the other three stages ($p<0.001$). Avian diversity was significantly different across stand stages ($p<0.05$). Average turnover was 0.31 across all surveyed years, with the highest turnover rates occurring during the young open canopy stage. These results suggest that managed forests and silviculture practices support a variety of avian species throughout the lifetime of a pine stand, though the species vary at different stand stages.

Analyzing the population structure of the Pacific Swallow, a highly dispersive island-inhabiting species

Grant Broyles, Brian Myers, and Elizabeth Scordato

Presenting author: **Grant Broyles**, California State Polytechnic University, Pomona, gbroyles@cpp.edu

The factors driving speciation and population divergence have been studied extensively by evolutionary biologists. Species found on islands have been a particular focus of this research because isolation across islands can lead to rapid population divergence. However, most studies showing strong effects of islands on speciation have focused on taxa with low dispersal propensity. The effects of islands on population structure and diversification are less clear for species with higher dispersal abilities. Here, I analyze the population structure of the island-dwelling, yet dispersive, Pacific Swallow (*Hirundo tahitica*). Pacific Swallows are widespread across the islands of Southeast Asia and Oceania and comprise seven different subspecies distinguished based on morphological traits. Due to the large geographic range of Pacific Swallows, there is great potential for population structure and diversification across islands. However, swallows are aerial insectivores that forage over bodies of water. These traits may lead Pacific Swallows to disperse readily between islands, increasing gene flow and slowing diversification. Although Pacific Swallows are common, evolutionary relationships within the species remain unstudied. Here, I analyzed whole-genome data from seventy-eight Pacific Swallows from seven different populations, comprising the entirety of the species range. Population genetic analyses show strong population structure, limited gene flow, and deep divergence between island populations. These findings suggest that even island-dwelling species with high dispersal propensity can be affected by island isolation.

On the importance of Department of Energy lands as habitat for birds

Joanna Burger and Michael Gochfeld

Presenting author: **Joanna Burger**, Rutgers University, burger@biology.rutgers.edu

There are many types of protected habitat, including National Wildlife Refuges, and National Parks and Forests, as well as state and local protected areas. We propose that some lands, such as those of the Department of Energy (DOE) hold some of the most highly protected lands that have been undisturbed by people for 75 years. When DOE acquired lands in the 1940s and 1950s for defense, they developed about 10 % of the land at the larger sites, and left the rest as buffer lands (National Security). We explore the importance of the lands at two large sites (Oak Ridge Reservation in Tennessee; Hanford Site in Washington State). Both have some of the most undisturbed native habitats in the region, with accompanying listed birds. Oak Ridge has the largest unbroken interior forest (and associated birds), and Hanford has the highest percentage of shrub-steppe, in their respective regions.

Time trends in Ugandan birds vary by habitat and land protection status

Ryan C. Burner, Christine Dranzoa, Lars Jørgen Rostad, Douglas Sheil, Herbert Tushabe, and Derek Pomeroy

Presenting author: **Ryan Burner**, Norwegian University of Life Sciences, ryan.c.burner@gmail.com

Populations of many bird species are declining in the most heavily studied regions (North America and Europe), but long-term studies in the tropics are more limited. For tropical Africa in particular, very little information is available to estimate trends in resident species. Yet the same stressors that operate in other regions—including climate change, habitat alteration, and insecticides—are present in Africa as well. In Uganda, tree cover has changed widely across the landscape, decreasing in some areas—typically due to clearance for agriculture and charcoal-making, but increasing in others including within several protected wooded savannas for reasons that remain a subject of debate. We surveyed birds from 1990 to 2010 in thirty sites across Uganda. Sites included both protected and non-protected areas and were grouped into four habitat classes: agricultural, savanna, scrubland, and forest. We hypothesized that resident forest-associated bird species would be decreasing in non-protected habitats due to a region-wide decrease in tree cover, but that they would be increasing in protected areas. We used Bayesian joint species distribution models to estimate time trends for each species by habitat and land protection status. Bird species that are more dependent on forest cover were more likely to be increasing in protected areas but most did not appear to be in decline outside of these areas, although most of our non-protected sites were unforested and so most forest species were already scarce in these areas. These results are consistent with the hypothesis that increasing woody cover in Ugandan protected areas is affecting bird communities. Managed burns may be helpful to maintain grassland habitat in some areas.

Socio-ecological factors and phenotype relative to neighbors shape the opportunity for polygyny in a migratory songbird

David Canal, Lotte Schlicht, Carlos Camacho, Jesús Martínez-Padilla, and Jaime Potti

Presenting author: **David Canal**, Centre for Ecological Research, dav.canal.p@gmail.com

Why females pair with already mated males and the mechanisms behind variation in such polygynous events within and across years remain open questions. We use a 19-year dataset from a European Pied Flycatcher (*Ficedula hypoleuca*) population to establish local networks of breeding pairs. We then test whether the probability of becoming socially polygynous and of mating with an already mated male (becoming a secondary female) is influenced by experienced socio-ecological factors and/or phenotype (as proxy of quality) relative to the neighbors. We also examined how the breeding contexts experienced by individuals shaped the spatio-temporal separation between polygynous males' broods. The phenotypic quality of individuals, by influencing their local breeding time, mediated the probability of being involved in a polygynous event. Middle-age individuals (2-3 years), with large wings and, in the case of males, with conspicuous sexual traits, bred earlier than their neighbors. By breeding locally early, males increased their chances of becoming polygynous, while females reduced those of becoming secondary. Further, the probability of polygyny decreased sharply with the distance between nests. Throughout the season, there was large variation in the temporal separation between primary and secondary broods, which was, in turn, related to the breeding time of the polygamous males (first nest) relative to the neighbors. Polygynous males that bred late relative to their neighbors had a short time window to attract a second female. Overall, the spatial proximity between polygynous males' broods and, if possible, their temporal staggering are compatible with a male strategy to maximize paternity and reduce the costs of caring for two broods.

The role of testosterone in regulating the movement behaviours of juvenile migrant songbirds

Garth W. Casbourn, Christopher D. Posliff, Chloe Henry, Elizabeth A. MacDougall-Shackleton, and Scott A. MacDougall-Shackleton

Presenting author: **Garth Casbourn**, University of Western Ontario, gcasbour@uwo.ca

The post-fledging period is a critical stage in the life of a juvenile migrant songbird. Juveniles must develop their foraging skills, as well as the flight, navigation, and orientation skills that will allow them to make their first migration. Movement across the landscape is critical to developing all of these skills, and there is likely individual variation in the propensity to move. Testosterone is related to individual differences in migration distance in adult sparrows, but it has not been studied in the context of other movement behaviours. This study used juvenile Song Sparrows (*Melospiza melodia*) to investigate the relationships among movement propensity in a novel environment, juvenile prospecting movements, and testosterone profile. Testosterone profile is here defined as the maximal level of circulating testosterone produced in response to an injection of gonadotropin-releasing hormone (GnRH). We introduced fledged, free-living juvenile birds to an artificial chamber (2.4 x 2.4 x 1.8 m) containing 5 artificial trees, and recorded activity for 10 minutes as an index of exploration behaviour. Following this, we injected birds with GnRH to trigger a surge in circulating testosterone, and collected blood samples 30 minutes post-injection. Finally, we radiotagged birds for 2-4 weeks to assess prospecting movements. Our findings do not show a relationship between individuals' movement/exploration propensity within a novel environment and on the natal landscape, and individual regulation of testosterone. This suggests that juvenile movement behaviours have regulatory mechanisms which are independent of the mechanisms underlying adult migratory behaviour.

Diversification and biogeography of the 'true brilliants' clade of Andean hummingbirds

Marialejandra Castro-Farias, Enrique Arbeláez-Cortéz, Christopher C. Witt, and Jorge L. Pérez-Emán

Presenting author: **Marialejandra Castro-Farias**, Univesity of New Mexico, mcastrof2@unm.edu

The 'Brilliants' are a diverse group of hummingbirds (54 species, >100 subspecies), mostly distributed in South American mountains and foothills. Within this clade, the 'true brilliants' include the genera currently known as *Heliodoxa*, *Clytolaema*, *Sternoclyta*, and *Hylonympha* (12 species, 21 subspecies). Beyond the species level, there is tremendous within-species diversity in this clade that can provide information on species limits, speciation, and biogeography. In this study, we sampled 193 individuals, including all phenotypically distinct populations and covering most of the geographical range of each species. We estimated the phylogeny using mtDNA and four nuclear genes. We found deep structure across geographic barriers in the lower montane taxa *H. schreibersii*, *H. jacula*, and *H. leadbeateri*, suggesting more species in this clade than recognized. H. aurescens, by contrast, is the only lowland species and it exhibited low haplotype diversity across a broad swath of Amazonia. The time-tree showed evidence of diversification pulses in the late Miocene and Pleistocene, respectively, corresponding with times of orogenic and climatic dynamism in northern South America. Highly distinct forms such as *Sternoclyta cyanopectus* and *Hylonympha macrocerca* diverged during the earlier pulse; the latter pulse was exemplified by pairs of taxa such as *branickii/gularis* and *schreibersii/whitelyana*. Our biogeographic analysis showed long-term eco-climatic niche stasis in the northern tropical Andes, with rare dispersal events to adjacent lowlands and other Neotropical mountain ranges. This clade should be considered a parable for montane hummingbird diversification and united into a single genus, *Heliodoxa*, with 14 species.

A molecular phylogeny and biogeographic analysis of Accipitridae: A test of the monophyly of the genus *Accipiter*

Therese A. Catanach, Shanta Hejmadi, and Jason D. Weckstein
Presenting author: **Therese Catanach**, Academy of Natural Sciences of Drexel University, tacatanach@drexel.edu

Although diurnal birds of prey are among the most charismatic bird groups, little is known about the phylogenetic relationships and biogeographic history within the family Accipitridae. We used a mix of publicly available and newly generated data to infer a subspecies level phylogeny of this family. We mined publicly available mitochondrial and nuclear data from GenBank and using information from museum vouchers from the data generating publications we determined subspecies for each of the sequences. We then supplemented this dataset with newly generated UCE and mitochondrial genomes from portions of the accipitrid phylogenetic tree with poor sampling, particularly within the genus *Accipiter*. Our resulting phylogenetic reconstruction includes approximately 400 recognized species and subspecies of Accipitridae (approximately 4/5ths of all valid species or subspecies). Our findings indicate that several taxa at the species and genus level are not monophyletic. For example, harriers in the genus *Circus* are embedded within the genus *Accipiter*. Conversely some taxa currently classified as *Accipiter* are not within this large *Accipiter* clade. Therefore, substantial taxonomic reorganization, particularly in the genus *Accipiter*, is required for the taxonomy in this family to reflect phylogenetic relationships.

Early- and late-breeding Tree Swallows experience different trade-offs between immune and reproductive investment

David A. Chang van Oordt, Conor C. Taff, Thomas A. Ryan, and Maren N. Vitousek
Presenting author: **David Chang van Oordt**, Cornell University, dac385@cornell.edu

The allocation of limited resources among life history traits creates trade-offs that constrain the range of possible phenotypes of all organisms. In animals, the cost of maintaining an effective immune response may trade-off against reproduction, resulting in altered susceptibility to disease. However, not all individuals face identical constraints because differences in resource allocation and acquisition as a result of varying individual quality or opportunity can influence the degree to which traits are negatively associated. Here, we evaluated how variation in individual quality may result in different patterns of trait associations between immunity and reproduction. We measured constitutive immunity in breeding female Tree Swallows (*Tachycineta bicolor*) using a bacteria killing assay with blood plasma to assess the relationships between bactericidal ability (BKA), reproductive effort and reproductive success. We found few relationships of BKA with reproductive effort, except when accounting for timing of breeding as an indicator of individual quality. Tree Swallows generally fed their nestlings less if investment in BKA was higher, and late breeders laid smaller clutches when their BKA was stronger. In general, reproductive success did not correlate with BKA, but late breeders with stronger BKA produced smaller young. We provide evidence that female Tree Swallows do not experience trade-offs equally among individuals and that quality likely plays a role in how costs of immunity are weighed. To understand how investment in immunity can limit life history traits, we must consider how variation among individuals influences the relative costs of immunity.

Origin and evolutionary history of the endemic Galapagos Rail: Museum specimens, genomes, and conservation

Jaime A. Chaves, Pedro J. Martinez-Torres, Emiliano A. Depino, Sebastian Espinoza-Ulloa, Jefferson García-Loor, Annabel Beichman, Daniel Chavez, Pooneh Kalhoori, and Martin Stervander
Presenting author: **Jaime Chaves**, San Francisco State University, jachaves@sfsu.edu

The biotas of the Galápagos Islands are probably one of the best studied island systems and have provided a broad model of insular species' origins and evolution. Nevertheless, some Galápagos species remain poorly characterized, such as the Galápagos Rail (*Laterallus spilonota*). This bird species is one of the less explored groups of endemic vertebrates on these islands, due to its elusive behavior, cryptic plumage and restricted distribution. To date there is no genetic assessment of its origins and sister relationships to other taxa, and importantly, there is no data on its current genetic diversity. This lack of information is critical given the adverse fate of island rail species around the world in the recent past. Here we examine the genetics of Galápagos Rails using a combination of mitogenome de novo assembly with multi-locus sequencing (mtDNA+nuDNA) from both modern and historical samples. We show

that the Galápagos Rail is part of the 'American black rail clade', sister to Black Rail (*L. jamaicensis*), with a colonization of Galápagos dated to 1.2 Mya. The separate analysis of cytb, ND2, and RAG-1 markers demonstrates shallow population structure across sampled islands, possibly due to elevated island connectivity. Additionally, birds sampled from Pinta possessed the lowest levels of genetic diversity, most likely reflecting the impact of past bottlenecks due to habitat loss caused by invasive goats grazing on sensitive habitat. The data presented here highlights the low genetic diversity in this endemic rail species and suggests the use of genetic data (both modern and historical) to guide conservation efforts.

Systematics and evolution of the tyrant-flycatcher tribe Contopini (Tyrannidae)

R. Terry Chesser, Jose G. Tello, Michael G. Harvey, and Elizabeth P. Derryberry
Presenting author: **Terry Chesser**, USGS Eastern Ecological Science Center, chessert@si.edu

The tribe Contopini, which includes the familiar genera *Contopus*, *Sayornis*, and *Empidonax*, is the most Nearctic group of suboscine birds, a group otherwise largely confined to the Neotropical region or the tropics of the Old World. We studied the systematics and evolution of the Contopini using a phylogeny based on sequencing of ultra-conserved elements (UCEs) for 61 individuals, sampling 41 of the 42 species. Our results indicated that the Contopini constitute a monophyletic group, and all genera were strongly supported as monophyletic, including *Empidonax*. All species for which more than one individual was sampled were found to be monophyletic except for *Contopus cinereus*, but divergence within some other species was notably higher than that typically found between sister species. Our results are consistent with the treatment of *C. cinereus* as three species, and support the idea that *Cnemotriccus fuscatus* consists of more than one species; however, a focused study will be needed before new species limits can be drawn within *C. fuscatus*. The tribe Contopini was estimated to have arrived in North America from Central America some 6 mya, and ancestral state reconstructions indicate that long-distance migration evolved four times, the earliest of these, in the ancestor to the *Empidonax-Sayornis* clade, roughly coincident with the colonization of North America. Subsequent shifts to breed in the Neotropics have occurred in several lineages.

Examining the patterns and drivers of bill shape evolution in Asian and African barbets

Vaibhav Chhaya, Sushma Reddy, and Anand Krishnan
Presenting author: **Vaibhav Chhaya**, Indian Institute of Science Education and Research, Pune, vaibhav.chhaya@students.iiserpune.ac.in

Birds exhibit remarkably diverse bills varying in size, shape, and structure. Besides foraging, these bills allow them to perform a wide range of functions including courtship, nest building, and thermoregulation. However, few studies have explored factors other than feeding ecology as drivers of bill morphology. Climatic conditions have been particularly overlooked, even though they may affect thermoregulatory demands as well as the mechanical properties of available nest substrates. In our study, we explore the evolutionary patterns and potential drivers of bill shape in African (Lybiidae) and Asian barbets (Megalaimidae), a pantropical clade of nest-excavating frugivorous birds. We use microcomputed tomography, landmark-based geometric morphometrics, and phylogenetic comparative methods to quantify bill shape variation and examine the influence of climate and allometry on bill shape and size. We study these influences separately for four different components of the bill- the outer rhamphotheca and inner bony core of the upper and lower mandibles. We find that, unlike in commonly documented adaptive radiations, the diversity in barbet bills has accumulated linearly over time and weakly driven by climate and allometry. In addition, the entire bill has evolved as a single integrated unit, with the four components of the bill showing a high degree of covariation. This finding contests the common assumption that bill evolution is driven by adaptation to feeding behaviors and highlights the need to explore other ecological, environmental, and evolutionary factors.

Phylogeography, hybridization, and eye color variation of the Boat-tailed Grackle (*Quiscalus major*)

Eamon C. Corbett, Brant C. Faircloth, and Robb T. Brumfield
Presenting author: **Eamon C. Corbett**, Louisiana State University, ecorbe5@lsu.edu

Boat-tailed Grackles (*Quiscalus major*) are endemic to the Eastern United States, where they are a conspicuous and characteristic inhabitant of coastal marsh habitats. Across their range, from Texas to New York, there are four grackle subspecies that differ largely in eye color and size. Neither the phylogenetic relationships among the subspecies nor the amount of gene flow between them have been previously resolved. Our field work in southeastern Louisiana, near the boundary between dark-eyed *Q. m. major* and light-eyed *Q. m. alabamensis*, has shown that eye color in adult males appears highly variable within populations, suggesting that there may be introgression between adjacent subspecies. Additionally, the closely related light-eyed Great-tailed Grackle (*Q. mexicanus*) has dramatically expanded its range during the last century, creating a new and growing area of sympatry with *Q. major*. While the two species have been reported to mate assortatively, morphological hybrids have also been identified, and the contact zone has not been studied using genetic techniques. To characterize geographic patterns of genetic variation, we sampled individuals of *Q. majo*r from localities throughout its distribution. We also sampled individuals of *Q. mexicanus* and putative hybrids from contact zone populations in Louisiana. We sequenced Ultraconserved Elements (UCEs) to sample thousands of SNPs across the genome for phylogeographic study. We will present these results and discuss the relationships and levels of gene flow between the four *Q. major* subspecies, the degree of hybridization between *Q. major* and *Q. mexicanus* in southwestern Louisiana, and how grackles can help us understand the genetics underlying variation in bird eye color.

Birds in the city: The use of artificial materials for nesting decreases nest daily survival

Josué Corrales-Moya, Gilbert Barrantes, Eduardo Chacón-Madrigal, and Luis Sandoval
Presenting author: **Josué Corrales-Moya**, Universidad de Costa Rica, Josuecorrales@hotmail.com

As the human population increases and urbanization expands, solid waste becomes more abundant in every place people inhabit. Some birds use those artificial materials instead of natural ones for nest building, but the consequences of using them remain poorly understood. For this reason, we evaluate if the exposed artificial materials on birds' nests affect the daily survival rate in a common urban species, the Clay-colored Thrush (*Turdus grayi*). We conducted an experiment using 28 previously collected nests with different amounts of artificial materials in the outer layers to quantify nest predation. Artificial nest material was measured using four pictures for each lateral nest side and one photo from above the nest. We then calculated the proportion of the total nest area covered by artificial material. We placed each nest with three artificial eggs (similar in color and size of study species) during the Clay-colored Thrush breeding season in trees inside of a 40 ha area composed of buildings, parking lots, roads and parks, soccer fields, and small nature reserves. Each nest was monitored with a camera trap for 12 days—the incubation period of this thrush. We evaluated nest survival using the program MARK and found that nest survival decreased with the proportion of exposed artificial materials in the external layer of each nest. We also found that 50% of nests were depredated and the principal predators were conspecifics. Some conspecific individuals collected materials from the experimental nests after eggs were depredated. The use of artificial materials could reduce reproductive success and population size in urban Clay-colored Thrushes because it makes nests more vulnerable to predation.

Movement patterns of the Orinoco Goose (*Oressochen jubatus*) on the Rio Branco, northern Amazonia

Bruna Mirely da Silva Costa, Lisa Devenport, Pedro Ivo Simões, and Luciano Nikolás Naka
Presenting author: **Bruna Costa**, Universidade Federal de Pernambuco, bruna.mirely@ufpe.br

Seasonal landscape changes, such as those created by the cyclical fluctuation of Amazonian rivers can result in migratory movements, particularly for beach-dwelling species that find their preferred habitats completely flooded during several months every year. Despite the seasonality of these habitats, little is known about such migratory movements within the Neotropics. In recent years, studies in the Peruvian Amazon unveiled previously unknown seasonal movements by the Orinoco Goose (*Oressochen jubatus*), a poorly known and threatened species. In this study, we used GPS technology to evaluate potential seasonal movements in this species on the Rio Branco, where an isolated population occurs. We captured three Orinoco Geese on the Lower Rio Branco to deploy ARGOS/GPS PTTs, which resulted in more than a year of data, unveiling previously undescribed seasonal movements in this population. Two females and a male were trapped during the dry season of 2020 and followed until the present. Our results showed that these birds leave the beaches of the lower Rio Branco when the water level rises and move ~ 400 km north to spend the high-water season on the rice fields of the upper Rio Branco, where they spend months at a time, together with multiple other species of wildfowl. Individuals seem to closely monitor the level of the water, and two of our tagged birds made several exploring trips back to the lower Rio Branco, only to fly back to the rice fields a few days later. This study presents the first migratory movements of this species in northern Amazonia, and suggests that these birds use human-made plantations during the high-water period and closely monitor environmental conditions throughout the year.

Seasonal plasticity in mitochondrial function of Yellow-rumped Warblers (*Setophaga coronata*)

Soren Z. Coulson, James F. Staples, and Christopher G. Guglielmo
Presenting author: **Soren Coulson**, Western University, scoulso8@uwo.ca

Birds metabolically remodel their flight muscle prior to migration to meet the energetic demands of migratory flight. Energy-provisioning enzyme activities are elevated during the migratory season, but changes in mitochondrial function are poorly understood. We hypothesize that mitochondrial function varies with season and predict higher substrate oxidative capacity and reduced reactive oxygen species formation during migration. We captured Yellow-rumped Warblers (*Setophaga coronata*) during their fall migration at Long Point, ON. Half of the birds were sampled within two to four weeks of capture (migratory phenotype) and the remaining birds were sampled in a non-migratory phenotype induced by short day photoperiod (9L:15D). We investigated differences in mitochondrial function by measuring oxygen consumption and hydrogen peroxide (H2O2) formation rates from oxidation of lipid and carbohydrate substrates in mitochondria isolated from the pectoralis major flight muscle. Oxygen consumption specific to electron transport system protein complexes was also measured using complex-specific substrates and inhibitors. Oxygen consumption did not vary with season, except that respiration was marginally more uncoupled in wintering birds ($p = 0.09$). When standardized to oxygen consumption, H2O2 formation rates were significantly higher in non-migratory warblers ($p=0.02$). Our findings partially support our hypothesis and indicate that seasonal plasticity in mitochondrial function is limited to oxidant balance in migratory songbirds. This plasticity is significant to migratory birds, as oxidative damage caused by reactive oxygen species may hinder flight performance during migration.

Decreased migration distances in North American geese linked to climate change

Shannon R. Curley and José R. Ramírez-Garofalo
Presenting author: **Shannon Curley**, The College of Staten Island, CUNY, shannon.r.curley@gmail.com

Anthropogenic climate change is driving changes in species distributions in a way that might impact the distance between breeding and wintering grounds during migration. In this study we evaluated changes in bird banding encounter records from the United States Geological Surveys Bird Banding Lab from 1950–2019 between breeding and winter locations for six species of migratory geese that breed in North America. We found that encounter distances between breeding and winter locations (as a proxy for migration distance) have significantly decreased over the time period for most species. These decreases in distance were primarily explained by encounter records in winter increasing in latitude over this same time period, consistent with warming trends in North America. For Canada Goose, we found that the proportion of encountered individuals of a population not migrating from their breeding grounds has significantly increased from 5% to 23% over this time, indicating that many individuals of this species are showing a propensity to remain year-round residents at a location. We demonstrate that migration distances and migratory behavior have been significantly altered in long and short-distance migratory geese.

Detecting potential nocturnal pre-migratory roost sites in Canada by Canadian weather radars

Marc-André Cyr, Edward Cheskey, Alex Bencke, and Gregory W. Mitchell
Presenting author: **Marc-André Cyr**, Environment and Climate Change Canada, marc-andre.cyr@canada.ca

Aerial insectivores declined dramatically in the last decades. Most species of swallows congregate at night in roosts of hundreds to thousands of individuals from July to September. Swallow roosts are typically formed in the tall vegetation of wetlands, where they have access to food and shelter. Roost sites are important stopover habitat for swallows, yet the location and size of most roosts are largely unknown, limiting our ability to protect them. The goal of this project was to identify potential locations and sizes of swallow pre-migratory roosts in Canada. Under contract with Environment and Climate Change Canada, Nature Canada analyzed Canadian weather radar images for the 2017-2019 period for 31 weather radars. Raw radar data were converted to georeferenced images for visual interpretation. Potential roost locations were identified from the characteristic 'croissant' or donut shape made by birds leaving a roost. Further, a temporal pattern of emergence, growth and dissipation was required to delineate the potential roost. Potential roosts were classified by size based on expert opinion. This study confirmed that Canadian c-band weather radar data can be used to detect potential roost sites, despite coarser resolution of images compared to s-band weather radar data used in the U.S. Roost locations were detected in southern Ontario at sites previously confirmed from field surveys and analysis of proximate U.S. weather radar data. New potential roost sites were identified and will require field validation. This work contributes to understanding the location and size of pre-migratory nocturnal roosts, an important step toward designating those sites under formal protection.

Life-history traits of alpine breeding songbirds predict early-life resilience to severe weather events

Devin R. de Zwaan, Anna Drake, Jennifer L. Greenwood, and Kathy Martin
Presenting author: **Devin de Zwaan**, University of British Columbia, drdezwaan@gmail.com

Inclement weather can severely constrain offspring size trait development with lasting fitness effects. Susceptibility to weather likely depends on the timing and intensity of weather events across early-life stages, while coping strategies may vary among species in predictable ways based on life-history traits. We assessed inclement weather effects on offspring growth for three alpine breeding songbirds that differ in breeding phenology and nest-site selection: Horned Lark (*Eremophila alpestris*), Dark-eyed Junco (*Junco hyemalis*), and Savannah Sparrow (*Passerculus sandwichensis*). Across species, we identified the clutch initiation and nestling stages as most critical to offspring size development. Cold temperatures experienced by the female during clutch initiation were associated with larger, heavier horned lark nestlings but the reverse for Savannah Sparrow, potentially indicating maternal effects. Larks were resilient to colder average temperatures during the nestling stage but were vulnerable to extreme cold events and multi-day storms. In contrast, juncos were robust to storms, but lower daily temperatures were associated with smaller nestling size and mass. We propose these differences may be linked to species life-history traits, such as: 1) thermal benefits accrued by larger horned lark nestlings, 2) greater nest site cover to buffer dark-eyed junco nestlings against precipitation, and 3) delayed clutch initiation by Savannah Sparrows to limit exposure to cold storms. We highlight stage-specific effects on early-life resilience to inclement weather with implications for reproductive success and discuss the potential to predict vulnerability of alpine species to increasingly volatile environmental conditions.

Opposing dominance within a color gene block is associated with maladaptive hybrid signal discordance

Devin R. de Zwaan, Jacqueline Mackenzie, Else Mikkelsen, and Silu Wang
Presenting author: **Silu Wang**, University of California, Berkeley, siluwang.evo@gmail.com

Color divergence is increasingly recognized as important for speciation in songbirds through its influence on social dynamics. However, the behavioral mechanisms underlying the eco-evolutionary feedback that acts across species boundaries is poorly understood. The hybrid zone between *Setophaga occidentalis* (SOCC) and *S. townsendi* (STOW) in the Cascade mountain ranges provides a natural observatory to test the interplay between genetics and social behaviour in maintaining species boundaries. Recently, we found that selection within a gene block underpinning color variation (ASIP-RALY) has maintained a stable and narrow hybrid zone. Here we investigated the social signaling roles of cheek darkness and flank streaking, two color traits linked to ASIP-RALY that reflect opposing dominance of SOCC and STOW alleles. We found that both traits act as honest badges of status, as they predicted male breeding quality. The opposing dominance effects of ASIP-RALY resulted in signal discordance for heterozygotes, which in turn was associated with inferior hybrid territorial performance, a fitness proxy quantified by vocal and physical responses of resident males to a decoy intruder. Taken together, this study highlights a potential behavioral mechanism underlying selection acting on a simple genetic architecture that has maintained a stable species boundary over decades despite significant gene flow.

Sex-ratio bias influences spring migration traits of male Yellow-rumped Warblers (*Setophaga coronata*)

Jessica E. Deakin, Christopher G. Guglielmo, and Yolanda E. Morbey
Presenting author: **Jessica Deakin**, Western University, jdeakin4@uwo.ca

Migration timing is believed to be endogenously controlled and fine-tuned by components of the physical environment such as photoperiod. The social environment may also provide important predictive information, but little is known about its influence on migratory decisions. We tested whether sex ratio, an important aspect of the social environment, effects the spring migration traits of male Yellow-rumped Warblers (*Setophaga coronata*). Birds were caught in fall 2019 at Long Point and brought to the Advanced Facility for Avian Research, ON. The birds were assigned to a male- or female-biased treatment in the winter and housed in flocks in large free-flight rooms. From the winter until their release, we took body mass measurements and standardized photos to monitor molt. In April, the birds were tagged, returned to their respective treatment room and photo-triggered to enter a migratory state. Using a novel approach, we measured the locomotor activity of the flocked birds over a 2-week period using automated radio-telemetry. In May, the birds were released at their capture site and Motus was used to determine stopover departure timing and track migratory movement. Sex ratio did not influence body mass or molt progression in males. However, males from the male-biased treatment had significantly less locomotor movement than those from the female-biased treatment. Additionally, a lower proportion of males from the male-biased treatment initiated migratory restlessness, an indicator of the urge to migrate. Finally, significantly fewer males from the male-biased treatment were detected north of the release site. Overall, our findings support the hypothesis that social environment influences the migratory behaviour of songbirds.

Genetic similarity of New Guinea parrotfinches suggests that they are not two species

Lucas H. DeCicco, Devon A. DeRaad, Paul M. Hime, Brett W. Benz, and Robert G. Moyle
Presenting author: **Lucas DeCicco**, University of Kansas, lhdecicco@gmail.com

There are multiple hypotheses related to the primary evolution of montane species, those taxa that occur in montane habitat but do not breed at sea level. The most widely accepted hypotheses are based on principles of competitive exclusion (either direct or diffuse), niche partitioning, and character displacement, resulting in a lowland species becoming adapted to a montane habitat. These populations occupy montane habitat after being excluded from the lowlands by increased competition of an invading species, as suggested under Wilson's taxon-cycle hypothesis or are drawn into the highlands by reduced competition, which is in line with the Mayr and Diamond push-pull hypotheses. Two *Erythrura* parrotfinch species in the New Guinea highlands have been proposed as exemplars of the taxon-cycle hypothesis, producing one endemic montane parrotfinch species *(E. papuana*) alongside a parapatric or broadly sympatric widespread species *(E. trichroa*). Mitochondrial data on these two species suggest that they are very closely related or identical, contrary to expectations under the taxon-cycle hypothesis. We investigated this system using ~4,000 genome-wide RADseq loci. Our results indicate that this is not an instance of the taxon-cycle hypothesis but a much more complicated and interesting scenario of two phenotypes (large-billed *E. papuana* and small-billed *E. trichroa*) occurring in juxtaposition of nearly identical genomic backgrounds. Our work suggests that this is a system at some stage of ecological speciation or an example of resource-based polymorphism, both likely being produced and maintained under strong divergent selection.

Do the major histocompatibility complex and the microbiome explain variation in fitness correlates in Dark-eyed Juncos (*Junco hyemalis*)?

Joee D. Denis, Danielle J. Whittaker, Tricia A. Van Laar, and Joel W.G. Slade
Presenting author: **Joee Denis**, California State University Fresno, denisjoee@gmail.com

Class II of the major histocompatibility complex (MHC) is an essential component in vertebrate immune systems since it recognizes pathogen-derived peptides from extracellular organisms, such as bacteria. In addition to its immunological role, MHC has previously been observed to be important for mate choice in several vertebrates, such that sexually selected traits may signal MHC diversity. Choosing mates that are highly diverse at MHC may provide direct benefits such as resource acquisition and defense and indirect benefits like genetically more diverse offspring. However, evidence of ornamental signals of MHC in birds is limited. Microbiome composition and diversity, which is posited to be mediated by class II MHC may also be essential to host health, as commensal bacteria may mediate host susceptibility to infection through increased resource competition against harmful bacteria. A candidate species to study signals of MHC diversity and microbiome is the Dark-Eyed Junco (*Junco hyemalis*). In our study, we found that MHC class II allelic diversity is positively associated with the percent of white plumage on junco tail feathers (a sexually selected trait). However, we found no association between MHC and body condition, nor did we find an association between microbiome species richness and the same fitness correlates. Our results add to the limited studies on MHC diversity and sexually selected traits in birds.

Genomic species delimitation of the Scrub-Jays

Devon A. DeRaad, A. Townsend Peterson, and Robert G. Moyle
Presenting author: **Devon DeRaad**, University of Kansas, devonderaad@gmail.com

Studying genomic variation amongst species can allow us to reconstruct evolutionary history and also broadly inform our understanding of lineage diversification under natural conditions. The Scrub-Jays are a well known North American avian species complex with multiple recently diverged lineages experiencing variable levels of isolation and gene flow, making them an ideal model system for testing evolutionary hypotheses. We sought to resolve the evolutionary history of the Scrub-Jays and test for differences in patterns of demography and diversification between the Z chromosome and autosomes. To do so, we used restriction-enzyme associated DNA sequencing to generate 16,307 high-quality genomic SNPs broadly shared amongst 95 samples from throughout the entire geographic distribution of the Scrub-Jays. We then used multiple methods of genomic species delimitation and species tree reconstruction to robustly resolve the evolutionary history of this group and tested for gene flow between identified lineages. Finally, we tested for differences in genetic diversity, interspecies divergence, and introgression between the Z chromosome and autosomes. Our efforts to resolve the evolutionary history of the Scrub-Jays with genome-wide resolution have important taxonomic implications including supporting the future recognition of a range-restricted endemic Scrub-Jay species in southern Mexico. Additionally, our comparative genomic analyses reveal that the Z chromosome serves as a significant barrier to gene flow in the Scrub-Jays, adding to the rapidly growing body of literature indicating that the avian Z chromosome plays a crucial role in the speciation process.

Local adaptation and gene flow across an alpine archipelago

Matt G. DeSaix, T. Luke George, Amy Seglund, Garth M. Spellman, Erika S. Zavaleta, and Kristen C. Ruegg

Presenting author: **Matt DeSaix**, Colorado State University, mgdesaix@gmail.com

Climate change is having profound effects on biodiversity and species distributions. Alpine species are some of the most climate-climate threatened taxa in North America and have already experienced significant declines. As the climate warms, alpine species are expected to shift their distributions northward and/or up in elevation. This distributional shift often results in range contractions in alpine species because they already inhabit the highest elevations locally. Local adaptation to rapidly changing environmental conditions may be a key component to the persistence of alpine species. Additionally, rapid range contraction may lead to inbreeding depression in small, isolated populations unless there is sufficient gene flow from dispersal that allows these populations to persist with limited genetic consequences. Here, we use a landscape genomics approach to investigate the consequences of climate change in the Brown-capped Rosy-Finch (*Leucosticte australis*), a near-endemic bird to the Colorado Rockies and one of the highest elevational breeding avian species on the continent. Whole-genome sequencing (~6x) of 116 blood samples from 11 sites across the range, revealed range-wide genetic connectivity, apart from a single isolated mountain, as well as high genetic diversity and low inbreeding despite their high elevation, sky island distributions. Characterization of local adaptation to high altitude environments is in progress. Overall, the results of this study will help inform persistence of high elevation sky island organisms in the face of climate change and other stressors.

Migratory physiology of the nomadic, irruptive Pine Siskin in captivity and the field

Joely G. DeSimone, Bret W. Tobalske, Megan A. Fylling, William M. Blake, and Creagh W. Breuner

Presenting author: **Joely DeSimone**, University of Montana, joely.desimone@umontana.edu

Facultative migrations are unpredictable in timing and destination, often in response to unpredictable variation in food availability. We propose two hypotheses about the physiological and behavioral responses of a facultative migrant, the Pine Siskin, to variation in food availability. Prepare Hypothesis: siskins increase fuel stores to prepare for departure, and elevations of baseline corticosterone (CORT) support increased activity. Escape Hypothesis: siskins do not prepare for departure, body condition declines as food availability declines, and stress-related levels of CORT induce escape. We took two approaches to test these hypotheses. In captivity, we manipulated food availability and measured changes in body composition, CORT, and hopping activity. In the field, we assessed how body condition and CORT related to feeding behavior (estimated via plasma triglycerides, TRIG), space use, and departure. Our captive study supports the Escape Hypothesis: body condition declined as food declined, baseline CORT increased with loss of body and fat mass, and birds increased activity when food availability was low. Our field results suggest an intermediate physiology, with neither preparatory nor escape behaviors. Birds in poor condition stayed longer near the field site and birds with higher TRIG were more likely to depart. However, above a threshold body mass, physiology did not predict departure, suggesting moderate energy stores are necessary for departure but movement decisions depend on other factors among birds with sufficient fuel. Together these studies demonstrate that facultative movements are physiologically distinct from seasonal migrations and are sensitive to both food availability and body condition.

Do male European Starlings advertise age through song?

Maheshi E. Dharmasiri and Colleen A. Barber

Presenting author: **Maheshi Dharmasiri**, Saint Mary's University, maheshidharmasiri@hotmail.com

Females from a range of taxa prefer to mate with older males as they may gain direct and/or indirect benefits that younger males are unable to provide. In avian species, direct benefits may consist of enhanced offspring provisioning while indirect benefits include good genes for their offspring. Male birds commonly use song to attract mates. Females assess male quality through song characteristics such as song complexity, song bout length, and song rate. Song repertoire size increases with age in a small number of species such as European Starlings (*Sturnus vulgaris*), which are open-ended learners. Variation within song types is less studied, but has been detected in a few species, including starlings, although its function in starlings is not known. We examined repertoire size, within-song type variation and song bout length with respect to male age in an eastern Canadian population of European Starlings. We predicted that song repertoire and bout length would increase with age while within-song type variation would decrease. We recorded twelve males and obtained two years of song data for eight males and three years of song data for one male. Repertoire size and song bout length did not increase with age in either the longitudinal or the cross-sectional analyses. However, younger males tended to have more within-song type variation than older males. These findings suggest that male song repertoire in European Starlings does not significantly increase over a one-year period. The number of within-song type variants decreased with age and could possibly play a role in mate attraction.

Hatching failure dissected: Examining factors that lead to embryonic mortality across altricial bird species

Alexander J. Di Giovanni, Michael J. Miller, Todd M. Jones, Thomas J. Benson, and Michael P. Ward

Presenting author: **Alexander Di Giovanni**, University of Illinois at Urbana-Champaign, digivnn2@illinois.edu

Juvenile mortality rates are high across taxa, and birds are no exception. While many studies on avian juvenile mortality have focused on the nestling and fledgling stages, little is known about the causes of non-predatory mortality of the embryo in the egg (i.e. hatching failure) despite reportedly high mortality rates during this stage. Our study used a non-invasive method (ballistocardiogram) to investigate factors driving variation in hatching failure across 14 free-living grassland and shrubland songbird species. We found that hatching failure varied among species ranging from 1.1% to 12.3%. We investigated several factors that may contribute to hatching failure and found that time of year, egg volume, incubation behaviors, and whether or not a nest was parasitized by a brood parasite (Brown-headed Cowbirds, *Molothrus ater*) did not impact hatching failure. The largest differences were associated with nest type (cavity vs. open-cup), clutch size, and the relative safety of a species' nest. Cavity nesting species, whose nests are the most likely to survive to produce young and which have the largest clutch sizes, also had the greatest rate of hatching failure. We dissected a subset of eggs that failed to hatch and found that the majority of hatching failure in cavity nesting species was due to embryonic death before or shortly after the onset of incubation. While more experimental approaches are needed to understand the variation in hatching failure across species, there may be tradeoffs of having a large clutch, specifically between the benefit of rearing more young, at the cost of a greater likelihood of egg hatching failure due to poor incubation, or the delayed onset of incubation.

Trends in bird abundance differ among protected forests but not bird guilds

Jeffrey W. Doser, Aaron S. Weed, Elise F. Zipkin, Kathryn M. Miller, and Andrew O. Finley

Presenting author: **Jeffrey Doser**, Michigan State University, doserjef@msu.edu

Improved monitoring and associated inferential tools to efficiently identify declining bird populations, particularly of rare species, is key to informed conservation and management across large spatio-temporal regions. We assess abundance trends for 106 bird species in a network of eight forested national parks in the northeast U.S.A. from 2006-2019 using a novel hierarchical model. Trends in bird abundance over time varied widely across parks, but species showed similar trends within parks. Three parks (Acadia National Park and Marsh-Billings-Rockefeller and Morristown National Historical Parks (NHP)) decreased in bird abundance across all species, while three parks (Saratoga NHP and Roosevelt-Vanderbilt and Weir-Farm National Historic Sites) increased in abundance. Bird abundance peaked at medium levels of basal area and high levels of percent forest and forest regeneration, with percent forest having the largest effect. Variation in these effects across parks could be a result of differences in forest structural stage and diversity. By sharing information across both communities and parks, our novel hierarchical model enables uncertainty-quantified estimates of abundance across multiple geographical (i.e., network, park) and taxonomic (i.e., community, guild, species) levels over a large spatio-temporal region. We found large variation in abundance trends across parks but not across bird guilds, suggesting that local forest condition might have a broad and consistent effect on the entire bird community within a given park. Research should target the three parks with overall decreasing trends in bird abundance to further identify what specific factors are driving observed declines across the bird community.

The costs of playing catchup: Songbirds with delayed spring departure migrate faster but pay the consequences

Bryant C. Dossman, Colin E. Studds, Amanda D. Rodewald, and Peter P. Marra
Presenting author: **Bryant Dossman**, Cornell University, bd342@cornell.edu

Timely arrival on the breeding grounds is vitally important for individual fitness and delays in arrival have largely been attributed to poor overwintering conditions. Yet despite the importance of this carry-over effect, few studies have investigated the extent to which individuals can modify their migratory behaviors to account for these delays. Given their limited reproductive opportunities, it follows that short-lived migratory passerines, should attempt to compensate for delays at the start of spring migration by migrating at faster paces. Since migrants make trade-offs between time, energy, and safety, speeding up migration in order to compensate for delays is likely to incur survival costs – yet the potential reproductive advantages are likely to outweigh these consequences. To investigate these hypotheses, we tracked individual American Redstarts (*Setophaga ruticilla*) departing their wintering grounds in Southwest Jamaica up through Florida and beyond using the motus wildlife tracking system. We leveraged long-term data on departure timing and annual return rates to quantify the relative departure dates (early vs delayed) of tagged individuals, to which we then related individual migration rates and annual survival. We found that individuals that departed relatively late migrated at a faster pace than individuals that departed relatively early. Furthermore, those delayed individuals were significantly less likely to return the following season. Our study supports the hypothesis that individual migrants attempt to compensate for delays in the start of spring migration and incur survival costs because of these compensatory behaviors—a potential mechanism underlying differential survival during spring migration.

The role of molt phenology divergence in maintaining reproductive isolation between taxa that hybridize in the Great Plains

Paul J. Dougherty and Matthew D. Carling
Presenting author: **Paul Dougherty**, University of Wyoming, pdoughe1@uwyo.edu

The outcome of hybridization between evolutionary distinct lineages depends largely on hybrid fitness. When hybrid fitness is low, parental populations will remain isolated and selection against heterospecific mating may eventually cease hybridization altogether. Adaptive divergence in molting behavior is a largely unexplored yet potentially consequential postzygotic isolating mechanism in birds. When parental taxa differ in molting behavior, recombination of adaptive complexes in hybrids may result in deleterious molt strategies, such as attempting to replace feathers during migration. Most of the avian hybrid zones in the Great Plains of North America feature dramatic divergence in molt phenology between parental taxa, with one taxon carrying out prebasic molt prior to fall migration and the other molting after departing breeding territories during an extended migratory stopover. To investigate the extent to which molt phenology divergence contributes to reproductive isolation between avian taxa that hybridize in the Great Plains, we captured Indigo Buntings (*Passerina cyanea*), Lazuli Buntings (*P. amoena*), and hybrids from wild populations and observed their molting behavior in a captive setting. Preliminary data indicate that the expected phenological differences between the parental species persist in a common environment, supporting a strong genetic basis for relative molt timing. Additionally, hybrid individuals exhibit a variety of molt and migration strategies, some of which incorporate elements from both parental phenotypes. The prevalence of putatively disadvantageous molt/migration strategies among hybrids supports our prediction that molt phenology divergence can promote speciation in birds.

Combining point counts and autonomous recording units improves avian survey efficacy in temperate mountain habitats of the Americas

Anna Drake, Devin R. de Zwaan, Tomás A. Altamirano, Scott Wilson, Kristina Hick, Camila Bravo, José Tomás Ibarra, and Kathy Martin

Presenting author: **Anna Drake**, University of British Columbia, drake.ae@gmail.com

Accurate biodiversity and population monitoring is a requirement for effective conservation decision-making. Survey method bias is therefore a concern, particularly when research programs face logistical and cost limitations. We employed point counts (PCs) and autonomous recording units (ARUs) to survey avian biodiversity within structurally comparable, high elevation, temperate mountain habitats: 9 mountains in British Columbia (BC), Canada and 10 in southern Chile. We assessed the performance and efficiency of single vs. combined methods by comparing species accumulation curves to multi-year species inventories (i.e. known community richness) and by incorporating time costs. We further examined method performance by modeling family-level detection probabilities. By extrapolating sampling curves using species incidence data, we estimated that ARUs capture ~93% of avian species present in BC but only ~58% in Chile, despite Chilean montane bird communities being less diverse. PCs capture equivalent diversity in both hemispheres (~72%). The presence of less-vocal species in Chile appears to drive poor ARU performance; PCs were better at detecting 11/11 families in Chile but 0/14 in BC. Combined methods were among the most efficient and accurate approaches to capturing diversity. In the presence of ARUs, PCs contributed little to detected diversity in BC, but significantly increased species detections in Chile, in both cases with negligible time costs. This study highlights the benefits of conducting PCs when ARUs are being deployed/retrieved in order to capture additional diversity with minimal additional effort and reduce methodological bias within a comparative framework.

Purple Martin diet is associated with habitat type but not foraging range

Julia Dunoyer, Kristen Lalla, Kevin Fraser, and Kyle Elliott

Presenting author: **Julia Dunoyer**, McGill University, juliadunoyer@gmail.com

Purple Martins (*Progne subis*), like many aerial insectivores, are declining at an alarming rate, possibly due to declines in insect populations. Understanding diet, and where they obtain their diet, could help understand why declines are occurring. Here, we quantified diet composition by DNA barcoding fecal samples collected from adults and used GPS biologgers to measure foraging range and habitat use. Foraging range did not have an effect on diet diversity or average prey size. Coleoptera was the most frequently detected prey order. Developed and cropland habitats were most frequently used while water and wetlands were least frequently used. Proportion of diets including Diptera decreased significantly with increased habitat use. In contrast, the proportion of diets including Odonata significantly increased with cropland habitat use. We conclude that Coleoptera is an important component of diet, and that Purple Martin houses might target areas with high concentrations of beetles. Moreover, houses installed near croplands with some wetlands or edges, ideal for dragonflies (Odonata), may also be successful, but that urban habitat can also be successfully used. Finally, shifting from insecticides to biocontrols such as beetles and flies can increase Purple Martin prey availability.

A retrospective analysis of methylmercury in the feathers of Indonesian avifauna

Sarah A. Dzielski, Subir B. Shakya, Dewi M. Prawiradilaga, and N. Roxanna Razavi

Presenting author: **Sarah Dzielski**, SUNY College of Environmental Science and Forestry, sadziels@syr.edu

Artisanal and small-scale gold mining (ASGM) is the largest anthropogenic source of mercury globally, though few studies have explored how the release of this toxicant into the environment is affecting avian wildlife in Indonesia, an ASGM hotspot. In this study, feather samples from Indonesian museum specimens were used to examine changes in methylmercury (MeHg), d15N, and d13C (diet and foraging habitat, respectively) through time. The following questions were assessed: 1. Do long term trends in MeHg through time in Indonesian bird specimens parallel global and local trends in ASGM Hg emissions? and 2. How does foraging guild and within-species variation in diet influence MeHg concentrations in Indonesian bird specimens? Feather samples from seven species collected between 1860 and 2019 were used to address these questions. We found that MeHg significantly varied by foraging guild, that some kingfisher specimens had feather MeHg concentrations above the threshold for sublethal effects, and that d15N and d13C depletion through time reflected isotopic changes due to anthropogenic activities over the past 150

years. This study is the first report of MeHg in Indonesian passerines, kingfishers, and woodpeckers. It provides critical data that is currently lacking on avian Hg exposure in a global avian hotspot severely impacted by Hg pollution.

Putting the speciation puzzle together: Looking at vocalizations between raven species

Victoria Eastham, Nandadevi Cortes-Rodriguez, and Rachel Sturge

Presenting author: **Victoria Eastham**, Ithaca College, tori.eastham@gmail.com

Birds have a number of identifying traits, for example, genetics, morphology, coloration and vocalizations, amongst others. From all of these traits, acoustic signals are used within species to communicate with members of the same species. These unique calls or songs are important in the identification of species and have the potential of being the first step in the speciation process. Ravens are a widespread large passerine that inhabits most of the world. They are considered species generalists with no specific set habitat and can be found on every continent except Antarctica and South America. Many studies have focused on Common Raven (*Corvus corax*) vocalizations and have found that there are between eighteen to twenty identified calls. However, vocalizations have not been exhaustively studied across different species of ravens nor is there a comparison between species. In this study, our goal is to see if there are changes in raven vocalizations between species as a way to understand the effect of isolation between different species. Here, we used songs from XenoCanto from four species of Ravens. We measured them using Raven Pro® and used PAST (PAlaeontological STatistics) to analyze the data. We also compared these songs to a previously made Corvus phylogenetic tree.

Point count offsets for population sizes of North American landbirds

Brandon P. M. Edwards, Adam C. Smith, Teegan Docherty, Marcel A. Gahbauer, Caitlyn Gillespie, Alexis Grinde, Taylor Harmer, Steve Matsuoka, Nicole Michel, Andy Murray, Gerald Niemi, Jon Pasher, Barry Robinson, Péter Sólymos, Diana Stralberg, and Edmund Zlonis

Presenting author: **Brandon Edwards**, Carleton University & Canadian Wildlife Service, brandonedwards3@cmail.carleton.ca

Bird monitoring in North America over several decades has created many open databases, housing millions of structured and semi-structured bird observations. These can be used as the basis for generating population estimates, but require accounting for variation in factors such as underlying field methods, timing, land cover, proximity to roads, and uneven spatial coverage. The QPAD approach considers probability of availability (p) and detection (q) of birds in relation to area (a) and density (d), allowing counts of birds from any stationary point-count survey to be translated into estimates of true density, facilitating integration of data from across disparate survey methods. Here, we introduce NA-POPS: Point Count Offsets for Population Sizes of North American Landbirds, a large-scale, multi-agency project aimed at generating an open-source database of detectability functions for all North American landbirds. To date, NA-POPS has collected over 6 million data points spanning 299 projects from across North America. This has allowed for the generation of detectability functions for over 300 species of landbirds so far. We describe how we curate these data while respecting data-ownership, the methods to generate the detectability functions, the open-access nature of the resulting database of offsets, and highlight some key spatial gaps that we are working to fill. We also describe our vision for use of the open-source detectability functions to improve population size estimates of North American landbirds.

Population genomics and hybrid detections between King and Clapper Rail populations in the eastern United States

Elisa C. Elizondo, Jonathan D. Clark, Susan B. McRae, Adrienne I. Kovach, and W. Gregory Shriver

Presenting author: **Elisa Elizondo**, University of Delaware, eelizo@udel.edu

The Clapper Rail (*Rallus crepitans*) and the King Rail (*Rallus elegans*) are secretive marsh birds with declining populations. These species freely hybridize, but the extent of hybridization and the genomic characterization of introgression are understudied. Unlike other marsh birds, surveys for Clapper and King rails using acoustic monitoring are hampered by substantial overlap in vocalizations between the two species, limiting the utility of auditory survey data. Hence, to increase our understanding of the connectivity of Clapper Rail populations and their introgression with King Rail, we adopted a genomic approach using molecular markers from populations along the East coast of North America. We obtained Clapper Rail samples from Connecticut (n = 24), Delaware (n = 46), North Carolina (n

= 22), South Carolina (n = 22), Georgia (n = 10), and Louisiana (n = 30) and King Rail samples from North Carolina (n = 30) and Louisiana (n = 18). We also included known hybrid birds from Louisiana (n = 15). Preliminary genomic analysis using RAD-seq on 80 individuals from Delaware, North Carolina, and Georgia identified two hybrid rails, both captured in Delaware saltmarshes. Our results suggest cryptic and on-going hybridization in Delaware.

Systematic map effort of using small Unmanned Aircraft Systems (sUAS) to monitor birds

Jared A. Elmore, Kristine O. Evans, Sathishkumar Samiappan, Meilun Zhou, Morgan B. Drabik-Hampshire (Pfeiffer), Bradley F. Blackwell, and Raymond B. Iglay

Presenting author: **Jared Elmore**, Mississippi State University, jae133@msstate.edu

Small Unmanned Aircraft Systems (sUAS) are replacing or supplementing manned aircraft and ground-based surveys in many monitoring situations due to better coverage at finer spatial and temporal resolutions, access, cost, bias, impacts, safety, efficiency, and logistical benefits. Various sUAS models and sensors are available with varying features and usefulness depending on survey goals. However, justification for selection of sUAS and sensors are not typically offered in published literature and existing reviews do not adequately cover past and current sUAS applications for monitoring birds nor their associated sUAS model and sensor technologies, taxonomic and geographic scope, flight conditions and considerations, spatial distributions of sUAS applications, or reported technology pitfalls. We conducted a systematic map to collect and consolidate evidence pertaining to sUAS monitoring of birds and investigate the current state of knowledge using an accurate, comprehensive, and repeatable search. We searched for peer-reviewed and grey literature as well as dissertations and theses using online publication databases, Google Scholar, and by request through a professional network of collaborators and publicly available websites. We used a tiered approach to article exclusion with eligible studies being those that monitor (i.e., identify, count, estimate, etc.) birds. Extracted data concerning sUAS, sensors, birds, methodology, and results were recorded and queried to produce tables, figures, and geographic maps. Our systematic map provides a useful synthesis of current applications of sUAS-bird related studies and identifies knowledge clusters and gaps that may influence future research directions and sUAS applications.

The evolution of Darwin's finches: Whole-genome sequencing of an entire community of finches on Daphne Island

Erik D. Enbody, C. Grace Sprehn, Ashley T. Sendell-Price, B. Rosemary Grant, Peter R. Grant, and Leif Andersson

Presenting author: **Erik Enbody**, Uppsala University, erik.enbody@gmail.com

Adaptive radiations provide a powerful comparative framework for studying the molecular basis of ecological diversity through comparative genomic analysis. Analyses that incorporate long-term monitoring and molecular analysis are needed to understand the contribution of both species' interactions and gene flow to diversification. Introgression may increase evolutionary potential through the sharing of adaptive alleles, but the contribution of gene flow to evolutionary change is difficult to establish in wild populations where gene variants contributing to phenotypic diversity are poorly known. We study a community of Darwin's finches on Daphne Island in the Galápagos archipelago by whole-genome sequencing of all individuals captured between 1983 and 2012 (*Geospiza*, n = 3,957). We use admixture mapping to confirm the role of two loci of large effect (ALX1 and HMGA2) on beak size and shape, and identify novel loci contributing to beak evolution in these species. We use individual-level haplotype data to track the frequency of causal alleles through time. In doing so, we show that allele frequency shifts in *G. fortis* at loci contributing to beak size track a decline in beak size over time in this species. We next show evidence for introgression of causative alleles having left lasting footprints on morphology over the time period, and discuss evidence for introgression between two species via a third conduit species. Our community-based investigation identifies several important genetic loci governing beak traits that have been subject to natural selection. They are transferred between species through introgressive hybridization, and may reflect a general mechanism for how gene exchange is contributing to biodiversity.

A review of scientific evidence on the impact of frightening devices to protect crops from avian pests

Janice K. Enos, Michael P. Ward, and Mark E. Hauber

Presenting author: **Janice Enos**, University of Illinois at Urbana-Champaign, jkkelly2@illinois.edu

Many bird species are considered agricultural pests and cause severe and costly damage to crops worldwide. Crop producers use several methods to reduce damage by birds, with frightening devices serving among the most popular approaches. Frightening devices, such as broadcast of conspecific alarm calls or placing predator models in fields, are considered effective because they can trigger antipredator behaviors that reduce foraging activities or abundances of target birds locally. However, it remains unclear which type of frightening device is most effective and whether some frightening devices work best against certain bird species or on certain types of crops. We reviewed the published scientific literature to fill in these knowledge gaps about using frightening devices for crop protection against avian pests. We found 46 experiments evaluating the impact(s) of frightening devices. However, only 26 experiments statistically tested their results from which to draw conclusions. We found that alarm call playback, eyespot balloons, and hawk-kites reduced avian abundance in all experiments. All experiments using alarm call playbacks, eyespot balloons and automated flying vehicles (drones) effectively reduced crop damage. However, only experiments on passerine birds and in row crops were well-represented in these experiments. We discuss potential biases in the literature that may limit our understanding of how birds respond to frightening devices and suggest future directions that researchers might take to fill knowledge gaps.

Concerted variation in melanogenesis genes underlies plumage patterning in capuchino seedeaters

Cecilia Estalles, Sheela P. Turbek, María J. Rodríguez-Cajarville, Luís F. Silveira, Kazumasa Wakamatsu, Irby J. Lovette, Pablo L. Tubaro, Darío A. Lijtmaer, and Leonardo Campagna

Presenting author: **Cecilia Estalles**, Museo Argentino de Ciencias Naturales Bernardino Rivadavia, ceciaguilares@gmail.com

Coloration is central to animal communication; it often governs mate choice, promotes reproductive isolation, and catalyzes speciation. Various studies have identified the genes responsible for particular changes in avian plumage coloration, yet less is known about how coloration patterns (which involve the combination of various color patches) are determined. Here, we study a recent avian radiation, the southern capuchinos, which comprise species with diverse color patterns despite remarkably low genomic divergence. To assess the genomic basis of color differentiation, we performed genome-wide association studies (GWAS) and correlated genotypic differences among species with concentration of melanin pigments (eumelanin and pheomelanin) independently in the feathers of six different color patches. Few genes are associated with color differences among three species that differ solely in their throats, and different genes are responsible for the transitions between different throat colors. Extending our analyses to the whole southern capuchino group, we found that differences in the coloration of each patch are associated with unique combinations of variants in multiple genomic regions. These regions include in most cases genes involved in the melanogenesis pathway, and differences among species were mostly in non-coding, presumably regulatory areas. Some genes are involved in color variation in various patches, but in some cases the SNPs associated with color changes in different patches clustered in different areas in the vicinity of the gene. We suggest that the combination of variants across multiple melanogenesis genes, and likely their interaction, generate the diverse coloration patterns of the southern capuchinos.

Breeding habitats, phenology and size of a resident population of Two-banded Plover (*Charadrius falklandicus*) at the northern edge of its distribution

Fernando A. Faria, Márcio Repenning, Guilherme Tavares Nunes, Nathan R. Senner, and Leandro Bugoni

Presenting author: **Fernando Faria**, Universidade Federal do Rio Grande do Sul, biofariaf@gmail.com

The central-peripheral hypothesis states that the demographic performance of a species decreases from the center to the edge of its range. Peripheral populations are often smaller and tend to occur under different and suboptimal conditions from those of core populations. Peripheral populations can also coexist during part of their annual cycle with populations from the core of the species' range. Studies of peripheral populations are thus valuable for understanding ecological and evolutionary processes. The Two-banded Plover (TWBP, *Charadrius falklandicus*) is an endemic South American shorebird that breeds in Patagonia and migrates northward during Austral winter. There are breeding records, however, from Lagoa do Peixe National Park in southern Brazil. In this study we (1) mapped nests, (2) characterized the reproductive biology, (3) evaluated the seasonal occurrence patterns, and, (4) estimated the size of the Brazilian TWBP population. We estimated that the Brazilian population has 55 (95% CI: 44.1 – 66.6) breeding pairs and the breeding season spanned the Austral spring and summer. The population was sedentary, and their nesting habitat differed and their apparent reproductive success was lower than those of core populations. These results indicate that the Brazilian TWBP population is isolated from the species' southernmost core populations, resulting in a heteropatric distribution. The differences in nesting habitat and year-round residency suggest they are ecologically distinct from other populations as well. The marked behavioral and ecological differences combined with the small size of the northern population supports the central-peripheral hypothesis.

Exploring parasite-mediated selection and MHC diversity of two seasonally sympatric subspecies of Dark-eyed Juncos (*Junco hyemalis*)

Esther M. Fernandez, Danielle Whittaker, and Joel W. G. Slade

Presenting author: **Esther Fernandez**, California State University, Fresno, esthermf@mail.fresnostate.edu

In birds, seasonal migration may increase exposure to a wide variety of pathogens, which can impose strong balancing selection (heterozygote advantage) on immune genes, such as the major histocompatibility complex (MHC). In contrast, sedentary species may exhibit good gene effects at MHC since they are likely exposed to local pathogens. The seasonally sympatric Dark-Eyed Juncos (*Junco hyemalis*) at the Mountain Lake Biological Station in Virginia are an excellent candidate study system to explore differences in MHC between the resident Carolina Juncos (*J. h. carolinensis*), and the overwintering migratory Slate-Colored Juncos (*J. h. hyemalis*). We hypothesized that the sedentary Carolina Junco will contain fewer, locally adapted MHC alleles in comparison to the migratory Slate-Colored Junco. In this study we explore how MHC class I diversity, patterns of molecular selection, and haemosporidian infection may be explained by migratory behavior in these seasonally sympatric Dark-Eyed Junco subspecies. We characterized MHC class I in each subspecies using next-generation sequencing, performed parasite-specific PCR to identify haemosporidian variants, and qPCR to determine infection levels. Contrary to our prediction, we found higher MHC class I diversity in the resident Carolina Juncos than the migratory Slate-Colored Juncos. Parasite data will be discussed. Ultimately, our results indicate that resident Juncos may experience more pathogen-mediated balancing selection at MHC class I than migratory Juncos.

On geographic vocal variation and its neuroethological implications in a Neotropical songbird

Ron A. Fernández-Gómez, Jorge E. Morales-Mávil, and J. Roberto Sosa-López

Presenting author: **Ron Fernández-Gómez**, Instituto de Neuroetología, Universidad Veracruzana, ronfernandezg@gmail.com

Acoustic signals are essential for mating, defending resources, and recognition. These signals may vary geographically under selective or random pressures, playing an essential role in species interactions, reproductive isolation, and speciation. In vocal learning species, the divergence in songs is complemented by cultural transmission, where both vocal production and auditory recognition abilities depend on a neural circuit that gives variability and complexity to vocal behavior. We explored the effects of geographic isolation in the song perception at behavioral and neuronal levels in the Olive Sparrow, *Arremonops rufivirgatus*, a Neotropical songbird with allopatric populations. We found geographic vocal variation in the song with divergence among populations within the complex. Then, we tested whether males recognized the song variations using playback experiments. We noticed an asymmetrical response pattern but with response intensity being predicted by the acoustic similarity, suggesting that males from the different populations may use a similar mechanism to recognize signals. We explore the neural response to species-specific songs assessing the activity of gene expression on the auditory forebrain areas and found that despite the current song divergence, it is not enough to promote differences in the neuronal activity. However, the magnitude of neuronal activity among some treatments was significant, supporting the idea that it may be fostered by specific acoustic features in the song. Our findings provide information from a neuroethological outlook about how song variations are perceived by populations with consequences for reproductive isolation and population differentiation.

The energetic 'pace of life' of tropical birds: Generally slow or widely diverse?

Timothy R. Forrester and Thomas E. Martin

Presenting author: **Timothy Forrester**, University of Montana, timothy.forrester@umontana.edu

Tropical species are thought to have a slower 'pace of life' than temperate species. Yet, tropical birds display diverse energetic strategies (e.g. baseline metabolic rates, offspring feeding rates, foraging speeds) and adult mortality rates that can overlap with temperate species. Daily energy expenditure (DEE) may have evolved in response to selection from extrinsic mortality, but the relationship between DEE and mortality is largely unexplored. We used a time-energy budget approach to quantify movement rates and foraging strategies to estimate DEE of nine coexisting species of tropical insectivorous passerines that span a gradient of annual adult mortality in Malaysia. We found that movement rates ranged from 2.7 ± 0.4 to 30.2 ± 1.5 (SE) movements/min among species and were predicted by their mortality rates. Species with high annual mortality rates made more movements/min and spent less time inactive than species with lower mortality rates. Moreover, high mortality species used energetically expensive foraging maneuvers (e.g. flutter chase, hover sally) for >50% of prey attacks, while low mortality species more commonly (>75%) used energetically cheaper maneuvers (e.g. glean). These behavioral differences yielded higher DEE in high mortality species than in low mortality species. Our results support the hypothesis that tropical species have evolved widely diverse 'metabolic niches' along the slow-fast life history axis, some as fast as those occupied by temperate species, via selection from extrinsic mortality.

Using integrated population models to understand drivers of population change over 55 years in two species of Finnish owls

Charles M. Francis and Pertti Saurola

Presenting author: **Charles Francis**, Environment and Climate Change Canada, charles.francis@canada.ca

Understanding drivers of population change and how they affect vital rates is necessary to predict how populations may change in the future and to understand conservation implications. We used integrated population models to examine impacts of climate and prey abundance on demographic parameters of two species of large owls that breed in Finland: Ural Owl (*Strix uralensis*) and Tawny Owl (*Strix aluco*). The Ural Owl has a predominantly northern range, while the Tawny Owl immigrated into Finland from the south last century. Both species have been targeted by Finnish bird-ringers for about 55 years, resulting in mark-recapture-recovery datasets with more than 55,000 ringed Tawny Owls and 70,000 ringed Ural Owls, along with >15,000 and >20,000 combined live recaptures and dead recoveries. We used joint recapture-recovery models, in a Bayesian framework with program MARK, to estimate annual variation in age-specific survival rates. We used annual monitoring of nest boxes to estimate breeding propensity and productivity, and an annual population survey to estimate numbers of breeding pairs each year. We combined data from each of these sources into integrated population models to estimate the relative importance of variation in age-specific survival, nesting propensity, reproductive success and recruitment on overall changes in population size. We found that all aspects of the owls' demography varied in relation to a ~3-year cycle in vole abundance, with increased nesting propensity, clutch size and fledging success in years when voles were abundant in spring and summer, and higher survival when voles were abundant in winter. Mean winter temperature and snow cover affected survival but differently in each species.

Spatio-temporal changes in fall waterfowl migration in the context of a rapidly changing world

Barbara Frei, Sarah Gutowsky, Frank Baldwin, and Christian Roy

Presenting author: **Barbara Frei**, Canadian Wildlife Service, barbara.frei@canada.ca

Changes in the phenology of migrating birds, or lack-thereof, in consequence of a rapidly changing world, have distinct implications for the success, survival, and management of migratory birds worldwide. Shift in phenology and migration movements may have extensive implications, including: loss of socioeconomic opportunities by waterfowl hunters and associated tourism, reduced efficacy of monitoring and management efforts by land managers and policy makers, and conservation implications of habitat overuse in key staging areas. Using nearly 60 years of banding and recovery data from three harvested waterfowl species across North America, we identified changes in migration phenology and patterns. The banding data included Mallards, Blue-winged Teals, and Northern Pintails that were banded from 1960 – 2019 in the three Prairie Provinces of Canada, and were subsequently shot or found dead (i.e., bands recovered) during the fall (September – December) hunting season across North America. We visualized spatiotemporal changes in the phenology and distribution of fall migration using kernel distribution estimation (KDE; Calenge et al. 2007) and assessed the spatial relationships using STAMP (Spatio-Temporal Analysis of Moving Polygons; Long et al. 2018). We found some species, such as the Mallard, are not only delaying fall migration, but are remaining in more northerly staging or overwintering areas, and even moving across different flyways than the same population in previous decades. Comparing these movements to changes in the climate and habitat cover provides further insight to possible human and climate-induced drivers of changing migration phenology of waterfowl.

Evidence of niche conservatism among pairs of allopatric avian taxa in two seasonally dry Neotropical forests

Lays V. de Freitas and Luciano N. Naka
Presenting author: **Lays Viturino de Freitas**, Universidade Federal de Pernambuco, laale.freitas@gmail.com

Adaptation, or the adjustment of organisms to their environment, represents a key feature for the survival and establishment of biological populations. Seasonally Dry Forests (SDF), located along the South American Dry Diagonal, represent a natural laboratory to understand the influence of ecological conditions on the evolutionary process of species. Numerous species of different biological groups (animals and plants) have allopatric populations in the Caatinga and the Gran Chaco, the two main blocks of Neotropical dry forests. The aim of this study is to understand whether these allopatric pairs of populations/taxa represent cases of niche evolution, and as such may be close to completing the speciation process, or represent cases of niche conservatism, and are more likely to have undergone non-adaptive mutations while in isolation. Aiming to answer this question, we tested hypotheses of divergence versus niche conservatism in 12 pairs of avian populations/taxa with allopatric distributions in these two dry forests. We used niche models and ordination methods to better understand the environmental preferences of these pairs and to evaluate their degree of niche differentiation. Our results indicated that in most cases (7/12), there is strong evidence of niche conservatism among allopatric populations. These results suggest that the current pattern of distribution of these populations fits with the natural tolerance of each lineage, and do not represent cases of ecological differentiation. Hence, our results suggest that the shared taxa between the Caatinga and the Chaco represent cases of niche conservatism of populations that continue to thrive in relatively similar environmental conditions.

A supergene underlies phenotypic variation in redpolls

Erik R. Funk, Nicholas A. Mason, Snæbjörn Pálsson, Tomáš Albrecht, Jeff Johnson, and Scott A. Taylor
Presenting author: **Erik Funk**, University of Colorado Boulder, erik.funk@colorado.edu

The genetic architecture of a phenotype can have considerable effects on the evolution of a trait or species. Understanding trait genetic architecture may provide insight into the complexity of a given phenotype and, potentially, the role of the phenotype in different evolutionary processes such as speciation. We use whole genome sequence data to investigate the genetic basis of phenotypic variation in redpoll finches (*Acanthis* spp.) and demonstrate that redpoll phenotype is broadly controlled by a ~55-Mb chromosomal inversion. Within this inversion, we find a number of candidate genes related to melanogenesis, carotenoid coloration, and bill shape, suggesting the inversion acts as a supergene controlling multiple linked traits. Given the latitudinal gradient in ecotype distribution, the supergene driven phenotypes are likely under environmental selection which appears to maintain supergene haplotypes as a balanced polymorphism. Our results provide a mechanism for the maintenance of ecotype variation in redpolls despite a genome that is widely homogenized by gene flow.

Epizootic of beak deformities worldwide: A review of avian keratin disorder in wild birds

Danielle E. Gerik, Caroline Van Hemert, Colleen M. Handel, Kate Risely, Jeff Walters, Kerry Brust, Anna Prinz, Andy Van Lanen, Jessie Schillaci, Clifford Anderson, Susan Cottrell, Cristian A. Gorosito, Víctor R. Cueto, and Maxine Zylberberg
Presenting author: **Danielle Gerik**, U.S. Geological Survey, dgerik@usgs.gov

An epizootic of debilitating beak deformities in wild birds has been documented in recent decades. Avian keratin disorder (AKD) is characterized by overgrowth of beak keratin and was first observed in clusters among Black-capped Chickadees (*Poecile atricapillus*) in Alaska. The prevalence of beak deformities is higher among Black-capped Chickadees and American Crows (*Corvus brachyrhynchos*) in Alaska than in any other population ever recorded. Reports of birds with similar beak deformities have recently emerged from across North America, in South America, and in Europe. We compiled reports from citizen-science programs, bird monitoring studies, and scientific literature to summarize the current geographic scope and bird species affected by AKD-like beak deformities. From 1979 to 2020, >3,300 citizen-science observers reported 290 species with beak deformities, comprising >4,000 birds in Alaska, 1,600 elsewhere in North America, and >900 from outside of North America. We also examined the occurrence of beak deformities in populations of Black-capped Chickadees in Alaska, Red-tailed Hawks (*Buteo jamaicensis*) in the Pacific Northwest, Red-cockaded Woodpeckers (*Dryobates borealis*) in North Carolina, and

Austral Thrushes (*Turdus falcklandii*) in Patagonia. Clinical signs of AKD in Black-capped Chickadees have been strongly associated with the occurrence of a novel picornavirus, which has now been detected in multiple species exhibiting morphologically similar beak deformities. Our detailed compilation, including geographic occurrence of individuals and species apparently affected, will help identify research and conservation actions required to evaluate and mitigate impacts of beak deformities on wild birds.

Soras over Illinois: Nocturnal settlement patterns in *Porzana carolina* are site-specific but show no evidence of visual or acoustic cues

Daniel L. Goldberg, Ashley M. Tauber, Michael P. Ward, and Angelo P. Capparella
Presenting author: **Daniel Goldberg**, Illinois State University, dlgoldb@ilstu.edu

Many birds migrate at night, but little is known about whether they base nocturnal settlement decisions on visual or acoustic cues. Studies of conspecific attraction have found that songbirds and seabirds are attracted by day to call playback or decoy models of their own species, and birds will also settle preferentially in certain environments based on the presence of vegetation or water bodies. Remotely-activated broadcasts and Autonomous Recording Units were applied to study whether Soras (*Porzana carolina*), common nocturnally-migrating rails in Central Illinois, could be promoted to settle in suboptimal farm field habitats in which Sora broadcasts, small ponds, both cues, or no cues were present. In our comparison of three different farms, Soras settling in experimental treatment sites at night were found to have no preference for conspecific playback or ponds relative to the control fields. However, there was a significant effect of site on calling rates. Franklin Farm had the majority of Soras heard during the study period, consistent with its status as a Nature Conservancy restored wetland. As nocturnal calls were detected at every farm sampled, these results can assist wetland managers in promoting Sora settlement in critical breeding habitats in Illinois and beyond.

Evaluating if human land disturbances break species barriers at continent-wide and regional scales

Kathryn C. Grabenstein, Theresa M., Burg, Ken A. Otter, and Scott A. Taylor
Presenting author: **Kathryn Grabenstein**, University of Colorado, Boulder, Kathryn.grabenstein@colorado.edu

Determining how species boundaries are maintained is critical for conserving biodiversity and understanding speciation. Hybridization following anthropogenic habitat disturbances (e.g., urbanization) has been detected globally in both terrestrial and aquatic species, and highlights the break-down of species barriers. However, while we have numerous records of the occurrence of disturbance-mediated hybridization, we lack information on the mechanisms by which disturbance breaks species barriers in most cases. Black-capped (*Poecile atricapillus*) and Mountain (*P. gambeli*) Chickadees are non-migratory birds that, despite broad range overlap, appear to hybridize predominantly in disturbed areas (e.g. logging sites or urban centers), including Colorado's Front Range. Using whole genome data from chickadees in Colorado, paired with reduced representation sequencing of a broader and larger set of samples spanning the majority of range overlap between Mountain and Black-capped Chickadees, we compare patterns of human-mediated habitat disturbances with hybridization rates to assess if human habitat disturbances correlate with hybridization. Assessing the conditions that correlate with broken species barriers between Black-capped and Mountain Chickadees will provide insight into the mechanisms maintaining reproductive isolation. Characterizing how human-altered landscapes change species interactions will expand our understanding of how anthropogenic changes promote hybridization in a rapidly changing world.

Acoustic, genetic, and morphological adaptations in song: A study of male and female tropical wren song

Brendan A. Graham, Luis A. Sandoval, and Daniel J. Mennill
Presenting author: **Brendan Graham**, University of Lethbridge, b.graham001@gmail.com

The signals used by animals in social and sexual communication vary with location, including acoustic signals, where acoustic traits vary from one region to the next. Acoustic variation between regions in song learning species likely involves cultural evolution, yet there is evidence that a number of other factors influence acoustic differences. Several hypotheses including the morphological, acoustic adaptation, and genetic adaptation hypotheses have been proposed to explain geographic song variation. In this study we examine geographic song variation for Rufous-and-

white Wrens (*Thryophilus rufalbus*) in the context of the morphological, genetic, and acoustic adaptation hypothesis. We examined frequency measurements from 126 wrens (53 females and 73 males) from four populations in Costa Rica. Songs varied between sexes, and song differentiation increased with genetic distance and increases in ambient noise, but acoustic differences did not change with increases in body mass. Larger wrens were found at higher elevations, where birds sing higher pitched songs. Overall males and females showed similar patterns, although there were some differences (e.g. trill pitch varied among females but not males). These results provide greater insight into the evolution of cultural traits in animals, and the interplay between vocalizations, environment, genetic differentiation, and morphology, and highlight the similarities and differences in sexually dimorphic traits.

Is hay for the birds? Investigating landowner willingness to time hay harvests for grassland bird conservation

Matthew P. Gruntorad, Katherine A. Graham, Nico Arcilla, and Christopher J. Chizinski

Presenting author: **Nico Arcilla**, International Bird Conservation Partnership, nico.arcilla@aya.yale.edu

Grassland bird populations are declining steeply worldwide, and effective grassland bird conservation strategies are urgently needed. In grasslands used for hay production, delaying hay harvest until at least July 15th allows most breeding birds to successfully nest and raise young for at least one breeding cycle. Most grassland bird populations nest on privately owned land rather than in public protected areas, and thus conservation strategies must engage private landowners to be widely effective. However, few studies have investigated private hay producers' willingness to alter their harvesting practices, a critical factor for bird conservation where most land is privately owned, such as in the North American Great Plains. We surveyed private landowners with hay production operations in the Nebraska Sandhills to learn whether they were willing to time their hay harvests for breeding bird conservation. We also investigated whether livestock production, wildlife knowledge, and/or hunting activity affected landowners' willingness to alter their haying practices for bird conservation. The majority (60%) of respondents expressed willingness to delay hay harvests to allow birds time to nest successfully. Livestock producers and those more knowledgeable about wildlife were more willing to delay hay harvests, whereas active hunters were less willing to do so. Our findings suggest that a majority of private producers show high potential for engaging in grassland bird conservation activities. Landowners' willingness to participate in bird conservation programs and actions could be further encouraged through extension and education efforts connecting hay producers with information and support for bird conservation.

Effects of space weather on radar-detected bird migration

Eric R. Gulson-Castillo, Benjamin M. Van Doren, Kyle G. Horton, Michelle X. Bui, Daniel T. Welling, Mark B. Moldwin, Kerby Shedden, and Benjamin M. Winger

Presenting author: **Eric Gulson-Castillo**, University of Michigan, ergc@umich.edu

Birds use Earth's magnetic field for navigation, but the magnetic field is regularly disrupted by solar storms. Whether this impacts bird navigation is unknown, so we test the hypothesis that navigation is negatively impacted by magnetic disturbances. We predict that magnetic disturbance causes changes in bird behavior during migration. We analyzed two decades (1995-2017) of weather radar from the US central flyway to measure bird migration volume and directionality. We compared this to a global index of magnetic disturbance collected during the same time period and a localized index specific to each radar station that we are developing. We used complex mixed-effect models to control for effects of weather and the effects of temporal and spatial autocorrelation. Our preliminary results suggest that magnetic disturbances are associated with a decrease in the dispersion of directions, with more birds flying in similar directions during geomagnetic storms. Furthermore, these effects seem to be amplified when there is high cloud cover and during the first portion of the night, when other celestial navigation cues are obscured and when magnetic disturbances are felt the strongest. We suggest that, when confronted by a geomagnetic storm, birds might drift with the wind instead of trying to navigate, leading to more similar flight directions. We are developing models to test these specific predictions and will use alternate modelling frameworks to confirm our first set of results.

Has artificial selection driven anatomical changes in the brain of the homing pigeon (*Columba livia*)?

Audrey E. M. Guyonnet, Kelsey J. Racicot, Ben Brinkman, and Andrew N. Iwaniuk

Presenting author: **Audrey Guyonnet**, University of Lethbridge, a.guyonnet@uleth.ca

Domestication is the process by which animals are artificially selected over time for specific, often divergent, behavioural and morphological traits. One of the most famous examples of selection for behavioural traits in a domesticated species is the homing pigeon. Homing pigeons can locate a home loft from a novel starting point and over unfamiliar terrain up to thousands of kilometres away. Homing is a spatial memory task dependent on the hippocampal formation (HF) in the brain. Despite the wealth of research on homing pigeon behaviour, whether the HF anatomy of homing pigeons differs from other breeds remains unclear. Based on intense selection for homing, we expect that homing pigeons have a relatively larger HF with more neurons than other breeds. Here, we provide initial data from a detailed comparison of HF anatomy across homing, feral, show, and sporting pigeons to test this prediction. Using unbiased stereology, we measured HF volume and neuron numbers in homing and feral pigeons, as well as several other sporting breeds. We then used generalized linear models to compare data across breeds in relation to the size of the brain and cerebral hemispheres. Preliminary analyses indicate that the homing pigeon HF is larger relative to the rest of the cerebral hemispheres and brain than feral pigeons'. This suggests that feral pigeons, descendants of homing pigeons no longer selected for homing, underwent a regression in HF size over a relatively short time frame. Analysing the brain anatomy of a wider range of domestic breeds will allow us to better understand the relationship between homing and hippocampal neuroanatomy and provide insight into how artificial selection for behaviour affects brain anatomy and function.

The importance of gene flow in archipelagos: Case study in a Pacific island flycatcher

Ethan F. Gyllenhaal, Luke B. Klicka, Lucas H. DeCicco, Robert G. Moyle, and Michael J. Andersen

Presenting author: **Ethan Gyllenhaal**, University of New Mexico, egyllenhaal@unm.edu

For over half a century, island biogeography has shaped how we think about biodiversity. Speciation within archipelagos is often viewed independently of classic island biogeographic predictions, as colonization of new islands is relatively easy within archipelagos. However, the same factors that dictate colonization chance also apply to individuals moving between islands, or gene flow. Gene flow is extremely important to the processes of speciation, as it often inhibits diversification. Therefore, island biogeographic theory should be considered when studying diversification within archipelagos. We test the impact of gene flow on diversification in the Solomon Islands using the 'Black-and-white' Monarch complex, which is composed of three to four allopatric species with several subspecies. Using genome-wide data from thirteen different island populations, we show that patterns of genetic divergence correspond to ease of movement between islands. At a shallow scale, the degree of connectivity during times of reduced sea level in the Pleistocene is the predictor of divergence between islands in the main chain of islands in the Solomons, which were connected at glacial maxima. At deeper scales, we uncover a phylogenetic pattern likely driven by post-colonization gene flow levels based on island parameters, which opposes predictions from colonization history. We used explicit tests of gene flow to confirm it occurred in levels consistent with our island-based predictions. Finally, as a proof of concept of gene flow after population divergence, we present evidence for a first-generation intergrade between distinct island taxa. Our results shine new light on the importance of gene flow in shaping island biodiversity.

The role of color perception and opponent processes in avian egg recognition

Daniel Hanley and Samantha Rutledge

Presenting author: **Daniel Hanley**, George Mason University, dhanley2@gmu.edu

Hosts of avian brood parasites are under intense selective pressure to prevent or reduce the cost of parasitism. Many have adapted refined egg discrimination abilities, which can spur a coevolutionary arms race with their respective parasites that lay increasingly mimetic eggs. Perceived differences in color and pattern can play a vital role in egg recognition. A classic assumption, supported by modern visual models, is that hosts reject parasitic eggs when there is a perceivable difference between the parasitic eggs and their own. However, while these models are very helpful at estimating color variation received, they do not provide specific insight into how colors are perceived. Color information received by the eye must be transmitted to the brain via a specific opponent channel, and then the bird may apply higher-order cognitive processes to make decisions based on that information. A growing body of evidence suggests that many hosts are more likely to reject browner eggs than bluer eggs, despite equal absolute perceived differences. Such behavioral responses to perceived color variation suggest that host egg recognition may be controlled via specific color opponent channels. Here we propose that birds use one opponent channel for egg recognition, which we support with field data and finally discuss implications this may have for our understanding of host brood parasite co-evolutionary dynamics.

Nest boxes vary in effectiveness as a tool to increase presence of American Kestrels (*Falco sparverius*) in agriculture

Melissa B. Hannay, Megan E. Shave, Olivia J. Utley, Sarah A. Groendyk, and Catherine A. Lindell
Presenting author: **Melissa Hannay**, Michigan State University, bradymel@msu.edu

Birds have the capability to provide vital ecosystem services such as pest reduction through their deterrence and consumption of crop pests. Landscape enhancements, like nest boxes, can attract birds to agricultural areas to provide these services, and are becoming a popular tool in pest management. However, there are large gaps in knowledge about how effectively these enhancements attract birds. From 2016 to 2018 we installed American Kestrel (*Falco sparverius*; hereafter, kestrel) nest boxes in a blueberry production region in western Michigan. From 2015 to 2018 we conducted surveys to monitor kestrel presence in sites along transects with and without boxes. We also monitored box occupancy and reproductive success. Kestrel presence appeared to increase over time in the study area. Kestrel presence in sites along transects increased when a box was occupied in a neighboring site. Box occupancy rates were positively influenced by occupancy of the same box the previous year. Percent successful nests and mean numbers of fledglings produced were high. A comparable nest box system in a sweet cherry production region in northern Michigan showed higher box occupancy and similar percent nest success and mean number of fledglings produced. However, the effect of nest boxes attracting kestrels was stronger in the sweet cherry study region. Our results show that nest boxes can serve as effective landscape enhancements to attract kestrels to agricultural landscapes although the degree to which kestrels occupy boxes can vary geographically. Local-scale pilot studies can provide information about the potential benefits and challenges of using nest boxes as a pest management tool.

The origin of the avian inner ear and its correspondence to flight and vocalization

Michael Hanson, Eva A. Hoffman, Mark A. Norell, and Bhart-Anjan S. Bhullar
Presenting author: **Michael Hanson**, Yale University, michael.hanson@yale.edu

Birds exhibit a markedly different inner ear structure from that of other extant reptiles, with highly elongated cochleae and dorsoventrally expanded semicircular canals—adaptations associated with sensitivity to high-frequency sound, permitting complex vocal communication, and bipedal locomotion including flight. We conducted geometric morphometric analyses of 3D digital endocasts from µCT scans of a large set of reptile and bird species (including fossil taxa from the early archosauromorphs to the closest relatives of crown birds) to investigate the origin of avian hearing acuity and locomotion. The semicircular canals and the cochlea are distinct evolutionary modules, with the former detecting acceleration and the latter detecting sound. Our analyses show three semicircular canal morphotypes corresponding to terrestrial quadrupeds, terrestrial bipeds and simple fliers, and high-maneuverability fliers. Bipedal non-avialan dinosaurs bridge the morphospace gap between quadrupedal reptiles and archosaurian fliers, while troodontid dinosaurs fall close to *Archaeopteryx* and among extant birds with low maneuverability flight. These taxa likely had locomotor control and three-dimensional mobility comparable to palaeognathous or gallinaceous birds. We also identified morphological signal for behavioral traits including aerial predation and semiaquatic habits. Analyses of cochlear shape data indicate a single instance of cochlear elongation in stem Archosaurs, likely coinciding in tandem with the rise of high-pitched juvenile vocalizations and adult responses to them, as in extant crocodilians and birds. These calls may have originated very early in the history of Archosauromorphs and suggest an early origin of parental care.

Translocation methods and post-release monitoring of reintroduced Brown-headed Nuthatch (*Sitta pusilla*) in Missouri pine woodlands

Kristen Heath-Acre, Sarah W. Kendrick, Frank R. Thompson III, Thomas W. Bonnot, Brian K. Davidson, and James A. Cox
Presenting author: **Kristen Heath-Acre**, University of Missouri, kristen.heath@missouri.edu

Brown-headed Nuthatches (*Sitta pusilla*) are presumed extirpated from Missouri due to near-total loss of pine woodlands in the last century. However, decades-long management of pine woodlands by Mark Twain National Forest and partners has restored Brown-headed Nuthatch habitat. In August and September 2020, we relocated 46 Brown-headed Nuthatches from Ouachita National Forest in Arkansas to Mark Twain National Forest in Missouri. We captured Brown-headed Nuthatches using conspecific playback and decoys and transported nuthatches in

individual ventilated cardboard mailing tubes with a perch and tulle cover. We flew nuthatches to release sites in a small aircraft to minimize transport time. We banded each nuthatch with an aluminum identification band and a unique color-band combination. We attached Lotek PicoPip Ag337 VHF radio transmitters to 23 individuals using a leg-loop harness method. We tracked radio-tagged individuals for 4 weeks post-release using radio telemetry and resighted individuals using color bands. To monitor occupancy and survival, we created a 250-m grid using known locations of reintroduced individuals with a 250-m buffer and conducted monthly playback surveys at each point beginning in November. Translocated Brown-headed Nuthatches have made movements up to 3 km from the release site, exhibited social behavior, and have begun to pair up and excavate nest cavities. Preliminary data suggests reintroduced nuthatches have a 6-month survival rate of 0.68 without accounting for possible emigration. Nest searches and nest-success monitoring are currently active. Reintroduction methods and post-release monitoring efforts will be replicated for the translocation of an additional 50 individuals in fall 2021.

Urbanization influences Wood Thrush abundance and nest success: A 25-year before-and-after study in 70 forest fragments

Karl T. Heide, Lyle E. Friesen, Virgil E. Martin, Edward D. Cheskey, Michael D. Cadman, and D. Ryan Norris

Presenting author: **Karl Heide**, University of Guelph, kheide@uoguelph.ca

Anthropogenic disturbances have resulted in the loss of nearly three billion North American birds over the past fifty years and a key contributor to these declines may be urbanization. While previous research has shown negative correlations between the amount of built-up land and the abundance and reproductive success of forest-breeding birds, most studies have been conducted along urban-rural gradients at a single point in time. Far fewer have compared population metrics at the same breeding sites before and after development of the surrounding landscape. The Wood Thrush (*Hylocichla mustelina*) is a steeply declining migratory songbird that breeds in temperate deciduous forest and winters in Central America. During the 1990's, Wood Thrush abundance and nest success data were collected in over 100 forest fragments across Waterloo Region, Ontario, Canada. Some of these fragments have since been surrounded by urbanization while others have remained rural. During the 2020 and 2021 breeding seasons, we re-assessed Wood Thrush abundance and nest success at 70 of these sites by replicating point-count and nest monitoring protocols used in the past. Our results suggest that Wood Thrush have (1) ceased to breed at more than half the sites they once occupied, (2) declined most steeply in areas with recent development in the surrounding landscape, and (3) experienced an increase in nest success that has been strongest at sites without development. Our findings provide rare before-and-after evidence that urbanization near breeding habitat may be contributing to a regional decline of a migratory songbird, as well as impeding the potential for reproductive output to improve in response to lower population densities.

Landscape structure and habitat change affects the abundance and distribution of wintering Neotropical migratory shorebirds

John A. Herbert, David Mizrahi, Grant Gunn, R.I.G. Morrison, R.K. Ross, and Caz M. Taylor

Presenting author: **John Herbert**, Tulane University, jherber4@tulane.edu

Coastal wetlands are inherently dynamic and therefore a need exists to understand how long-term coastal habitat change affects wildlife populations. The coastal mudflats of the Guiana coast in South America support millions of wintering Nearctic-Neotropical migratory shorebirds, yet little is known how the coastal dynamics affect these shorebird population declines. We investigated the coastal habitat change on the Guiana coast from 1984-2017 and the spatio-temporal distributions of wintering Semipalmated Sandpipers (*Calidris pusilla*) and yellowlegs (*Tringa* sp.) using remotely sensed data and repeated aerial surveys. The area of tidal mudflats and coastal wetlands decreased during the 1990s into the early 2000s, while forest land cover increased. Tidal mudflats followed a long-term cyclical dynamic and increased in the 2010s, but coastal wetlands continued to decrease. The populations of both Semipalmated Sandpipers and yellowlegs decreased by over 80% from 1982 to 2017. The spatio-temporal distributions of mud and wetlands were positively associated with the distribution of the winter shorebird populations. The models found correlation of habitat change and the overall declines of these populations. Our study found that the dynamic habitat of the Guiana coast did affect the spatio-temporal distributions of shorebirds in the winter, but we conclude that other events during the annual cycle are more likely to be responsible for overall population declines.

Irruption of White-breasted Nuthatches when mast yields are low in the northeast

Paul H. Heveran, Andrew Dreelin, Erica H. Dunn, Derek Potter, Andra Florea, and Joseph P. Gyekis
Presenting author: **Paul Heveran**, DeSales University, birdmeister.paul@gmail.com

White-breasted Nuthatch (*Sitta carolinensis*) is generally considered a resident species, with local juvenile dispersal as the main source of movement in the species. Historically, local and sporadic instances of irruptive behavior have been reported. We used community science and long-term migration monitoring data to show that some White-breasted Nuthatches in northeastern North America show a biennial, region-wide pattern of irruption. White-breasted Nuthatch migration monitoring data came from three major migration count sites: Long Point Bird Observatory, Hawk Mountain Sanctuary, and Cape May Bird Observatory. We found that abundance at these sites was most strongly correlated with numbers of three classic irruptive songbird species: Red-breasted Nuthatch, Purple Finch, and Pine Siskin. Fall migrant abundance surges of White-breasted Nuthatches coincided with low mast yields in a wide variety of plant species across southern and central Ontario. These findings suggest links among mast production and fall irruptions that are regionally synchronized and oscillate in a biennial pattern. Facultative migration in the species has been largely overlooked in the past because migrant nuthatches are difficult to notice amid resident populations. We suggest closer study of widespread species with potential for facultative movements will yield valuable insight into migratory ecology.

Working hard or hardly working: A review of diurnal and nocturnal activity budgets suggests inactivity is a common behavior in free-living birds

Brett L. Hodinka and Tony D. Williams
Presenting author: **Brett Hodinka**, Simon Fraser University, bhodinka@sfu.ca

How hard do free-living animals truly work? There are several reviews linking metabolic rate, as a measure of workload, to performance and survival across a range of taxa. However, these studies have focused on resting metabolic rate (RMR) and basal metabolic rate (BMR), thus ignoring the behavioral component of daily activities responsible for generating most of the energy expenditure of free-living animals. While RMR and BMR are traditionally used as proxies for daily energy expenditure (DEE), costs should be activity driven; so incorporating behavior into our understanding of variation in DEE and metabolic scope, which do incorporate putative costs of activity, will be valuable. Therefore, we asked how common is inactivity (e.g., rest, sleep) in the diurnal and nocturnal time budgets of free-living birds? In a Web of Science literature search—using key phrases, 'time-activity budgets,' 'birds,' and 'activity patterns'—we compiled 150 peer-reviewed papers on 230 avian species and extracted diurnal and nocturnal activity data, including time spent engaging in several common behaviors. Preliminary results suggest inactivity is a common behavior across the annual cycle and at different life-stages: birds spend approximately 37.0% of daylight hours and 42.8% of nighttime hours inactive. The highest percentage of inactivity occurred during pre-breeding (43.9%) and molt (43.5%) and lowest, but still high inactivity, during non-breeding (37.7%) and breeding (32.5%). We will explore sources of variation in this 'ecology of inactivity' and integrate activity-specific metabolic rate estimates with daily activity budgets to investigate the degree to which low-cost behaviors influence commonly held estimates of metabolic scope.

Levels of predation at two Leach's Storm Petrel (*Hydrobates leucorhous*) breeding colonies

Rielle Hoeg, Dave Shutler, and Ingrid L. Pollet
Presenting author: **Dave Shutler**, Acadia University, dave.shutler@acadiau.ca

Seabirds are declining worldwide, and predation by introduced and endemic species is one threat that affects many of them. Leach's Storm Petrel (*Hydrobates leucorhous*, hereafter LHSP) populations are declining in a number of locations for reasons that are likely multicausal, and perhaps local or regional, but relative contributions of individual causes are poorly understood. To help understand causes, we quantified predation at two Nova Scotian LHSP breeding colonies that differ in predator management: no management occurs on Bon Portage (BP) Island, whereas management is used on Country Island (CI). Transects were monitored for evidence of predation approximately biweekly on BP and CI in 2018 and 2019, during May–October on BP and May–July on CI. We did not have data on predator densities, but in both colonies, predator density would have been very location-specific. Evidence, such as LHSP carcasses, feather piles, dug up nest burrows, and gull and owl pellets, was removed or destroyed during each visit. Predation of eggs and nestlings was scarcely detected. Similarly, adult predation on CI was seldom detected. We estimated that 4,000 individuals were depredated on BP in each year of this study. Approximately 42% of predation events were ascribed to gulls and 10% to owls; 48% of remains could not confidently be ascribed to a particular predator. We do not know how general these rates will be because of differences among colonies in predator communities. In any case, LHSP are listed as 'Vulnerable' globally, and although up to a 5% annual loss of adults may be sustainable for a healthy population, such losses may exacerbate population declines if other factors are additive.

Rethinking invasion theory and practice: A case study in the European Starling (*Sturnus vulgaris*)

Natalie R. Hofmeister

Presenting author: **Natalie Hofmeister**, Cornell University, nrh44@cornell.edu

Debates around the goals of invasion biology surface every few years, but most invasion biologists ask how 'invasive alien species' upset ecological balance and harm native species. Invasion success depends on both favorable external conditions and intrinsic characteristics (e.g., genetics or physiology) suited to those conditions. The European Starling was introduced to Australia and North America by acclimatization societies in the 19th century. Given that starlings invade most non-native areas with help from humans, it is remarkable that some now view management of invasive species as a nativist, xenophobic, and/or futile effort to control the inevitable spread of species. No matter one's perspective, scientific knowledge and power determines the future of an invasive species, and the value-based claims embedded in invasion biology may guide scientific methods and interpretation. Using the starling as a case study, I will suggest how invasion biologists might engage debates around the goals and assumptions of invasion theory and practice even in interpreting genomic surveys. Both methodological limitations and cultural biases may encourage invasion biologists like myself to separate our interpretations of demographic shifts and localized selection. This talk will reflect on my own genomic work to understand starlings' invasion success, and suggest adjustments to how biologists measure and interpret invasion success. I argue that reconsidering what counts as an intrinsic and extrinsic driver of invasion success produces more thoughtful and just science, refining scientific methods and engaging with social implications of invasion biology.

Genetic constraint on song learning ability in songbirds

Daniel M. Hooper, Cécile Issard, and Sarah M. N. Woolley

Presenting author: **Daniel Hooper**, Columbia University, danielmhooper@gmail.com

The songs of oscine songbirds have classically been used to examine the behavioral, neural, and genetic mechanisms responsible for vocal learning. In songbirds, song learning is achieved through auditory and vocal motor processes that integrate early life experience with a genetically-determined neural circuitry. A young songbird is tasked with the challenge of accurately and selectively learning the songs of its own species; species boundaries and its own reproductive fitness depends on it. Empirical work shows however that 1) erroneous learning from other species is common in nature but 2) that many species of songbird possess a learning preference for the songs of their own species. To what extent the seemingly open-ended nature of song learning is under genetic constraint remains an open question. Here we examine evidence of genetic constraint on song learning fidelity in three closely-related species of Estrildid finch (family Estrildidae) and their F1 hybrid offspring. We compare differences between groups in the acoustic features (syllables) and the temporal patterns (syntax) of their songs. We use this multi-species cross-foster tutoring and hybridization scheme to try and disentangle the respective limits to song learning and production brought about by a bird's early learning experience and their genetic ancestry.

Near-term ecological forecasting for dynamic aeroconservation of migratory birds

Kyle G. Horton, Benjamin M. Van Doren, Heidi J. Albers, Andrew Farnsworth, and Daniel Sheldon

Presenting author: **Kyle Horton**, Colorado State University, kyle.horton@colostate.edu

Near-term ecological forecasting has potential to mitigate the negative impacts of human modifications on wildlife by directing efficient dynamic conservation action through relevant and timely predictions. We use the North American avian migration system to highlight ecological forecasting applications for aeroconservation. We use millions of observations from 143 weather surveillance radars to construct and evaluate a migration forecasting system for nocturnal bird migration over the contiguous United States. We identified the number of nights of mitigation action required to reduce risk to 50% of avian migrants passing a given area in spring and autumn based on dynamic forecasts of migration activity. We also investigated an alternative approach, employing a fixed conservation strategy using time windows that historically capture 50% of migratory passage. In practice, during both spring and autumn, dynamic forecasts required fewer action nights compared to fixed window selection at all locations (spring: mean of 7.3 more alert days; fall: mean of 12.8 more alert days). This pattern resulted in part from the pulsed nature of bird migration captured in the radar data, where the majority (53.4%) of birds move on 10% of a migration season's nights. Our results highlight the benefits of near-term ecological forecasting and the potential advantages of dynamic mitigation strategies over static ones, especially in the face of increasing risks to migrating birds from light pollution, wind energy, and collisions with structures.

Effects of experimental malaria infection on migration of Yellow-rumped Warblers (*Setophaga coronata*)

Rebecca Howe, Chris Guglielmo, Leticia de Souza Soares, Yolanda Morbey, and Elizabeth MacDougall-Shackleton

Presenting author: **Rebecca Howe**, University of Western Ontario, rhowe6@uwo.ca

Whether and how avian malaria affects bird migration, particularly during stopover (an important step in migration where birds spend most of their migratory period), has received much attention, but little experimental study. Forty Yellow-rumped Warblers (*Setophaga coronata*) were captured during fall migration at the Bruce Peninsula Bird Observatory and transported 300 km south to the Advanced Facility for Avian Research in London, Ontario, Canada. Twenty-five birds were experimentally inoculated with avian malaria (*Plasmodium cathemerium*) while fifteen birds were inoculated with uninfected blood as a control. All birds were fitted with radio-transmitters and kept in conditions similar to a migratory stopover before being released an additional 100 km south at Long Point, Ontario to continue their migration. Activity was measured in captivity using radio signal strength variability and birds were radio-tracked after release using handheld radio-telemetry and the Motus Wildlife Tracking System. Six of the treatment birds (24%) developed *P. cathemerium* infections after inoculation (Successful) but did not have statistically different captive activity levels from birds that were inoculated but did not develop infections (Unsuccessful) or Control birds. Stopover duration (time to departure after release) was not significantly different between groups. This research addresses the migratory implications of exposure to and infection with a common bloodborne pathogen, suggesting that birds do not alter their migratory strategies in response to infection.

Does ecological specificity impact differentiation across a barrier? Insights from an avian pine-oak assemblage

Jack P. Hruska and Joseph D. Manthey

Presenting author: **Jack Hruska**, Texas Tech University, jackphruska@gmail.com

Comparative phylogeography has emphasized the incorporation of species-specific traits when testing hypotheses about diversification across a shared biogeographic barrier. However, most studies to date have focused on a narrow subset of species-specific traits, largely assessing the impact of morphology, often used as a proxy for dispersal capacity, on diversification. We incorporate a rarely used phenotype, ecological specificity on a habitat type, and ask whether the degree of specificity predicts patterns of demography and genetic diversity across a barrier. We evaluate the demography and genetic diversity of populations of two pine-oak specialists, the Azure-crowned Hummingbird and Acorn Woodpecker, and two pine-oak generalists, the Gray-crowned Yellowthroat and House Wren, all of which span a biogeographic barrier in northern Central America. We predicted that pine-oak specialists, in accordance with the specialist-generalist variance hypothesis, will show more genetic structure and have demographic histories that are concordant. We used whole-genome data from 20 individuals (5 per species) of populations spanning this barrier and evaluated patterns of genetic diversity (FST, heterozygosity), population structure, and demographic and divergence history. Population structure was evaluated using the clustering program STRUCTURE, historical demography was evaluated using the coalescent program MSMC2 and divergence history was assessed using the Bayesian program ecoevolity. We find that ecological specificity is not predictive of genetic structure and variation. However, we find that populations of specialists have more similar demographic and divergence histories, while those of specialists are idiosyncratic.

Early environment and condition dependence in a lifelong sexual signal: Gene expression and melanin color in Barn Swallows

Amanda K. Hund, Sheela P. Turbek, Rebecca J. Safran, and Scott A. Taylor
Presenting author: **Amanda Hund**, University of Minnesota, ahund@umn.edu

The condition dependence of sexual traits is hypothesized to maintain signal honesty. Melanin-based sexual traits, however, are thought to be mostly under genetic control and often lack condition dependence when they are expressed in adults. One explanation is that condition dependence for some melanin traits is limited to certain time periods, such as early development. In North American Barn Swallows, *Hirundo rustica* erythrogaster, melanin breast plumage is sexually selected, yet color changes little within individual males as adults, despite annual molting of feathers. Yet heritability studies find that a large fraction of variation in color can be attributed to the developmental environment. To better understand the gene by environment interactions that generate this pattern, we cross-fostered eggs and collected data on nest environment, maternal investment in egg composition and incubation, as well as nestling condition and physiology. We then collected developing feather quills from nestlings for RNA analysis and compared gene expression profiles with the color of emerged feathers when nestlings fledged. From these data, we identify how gene expression and environmental variation during development shape melanin color expression. This work provides new insight into the condition-dependence of melanin traits during development, and what females gain by using melanin-based signals during mate choice.

National population trends of Blackpoll Warbler: An integrated analysis of migration counts and stable isotopes

David T. Iles, Erica H. Dunn, Steven L. Van Wilgenburg, Kevin J. Kardynal, Danielle M. Ethier, Diana Stralberg, Péter Sólymos, Adam C. Smith, and Charles M. Francis
Presenting author: **David Iles**, Environment and Climate Change Canada, david.thomas.iles@gmail.com

Estimated declines of Blackpoll Warblers are among the steepest of any landbird over the last 50 years. However, the reliability of these trend estimates is uncertain, owing to the absence of Breeding Bird Survey coverage throughout the core of this species' boreal breeding range. Migration monitoring is a complementary method for evaluating population changes for species that are costly to monitor during the breeding season, such as Blackpoll Warbler. Here, we describe a novel Bayesian state-space population model that integrates stable isotopes (to determine breeding origins of migrations) and migration counts (to evaluate population trends) across an international network of monitoring stations. Simulations confirm the ability of our model to reliably estimate trends under realistic monitoring effort. Our empirical analysis of Blackpoll Warbler fall migration reveals a distinct longitudinal gradient in population trends; western populations have experienced 20-year increases in abundance, while eastern populations have likely experienced steep declines. Our analysis can be readily applied to other species that are detected at migration monitoring stations and is potentially capable of providing critical trend information for many boreal bird species.

Full annual cycle of a small migrating songbird species, the Golden-crowned Sparrow, tracked with GPS

Autumn R. Iverson, Renée L. Cormier, and Diana L. Humple
Presenting author: **Autumn Iverson**, University of California Davis, ariverson@ucdavis.edu

The importance of understanding the full annual cycle has been increasingly recognized, especially for migratory birds as details of migration are not well understood for many species. Migrating songbirds in North America have shown sharp declines and knowledge of their migration has been limited by the ability to track them. We used miniaturized GPS technology that allows long-term tracking on small birds. Golden-crowned Sparrows (*Zonotrichia atricapilla*; GCSP) are just large enough for the smallest GPS tags currently available (~1g), making them one of the smallest species to be tracked with GPS. We deployed 50 GPS tags on GCSP over two years between two California sites: Point Reyes National Seashore on the coast and Davis in the Central Valley. Of these, 29 were recaptured (58%) after migration. Some tags were lost or malfunctioned, and in total 22 tags successfully recorded data. Birds traveled along primarily coastal routes to breeding grounds in Alaska, except for one bird that bred in British Columbia. Birds from the same wintering grounds bred in similar regions, but not at the same sites. Breeding home ranges and stopover locations were identified. Additionally, data from three individuals that were tagged in two consecutive years provided the first time to our knowledge that individual birds of this size have been tracked in multiple years with GPS. On average, birds traveled faster on spring migration (Davis: 28 days, ~120 km/day; Point Reyes: 33 days, ~123 km/day) than fall migration (Davis: 33 days, ~104 km/day; Point Reyes: 43 days, ~97 km/day) for up to >4000 km traveled on migration. This study provides previously unknown fine-scale details on the migration ecology for this species.

Body temperature and reproductive effort in a long-lived tropical songbird

Holly R. Jackson and Thomas E. Martin
Presenting author: **Holly Jackson**, University of Montana, hollyjackson595@gmail.com

High body temperatures resulting from activity and exposure to warm environmental temperatures are thought to constrain reproductive success in endotherms. However, support for heat constraints on reproduction have come from temperate endotherms that have high reproductive effort. Tropical endotherms provide an interesting contrast for the generality of such constraints. On the one hand, narrow thermal tolerances thought to be typical of tropical organisms may readily cause heat constraints for reproductive activity. On the other hand, the low reproductive effort of long-lived tropical species may not generate enough heat to create constraints. We sought to understand why body temperature (Tb) varies and how this variation influences constraints on reproductive effort in a long-lived breeding tropical songbird. We performed a feather-trimming experiment that increased heat dissipation to assess whether parental provisioning and brooding activity were constrained by the need to offload excess body heat. We found parent Tb increased with environmental temperature (Te), with adults becoming warmest during mid-day when Te was highest. Adults caring for older or more offspring reached higher Tbs, while birds that stayed on the nest longer to brood or incubate were able to cool more than those that left the nest sooner. Experimentally trimmed parents were cooler than untrimmed parents when caring for eggs, but not nestlings. Adult behavior data are nearly compiled and will be presented. Results from this study can provide critical insight into the generality of heat constraining reproductive effort in endotherms. Such constraints are becoming increasingly important to understand given climate warming.

Changes in forest structure and nesting behavior of Hawai'i 'elepaio over 25 years

Kelly A. Jaenecke and Paul C. Banko
Presenting author: **Kelly Jaenecke**, Hawaii Cooperative Studies Unit, kaj352@nau.edu

Long-term ecological studies are valuable for detecting changes over time. We compared forest composition and Hawai'i 'elepaio (*Chasiempis sandwichensis*) nesting behavior over a 25-year period in Hawai'i Volcanoes National Park (HAVO). Both forest composition and ʻelepaio nest tree characteristics changed over time, suggesting a response to habitat restoration efforts. In 1993–1994, Sarr et al. (1995) studied Hawai'i 'elepaio nest site selection, territory size, and forest structure in mesic montane forest recovering from ungulate damage along Mauna Loa Road in HAVO. We used similar methods at the same site in 2016 to compare nest site selection (tree species, tree and nest height) and map territories held by nesting pairs. In 2019, we repeated the same point-center-quarter method to quantify forest composition (tree density, relative abundance, height, and DBH). Twice as many nests were found in aʻaliʻi (*Dodonaea viscosa*) as in koa (*Acacia koa*) in both time periods. On average, Hawai'i 'elepaio territory size was 0.57 ha per pair in the earlier study, and 0.69 ha more recently. Our measurements suggested that heights of nests and nest trees were greater for aʻaliʻi and koa in the earlier study, but DBH of non-nest trees trended upward for both species over time. Overall tree density was 0.16 trees/m2 earlier and 0.26 trees/m2 later. Koa relative abundance was 0.53 trees/m2 earlier and 0.45 trees/m2 later, but aʻaliʻi remained constant at 0.47 trees/m2 over time. The relative abundance of mamane (Sophora chrysophylla) was not recorded earlier but was 0.08 trees/m2 in 2016. Our results suggest that changes in forest structure may affect nesting behavior, but in ways that are not necessarily simple or consistent.

How common ravens (*Corvus corax*) exploit anthropogenic food sources through time and space in a semi-transformed, alpine environment

Varalika Jain, Petra Sumasgutner, Susan J. Cunningham, Thomas Bugnyar, and Matthias C. Loretto
Presenting author: **Varalika Jain**, University of Cape Town, veera.jain@gmail.com

In human-transformed landscapes, the behaviourally flexible and adaptable common raven (*Corvus corax*) has thrived by exploiting anthropogenic food sources (AFSs), which are often more spatially concentrated, easily accessible, abundant and stable than natural ones. Consequently, raven population numbers have increased across their range, raising conservation concerns including increased predation on threatened species and human-wildlife conflict. Using data from a long-term GPS-tracking initiative in the Upper Austrian Alps, we investigated which AFSs were most extensively used by non-breeding ravens, and which factors predicted individual variation in their usage of AFSs. Individuals exhibited great variation in their movement patterns and AFS-use varied based on traits (i.e., age, origin and ranging behaviour), season and type of AFS. Juveniles, captive bred-released and local birds visited fewer AFSs than adults, wild-caught and vagrant birds, but did not have a lower probability of being at one at any given point in time, suggesting experience affects AFS-use. In winter, individuals visited the most sites, but also had the lowest probability of being at a specific site, indicative of high foraging competition under harsh environmental conditions. In spring, individuals visited many AFSs and had a high probability of being present at a specific site, perhaps due to decreased competition and increased food availability. From 44 AFSs, ravens had a higher probability of being present at game parks and refuse sites than huts, likely due to differences in resource quality, quantity and replenishing rate. Overall, strategies to manage ravens in this system should consider these differences and focus on controlling food supply at sites on a regional scale.

Foraging and aggression of non-breeding shorebirds on a habitat mosaic — Bulls Island, South Carolina

Ellen G. Jamieson, Felicia Sanders, and Erica Nol

Presenting author: **Ellen Jamieson**, Trent University, ellenjamieson@trentu.ca

Shorebirds who spend their non-breeding season in coastal environments are vulnerable to habitat loss and disruption in prey availability from rising sea levels and temperatures, frequent storms, and human development. We examined shorebird abundance and distribution on Bulls Island, South Carolina, a minimally disturbed barrier island on the mid-Atlantic coast of the United States, by conducting ground surveys during the non-breeding season in 2018 and 2019. We further investigated habitat use and foraging behavior of Dunlin (*Calidris alpina*), Sanderling (*Calidris alba*), Semipalmated Plovers (*Charadrius semipalmatus*), and Piping Plovers (*Charadrius melodus*), while also considering the effect of prey availability. We recorded 21 shorebird species on Bulls Island. Average survey counts were 1770 birds in 2018 and 1437 in 2019. Foraging behavior varied across available habitats and was associated with invertebrate availability and proximity of other foraging shorebirds. Invertebrate availability varied across habitats and exhibited seasonal increases. Despite some differences between species, foraging rate was highest in the marsh relict and mudflat, in March and April, and lowest at high tide. There was a higher incidence of competition in habitats with greater invertebrate availability and with higher densities of foraging birds. This study shows how shorebird foraging behavior can vary across habitats on unaltered beaches, which may provide a range of opportunities and niche partitioning of the shorebird community. Future research could examine potential consequences of habitat loss or homogenization of beach fronts and density-dependent processes on shorebird communities, foraging efficiency, and seasonal survival.

Smells like home: Bird-scented nests as a mechanism for olfactory homing in a burrow- nesting seabird

Sarah L. Jennings and Susan E. Ebeler

Presenting author: **Sarah Jennings**, University of California, Davis, slejennings@ucdavis.edu

Homing to and from a familiar site, such as a nest, is a common behavior in animals. Many species rely on chemical information to assist with homing, either in the form of environmental chemicals associated with a specific location or chemicals deposited in the environment by an individual or their conspecifics. While olfaction is an underappreciated sensory modality in birds, it may facilitate homing and nest recognition in a range of avian species. This is best studied in nocturnal burrow-nesting seabirds, which use their excellent sense of smell to locate their breeding colony and to identify their nest. We examined the chemical information present at a colony of Leach's storm-petrels (*Oceanodroma leucorhoa*) to determine whether environmental chemicals, bird-produced chemicals, or a combination of the two facilitate olfactory homing and nest recognition in this species. We characterized the chemical profiles associated with the colony landscape and the storm-petrels occupants using gas-chromatography mass-spectrometry. We found that the colony contains gradients of environmental odorants, which may aid homeward navigation. We also show that each storm-petrel burrow is uniquely scented with the odor of its occupants. Moreover, we found that mated pairs and their nest possess a common odor, which may reinforce olfactory nest recognition in this species. Our findings also have implications for avian communication as bird-scented nests may function to transfer information between conspecifics, analogous to scent marks in other taxonomic groups.

Morphological consequences of climate change for resident birds in intact Amazonia

Vitek Jirinec, Ryan C. Burner, Richard O. Bierregaard Jr., Angélica Hernández-Palma, Erik I. Johnson, Thomas E. Lovejoy, Luke L. Powell, Cameron L. Rutt, Jared D. Wolfe, and Philip C Stouffer
Presenting author: **Vitek Jirinec**, Louisiana State University, vjirin1@lsu.edu

Warming from climate change is expected to reduce body size of endotherms, but studies of temperate birds have produced equivocal results. We collected mass and wing measurements over four decades on an Amazonian bird community (n = 77 species) sampled in the understory of primary, continuous forest with little to no local disturbance. We found that, since 1966, mean precipitation increased by 13% in the wet season and fell by 15% in the dry season. In contrast, mean temperature increased linearly in both seasons, with temperatures increasing by 1.00 °C in the wet season and 1.65 °C in the dry season. These results represent climate change that overlaps spatiotemporally with bird morphometric data. Over the last 40 years, all 77 species showed lower mean mass—nearly half with 95% confidence. A third of species exhibited concomitant increases in wing length, driving a decrease in mass:wing ratios for 69% of species. Lower mass was associated with hotter, drier dry seasons. However, unlike for mass, long-term trends in wing and mass:wing ratios persisted after controlling for annual seasonal conditions. Both seasonal and long-term morphological shifts suggest response to climate change and highlight its pervasive consequences, even in the heart of the world's largest rainforest.

Slight differences, dramatic consequences: Contrasting patterns of sociality along an environmental gradient in two cooperatively breeding species

Allison E. Johnson, Joseph Welklin, Ian R. Hoppe, and Daizaburo Shizuka
Presenting author: **Allison Johnson**, University of Nebraska-Lincoln, aj.petrochelidon@gmail.com

Cooperative breeding in birds has been described as an adaptation to environmental conditions. Explanations for the presence of helpers at the nest have classically been organized into two categories; resource constraints hypotheses predict that cooperative breeding should occur in high-quality habitats, while social benefits hypotheses predict cooperative breeding should occur in low-quality environments. The extensive body of work on cooperative breeding birds has helped to reconcile these hypotheses, indicating that different costs and benefits accrued through sociality might promote social living in different species in different environments. However, little work has examined whether the interplay between social benefits and environment can explain social variation across ecological gradients within species. Using a combination of transect observations and eBird data, we examine social group size in two closely related species with different documented benefits to social living, the Superb Fairywren (*Malurus cyaneus*) and the Purple-backed Fairywren (*M. assimilis*). We show that these species exhibit opposing patterns of group size variation across the same ecological gradient, with Superb Fairywrens having the largest groups in wet, stable habitats and Purple-backed Fairywrens having the largest groups in dry, variable environments. These findings suggest the nuanced differences in the benefits of helping and dispersal behavior observed in these two species likely contribute to misaligned ecogeographic patterns of variation in group size across species, and suggest integration of ecogeographic studies within and between species can provide novel insight into social trait evolution.

Evidence of nomadic behavior in Black-billed and Yellow-billed Cuckoos and implications for conservation strategies

Claire Johnson and Thomas J. Benson
Presenting author: **Claire Johnson**, University of Illinois Urbana-Champaign, cjohnsn4@illinois.edu

Black-billed Cuckoos and Yellow-billed Cuckoos have experienced extensive range-wide population declines over the last several decades. However, as cuckoos are patchily distributed and hard-to-detect, their habitat requirements are poorly understood. Prior observations indicate these species may range widely both within and between breeding seasons, potentially contributing to low detection and weak habitat associations. We set out to examine habitat variables driving occupancy and movement dynamics at both temporal scales. We performed passive and call-broadcast surveys for cuckoos at 41 sites throughout northern Illinois in 2019 and 2020 and used a dynamic occupancy modelling framework to estimate occupancy, immigration, and emigration probability within and between seasons while also accounting for imperfect detection. We found strong support for wide-ranging movement both within and between seasons. Top habitat predictors of occupancy and movement dynamics also indicated

Black-billed Cuckoos use early successional habitat while Yellow-billed Cuckoos use older successional or forested habitat. However, while these species are associated with distinct habitat types, they were more likely to occur together at a site than alone in both survey years. This suggests a common factor plays a role in site level turnover, and due to these species' reliance on ephemeral insect abundance, we believe food availability may also contribute to movement dynamics. Evidence of wide-ranging movements also implies the need for coordinating management actions within a broader spatial context to allow these species to adjust to changes in ephemeral habitat availability and insect abundance.

The role of ecological divergence on time to sympatry in suboscine passerines

Oscar Johnson, Rob Barber, Gustavo A. Bravo, Santiago Claramunt, Elizabeth P. Derryberry, Michael G. Harvey, Rafael S. Marcondes, Marco A. Rego, Joseph A. Tobias, and Robb T. Brumfield.

Presenting author: **Oscar Johnson**, Louisiana State University, henicorhina@gmail.com

The transition to sympatry following allopatric speciation is an important step in the speciation process, because it allows for the buildup of alpha diversity. Sympatry after secondary contact is possible if reproductive barriers and ecological divergence have evolved sufficiently to allow both species to occur within a defined geographic region. Ecologically diverged sympatric species can be subdivided into those that have diverged in habitat (i.e. sympatry without syntopy) and those that have not (i.e. sympatry with syntopy). The latter group is predicted to have diverged in ecological traits that minimize competition, such as song, plumage color, morphometrics, behavior, or other life history traits. Here, we investigate which mode of ecological divergence evolves first using a species-level phylogeny of suboscines, and examine the rate of divergence in a suite of ecologically important traits. We assembled a database for all 1,323 suboscine passerines of song, plumage, morphometric, and life history traits, and calculated the degree of divergence in each trait for each pair of species. We calculated the degree of co-occurrence for pairs of species using published distributional information and community science databases. Preliminary analyses suggest that sympatry with syntopy evolves more rapidly than sympatry without syntopy, consistent with previous studies that found phylogenetic conservatism of habitat preference in birds.

A post-fledging perspective: Does parent-offspring conflict help mediate the age of fledging in songbirds?

Todd M. Jones, Jeffrey D. Brawn, Ian J. Ausprey, Andrew C. Vitz, Amanda D. Rodewald, Douglas W. Raybuck, Than J. Boves, Cameron J. Fiss, Darin J. McNeil, Scott H. Stoleson, Jeffery L. Larkin, W. Andrew Cox, Amy C. Schwarzer, Noah Horsley, Evalynn M. Trumbo, and Michael P. Ward

Presenting author: **Todd Jones**, University of Illinois at Urbana-Champaign, toddmj@illinois.edu

Songbird species show considerable variation in the age at which they fledge, but the reasons why remain unclear. The bulk of past research suggests that mortality risk plays a key role in driving variation in the age of fledging among species, but other factors are thought to mediate the process as well. For example, ecologists have long debated the role of parent-offspring conflict on the age of fledging—do parents manipulate offspring into fledging to optimize their own fitness or do offspring choose when to leave? To provide greater insight into this question, we compared nesting and post-fledging survival rates across 18 species from 8 studies in the continental USA. For the majority of species, we found that offspring leave relatively safe nesting environments for more dangerous post-fledging ones, resulting in so-called 'post-fledging bottlenecks'. This raises an important question: if offspring would benefit in terms of survival and development by staying in the nest longer, why then, do they fledge so early? Our findings suggest that parents manipulate offspring into fledging earlier for their own benefits (14% increase in brood survival), but at the cost of survival (13.6%) for each individual offspring. Additionally, benefits of earlier fledging were uneven across species and predicted the age of fledging among songbirds. Collectively, our results suggest that parent-offspring conflict and associated parental benefits explain variation in fledging age among songbird species and why post-fledging bottlenecks occur. Furthermore, our findings highlight important avenues of future research on aspects of fledging in songbirds and other avian taxa.

Variation in breeding timing and habitat drive age-specific reproductive success of the endangered Golden-cheeked Warbler (*Setophaga chrysoparia*)

Gabriella L. Jukkala, Jinelle H. Sperry, and Michael P. Ward

Presenting author: **Gabriella Jukkala**, University of Illinois, gjukkala@illinois.edu

Age-specific reproductive success has been well-documented across avian taxa. In passerines, the lowest success is typically observed in the first breeding season and is often attributed to young birds being less developed in the intrinsic and extrinsic qualities necessary to reproduce. However, the qualities that improve with age and their impact on reproductive performance vary among species, making it necessary to identify the proximate drivers of age-dependent success for individual species. We investigated age-specific reproductive success and its intrinsic and extrinsic drivers in the endangered Golden-cheeked Warbler (*Setophaga chrysoparia*) in central Texas, USA. We used a long-term demographic dataset (2000-2020, n=1060 nests) and habitat data collected in 2019-2020 to determine how nest survival, productivity, pairing success, clutch characteristics, and nest site selection vary between Second Year (SY) and After Second Year (ASY) males and relative to temporal and habitat factors. ASY males had higher nest survival and produced more fledglings overall than SY males. Pairing was strongly age-assortative and ASY pairs initiated their first clutches earlier in the season than SY pairs, but clutch sizes and productivity of successful nests did not differ. For both age classes, nest survival and productivity declined seasonally and with increasing oak basal area, but these factors especially affected SY males, which nested later and in greater oak cover. Our results indicate that both intrinsic and extrinsic factors result in reduced reproductive success for SY birds compared to ASY birds, suggesting that conservation measures aimed at improving nest survival for younger birds could contribute to population goals.

Great Lakes Basin avian biodiversity and changes in species-area relationships with watershed position

Adisa Julien and Stephanie Melles

Presenting author: **Adisa Julien**, Ryerson University, adisa.julien@ryerson.ca

Species-area relationships (SAR) that incorporate sampling effort are familiar models of how biodiversity could change when habitats are lost. In land-based systems, the consistent pattern of increased species richness with increasing area sampled is an ecological norm. In freshwater systems, fish species discharge relationships are analogous to species-area relationships in terrestrial systems, but the relationship between terrestrial species and discharge remains largely unexplored. We tested whether bird species-area relationships vary with watershed position, majority land cover class, and distance from rivers. Using data from the Ontario Breeding Bird Atlas (2001-2005), we created bird SARs to explore how increases in diversity with sampled area varies with watershed position on the Canadian side of the Great Lakes Basin (GLB). The mosaic landscape of the GLB was further summarized into six majority cover classes at varying spatial scales (i.e., within 15, 70 and 135 m). Using Generalized Linear Modeling we tease apart the relationships between variables to explore how watershed position affects our interpretation of species diversity in different habitats, including, forested, agricultural, undifferentiated greenspace, and urban land cover classes.

Reduced habitat suitability and landscape connectivity in a migratory divide

Hannah Justen, Julie Lee-Yaw, and Kira Delmore

Presenting author: **Hannah Justen**, Texas A&M University, hjusten@bio.tamu.edu

Migratory divides are hybrid zones between closely related populations that use different migratory routes. Hybrids in divides take intermediate routes and it has long been predicted that they will be inferior, bringing hybrids over terrain avoided by pure forms. We provide the first test of this prediction, combining ecological niche models and landscape connectivity analyses with empirical tracking data from a well-characterized divide between coastal and inland subspecies of Swainson's Thrushes. Our models predict lower habitat suitability in the intermediate area between the migratory ranges of pure birds and optimal migration routes that avoid this intermediate area. Furthermore, birds taking intermediate routes used stopover sites of lower predicted habitat suitability than birds migrating on either side of the divide and routes overlapped less with optimal paths. Our results support the prediction that intermediate routes of hybrids in migratory divides are ecologically inferior to those of parental forms. This finding suggests ecological differences are helping to maintain divides and could have broad implications, with divides shaping the distribution and maintenance of species boundaries globally and across many taxonomic groups.

Ecosystem restoration and partnerships: Reintroduction of Brown-headed Nuthatch (*Sitta pusilla*) to Missouri pine woodlands

Sarah W. Kendrick, Thomas W. Bonnot, Frank R. Thompson III, Kristen M. Heath-Acre, James A. Cox, and Brian K. Davidson

Presenting author: **Sarah Kendrick**, Missouri Department of Conservation, sarah.kendrick@mdc.mo.gov

Conservation partners from multiple agencies and non-governmental organizations recently planned and executed the return of Brown-headed Nuthatch (*Sitta pusilla*) to Missouri pine woodlands by translocating birds from Arkansas in August and September 2020, with a second translocation planned in fall 2021. Brown-headed Nuthatches were presumed extirpated in the early 1900s due to the near complete loss of Missouri's pine woodlands. Over 20 years of shortleaf-pine woodland management has occurred on the Mark Twain National Forest which was recently accelerated as part of the national Collaborative Forest Landscape Restoration Program. Given the success of pine woodland restoration, we began investigating the potential to restore a population of Brown-headed Nuthatch to this natural community. We assessed habitat suitability of Missouri's pine woodlands by fitting a habitat model using monitoring data from Arkansas and determined enough suitable habitat was present to support a population in Missouri. We also assessed population trends and abundance of the potential source population on Ouachita National Forest in Arkansas, determined birds were abundant, and identified potential trapping sites. We shared these results with diverse project partners at a 2019 meeting in Missouri and got support for moving forward with the reintroduction effort. Soon after, we received all necessary permits and permissions. In August and September 2020, in the middle of a pandemic, we successfully translocated 46 birds to Missouri.

Influenza prevalence in wild waterfowl inhabiting the continental United States throughout the annual cycle

Cody M. Kent, Jennifer M. Mullinax, Andrew M. Ramey, Jeffery D. Sullivan, and Diann J. Prosser

Presenting author: **Cody Kent**, University of Maryland, codymkent@gmail.com

Avian influenza poses risks to human health, agricultural production, and wildlife. Of particular interest is the risk of outbreaks at poultry farms from viruses introduced from wild waterfowl. Though it is generally recognized that influenza prevalence peaks in waterfowl in late summer through fall, temporal and spatial variation has not been fully characterized. Here, using two databases surveilling for influenza in wild birds, we applied a spatiotemporal Bayesian hierarchical model to explore patterns in influenza prevalence throughout the annual cycle and across the continental United States for 30 species of waterfowl. As sampling effort varied greatly by season for many species, we used correlated stratum-specific smoothing priors to allow species to vary independently while also providing reasonable predictions when data were limited. We confirmed peaks in influenza prevalence in late summer through fall for dabbling ducks in the genera *Anas* and *Spatula* as compared to other species, but not for *Mareca*. Many species exhibited a smaller peak in prevalence during the spring, possibly linked to staging or migration. Spatial trends appeared to be correlated with regional duck density, with the highest prevalence found across the upper Midwest during late summer and fall. We also found evidence for elevated levels of influenza prevalence in the Mississippi Alluvial Valley in late winter and early spring, possibly from either the high density of wintering ducks or the influx of migrants from the Neotropics. Our results suggest that spatiotemporal peaks in prevalence beyond autumn staging areas may play an important role in the maintenance of influenza viruses within the wild bird reservoir.

Community characteristics of forest understory birds along an elevational gradient in the Horn of Africa: A multi-year baseline

Kyle D. Kittelberger, Montague H.C. Neate-Clegg, Evan R. Buechley, and Çagan H. Sekercioglu

Presenting author: **Kyle Kittelberger**, University of Utah, kyle.kittelberger@utah.edu

Tropical mountains are global hotspots for birdlife. However, there is a dearth of baseline avifaunal data along elevational gradients, particularly in Africa, limiting our ability to observe and assess changes over time in tropical montane avian communities. In this study, we undertook a multi-year assessment of understory birds along a 1,750 m elevational gradient in an Afrotropical moist evergreen montane forest within Ethiopia's Bale Mountains. Analyzing 6 years of systematic bird-banding data from 5 sites, we describe the patterns of species richness, abundance, community composition, and demographic rates over space and time. We found bimodal patterns in observed and estimated species richness across the elevational gradient, although no sites reached asymptotic species richness throughout the study. Species turnover was high across the gradient, though forested sites at mid-elevations resembled each other in species composition. We found significant variation across sites in bird abundance in some of the dietary and habitat guilds. For the majority of analyzed species, capture rates did not change over time and there were no changes in species' mean elevations. Population growth rates, recruitment rates, and apparent survival rates averaged 1.02, 0.52, and 0.51 respectively, and there were no elevational patterns in demographic rates. This study establishes a multi-year baseline for Afrotropical birds along an elevational gradient in an under-studied international biodiversity hotspot. These data will be critical in assessing the long-term responses of tropical montane birdlife to climate change and habitat degradation.

Origins of harvested American Black Duck (*Anas rubripes*): Testing the flyover hypothesis

Jackson W. Kusack, Douglas C. Tozer, and Keith A. Hobson

Presenting author: **Jackson Kusack**, Western University, jkusack@uwo.ca

For harvested waterfowl, such as the American Black Duck (Anas rubripes), effective management requires detailed information on connectivity between breeding, wintering, and stopover sites. Within Canada, leg-band returns and stable isotopes show that hunters in Atlantic Canada are more likely to harvest black ducks produced locally compared to those harvested in Ontario and Quebec which likely originated in the boreal. For these northern black ducks, which migrate south later in the season, it is hypothesized that they are more likely to be harvested by American hunters (i.e., the 'flyover hypothesis'), but data are lacking. To test this, we used feather stable hydrogen isotopes (d2H) to infer natal/moult origin, utilizing continental trends in GNIP-based precipitation d2H. We collected feathers from wings submitted by hunters to the species composition and parts collection surveys and applied a likelihood-based assignment method of feather d2H to assign probable origin. Supporting the flyover hypothesis, black ducks harvested in Atlantic Canada showed a predominantly southern origin while those harvested in the US were primarily boreal produced. This research directly informs regulation and management decisions, promoting more effective conservation of American Black Ducks.

Population genetic differentiation and hybridization of Glaucous Gull (*Larus hyperboreus*)

Emma Lachance Linklater, Greg Robertson, Sarah Sonsthagen, Freydís Vigfúsdóttir, and Vicki Friesen

Presenting author: **Emma Lachance Linklater**, Queen's University, 13emll@queensu.ca

To effectively conserve Arctic species, genetically differentiated populations must be defined for genetic variation to be appropriately managed. This project examined population genetic differentiation in the Glaucous Gull (Larus hyperboreus) and assessed hybridization between Glaucous Gulls and three closely-related species. ddRAD sequencing was conducted on 62 Glaucous Gulls, 18 American Herring Gulls (*L. smithsonianus*), 6 European Herring Gulls (*L. argentatus*), and 15 Glaucous-winged Gulls (*L. glaucescens*). Molecular assignments and principal coordinates analysis suggested only weak population differentiation between sampled colonies of Glaucous Gull. Interspecific analyses showed that Glaucous Gull and Glaucous-winged Gull are genetically distinct species but that Glaucous Gull and the two species of Herring Gull are only weakly differentiated. Detailed information on population genetic structure and hybridization will help conservation practitioners effectively manage the long-term persistence of Glaucous Gull populations. Proactive management strategies for this species will benefit both Glaucous Gull and the entire Arctic ecosystem.

Enhancing tropical avian behavioral ecology via ddRAD-seq: Genetic mating system of the Black Catbird (*Melanoptila glabrirostris*) as a case study

Joshua B. LaPergola, Christina P. Riehl, Blanca Roldán-Clarà, Juan E. Martínez-Gómez, and Robert L. Curry

Presenting author: **Joshua LaPergola**, Princeton University, jlapblca@gmail.com

Avian behavioral ecology suffers from a temperate zone bias: most empirical work has involved species at northern temperate latitudes despite most avian diversity occurring in the tropics. In particular, the mating and social systems of tropical species remain poorly known, reducing the generalizability of comparative studies attempting to test broader theories. Robustly describing mating and social systems depends, in part, on the use of genetic resources for parentage assignment and quantifying the relatedness of group members. One means of addressing this bias is by

leveraging a next-generation sequencing technique, double-digestion restriction associated DNA sequencing (ddRAD-seq), to develop genetic resources for poorly studied and 'non-model' tropical species. We will present a case study from the Riehl lab to demonstrate the utility of ddRAD-seq to identify single nucleotide polymorphisms (SNPs) in poorly known tropical species. We characterize the genetic mating system of the Yucatán Peninsula endemic *Melanoptila glabrirostris* (Black Catbird) using samples collected over one decade ago from two populations, one continental and one insular. In this species, the use of SNP data permitted parentage analyses without the need for the expensive and time-intensive steps of microsatellite loci discovery. We advocate for the application of ddRAD-seq to the study of tropical avian behavioral ecology. The Riehl lab encourages tropical ornithologists with the necessary samples for parentage and/or relatedness analyses but lacking the institutional and/or genomic resources to contact us regarding the possibility of collaboration.

Call rate as an index of nest abundance and provisioning rates in wading bird colonies

Rachel C. Larson and Dale E. Gawlik

Presenting author: **Rachel Larson**, Florida Atlantic University, larsonr@fau.edu

Wading birds are often used as indicators of wetland quality due to their high trophic level positions and sensitivity to hydrologic conditions. However, traditional colony monitoring methods, such as nest counts, can be time-intensive, disruptive to nesting birds, and limited by colony accessibility. Our study aims to improve the efficiency of wading bird monitoring by using passive acoustic sampling to estimate colony nest abundances and provisioning rates, while identifying variables that affect call detection. We deployed autonomous recording units in colonies of Snowy Egrets (*Egretta thula*), Tricolored Herons (*E. tricolor*), and Great Egrets (*Ardea alba*) on Lake Okeechobee, Florida to detect chick begging calls and used automatic call recognition software to measure call rate and acoustic parameters. Generalized linear mixed models showed that call rates increased with daily nest abundance for all species. Snowy Egret and Tricolored Heron call rate was also dependent on the number of days since colony initiation, whereas Great Egret call detection increased with nest height and decreased with the density of vegetation surrounding nests. The timing of begging calls correlated with provisioning events ($P<0.01$, $R^2=0.45$), with begging occurring at higher amplitudes and faster rates during provisioning, compared to non-provisioning periods (ANOVA, $P<0.01$). We showed that wading bird nest abundances and provisioning rates can be estimated using passive acoustic sampling, reducing the need for manual colony surveys. These methods enable long-term monitoring of wading bird colony sizes and nesting trends, which are important measures of wetland restoration in south Florida and worldwide.

Repeated burning undermines the conservation value of restored cattle pastures in Guatemala for tropical resident birds

Anna Lello-Smith, Amanda D. Rodewald, Viviana Ruiz-Gutierrez, and Victor Hugo Ramos

Presenting author: **Anna Lello-Smith**, Cornell University, aml442@cornell.edu

Restoring degraded forest is a priority for global biodiversity conservation strategies. Forest restoration is critical in the face of threats to ecosystem resilience like drought and fire that are being exacerbated by climate change. Fire is emerging as a novel pressure in humid tropical systems due to increasing frequency and severity of droughts and to agricultural expansion into previously undisturbed forest. Repeated burning within restored tropical landscapes is an increasingly likely scenario that may undermine their conservation potential; yet we lack even a basic understanding of how recurrent fires impact the conservation value of second growth. We asked how repeated burning of naturally regenerating cattle pastures in Guatemala during the first decade of regrowth affects their use by resident forest-dependent and threatened bird species. To explore what drives use patterns of burned and unburned restored pastures, we asked how species' opportunistic use of restored pastures relates to the degree of vegetation succession at a local scale. We found that pastures have accrued value as habitat for forest birds during the first decade of regrowth, with 38 highly forest dependent species detected in decade-old pastures. Repeated burning has significantly reduced their conservation value: a majority of forest species used burned sites less than unburned sites or were excluded entirely from burned sites. By looking at underlying dynamic rates, we established that a potential mechanism through which burning excludes species from restored pastures is by impeding vegetation growth. The capacity of restored pastures to support threatened forest-dependent birds depends on effectively protecting restored areas from fire.

Do female-specific social interactions influence timing of egg-laying in European starlings?

Kathryn M. Leonard and Tony D. Williams

Presenting author: **Kathryn Leonard**, Simon Fraser University, kathryn_leonard@sfu.ca

Social factors are thought to be important 'supplemental cues' for timing of egg-laying in females, but most research has focused on the roles of male song and display. Although male and female vocalisations can have similar functions, the role of female communication in breeding phenology is still poorly understood. In theory, positive social interactions between females might arise if this provides information on environmental conditions, matching food availability with provisioning or via group foraging to locate food, and stimulation of ovarian development and reproductive behavior. Conversely, negative female social interactions (stress, territorial aggression, nest box takeovers) will likely disrupt social networks and breeding synchrony. We investigated how female-specific social interactions related to timing of laying in European Starlings (*Sturnus vulgaris*), highly social birds that exhibit semi-colonial living and synchronous breeding. First, we compared residual, temperature-independent variation in egg-laying date with annual variation in nearest neighbor distances and found no simple relationship between the two. To further explore this, we will use social network analysis including proximity to, and familiarity with, other females to determine if female social interactions explain residual variation in laying date at both the individual and population level. Second, we used an experimental approach with female-specific call playback from inside nest boxes during the pre-laying period. Our goal was to manipulate laying date by inducing positive social stimulation (advancing laying) or negative social stimulation (delaying laying date) focusing on female-female communication.

Estimating population trends of gulls and cormorants for coast-wide aerial imagery in Maine

Meredith A. Lewis, Logan R. Kline, Lauren Maher, Daniel J. Hayes, and Cynthia S. Loftin

Presenting author: **Meredith Lewis**, University of Maine, meredith.a.lewis@maine.edu

Long-term monitoring is integral to understanding avian population shifts and trends, gaining insight into large-scale patterns, and informing species and ecosystem management practices. However, financial costs combined with relative remoteness, number of colonies, and disturbance during surveys limit frequent surveys for many species. Aerial surveys are an important tool for surveying colonial seabird and wading bird species, as large areas can be covered in a short period of time while minimizing disturbance and imagery collected via planes provides a permanent record of survey. We used a multiple-observer approach to count nesting Herring Gulls (*Larus argentatus*), Great Black-backed Gulls (*Larus marinus*), and Double-crested Cormorants (*Phalacrocorax auritus*) in aerial imagery collected in 2019 of 274 islands off Maine's coast. We compared 2019 estimates to counts derived from coastal Maine imagery collected in 2008 and 2013, to evaluate change in nesting bird numbers and their distributions along the coast and within individual islands. Using cluster analyses, we tested whether or not islands in decline were more or less likely to occur close together and indicate regional patterns to population changes. Coast-wide trends varied by species, with Great Black-backed Gulls in particular experiencing declines on islands surveyed in 2013 and 2019 while other species remained stable between 2013 and 2019. Understanding seabird population trends and mechanisms contributing to changes in distributions and abundances is enhanced with data collected across temporal and spatial scales.

Origins and diversification of endemic birds in the Caatinga dry forest

Hevana Lima, Gustavo A. Bravo, Diego Astúa and Luciano N. Naka

Presenting author: **Hevana Lima**, Universidade Federal de Pernambuco, hevana.lima@ufpe.br

The increasing availability of genetic data and the genealogical relationships of species has allowed us to study, in unprecedented detail, the history of biomes and the biogeographical histories and affinities of its biotas. The Caatinga dry forest, in northeast Brazil, represents the largest and most biologically diverse patch of Seasonally Dry Tropical Forest in the Neotropics. Previously considered a species-poor domain, it presents a fairly rich avifauna, with more than 500 species, 10% of which are endemic. Preliminary data suggests that this endemic avifauna is formed by three groups of species, including: i) endemic species with sister species in different South American regions; ii) species that originated in adjacent ecosystems; and iii) species widely distributed in South America. In this study, we use 51 Caatinga avian endemic taxa to evaluate the origins of its avifauna. Our study aims to use ancestral habitats reconstruction and time-calibrated phylogenies to i) investigate the biogeographical origins of the Caatinga avifauna, and ii) understand the timing and diversification of its endemic avifauna. Preliminary analyses suggest a mixed origin of the Caatinga endemic avifauna. Most avian endemics are related to lineages from open habitats, such as other dry forests or savannas, but a number of species likely arrived from adjacent humid forests. Whereas we detected relatively old lineages that likely occupied these dry landscapes prior to the Pleistocene, other endemics seem to represent new arrivals from adjacent habitats. This study represents the first effort to describe the biogeographical origins of the Caatinga avifauna, thus providing new data about the history of this endemic and threatened domain.

Searching for gold: Using a novel land cover classification to identify multi-scale drivers of site occupancy by a flagship species for early-successional habitat conservation

Baron H. Lin and Lesley P. Bulluck

Presenting author: **Baron Lin**, Virginia Commonwealth University, linb5@vcu.edu

Understanding habitat selection at multiple scales is an important step in guiding conservation programs and reversing species declines. This, however, is difficult for species that occupy early-successional habitats (ESH) due to a lack of accurate representation of shrub cover in publicly available land cover data. The Golden-winged Warbler (*Vermivora chrysoptera*; GWWA) is a threatened species of conservation concern and a flagship for ESH conservation. We used a novel, LIDAR-derived land cover classification that accurately identifies shrubs at a fine resolution (1m) to investigate how habitat composition and configuration influence GWWA site occupancy. We aggregated this same land cover data to 30m resolution to compare with models using commonly used spatial data. Our results confirm that elevation, forest and shrub cover are important habitat features for GWWA and suggest specific extents and optimum amounts that these cover types should be maintained: elevation 900-1000m, 10-15% shrub cover at 500m, and 50-60% forest cover at 1km. Models using coarse resolution data identified the same cover types and extents as important for GWWA. Our results can improve communication and implementation of GWWA conservation efforts. Widely available land cover data that includes an accurate representation of shrub cover are needed to extend these results across the Appalachian region. We projected GWWA occupancy probability across a five-county region to plan future surveys and recruitment for ESH management. Our study highlights the importance of understanding habitat selection at multiple scales and integrating freely available spatial data to guide conservation programs.

What is trend?

William A. Link and John R. Sauer

Presenting author: **William Link**, Eastern Ecological Science Center, wlink@usgs.gov

The purpose of the North American Breeding Bird Survey (BBS) as stated at its USGS website is 'to monitor the status and trends of North American bird population.' The survey has been the only source of reliable data for >500 species over the last 55 years. During this time, a variety of statistical analyses have been developed for the data, controlling for irrelevant sources of variation and accounting for spatial variation in population change. Still, there remains a surprising amount of controversy about estimating trend. Analysts desire estimates that are precise, and stable (i.e. not excessively influenced by year-to-year variation in population size). These are reasonable goals, but sometimes achieved by changing the quantity estimated, or by using models which ignore components of variation. We argue for the necessity of a formal definition of trend, as a function of model parameters. Reasonable definitions leading to stable estimates are possible, but it is crucial that there be a proper accounting of all sources of variation in reporting precision. We compare candidate definitions of trend and illustrate the effects of ignoring sources of variation in estimation.

Anthropogenic effects on European Starling nestlings’ growth and cholesterol

Courtney L. Linkus and Sarah Guindre-Parker

Presenting author: **Courtney Linkous**, Kennesaw State University, clinkou1@students.kennesaw.edu

Urbanization is a leading threat to wildlife, and anthropogenic habitat modifications may alter the resources that wildlife have access to. For example, urban centers may provide animals with abundant anthropogenic food sources, though these foods may be lower in quality than natural food sources. The impact of living in urban centers on the growth, physiology and behavior of birds remains equivocal and can vary across species. We studied two free-living populations of European Starlings (*Sturnus vulgaris*); one at an urban farm (high human density) and one at a rural farm (low human density) in Kennesaw, GA. We monitored 100 nestlings across both sites and collected weight measurements to generate growth curves and collected blood samples to measure nestling cholesterol (index of dietary fats) and triglycerides (index of fattening rate). We hypothesized that urban nestlings will have slower growth rates, lower triglycerides, and higher cholesterol than rural nestlings. We also hypothesized that chick growth rates will be correlated to their behavioral coping style, where slower growing nestlings will have slower breathing rates and reduced struggling rates when handled. Future research will increase sampling at additional sites along an urban to rural gradient, examine parental behavior in selecting food sources for their nestlings, and assess additional indices of health and fitness.

Exploring how different suites of nest predators (birds, mammals, and reptiles) respond to the playback of the begging calls of bird nestlings

Shilong Liu, Qiao Xie, Eben Goodale, and Aiwu Jiang

Presenting author: **Shilong Liu**, College of Forestry, 15090690023@163.com

Begging brings both benefits and costs for nestling birds: it can indicate their needs to their parents, but it can also be a cue used by predators to find the nest. The costs, like many variables related to nest predation, can be specific to what kinds of predators are present and their auditory capabilities. These costs and benefits could also be affected by human noise, as noise could disrupt communication to parents and eavesdropping by predators, although human-produced noise might be easily ignored if predators can hear high-frequency components of the begging. We studied nest predation on a generalist bird, the Red-whiskered Bulbul *Pycnonotus jocosus*, in a subtropical rainforest in which there was a variety of nest predators, including birds, mammals and reptiles. At natural and, later, artificial nests (total n = 160), we broadcast recordings of begging nestling, with and without traffic noise, at two volumes. We hypothesized that playback would increase predation relative to a silent control, and that traffic noise would decrease predation, as the begging signal was degraded, but could be ignored by mammalian predators with sensitive high-frequency hearing. We found that predation was lowest for the control treatment, and lower for treatments mixed with traffic noise than for those without traffic noise. However, this result was primarily produced by mammals avoiding all trials with traffic noise. Our results demonstrate the human-associated noise can disturb nest predators and change patterns of nest predation. Further studies, especially in areas where human noise is more common than our rainforest study site, should look further at how noise can affect begging behavior.

Hybridization dynamics of a manakin hybrid zone

Kira M. Long, Michael J. Braun, and Jeffery D. Brawn

Presenting author: **Kira Long**, University of Illinois Urbana-Champaign, kiralong778@gmail.com

Hybrid zones form when individuals from two species interbreed. How and why these zones change over space and time is an important and complex issue in evolutionary biology. Hybrid zones are dynamic systems that can move across a landscape or remain spatially stable, depending on the fitness of hybrid individuals. The Golden-collared Manakin (*Manacus vitellinus*) and the White-collared Manakin (*Manacus candei*) hybridize in western Panama where females preferentially select males with yellow throats. Despite this female preference, the yellow-throated phenotype has not spread to fixation across the hybrid zone. First, we confirm through the use of population genomics and Restriction site-Associated DNA sequencing (RADseq) that this hybrid zone is spatially stable and not continuing to introgress like predicted. Then, we investigate if the stability of this hybrid zone is caused by hybrids having lower fitness than the parental species. Thus, we test two avenues that may cause lower hybrid fitness: higher rates of avian malaria infections and lower egg hatching success in hybrid populations. Preliminary data on avian malaria infection rates finds only a single individual with an infection, indicating that avian malaria may not play an important role in selecting against hybrids to maintain hybrid zone stability. However, we find that hybrid nests have lower hatching rates than non-hybrid nests, possibly indicating hybrid inviability and lowering recruitment in the hybrid populations.

The evolutionary history of the troupials unveils hidden diversity within the *Icterus icterus* species complex

Layse A. S Lucas, Maria W. Pil, Leilton W. Luna, and Luciano N. Naka

Presenting author: **Layse Lucas**, Federal University of Pernambuco, laysealbuquerque00@gmail.com

Delimiting species boundaries and understanding the distribution of independent evolutionary units within a species complex can shed light on the evolutionary history of such groups and help unravel the history of the landscape. With that in mind, we studied the genetic structure of the Neotropical troupials, a species complex formed by three allopatric species that inhabit mostly dry Neotropical lowlands. We used DNA sequencing of Ultraconserved elements (UCE) and the mitogenome to sample 21 individuals within the complex across its range. Based on 1,500 loci, and ~1,000 independent SNPs, we identified four distinct genomic clusters, including i) *Icterus icterus*, from the W Colombian/Venezuelan lowlands; ii) *Icterus I. c. croconotus*, from western South American dry lowlands and part of W Amazonia; iii) *Icterus I. jamacaii*, from NE Brazil; and iv) an isolated population of *I. c. croconotus*, from the Roraima-Rupununi savannas. The mitogenomic tree indicated a fifth distinct group, separating the two forms of I. croconotus in western South American dry lowlands. These two subspecies, *I. c. croconotus* and *I. c. strictifrons*, diverged from another more recently, during the Late Pleistocene (~0.5-0.7 Ma). Our results provide evidence for the existence of an undescribed lineage from the Roraima-Rupununi savannas, which diverged during the middle Pleistocene (~0.9-1.48 Ma) and indicate genetic introgression between *I. jamacaii* and *I. c. croconotus* in central Brazil. Despite lack of morphometric divergence (little or no differences in body size) the four genetic clusters identified are readily diagnosable and seem to represent independent evolutionary lineages.

The hormone ghrelin affects migratory behaviour in a migratory wood-warbler

Sara Lupi, Yolanda E. Morbey, Hiroyuki Kaiya, Scott A. MacDougall-Shackleton, Leonida Fusani, and Christopher G. Guglielmo

Presenting author: **Sara Lupi**, Western University, slupi@uwo.ca

Every year, migratory birds fly long distances between breeding and wintering grounds. During migratory flights, birds almost exclusively utilize fat stores as energy source. In most cases, birds combine non-stop flights and stopovers, i.e. breaks to rest and refuel. There is growing evidence that metabolic hormones play a key role in modulating the physiological and behavioural adjustments required to switch between stopover and flight phase. We recently showed that the hormone ghrelin, mostly produced by the gastrointestinal tract, is involved in the regulation of migratory disposition and food intake in captive birds during spring stopover. Here, we present our new field radio-tracking experiment where we studied the effects of experimentally elevated ghrelin on migratory behavior in free-living yellow-rumped warblers (*Setophaga coronata coronata*) caught during spring stopover on the north shore of Lake Erie (Ontario, Canada). Specifically, we tracked birds using the Motus Wildlife Tracking System to investigate the role of acylated and unacylated ghrelin in regulating stopover behavior, departure decisions and post-departure migratory behavior. The results show that injections of both acylated and unacylated ghrelin stimulated a quick movement away from the field site, indicating that the hormone ghrelin triggers a behavioural switch between stopover and flight phases of migration. The hormone manipulation caused short-term effects on departure decisions and did not affect the overall rate of migration. This study provides experimental evidence for a key role of ghrelin during spring migration and shows that hormones regulating peripheral metabolism mediate departure decisions centrally in migratory birds.

Limited evidence for distance decay across terra firme rainforest in Amazonia

Cameron Rutt, Justin Cooper, Phil Stouffer, Mario Cohn-Haft, Christian Andretti, Claudeir Vargas, Thiago Costa, and David Luther

Presenting author: **David Luther**, George Mason University, dluther@gmu.edu

The Amazon rainforest is known for its high levels of biodiversity, but the relative contributions of alpha and beta diversity are not known. Distance decay is often cited as a major contributor to species turnover, but most studies span environmental gradients (habitat, soil, elevation, precipitation, temperature), and little is known about the relative contribution of beta diversity to overall species diversity within the same environment. The combination of high species richness, large tracts of continuous terra firme forest, and minimal changes in elevation, precipitation, and temperature make the Amazon an ideal location to test the influence of distance decay on species diversity and turnover. Here, we assess the effect of distance decay on avian communities of the central Amazon of Brazil and predict that distance decay is not an important driver of species turnover within the same habitat. We used avian point count data from pairs of 100-ha plots in three disparate locations to sample 600 ha of primary forest. In all, 216 points were sampled throughout the wet and dry season. We detected an average of 59 species per point, 190 species per plot, and 213 per site. Dissimilarity indices showed minimal differences between plots, but dissimilarity did increase slightly with distance. The difference was primarily driven by a reduction in the number of vulnerable understory insectivores at the most disturbed site, suggesting that disturbance and not distance is at play across wide swaths of forest within the same Amazonian interfluve.

The cost of reproduction does not affect moult feather quality in Thick-billed Murres (*Uria lomvia*)

Emily C. MacDonald, Allison Patterson, and Kyle H. Elliott

Presenting author: **Emily MacDonald**, McGill University, emily.macdonald2@mail.mcgill.ca

Seasonal environments constrain time and energy for migratory birds that schedule reproduction and moult in sequence. Accordingly, increased investment into reproduction can restrict post-breeding moult, resulting in a speedy moult in of poorer quality feathers. The reduced quality in feathers can hinder an individual's fitness until the following moult, and lower future reproductive success. We studied feather quality as a reproductive cost in Thick-billed Murres (*Uria lomvia*), an Arctic seabird with high energetic flight costs and a restricted, synchronous moult period performed post-reproduction. Further, we wish to test if effects are sex-dependent, due to male-only post-fledgling care. Thick-billed Murre feathers were most variable in feather area, feather length and barb density. Experimental variation in reproductive costs (wing-clipping, forced relaying) did not influence the feather traits, nor the rate of feather moult. The average speed of feather growth was conserved around 1.21 mm/day, although average days taken to grow one feather (~66 days) was variable. Additionally, feather traits significantly differed between the sexes. Thus, Thick-billed Murre sexes may experience disparate selection pressures for feather traits. Also, Thick-billed Murres, like other long-lived birds, appear to favour future reproductive success and survival over current reproduction activities so that feather quality was maintained regardless of time and energy spent in breeding.

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grinnell: A package for dispersal simulations across geography and time to estimate calibration areas for niche and distribution models

Fernando Machado-Stredel, Marlon E. Cobos, and A. Townsend Peterson

Presenting author: **Fernando Machado-Stredel**, University of Kansas, fmachadostredel@ku.edu

Ecological niche models (ENM) and species distribution models (SDM) are tools that have seen considerable use and improvement during the last twenty years, especially in ornithology. The choice of calibration areas is known to have strong effects on model outcomes, as well as on their transferability to different climates. These models should be calibrated within areas that the species has explored via dispersal, including suitable and unsuitable regions, during its recent history (the accessible area M). Here, we provide simulations for estimating such areas within a new R package (grinnell). We consider dispersal, colonization, and extinction processes in current and past climates using four *Aphelocoma* jay species (Corvidae). We explore different parameters of our simulations and compared them to current approaches for accessible area selection (buffers, hulls, ecoregions) in terms of model performance and risks of extrapolation using the Maxent algorithm and mobility-oriented parity analyses, respectively. Our simulations generated accessible areas consistent with the *Aphelocoma* species distributions, including a moderate proportion of unsuitable regions for calibration. In general, simulated areas were better suited in finding regions of extrapolation and in producing Maxent models with low omission. Important factors to consider within our simulations were layer resolution, dispersal features, and inclusion of changing climatic conditions (glacial-interglacial cycles). This work represents the first simulation-based method for selecting calibration areas for ENM and SDM, offering an approach to estimate accessible areas of species while considering changing patterns of climatic suitability during recent history.

Morphology of migration: Associations between wing shape, bill morphology, and migration in kingbirds (*Tyrannus*)

Maggie MacPherson, Alex Jahn, and Nicholas Mason

Presenting author: **Maggie MacPherson**, Louisiana State University, maggie.macpherson@gmail.com

Morphology is closely linked to locomotion and diet in birds, such as in species that undertake long-distance migrations, where wings are under selection to maximize mobility and minimize energy expenditure. Migratory behaviors also interact with diet, such that migratory taxa tend to be dietary generalists, while sedentary taxa tend to be dietary specialists. Despite a hypothesized link between migration status and morphology, phylogenetic comparative studies have yielded conflicting findings. In this study, we tested for evolutionary associations between migratory status and limb and bill morphology across kingbirds (*Tyrannus* spp.), a pan-American genus of birds with migratory, partially migratory, and sedentary taxa. We found that migratory kingbirds had longer and more pointed wings, in agreement with expectations of selection favoring improved aerodynamics for long-distance migration. We also found an association between migratory status and bill shape, such that migratory taxa had wider and deeper bills and sedentary taxa had longer bills. However, there was no difference in levels of intraspecific morphological variation among migrants, partial migrants, and residents, suggesting that dietary specialization has evolved independently of migration strategy. Evolutionary links between migration, diet, and morphology in kingbirds further strengthen ecomorphological associations that underlie long-distance seasonal movements in animals.

Guidance for analytical methods to cumulative effects assessment for terrestrial bird species

C. Lisa Mahon and Shawna Pelech

Presenting author: **C. Lisa Mahon**, Canadian Wildlife Service & Environment and Climate Change Canada, Lisa.Mahon@canada.ca

Landscapes in Canada are undergoing rapid change due to resource, land use, and climate stressors. Understanding the cumulative effects of these stressors is challenging because of ecosystem complexity, stressor variability, and species response to individual or multiple stressors. A challenge within the field of cumulative effects assessment (CEA) is guidance that describes and evaluates analytical methods. In this review we discuss four broad categories of methods with current or potential use for project-based and effects-based CEA for species in terrestrial systems: (1) qualitative review, (2) habitat supply models, (3) empirical species-stressor models, and (4) decision support models. We describe each method and provide examples, highlight advantages and limitations, identify how methods address key science-based CEA questions, and provide direction on when and why to use specific CEA methods. Empirical species-stressor models and decision support models are analytical approaches that provide answers to many science-based CEA questions including how multiple stressors combine to affect individual species. We provide recommendations for using one or more methods as complementary building blocks to fill data gaps, improve understanding and communication, engage diverse partner groups, and increase the quality and credibility of the CEA. Our review supports a move toward regional scale, effects-based CEA where partner collaboration to design, implement, and analyze comprehensive assessments of multiple stressors will (1) expand our knowledge of terrestrial species response to stressors, and (2) inform best management for resource industries and conservation actions for land managers.

Sex-specific contributions to nest building in birds

Mark C. Mainwaring, Jeno Nagy, and Mark E. Hauber

Presenting author: **Mark Hauber**, University of Illinois at Urbana-Champaign, mhauber@illinois.edu

The causes and consequences of interspecific variation in sex-specific contributions to animal parental care are relatively well understood during pregnancy or incubation and during offspring provisioning, but comparative patterns of sex-biased investment during nest-, den-, or other shelter-building have been almost completely overlooked. This is surprising because birthing shelters' protective properties have important fitness consequences for both parents and offspring. Here, we address this gap in our knowledge by testing predictions concerning sex-specific contributions to avian nest building in more than 500 species of Western Palearctic birds in relation to the time available to breed and sex-specific reproductive effort, whilst also examining correlates with nesting site and nest structure. Using multivariate phylogenetic comparative and path analysis approaches, we found that, opposite to what had been predicted, species in which females build nests alone have shorter breeding seasons and breed at higher latitudes. In addition, species in which females lay larger clutch sizes and incubate eggs alone are more likely to have nests built by females alone, again countering predictions that reproductive contributions are not traded-off between the sexes. Finally, however, sex-specific nest building contributions were predictably related to nest site and structure, as species in which females built nests alone were more likely to have open cup nests relative to enclosed, domed nests of species in which both parents build. Our study generates several new questions for experimental research into the adaptive dynamics of sex-specific contributions prior or at the onset of breeding and parental care.

Comparative genomic analysis of population history and inbreeding in the Neotropical falcons *Falco deiroleucus* and *Falco rufigularis*

Audrey M. Martin, Robert B. Berry, Paige A. Byerly, Jaime Gasca-Pineda, Jeff A. Johnson, and Matt D. Carling

Presenting author: **Audrey Martin**, University of Wyoming, amarti83@uwyo.edu

Genomic resources are increasingly valuable in assessing population characteristics of non-model species, particularly where sister taxa present different demographic histories for comparison. We evaluated population trends and inbreeding status in the Orange-breasted Falcon and their more common sister species, the Bat Falcon. For both species, we aligned our samples to the Peregrine Falcon reference genome and generated approximately 6.5 million single nucleotide polymorphisms per individual. Our initial metrics suggested low genetic diversity within Orange-breasted Falcons and the possibility of population structure within Bat Falcons. Individual inbreeding coefficients indicated that all sampled Orange-breasted Falcons were significantly more inbred than the sampled Bat Falcons, with values similar to those seen in island-mainland species pairs. The distribution of runs of homozygosity showed variation suggesting persistent low population size and the possibility of bottlenecks in Orange-breasted Falcons—contrasting with consistently larger populations in the genetic history of the Bat Falcon. Taken together, inbreeding coefficients and runs of homozygosity highlight differences in the historical demography of these species.

To the beat of their own drum: Temporal and environmental factors influence drumming display activity in the Ruffed Grouse (*Bonasa umbellus*)

Michelle J. Martin, Eloïse C. Déaux, and Andrew N. Iwaniuk

Presenting author: **Michelle Martin**, University of Lethbridge, martinm@uleth.ca

The Ruffed Grouse is a widespread gamebird species that is heavily managed in many regions, but its cryptic coloration and behavior makes it difficult to census. Frequently, Ruffed Grouse population estimates are therefore derived from counting the number of males actively drumming: a wingbeating display that generates a loud, low frequency sound. While drumming surveys have been used for over 60 years, the timing of surveys relative to drumming activity and the effects of weather on drumming activity remain unclear. We analyzed drumming activity across several years and used generalized additive mixed models to determine the relationship between drumming activity and time of day, date, temperature, and precipitation. The dates of peak activity were similar across years, despite inter-annual variation in weather patterns. The hourly drumming activity model yielded two activity peaks: a large peak at 1.5 hours before dawn and a second, smaller peak 1 hour before sunset. Temperature range formed a u-shaped curve relative to drumming activity with low and high temperature extremes associated with increased activity. Minimum temperature was not associated with changes in drumming activity, but drumming activity increased gradually with higher daily maximum temperatures. These results suggest large temperature increases and decreases throughout the day and high daily maximum temperatures increase daily drumming activity rates. In addition, morning drumming surveys should begin 2 hours prior to sunrise, and evening drumming surveys could be a useful addition to accurately census Ruffed Grouse populations.

Rate of avian telomere shortening across DNA sample types

Noelle M. Mason

Presenting author: **Noelle Mason**, Colorado State University, masonnm@colostate.edu

Avian conservation research is becoming increasingly more important as our environment continues to change due to anthropogenic impacts. As environmental changes accumulate, quantifying the extent that human-caused climate stressors are affecting bird populations remains a priority, and populations found to be most vulnerable to these stressors can be given conservation priority. Genomic tools, such as measuring the rate at which telomeres shorten, can be used to assess vulnerability in bird populations. Telomeres cap the ends of the chromosomes, thereby protecting the genome and shortening with cell division. Recent research suggests shortening can be accelerated by environmental stress. A blood or feather sample is needed to extract DNA for telomere measurement. Comparison between the rate of telomere shortening in blood versus body and tail feathers will be significant in informing the methods of researchers using telomeres as a measure of stress in avian life history. I hypothesize that the rate of telomere shortening in feathers will reflect the telomere length at the time the feather was molted because tissue gets trapped in the shaft of the feather, while blood will offer a real-time snapshot of an individual bird’s telomere length. Results from this study will help to inform researchers' decisions in the field when it comes to collection of blood and/or feathers for use in avian life history research.

Sex-linked inversion underlies divergence between the Golden-crowned Sparrow (*Zonotrichia atricapilla*) and the White-crowned Sparrow (*Zonotrichia leucophrys*)

Quinn McCallum, Kenneth Askelson, Finola Fogarty, Libby Natola, Ellen Nikselski, Andrew Huang, and Darren Irwin
Presenting author: **Quinn McCallum**, University of British Columbia, quinn.a.mccallum@gmail.com

Sympatric species pairs provide an opportunity to study the late stages of genomic divergence during speciation and may allow for the identification of genomic regions underlying reproductive isolation. The Golden-crowned Sparrow (*Zonotrichia atricapilla*) and the White-crowned Sparrow (*Zonotrichia leucophrys*) are sister species that are broadly sympatric in western North America and largely reproductively isolated despite recent mitochondrial introgression. We used a genotyping-by-sequencing approach to investigate genomic divergence between these species, as well as between two hybridizing subspecies of *Z. leucophrys*, across more than 45,000 single nucleotide polymorphisms. The two species showed strong clustering, high levels of relative differentiation, and genomic patterns consistent with a history of divergence in allopatry. The two *Z. leucophrys* subspecies showed moderate clustering and levels of relative differentiation, and patterns consistent with a history of divergence in allopatry and recurrent selection between ancestral and daughter populations. In all comparisons, macrochromosomes showed increased divergence and reduced nucleotide diversity relative to microchromosomes. Furthermore, patterns of relative and absolute divergence and linkage disequilibrium strongly suggest a large inversion on the Z chromosome, with inversion haplotypes that segregate between *Z. atricapilla* and *Z. leucophrys*. This putative inversion has implications for reproductive isolation between these species and adds to a growing body of evidence for the importance of inversions and the Z chromosome in speciation.

Multi-scale drivers of restoration outcomes for an imperiled songbird

Darin J. McNeil, Amanda D. Rodewald, Viviana Ruiz-Gutierrez, Kirsten E. Johnson, Matt Strimas-Mackey, Sharon Petzinger, Orin J. Robinson, Gerardo E. Soto, Andre A. Dhondt, and Jeffery L. Larkin
Presenting author: **Darin McNeil**, University of North Carolina - Wilmington, darin.j.mcneil@gmail.com

Habitat restoration is a cornerstone of conservation, particularly for habitat-limited species. However, restoration efforts are seldom rigorously monitored at meaningful spatial scales. Poor understanding of how species respond to habitat restoration programs limits conservation efficacy for habitat-restricted species like the Golden-winged Warbler (*Vermivora chrysoptera*, GWWA). We provide one of the first concerted assessments of a national conservation program aimed at restoring songbird habitat across its breeding range. We studied GWWA response to forest habitat restoration across two broad regions with opposing population trajectories and assessed factors driving species use of restored habitats across multiple spatial scales. From 2015-17, we conducted 1,145 (n = 457 locations) and 519 point counts (n = 215 locations) across the Appalachian Mountains and Great Lakes (respectively) within restored habitats. In the Appalachian Mountains, occupancy (ψ) varied with longitude, elevation, forest type, and number of growing seasons. Detections were restricted to areas within close proximity to population centers (usually < 24 km) in the Appalachian Mountains, where GWWAs are rare ($\psi = 0.22$, 95%CI: 0.20 – 0.25), but not in the Great Lakes, where GWWAs remain common ($\psi = 0.87$, 95%CI: 0.84 – 0.90). Our study suggests that, even when best management practices are carefully implemented, restoration outcomes vary within/across regions and with multi-scale habitat attributes. Although assessments of concerted habitat restoration efforts remain uncommon, our study demonstrates the value of monitoring data in the adaptive management process for imperiled species.

Nestling provisioning of Gray Catbirds: Do males play a larger role than expected?

Joseph J. Medica and Lucas J. Redmond
Presenting author: **Lucas Redmond**, Penn State Schuylkill, ljr5322@psu.edu

Birds typically provide intensive parental care to their young throughout the nest cycle in the form of incubation, brooding, provisioning of young, and nest sanitation. These behaviors represent trade-offs because although they represent a cost to the parents in both time and energy, they increase the chance of successful reproduction. Although some of these behaviors may be exhibited by both sexes (e.g., nest sanitation, provisioning), some behaviors may only be performed by one of the sexes (e.g., only females incubate eggs in many species). Furthermore, some of these behaviors may be primarily performed by one sex and not the other. For example, females of some species may provision offspring at higher rates than the males they are paired with. We studied parental care in a population of Gray Catbirds in southeastern Pennsylvania from 2017 to 2019. Catbirds are socially monogamous, multiple-brooded, open-cup nesting songbirds that exhibit biparental care. We used remotely placed cameras at catbird nests to record and quantify parental behavior during the nestling phase of the nest cycle. Based on patterns observed in other songbirds, we predicted that female catbirds would feed at higher rates than males. We found no difference in feeding rates among years, and within years, feeding rates did not change across the breeding season. Male catbirds fed their young at rates approximately 1.5 times greater than the females they were paired with. Further, male feeding rates were positively related with nest success. Our results suggest that male catbirds have a much larger role in parental care than was previously anticipated, as well as an integral role in determining the fate of their young.

Parental behavior differs by moonlight intensity in a diurnal bird species

Colleen R. Miller, Conor C. Taff, Jennifer J. Uehling, and Maren N. Vitousek
Presenting author: **Colleen Miller**, Cornell University, ccm246@cornell.edu

Light cycles control the timing of daily activities that can affect the success of an organism. With a continually brighter night sky, it is necessary to understand how organisms exhibit light-based biological rhythms. While rhythms entrained to solar cycles are well understood in diurnal animals, we know less about how lunar light affects most organisms. Some research has found lunar rhythms influence diurnal vertebrates' life history, including aspects of reproduction such as hormone circulation and mating success. However, little is known about the impacts of lunar light on parental care, a key element of reproductive performance. We studied the relationship between moonlight intensity and the timing of offspring provisioning in Tree Swallows (*Tachycineta bicolor*) using radio frequency identification networks over several breeding seasons. We predicted that activity would begin earlier on days following brighter nights in a pattern following the lunar cycle. We found strong relationships between moonlight intensity and onset of daily activity, after controlling for dawn time. Parents began provisioning young earlier on days following full moons. Provisioning also began earlier on days with earlier dawns; however, on nights when the moon was brightest, dawn timing was unrelated to the onset of activity. This study exemplifies the importance of understanding how moonlight influences reproductive behavior, and potentially fitness, of breeding birds during an era of unprecedented light pollution in natural areas.

Thermal ecology of Trumpeter Swan incubation

Paige C. Miller and David J. Delehanty
Presenting author: **Paige Miller**, Idaho State University, millpai2@isu.edu

Trumpeter Swans underwent severe population decline during Euro-American settlement of North America and since have been rescued from extinction by nearly a century of conservation management. Trumpeter Swans now number approximately 63,000 wild adults, providing substantial opportunity for scientific investigation. Trumpeter Swans construct unusually large nest mounds in northern marshes that are characterized by large daily and seasonal thermal fluctuation, where they incubate clutches averaging 3-6 eggs. We measured Trumpeter Swan incubation behavior and nest thermal characteristics at active nests within the Red Rock Lakes National Wildlife Refuge in southwestern Montana, USA, the location where the last wild breeding population of Trumpeter Swans within the contiguous United States was preserved. We deployed thermal data loggers within nest mounds, as well as around-the-clock video monitoring devices and a remote weather monitoring station to measure swan incubation and nest temperatures in relation to the external environment. Our measurements revealed fine-scale association of incubation behavior relative to the thermal environment. Swans were acutely sensitive to their thermal environment, incubating persistently at night and other cool periods, and preventing eggs from overheating during incubation recesses which they performed during warm daylight hours. The nest mound acted as a large thermal body moderating thermal flux at nests. Nest mounds were cooler than environmental temperature during the hot periods and warmer than environmental temperature during cool periods. Regardless of environmental temperature, during active incubation, swans maintained an egg incubation temperature of 35.70 ± 0.27 °C.

Understanding the effects of sampling on inferred population histories in two North American songbirds

Nicholas R. Minor and Matthew D. Carling
Presenting author: **Nicholas Minor**, University of Wyoming, nminor1@uwyo.edu

Estimates of population size, both current and into the past, are crucial for understanding population-level microevolution as well as species-level macroevolution. A variety of approaches exist for inferring histories of population growth, contraction, and stasis with genomic data. However, still little is known about how sub-optimal sampling or population structure, common characteristics of non-model organism datasets, produce consistent forms of bias in demographic inferences. Here, using a genomic dataset of Indigo (*Passerina cyanea*) and Lazuli Buntings (*P. amoena*), we explore the effects of sampling and population structure on population histories inferred with multiple methods. We compare full-dataset histories, pruned-dataset histories, and simulation-based histories to disentangle the artefacts of sub-optimal sampling and population structure on demographic inferences. Our findings show that sub-optimal sampling and population structure can distort histories of population size change in consistent ways. Moreover, we find that simulation offers a promising means of accounting for these biases in demographic inference studies.

Songbird parents modify their behavior in open but not enclosed nests to mitigate energetic effects of rain on nestlings

Adam E. Mitchell, Blair O. Wolf, and Thomas E. Martin

Presenting author: **Adam Mitchell**, University of Montana, adamemitchell@gmail.com

Understanding the ecological effects of rainfall will be critical for predicting how species might respond to climate change, given expected shifts in frequency and magnitude of rain events. Rainfall creates challenges for breeding animals through physiological costs of heat loss on developing young, but parents in altricial species can potentially ameliorate such costs through shifts in behavior. In addition, most birds build nests to raise young, and nest structure may influence the impact of rain on offspring and parents. Studies of the effects of rain on offspring and parents have generally been correlational, which do not separate direct physiological effects of rain from indirect effects of other ecological factors that shift with rain (e.g., food, predation). At a field site in Malaysian Borneo, we experimentally simulated rain above the nests of five songbird species using the two most common nest types, cup-shaped and enclosed. We measured parental brooding and food provisioning behaviors, and offspring energy expenditure in response to simulated rain. Experimental rain caused parents in open, but not enclosed nests to increase their brooding time, which resulted in no effect of rain on energy expenditure of nestlings in either nest type. Offspring provisioning rate also did not change with experimental rain. These results illustrate an important influence of nest type on parental activity during rainfall. Our results also suggest that substantial shifts in parental behavior should be expected in open-nesting songbird species in regions that are predicted to experience heavier rainfall as climates change.

Occupancy probability of bird species in relation to the structural vegetation complexity of a coffee landscape in Costa Rica

Ingrid Molina-Mora, Viviana Ruiz-Gutierrez, Luis Sandoval, and Alejandro Quesada

Presenting author: **Ingrid Molina-Mora**, Universidad de Costa Rica, molinam.ingrid@gmail.com

Productive landscapes in tropical areas are dominated by monocultures, which reduce habitat heterogeneity for birds and consequently species richness. However, coffee producers often plant trees to provide shade to the crops and divide the plots within a farm. Those trees could increase structural complexity in the farms and at landscape level, and provide food, refuge, and a corridor to birds and other animals. We conducted 160 bird point counts twice a year for two years (2019-2020) at San Ramon coffee region, Costa Rica, to identify thresholds where the occupancy probability of bird species increases as a function of the contribution of shaded-coffee farms to structural vegetation complexity of the landscape. In each point count we estimate the structural vegetation complexity using Light Detection and Ranging (LIDAR) images. In each point we measured canopy height, coverage, and the above ground biomass. Preliminary results show that species such as the Streaked-headed Woodcreeper and the Long-tailed Manakin are more likely to occur with increased above-ground biomass in coffee plantations. Meanwhile, the Orange-billed Nightingale-thrush occurs more in habitats with high structural complexity (e.g. forest remnants). In general we found that species occurrence is positively related to vegetation complexity. Therefore, management practices such as increasing overall tree cover and restoring riparian forests corridors through the coffee farms and other monocultures will benefit bird species occurrence and conservation.

Evolutionary implications of genetic variation around Amazonian rivers: A case study of the Blue-crowned Manakin

Andre E. Moncrieff, Brant C. Faircloth, and Robb T. Brumfield

Presenting author: **Andre Moncrieff**, Louisiana State University, amoncr2@lsu.edu

Studies of Amazonian understory forest birds, including manakins (Pipridae), have established that rivers play an important role in defining geographic distributions of species as well as forming the boundaries of intraspecific genetic clusters. A few recent studies have also documented the presence of hybridization between river-delimited taxa across narrow headwater regions. To further explore patterns of genetic variation across the Amazon Basin, we examined the Blue-crowned Manakin, which is found throughout the western Amazon Basin, Chocó forests west of the Andes, and in Panama and Costa Rica. Previous phylogeographic studies of this species using mitochondrial and nuclear loci demonstrated deep divergence between populations separated by large Amazonian rivers. However, limited sampling around the headwater regions of these rivers and limited resolution among markers made it difficult to assess the occurrence of hybridization between cryptic populations. Thus, we included extensive sampling from headwater regions, including from our recent fieldwork along the upper Ucayali River, to further explore fine-scale patterns of gene flow around river barriers. We obtained next-generation sequence data (RADcap) for 764 Blue-crowned Manakins and found that broad geographic patterns of genetic structure indicate that major Amazonian rivers are important dispersal barriers. We also found that genetic divergence in headwater regions was reduced, highlighting the importance of these regions as genetic conduits between otherwise isolated populations.

Parallel genomic signatures of local adaptation across a continental-scale environmental gradient in two North American woodpeckers

Lucas R. Moreira and Brian T. Smith

Presenting author: **Lucas Rocha Moreira**, Columbia University, lr2767@columbia.edu

Genomic parallelism provides a window into the role of constraint and stochasticity in adaptive evolution. While most studies investigating parallel local adaptation focus on closely related lineages distributed across sharp environmental contrasts, little is known about adaptation across continental scales. We investigated the genomic architecture of parallel local adaptation in Downy (*Dryobates pubescens*) and Hairy Woodpecker (*D. villosus*), two ecologically similar species that co-occur across a complex environmental gradient in North America. Downy and Hairy Woodpecker exhibit remarkably parallel patterns of geographic variation in plumage and body size and have experienced very similar biotic and abiotic selective pressures throughout their evolutionary history. We compared signatures of selection across several populations of Downy and Hairy Woodpecker using whole-genome resequencing data and uncovered limited evidence of genomic parallelism at the SNP level, but an exceedingly large overlap in candidate genes. We found a number of SNPs showing correlation with temperature and precipitation, most of which were in non-coding regions, suggesting a dominant role of regulatory change in adaptation. Population comparisons detected several candidate genes exhibiting evidence of selective sweeps, including genes related to immune response, nutrition, respiration, and embryonic development. We also identified potential candidates associated with key phenotypic traits in Downy and Hairy Woodpecker, such as differences in body size and plumage variation. Our results provide compelling evidence of the significant role of genomic parallelism in local adaptation across a broad-scale environmental gradient.

Color insights in mixed-species flocks from Costa Rican highlands: Revisiting the social mimicry hypothesis

Pablo Muñoz, Pierre-Paul Bitton, and Luis Sandoval

Presenting author: **Pablo Muñoz**, Universidad de Costa Rica, pablomgl94@gmail.com

The factors that contribute to the cohesion of mixed-species flocks are not yet well understood. An evolutionary approach might give us insights into how species-specific traits could be selected at higher levels, such as in the context of a mixed flock. Moynihan's social mimicry hypothesis states that birds in mixed-species flocks may present a convergence in coloration, which will make them less conspicuous compared to other bird species, as a way to compensate for the flock's acoustic conspicuousness. Our objective was to test Moynihan's social mimicry hypothesis in mixed-species flocks from Costa Rican highlands by comparing species that form mixed-species flocks to those that do not. We measured plumage reflectance in 20 flocking and 20 non-flocking species that are phylogenetically close to the flocking species. In each species we measured 8 body parts (crown, nape, mantle, rump, breast, sides, and dorsal side of external rectrices and primaries) of 6 adult individuals (3 per sex) using reflectance spectrophotometry. We used a tetrahedral colorspace visual model and alpha shapes to calculate color volumes and compare plumage patches among species. The color spectral data evidence suggests that social mimicry has not been an important selective factor in promoting formation of mixed-species flocks in Costa Rican highlands, because the color volumes occupied by flocking species is not different from that of the non-flocking species. Both the diverse evolutionary origins of Costa Rica's endemic species and their isolation have likely been important in the composition of mixed-species flocks, rather than social mimicry.

What do we really know about the water repellency of feathers?

Frank M. Muzio and Margaret A. Rubega
Presenting author: **Frank Muzio**, University of Connecticut, frank.muzio@uconn.edu

Feathers are unique and complex structures that serve a variety of vital functions, including flight, thermoregulation, visual displays, crypsis, and water repellency. Among these, water repellency is crucial; its loss can eliminate the other functions. Past research has attempted to explain how exactly feathers repel water, but important gaps in our understanding of what is happening at the water-feather interface remain. Some previous research places emphasis on the size of, and distance between, barbs. Surprisingly, the role of barbules in water repellency has been almost completely ignored, and direct measures of the wettability of feathers has been largely overlooked in favor of theoretical indices using barb characteristics alone. Barbules make up a large portion of the surface area of a feather and play a key role in keeping the barbs and the overall feather structure intact. Past work has demonstrated that barbule morphology can vary drastically, even across different feathers of an individual, and we present evidence that these differences play a part in a feather's ability to shed water. We suggest that a reevaluation of our understanding of how feathers keep a bird dry, and how and why their water repellency varies with phylogeny, life history, and habitat, is necessary.

Demographic inference of commensal swallows in southeast Asia and Oceania

Brian M. Myers, Amanda K. Hund, Nicholas Friedman, Dency Gawin, Farah Modh-Taib, Robert Ong, Chamalka Da Silva, Sampath Seneviratne, Thilini Thakshila, and Elizabeth S.C. Scordato
Presenting author: **Brian Myers**, California State Polytechnic University, Pomona, bmyers62622@gmail.com

Species are sensitive to environmental and anthropogenic phenomena that lead to fluctuations in population sizes and shape evolutionary events over time. Such phenomena have likely shaped the evolutionary history and current distribution of the Pacific Swallow (*Hirundo tahitica*), a dispersive, commensal species that nests on human-made structures such as buildings and bridges. There are seven subspecies of Pacific Swallow distributed across island and coastal mainland Southeast Asia and Oceania. Here, we perform demographic analyses using whole-genome sequence data on island populations of five subspecies of the Pacific Swallow from Borneo, Fiji, Malaysia, Japan, Sri Lanka, and Papua New Guinea. The islands in the Pacific Swallow range vary in size and proximity to one another, enabling investigation of how different populations have responded over time to an ever-changing environment. Specifically, we focus on changes in population size in response to rapid anthropogenic development over the last several thousand years, and investigate potential drift, gene flow, and divergence events between these populations. If human development has created new nesting habitat for Pacific Swallows, we should observe an increase in population sizes of Pacific Swallows that correlates with increases in human development over time.

Ecomorphological data suggests variable impacts of adaptation, allometric change, and historical contingency during the evolution of skull shape in shorebirds (order: Charadriiformes)

Rossy N. Natale and Graham J. Slater
Presenting author: **Rossy Natale**, University of Chicago, rnatale@uchicago.edu

The diverse morphologies of the avian skull have been heavily studied, but little consensus has been reached in regards to why various factors such as adaptation for foraging ecology, allometric change (shape change due to body size changes), and historical contingency are recovered as more significant predictors of skull shape in certain clades. By collecting comprehensive, three-dimensional morphological data from the skulls of 270 species or ecologically diverse shorebirds (order: Charadriiformes) and investigating this data in light of body size, phylogeny, and ecology, we demonstrated that while there is a significant relationship between skull shape and foraging ecology, it is weaker than may be expected and that this relationship is heavily influenced by phylogenetic history. Additionally, we found that in certain Charadriiform families, allometric change explained a large proportion of the variation in shape within these families, but that allometric influence was weak when we analyzed the size and shape relationship at the level of the whole order. This work highlights both the need to investigate various influences on skull shape when exploring the evolutionary history of any given avian clade and stresses the insights that can be gained from analyzing data at both relatively broad and fine taxonomic scales.

Variable hybridization across multiple Red-breasted x Red-naped Sapsucker hybrid zones

Libby Natola, Shawn M. Billerman, Sampath S. Seneviratne, Matthew D. Carling, and Darren E. Irwin
Presenting author: **Libby Natola**, University of British Columbia, natola@zoology.ubc.ca

Evolutionary biologists study natural hybrid zones because they allow us to quantify the degree of reproductive isolation between species and identify the different barriers to reproduction between two forms, particularly in non-laboratory settings. However, empirical hybrid zones are difficult to replicate or study under varying environmental conditions because they are often geographically limited and singular in occurrence. Replicate transect analysis, wherein multiple hybrid zones among two species are compared across independent transects, is seldom possible but can be a powerful tool in decoupling intrinsic (e.g. genetic incompatibilities) from extrinsic (e.g. environmental factors) barriers and identifying environmental features associated with reproductive barriers. Here, we have combined sampling and genomic data from three replicate hybrid zones among Red-breasted and Red-naped Sapsuckers (*Sphyrapicus ruber* and *S. nuchalis*). We provide evidence that the two species exhibit variable hybridization rates, zone widths, and genomic patterns among replicate hybrid zones. These data suggest a strong role of extrinsic barriers maintaining reproductive isolation among Red-naped and Red-breasted Sapsuckers.

Investigating the role of the gut microbiome in susceptibility to avian malaria in Hawaiian honeycreepers

Amanda K. Navine, Kristina L. Paxton, Eben H. Paxton, Patrick J. Hart, Jeffrey T. Foster, Nancy McInerney, Robert C. Fleischer, and Elin Videvall
Presenting author: **Amanda Navine**, University of Hawaii at Hilo, navine@hawaii.edu

High extinction rates among Hawaiian honeycreepers (subfamily Drepanidinae) due to mosquito-vectored avian malaria (*Plasmodium relictum*) showcase how introduced diseases can devastate naïve species. Most honeycreepers persist in high-elevation refugia from disease, where lower temperature limits development of mosquitoes and malaria parasites. However, as climate change raises global temperatures there is a risk that *P. relictum* may move up in elevation and cause a rapid loss of such avian refugia. Hawaii Amakihi (*Chlorodrepanis virens*) are the only honeycreepers found at high densities in low-elevation areas of Hawaii where malaria prevalence is high. We hypothesize that amakihi persistence in disease hotspots may be partially due to increased immunity to *P. relictum* conferred by their gut microbiota. To test this, we collected cloacal swabs and blood from wild amakihi (n = 185) and malaria-resistant Warbling White-eyes (*Zosterops japonicus*, n = 179), at 16 sites of variable elevation (50-1750m) and malaria prevalence (20.0-67.3%) across Hawaii Island. We used 16S rRNA gene sequencing to characterize the gut microbiome and qPCR to quantify *P. relictum* parasitemia intensity for each bird. Using an established bioinformatics pipeline and PERMANOVA model we assessed the relationship between microbiome composition and *P. relictum* infection and determined which bacterial taxa are associated with lower parasitemia intensity. Elucidating if microbial species are associated with increased protection against avian malaria in amakihi is an essential first step in understanding host-microbiota-disease dynamics in this system and ultimately determining if probiotic based conservation strategies could mitigate honeycreeper decline.

Do migrating songbirds track the 'green wave' of emerging vegetation in spring?

Claire Nemes, Steven Guinn, Samantha Collins, Bryant Dossman, Alex Gerson, Camila Gómez, Ana María González-Prieto, Joseph Marty, Mariamar Gutierrez Ramirez, Sarah A. Hamer, Peter P. Marra, Philip Vasseur, Theodore J. Zenzal, and Emily Cohen
Presenting author: **Claire Nemes**, University of Maryland Center for Environmental Science,
claire.nemes@umces.edu

Temperate spring can be envisioned as a 'green wave' of emerging vegetation moving from low to high latitudes, with the movement of the wave's leading edge deemed the start of spring. Birds time their migrations to exploit this resource wave, but the extent to which individuals adjust the pace of migration in response to conditions en route is unclear. Uncertainty is expected to grow as spring phenology shifts with climate change. In response, we used the Motus network to track songbirds on migration between the US Gulf Coast and points north to test the hypothesis that migration rate and timing is related to the phenological wave. We expect that birds adjust their migration rate to either maintain or change their relationship to the green wave in spring. We measured the green wave with the annual and expected start of spring day from a 16-year time series and calculated the speed of the wave relative to avian detection points. We found birds did not travel at a constant rate based on 'expected' start of spring, but instead adjusted the pace of migration according to the phenology encountered en route. All birds arrived after the yearly start of spring occurred on the Gulf Coast, trailing behind the leading edge of the green wave. As they approached northern breeding areas, a few individuals overtook the wave, while most closed the gap but continued to trail behind. Counter to our expectation that songbirds 'surf' the green wave within North America, data suggest that they may track a phase of the wave behind the leading edge. Individuals that jump the wave and arrive to their destination before the start of spring risk suboptimal conditions but are positioned to take advantage of spring's arriving resources.

Comparing migration timing, rate, and routes between populations of Canada Geese (*Branta canadensis*) and Cackling Geese (*Branta hutchinsii*) breeding at different latitudes

Leanne R. Neufeld, Frank Baldwin, and Kevin C. Fraser
Presenting author: **Leanne Neufeld**, University of Manitoba, umneu267@myumanitoba.ca

Migration timing is important to the reproductive success of birds, as mismatches with peak food abundance can lead to reduced fitness and population declines. Birds breeding further north may be more susceptible to mismatches, as their timing may be more constrained by shorter seasons with increasing latitude. The migration and breeding of migratory geese may be strongly influenced by seasonal phenology, but how timing may vary for populations breeding at different latitudes is little known. Using light-level geolocators, we tracked 88 individuals from three populations of migratory geese breeding across 20 degrees of latitude; a giant Canada Goose population *Branta canadensis maxima* (n = 34) breeding in southern Manitoba, a Southern Hudson Bay population B. c. interior (n = 39), and arctic-breeding Cackling Geese *Branta hutchinsii* (n = 15). We ran generalized linear mixed models to test for differences in migration departure timing, arrival timing, and rate for both fall and spring migration, and for differences in the timing of breeding. During spring migration, more southern-breeding Canada Geese departed on their spring migration 9-13 days earlier and arrived at their breeding grounds 32-57 days earlier than Cackling Geese, but departed 20-26 days later on fall migration. Generally, there were no differences in migration rate among the populations. The breeding period was later and shorter for more northern-breeding birds. Canada Geese spent 50-90 more days at their breeding sites than Cackling Geese. Overall, we found large differences in timing for populations breeding at different latitudes that extended across the annual cycle. This variation will be important to consider in ongoing conservation and management.

Malaria parasites of the Saltmarsh Sparrow (*Ammodramus caudacutus*) and patterns of infection with mercury exposure

Alyssa P. Neuhaus, Ellen Martinsen, Oksana Lane, Adrienne Kovach, and Michelle Kneeland
Presenting author: **Alyssa Neuhaus**, University of Vermont, apneuhaus@gmail.com

Avian malaria parasites (genus *Plasmodium*) are extremely common in birds worldwide and have the ability to dramatically impact sensitive populations. Mercury, a heavy metal that accumulates in the tissues of birds, is a common environmental pollutant that may reduce immune system function and impact susceptibility to malaria parasite infection. We surveyed the endangered Saltmarsh Sparrow (*Ammodramus caudacutus*), a species with high exposure to mercury, for malaria parasite infection to investigate the diversity and distribution of malaria parasites in the species and the relationship between blood mercury levels and infection status. Overall, 16.5% of Saltmarsh Sparrows were found to be infected with a total of six *Plasmodium* lineages, and there was a greater prevalence and diversity of parasites in northern states. We found an unexpected negative correlation between blood mercury levels and infection status, suggesting that low levels of blood mercury may increase the likelihood of malaria parasite infection. The discovery of a relatively high prevalence and diversity of malaria parasites in the northern portion of the breeding range of the Saltmarsh Sparrow, a species in rapid decline across its range and considered endangered by the IUCN, and the relationship between mercury exposure and malaria parasite infection status, suggest the need for continued study as environmental contamination combined with climate change may heavily impact host, vector, and parasite distributions and host-parasite dynamics.

Resource and rainfall thresholds structure reproductive phenology of tropical montane bird communities

Felicity L. Newell, Ian J. Ausprey, and Scott K. Robinson

Presenting author: **Felicity Newell**, Florida Museum of Natural History, fnewell@ufl.edu

Montane systems provide a unique opportunity to examine effects of climate at small spatial scales, given that endemic mountaintop species may be especially sensitive to climate change. Here, we employ spatiotemporal variation in montane climate as a natural experiment to examine how rainfall regulates reproduction across tropical food webs. The classic 'Diet-Breeding' hypothesis (Skutch 1950) predicts that reproductive timing of income breeders such as birds depends on trophic interactions and peak availability of rainfall-driven resource supplies. From 2015–2019, we studied eight cloud forest landscapes from 1700–3100 m in northern Peru, collecting comprehensive datasets on phenology and abundance of montane birds, arthropods, and plants along with concurrent in situ weather data. Consistent with peak abundance of bird-pollinated flowers and bird-dispersed fruits, we found nectivores (23 species in 2 families) nested at the beginning of the dry season whereas frugivores (11 species in 5 families) nested primarily during the rainy season. For invertivores (48 species in 11 families) and omnivores (4 species in 1 family), we found local shifts in breeding from the beginning of the dry season to the beginning of the wet season. Abrupt phenological shifts were driven by resource thresholds stemming from decreasing April–June rainfall and reduced dry-season arthropod biomass. For the first time, we document repeated 5-month phenological shifts for the same species across < 100 km. These results have implications for population dynamics and connectivity of montane birds.

Few genomic regions underlie phenotypic differentiation in *Sporophila beltoni*, a recently described seedeater species from southern Brazil

Tram N. Nguyen, Márcio Repenning, Carla Suertegaray Fontana, and Leonardo Campagna

Presenting author: **Tram Nguyen**, Cornell University, tn337@cornell.edu

Recent speciation events can allow researchers to associate phenotypes with their causal genotypes, thus providing insights into the process of speciation. Finding recent species that diverge in traits relevant reproductive isolation is therefore crucial to our ability to search for the genetic basis of such phenotypes. Here we investigate the genetic underpinnings of the phenotypic differences between a pair of species from the genus *Sporophila*, two seedeaters that are thought to have speciated very recently. Once thought to be the same species, *Sporophila plumbea* and *Sporophila beltoni* have only recently (2013) been distinguished as sister species based on morphology, plumage pattern, breeding habits and song variation. Most notably, second-year males of S. beltoni develop yellow bills while males of S. plumbea have black bills. Sequencing of mitochondrial markers for 28 individuals showed that both species share mtDNA haplotypes, either through hybridization or incomplete lineage sorting, and consequently lack reciprocal monophyly. Whole-genome sequences from 36 individuals (18 of each species) revealed low levels of genetic divergence (average FST = 0.0018), yet we found 40 SNPs of high divergence encapsulated in just three narrow divergence peaks (average length of 60 kb) along the genome. These differentiated regions harbor six genes, one of which is a well-known pigmentation gene (EDN3 which encodes the protein Endothelin-3), which controls skin coloration in chickens. This study contributes to the growing body of literature indicating that genes potentially involved in traits related to prezygotic isolation are important in the early stages of speciation.

So you want to write research-based fiction

Amanda C. Niehaus

Presenting author: **Amanda Niehaus**, The University of Queensland, amandacniehaus@gmail.com

As scientists, we are trained to present data and observations with as little subjectivity as possible. Yet, clearly, cold facts alone can't incite action on the major scientific issues of our time, including Covid-19, vaccination, or climate change. Ironically, fiction can help us connect our ideas with diverse readers, by showing what facts mean in everyday—even made up—lives. But after all these years of academic writing, where do we even start? In this talk, you will learn how Amanda transitioned from life as a full-time research scientist to a full-time writer—including how she wrote and published an award-winning short story and novel called The Breeding Season that translate her scientific research on semelparous marsupials into a contemporary, very-human love story; you will explore different approaches to science-in-fiction; and you will come away with new ideas, resources, and practical tools to help you get started writing your own research-based fiction.

Temporal niche partitioning of a plant-hummingbird network in the Atlantic forest of southeastern Brazil

Andrea V. Nieto, Rafael O. Wüest, Catherine H. Graham, and Isabela G. Varassin

Presenting author: **Andrea Nieto**, Universidade Federal do Paraná, andreanieto87@gmail.com

Niche partitioning is one of the mechanisms that allows species to coexist. Within mutualistic interaction networks, this mechanism has been studied at broad spatial and seasonal scales, while at fine temporal scales, i.e., throughout the day, it has been little addressed. We explored the temporal niche partitioning, throughout the day, of a plant-hummingbird interaction network in the Atlantic forest of southeastern Brazil. Over nine months, we set up time-lapse cameras on flowers to evaluate hummingbird visitation patterns. We collected data on flower morphology, nectar production, and floral resource availability to evaluate the relationships between these variables and the temporal pattern of hummingbird visitation. From the hummingbird perspective we found no temporal partitioning, instead hummingbirds foraged on distinct flower species. From the plant perspective, some species flowered at the same time and often were visited by more than one hummingbird species. Morphologically similar plants produced nectar during the same time of day. These results suggest that the plants are not partitioning the pollination niche (i.e., hummingbird visitors). Taken together, our results indicate that hummingbird and plant assemblages are likely structured by different mechanisms. Patterns of visitation of hummingbirds to plants are consistent with facilitation among plants, while hummingbirds partition forage on distinct flowers, a pattern possibly driven by competition. In sum, our focus on fine-scale temporal patterns provided a more nuanced and detailed view of mechanisms influencing plant-hummingbird interactions.

Using citizen science to optimize spatial conservation planning for grassland birds

Laura A. Nunes, Christine A. Ribic, and Benjamin Zuckerberg

Presenting author: **Christine A. Ribic**, U.S. Geological Survey, caribic@wisc.edu

Grassland birds are experiencing steep population declines due to loss and degradation of grassland habitats. In 2010, Wisconsin Department of Natural Resources established a statewide hierarchical conservation design for grassland birds consisting of smaller targeted management areas (Grassland Bird Conservation Areas, GBCAs) strategically placed within larger landscapes of private and public grasslands (Focal Landscapes). To date, this conservation network lacks state-wide baseline information against which to evaluate the effectiveness of this conservation design. We used data from avian point count surveys conducted as part of Wisconsin's Breeding Bird Atlas II to estimate density hotspots of 10 obligate grassland bird species and used spatial randomization tests to evaluate 3 Focal Landscapes for grassland bird conservation. Across all species, mean population densities in the Focal Landscapes were similar to or higher than statewide average estimates Overall, we found that the Focal Landscapes were better aligned with conserving hotspots for species requiring moderately tall grass (e.g., Bobolink, Eastern Meadowlark, Savannah Sparrow), but less aligned with species associated with short grass (e.g., Horned Lark) or tall grass (e.g., Sedge Wren). We suggest that citizen science data, such as those derived from biological atlases, may provide rigorous assessments of threatened populations over broad spatial scales and could be important for informing conservation planning aimed at reversing the decline of vulnerable taxa.

Battle for the nest: Interactions between an obligate brood parasite and its host during laying events

Jack O'Hara, Patrick Page, and Brian D. Peer

Presenting author: **Brian Peer**, Western Illinois University, BD-Peer@wiu.edu

Avian brood parasites rely on hosts to raise their young. The parasite must first locate a nest and then access it to lay its eggs. Hosts may respond to parasitism by investing in frontline defenses to prevent being parasitized. Relatively little is known regarding the interactions between the parasitic Brown-headed Cowbird (*Molothrus ater*) and its hosts during cowbird laying events because they occur prior to sunrise. We investigated the behavior of cowbirds and the Prothonotary Warbler (*Protonotaria citrea*), which is the only host reported as a victim of cowbird mafia behavior. Because mafia cowbirds destroy nest contents after a host has rejected a cowbird egg, we predicted that warblers should invest in frontline defenses to reduce the likelihood of parasitism and subsequent mafia enforcement. We recorded >1,000 hours of video and observed >100 visits by cowbirds at nests. Prospecting occurred after sunrise when cowbirds visited nests to determine if they were ready to be parasitized. We observed >20 laying events and

found cowbirds that arrived earliest in the morning (<13 min prior to sunrise) encountered little resistance from warblers. Cowbirds arriving closer to sunrise were more likely to be confronted, and while some were repelled, the majority laid successfully despite being viciously attacked by hosts. These observations indicate that warbler frontline defenses are largely ineffectual in reducing parasitism because warblers do not typically arrive at their nests until after cowbirds lay. When warblers are present, cowbirds withstand the attacks and when repelled, they return and successfully parasitize the nests. The lack of investment in frontline defenses by a host subjected to mafia behavior is puzzling.

Reproductive performance increases with age in European Starlings

Nii T. Obodai and Colleen A. Barber

Presenting author: **Colleen Barber**, Saint Mary's University, colleen.barber@smu.ca

The most energetically costly event in a bird's life cycle is reproduction, particularly for females who lay nutrient-rich eggs. Females invest more into breeding and choose higher-quality mates when possible for the benefits they provide. Males would also choose to pair with a high-quality female whenever possible. Studies have found that high-quality mates were typically older. Older females might be in better condition and therefore lay more eggs than young females. European Starlings (*Sturnus vulgaris*) are cavity-nesting passerines with biparental care. Both sexes have hackles whose length of iridescence allows classification into one of two age categories (Second Year, SY, who are breeding for the first time, and After Second Year, ASY, who likely bred at least once before). The objective of our study was to determine whether older females had higher reproductive performance than younger females, using four years of data. We predicted that ASY females would be in better condition than SY females, and that they would have larger clutch sizes, a higher mean egg mass, and greater hatching and fledging success. In support of our predictions, ASY females were in significantly better condition than SY females and laid larger clutches. ASY females also tended to have higher fledging success, although mean egg mass and hatching success did not differ between ASY and SY females. Condition and reproductive performance in this population of European Starlings were higher for older females than first-time breeding females, suggesting that these older females might be expected to be preferred as mates.

Evolutionary history of the Variable Seedeater (*Sporophila corvina*)

Diego Ocampo, Kevin Winker, Mathew Miller, Luis Sandoval, and J. Albert C. Uy

Presenting author: **Diego Ocampo**, University of Miami, ocampov.diego@gmail.com

Understanding the origin of biological species requires uncovering the evolutionary history of the diversifying lineage. However, because of low genetic differentiation and potentially high levels of gene flow among taxa, disentangling the evolutionary relationships of recently radiating clades is often challenging. Here, we used a phylogenomic approach to study, for the first time, the evolutionary history and population structure of *Sporophila corvina*, a variable species of small Neotropical birds that exhibits striking geographic variation in song and plumage color. Previous work on this genus indicated that variation in secondary sexual traits is important in generating premating sexual isolation. Using over 30,000 genome-wide SNPs and a mitochondrial marker (ND2), we confirmed that the *S. corvina* complex (i.e., *S. corvina*, *S. intermedia*, and *S. americana*) forms a monophyletic clade. We also found that the entirely black subspecies, S. c. corvina, is derived recently within a pied-colored clade. Further, our structure analyses identified three distinct genetic groups (K=3) within *S. corvina*; interestingly, we found that the subspecies *S. c. hoffmanni* and *S. c. hicksii* form a single genetic cluster despite their discontinuous distribution and significant phenotypic differences. Finally, we found strong evidence of gene flow across the whole species' distribution, but with reduced rates at the geographic limits between the entirely black and pied subspecies, which suggests an important role of phenotypic divergence in limiting gene flow. Overall, these findings shed light into the patterns and drivers of evolution of this rapidly diversifying genus.

Using range edges to understand drivers of avifaunal divergence on the Thai-Malay Peninsula

Zheng Oong and Sushma Reddy

Presenting author: **Zheng Oong**, University of Minnesota, Twin Cities, oong0001@umn.edu

Biogeographers have long recognized the Thai-Malay Peninsula as a biogeographical transition zone between assemblages of mainland Southeast Asia ('Indochina') and those of the Sunda Shelf. However, the exact position of the transition on the peninsula varies from taxon to taxon. Even within birds, results have varied across groups, suggesting an intricate interplay between factors like geomorphology and species ecology to generate the biogeographic patterns we see today. We performed a novel analysis of range edges to evaluate the potential drivers of the Indochinese-Sundaic avifaunal divergence. We spatially analyzed species distribution edges to examine the degree of overlap and consistency in range limits and assess the correspondence of 'barriers' with an analysis of areas of endemism. As range edges are shaped by a complex interaction of factors related to species' macroevolutionary histories, we evaluated the correlation between range edges and biotic (habitat, elevation, feeding ecology) and abiotic parameters (climate, seasonality, geomorphology). Given that the Indochinese-Sundaic biogeographic transition is still poorly understood, our study represents an important first step in understanding the drivers of avifaunal divergence at a broad geographic and taxonomic scale in this region.

Fire and ice increase nest success in a mountain-endemic South African bird

Krista N. Oswald, Elizabeth F. Diener, John P. Diener, Susan J. Cunningham, Ben Smit, and Alan T. K. Lee

Presenting author: **Krista Oswald**, Rhodes University, knoswald@gmail.com

A major cause of reproductive failure in birds is nest predation. Predation risk depends on predator type, as predators vary in their ecology and sensory modalities (e.g. visual vs. olfactory). Snakes (generally olfactory predators) are a major nest predator for small birds, with predation strongly associated with higher temperatures. We investigated nest survival in a ground-nesting species endemic to the South African mountains, the Cape Rockjumper. We collected 3 years of nest data, testing whether nest survival was related to (1) habitat stage (early post-fire vs. late post-fire habitat, = 3 and > 3 years since fire respectively), (2) nest concealment, and (3) temperature. We found that nests had better survival at lower temperatures, with snake predation (our main source of predation) increasing in higher temperatures.

Stable isotope evidence shows key farmland structure features driving Eastern Wild Turkey food selection

Nickson E. Otieno and Laurent Frenette

Presenting author: **Nickson Otieno**, National Museums of Kenya, otieno_nickson@yahoo.com

The Eastern Wild Turkey (EWT, *Meleagris gallopavo silvestris*) is frequently cited as a corn pest throughout North America, but little tangible evidence exists to support this factually, although it is occasionally observed consuming bits of corn left on the ground, or corn grains may be found in its crop after slaughter. To test the corn pest paradigm, we tested linkages of land cover patterns to EWT dispersal and corn consumption rates using analyses of δ13C and δ15N isotopes across an intensively farmed landscape in south-east Quebec, a cornfield-dominated croplands region. Mean abundance of EWT encountered were highest in regions with greater mix of forest, cropland and open space matrices, particularly with high crop-field cover and proximity to water bodies. However, isotopic analyses indicated that contribution of corn to EWT diet was primarily correlated with forest cover rather than overall crop-field size, suggesting that corn was not the primary attractant. Regions with extensive road networks also supported high rates of corn consumption, suggesting that such features may be facilitating cornfield raids by true corn pests which may then leave remnants that EWT subsequently consume. Adult EWT predominantly consumed plant-based food, particularly C3 plants, while juveniles mostly consumed invertebrates, several of which constitute crop pests. These results imply that corn constitutes only an opportunistic and supplemental component of EWT diet, especially where cornfields neighbour forests. Furthermore, EWT foraging flocks may in fact collectively contribute significantly to arthropod pest regulation across the landscape, rather than being corn pests.

Offspring provisioning effort in European Starlings (*Sturnus vulgaris*) during the nestling rearing period

Sara Ozbek and Colleen Barber

Presenting author: **Sara Ozbek**, Saint Mary's University, sarozbek1@gmail.com

Rearing offspring is a critical but energetically costly period for birds. Socially monogamous species typically have biparental care, although females invest more heavily in the offspring. Some studies have found that in the socially monogamous yet facultatively polygynous European Starling (*Sturnus vulgaris*), females provisioned the offspring at similar rates as the males, with provisioning rates higher in the mornings than the afternoons. One study also found that provisioning rates tended to increase mid-way through the nestling cycle before declining. This study was conducted to confirm whether the findings in the literature also pertain to our European Starling population as there are many differences among populations. Parental provisioning by eight European Starling pairs was studied over the nestling period using GoPro cameras. Two observation sessions (morning, afternoon) per pair were done on five different days through the nestling period. I predicted that male and female offspring provisioning would be similar. I also predicted that offspring provisioning rates would be higher in the mornings than afternoons, as studies found a negative correlation between summer temperatures and provisioning rates. Finally, I predicted that as nestlings aged, provisioning visits would increase. Females provisioned offspring significantly more often than males. Moreover, parents provisioned at higher rates in the mornings than afternoons. Finally, as nestlings aged, provisioning rates continued to increase. This study has implications in further understanding avian investment in offspring provisioning behaviours.

Initial evaluation of avian use of agricultural cover crops during the winter, migration stopover, and the breeding season in Tennessee

Brittany Panos, David Buehler, and Craig Harper

Presenting author: **Brittany Panos**, University of Tennessee - Knoxville, bpanos@vols.utk.edu

The U.S. Department of Agriculture Natural Resources Conservation Service administers the winter cover crop program to provide financial incentives to agricultural producers to sow herbaceous plant seeds to protect agricultural fields from soil erosion during the non-growing season (late fall through spring). As of fall 2020, 58,643 hectares were certified as planted with cover crops through NRCS in Tennessee. Although benefits related to soil retention and water quality improvements have been documented, potential benefits to birds remain largely unknown. We are investigating use of cover crop fields by birds during the stationary non-breeding period, migration, and the breeding season by comparing bird use of cover crop fields with no-till row-crop fields without cover crops. We selected 77 fields with cover crops and 30 control fields without cover crops for evaluation in four counties across middle and western Tennessee. We monitored avian use along two 100-m line transects in each field in a distance-sampling framework every three to four weeks, January – June 2021. We also employed supplemental drive netting with mist nets and banding to further quantify avian use. We will nest-search during the breeding season for focal grassland species to document how these fields support breeding birds. During the winter 2021 season, we detected 46 species (96%) on cover crop fields and 24 species (50%) on control fields. We will present results from the full 2021 field season, describing avian use of no-till crop fields with and without cover crops, and how vegetation cover influenced use.

Vocal coordination between male and female Carolina Wrens (*Thryothorus ludovicianus*)

Rustin Pare and J. Jordan Price

Presenting author: **Rustin Pare**, St. Mary's College of Maryland, rwpare@smcm.edu

Duetting by female and male songbirds is much more common in tropical than in temperate regions. Furthermore, in temperate species in which only males sing female singing behavior appears to have been lost in an ancestral species. My research focused on female vocal behavior in the Carolina Wren (*Thryothorus ludovicianus*), a temperate species whose females do not perform the highly coordinated duets with males for which other tropical members of the wren family (Troglodytidae) are known. I recorded the vocalizations of male and female wrens on their territories, then used a software program to quantify whether these vocalizations are coordinated more or less than expected by random chance. This analysis showed that male and female wrens perform a coordinated duet which is not dissimilar to those performed by tropical wren species even though female Carolina Wrens appear to have lost complex songs. Further study should investigate the function of this vocal coordination in territorial Carolina Wrens.

Long-distance migrants experience slower molecular evolution

Teresa M. Pegan, Jacob S. Berv, Eric R. Gulson-Castillo, and Benjamin M. Winger

Presenting author: **Teresa Pegan**, University of Michigan, tmpegan@umich.edu

Molecular substitution rates are correlated with life history traits such as mass and generation time across the tree of life. On the slow end of the life history continuum, large-bodied species prioritize adult survival over high annual fecundity, and these tend to have slow rates of molecular evolution. Life history strategy in birds is also influenced by seasonal migration, which allows individuals to prioritize over-winter survival at the cost of time spent breeding.

In North American boreal birds, which share broadly similar mass and generation time, long-distance migrants have higher survival and lower fecundity than short-distance migrants. We therefore expect that long-distance migrants should also experience slower rates of molecular evolution. Here, we test this hypothesis using synonymous substitution rate (dS), which reflects substitutions that are not strongly influenced by selection. We used the program Coevol to test for correlated evolution between migration distance and dS in 38 small-bodied North American boreal birds using 5 mitochondrial genes. Our results suggest that long-distance migrants experience lower dS than short-distance migrants. The patterns we detect may be influenced by selection for mutation-avoidance, which has been hypothesized as a link connecting life history and molecular rates. We will also discuss whether our results are influenced by effective population size, which is thought to affect dS under nearly neutral theory. Our results further emphasize the role of migration in avian life history and demonstrate that life history variation influences mitochondrial rate of evolution even among species with broadly similar mass and generation length.

Comparative analyses of vocalization and genomic divergence in Nashville Warblers

Lan-Nhi Phung and David P. L. Toews

Presenting author: **Lan-Nhi Phung**, The Pennsylvania State University, phung@psu.edu

The Nashville Warbler (*Leiothlypis ruficapilla*) has a breeding ground in North America that is separated into two ranges with no overlap. Coupled with their subtle differences in plumage color, behavior, and calls, they are considered two subspecies, *L. r. ruficapilla* in the East and *L. r. ridgwayi* in the West. As opposed to other well-studied warblers, this species, especially the western group, has not received much study, including whether there are strong differences between the two subspecies in vocal characteristics. Moreover, genetic data from the group is limited. This project aims to quantify any differences between the Nashville Warbler subspecies from two independent characters: vocalizations and nuclear genetic markers. First, we analyzed several acoustic components of the Nashville Warbler primary song, which provided evidence that the subspecies songs are highly diagnosable. Within each subspecies we did not find evidence that either has vocal geographic variation in the form of song dialects. Second, we used low-coverage whole-genome resequencing from 12 individuals of each subspecies (n = 24) to quantify differences in the nuclear genome. This allowed us to estimate the current and historical level of gene flow and provide insights into their demographic history and taxonomic status. With this data, we also inferred the magnitude and timing of the differentiation across the genomes of the two subspecies and compare it to that of previously sequenced genomes of parulid warbler species-pairs.

An evaluation of the importance of Delaware Bay near-shore habitats to migratory songbirds

Aya Pickett and Christopher M. Heckscher

Presenting author: **Aya Pickett**, Delaware State University, ayapickett@gmail.com

The Delaware Bayshore has long been recognized as a globally important stopover region for shorebirds and waterfowl. However, the bay's coastal habitats host large volumes of songbirds during north and southbound migration. In particular, several species of boreal-breeding songbirds, many of which are in decline, use the bayshore's many wooded coastal marsh hummocks. Thus, although the bay's coastal marshes are severely threatened by sea-level rise (SLR), they may support globally important stopover habitat. To date, little research has been conducted on the use of these coastal marshes by migratory songbirds, and we are not aware of any specific conservation policies geared toward the preservation of songbird habitat whereas shorebird and waterfowl conservation efforts are commonplace. Because of the threat of SLR, in 2020 we initiated a banding station on a typical (<5 ha) coastal saltmarsh hummock to investigate its use by migratory songbirds. Tissue and feather samples were collected to determine songbird refueling performance and breeding origin, respectively. A total of 548 individuals were captured representing 47 species, 23.53% of species were boreal breeders. Our most abundant species was Yellow-rumped (Myrtle) Warbler (*Setophaga coronata coronata*, 36.5%) – a boreal breeding songbird. In addition, Gray Catbird (*Dumetella carolinensis*, 19.71%), and Common Yellowthroat (*Geothlypis trichas*, 11.13%) were the next most abundant transient species. These and other preliminary results will be presented and suggest high use by both boreal and temperate breeding passerines similar to that of other globally recognized coastal stopover regions (e.g., Gulf of Mexico, Great Lakes, Gulf of Maine).

A newly discovered song type in Connecticut Warblers (*Oporornis agilis*) is variable in versatility and diel song rate at both inter- and intra-individual levels

Kaitlyn E. Plastino, Kevin C. Hannah, and Jennifer R. Foote

Presenting author: **Kaitlyn Plastino**, Algoma University, kplastino@algomau.ca

The Connecticut Warbler (*Oporornis agilis*) is one of the least studied passerines in North America. This species is secretive in nature and utilizes low-elevation habitats within boreal forests. Due to their relatively inaccessible environment, their vocal behaviour has not been well studied. Using autonomous recordings made in the Northwestern Ontario boreal forest, we examined this species' vocal repertoire. We report a novel but rarely used, second song type: an extended song that covers a broader frequency range and is significantly longer and more variable than the species' primary song. The extended song is similar in composition to the Ovenbird's (*Seiurus aurocapilla*) flight song; It includes an introductory segment, several notes from its primary song, and a terminal segment. We predicted we would find variation within and among individuals in song characteristics and diel separation of song type use as is observed in Ovenbirds. First, we found that song length and syllable versatility index varied within and among individuals. We also found that primary songs peaked at dawn and declined through the day while extended songs peaked in evening, suggesting temporal separation. Our work highlights the value of environmental recordings created for survey purposes so that we may answer questions about the vocal behaviour of difficult to study species, in addition to expanding our knowledge of natural history. While the vocal repertoires of most North American passerines are considered to be well characterized, we demonstrate that novel vocalizations are still waiting to be discovered, particularly for boreal species.

Habitat factors influencing avian community richness on Wetland Reserve Program easements vary across seasons

Jon Podoliak, David Hicks, and Lisa Webb

Presenting author: **Jon Podoliak**, University of Missouri, jmpk96@mail.missouri.edu

Bottomland hardwood (BLH) forested wetlands provide vital habitat for waterfowl and neotropical songbirds and were once dominant in the Lower Mississippi Alluvial Valley (LMAV). However, conversion to agricultural land reduced BLH area across the LMAV by >75% between 1800-1980. The Wetland Reserve Program (WRP) began in 1990 to restore marginal agricultural lands to wetlands in response to wetland loss; in the LMAV, the WRP focuses on restoring BLH wetlands for wildlife habitat. Our objective was to assess habitat factors on WRP sites that affect avian richness across seasons. We sampled 20 WRP easements across western Tennessee and Kentucky from autumn 2019-spring 2020. Bird species richness ranged from 1-11 species in autumn, 1-16 species in winter, and 5-20 species in spring. We evaluated forested habitat factors important for explaining variation in avian richness using generalized linear models. Our autumn model indicated avian richness was positively associated with average forb, leaf litter cover, and water depth. Our winter model indicated avian richness was positively associated with average DBH and bare ground, and negatively associated with average shrub cover. Our spring model indicated avian richness was positively associated with average shrub cover and DBH and negatively associated with average leaf litter. Our preliminary results indicate seasonal variation in habitat factors explaining avian richness, which may be linked to different bird communities using BLH wetlands across seasons, with different habitat requirements. Our findings may aid in improving restoration efforts of BLH wetlands to maximize avian richness across the full annual cycle. Data from 2020-2021 at additional sites are forthcoming.

Assessing the long-term effects of two expanding gap silvicultural systems on the forest avian assemblage in central Maine

Carl K. Pohlman

Presenting author: **Carl Pohlman**, University of Maine, carl.pohlman@maine.edu

Forests of the northeastern United States and eastern Canada represent vital breeding habitat for imperiled forest birds. Forest management for a diverse assemblage of breeding birds is difficult due to the varied and often idiosyncratic species-level responses to forest management techniques, though forest management and avian conservation are not mutually exclusive. The University of Maine's Acadian Forest Ecosystem Research Program (AFERP) consists of two expanding gap treatments in addition to unharvested reference stands representing a unique long-term ecologically-based silvicultural system. Avian surveys were first conducted in the mid-90s and coincided with the first AFERP harvests. The goal of this project is to compare the avian assemblage in response to the two expanding-gap harvest treatments over the course of several timber harvests. This is accomplished by comparing bird assemblages at harvested sites to those at unharvested sites and multiple survey periods over the full rotation. Based on territory mapping of all species, preliminary results of a two-way ANOVA on treatments and survey period indicate there was no significant difference (p>0.05) in the bird assemblage among treatments, indicating that the two expanding gap treatments did not impact forest bird assemblages. However, when compared to initial surveys, a significant (p<0.05) decline in Shannon's H and species richness was observed. The findings of this project can be used to develop best management practices for applying ecological forestry to bird habitat.

The mechanical design of woodpecker tails as an adaptation to scansorial habits

Brenda L. Poledri, Darío A. Lijtmaer, and Pablo L. Tubaro
Presenting author: **Brenda Poledri**, Museo Argentino de Ciencias Naturales Bernardino Rivadavia, brendapoledri@gmail.com

Woodpeckers (Picidae) typically move vertically on tree trunks using the tail as a support for body weight. This unusual means of support (scansorial) correlates with several putative morphological adaptations including an increase in the flexural stiffness of rectrix rachices. However, a rigorous test of the adaptive value of these characters is still lacking. Here we present the results of a comparative morphological study focused in woodpeckers, including other scansorial and non-scansorial bird groups. Rachis diameter was positively associated with body mass as expected if tail structure was a simple allometric product of body size. Scansorial birds had larger rachis diameters for a given body mass than cursorial birds, and an increased proportion of cortex. However, woodpeckers differed from woodcreepers in several critical aspects: 1) they had significatively shorter tails; 2) they evidenced a faster decrease of the dorso-ventral diameter of rachices towards the tip, and 3) they had a larger proportion of cortex and a smaller proportion of medullary tissue along the distal parts of their rachices. These results indicate that woodpecker tail feathers are not designed to resist Euler buckling (i.e. the tendency to collapse by arching along their length when the feather is loaded axially by body weight) as in woodcreepers, but to allow a 'controlled' distal buckling that increase tail adherence to the trunk surface as well as the body weight that the proximal part of the tail can support without significant deformation.

Origin of novel population dynamics through behavioral feedbacks in a passerine bird

Ahva L. Potticary, Stephanie M. Aguillon, and Renée A. Duckworth
Presenting author: **Ahva Potticary**, University of Arizona, apotticary@email.arizona.edu

Population responses to environmental change are difficult to predict because the mechanisms by which pre-existing adaptations drive dynamics in a novel context are not known. Here, we use a combination of field experiments and long-term data from Western Bluebird populations to show that maternal effects that evolved in response to successional dynamics produced novel feedbacks in a human-altered stable habitat. In crowded years, females produced more dispersive and aggressive offspring leading to lower offspring recruitment, a decline in population density and a rise in population aggression in the subsequent year. In turn, low population density led females to produce more philopatric, nonaggressive offspring which increased recruitment and population density, starting the cycle anew. These reciprocal feedbacks between population density and offspring behavior emerged spontaneously in the novel context, providing evidence that self-organizing properties of ecological systems are generated by individual differences in behavior that arise from local scale responses.

Big-data bioacoustics, biogeography, and biases in birds

Kaiya L. Provost, Jiaying Yang, and Bryan C. Carstens
Presenting author: **Kaiya Provost**, The Ohio State University, provost.27@osu.edu

Birds show an astonishing array of songs and calls, the diversity and functions of which have been studied across many facets of biology, including neurobiology, behavioral ecology, reproductive isolation, and so on. One lingering gap in these studies is understanding what the spatiotemporal dynamics of song are at the community level, as the majority of approaches study a single species at a time. Here we look across multiple co-distributed species simultaneously to examine how these dynamics correspond to genetic and phenotypic patterns. We develop a 'big-data' approach to explore the relationships between vocalizations, genetics, and multiple evolutionary forces in the North American avifauna. We leverage existing bioacoustic and genetic repositories (e.g., Xeno-Canto, the Borror Lab of Bioacoustics, GenBank) as well as environmental data (e.g., WorldClim) to investigate global and local biases in collection of these data types. We highlight global gaps in sampling in both bioacoustic and genetic data and metadata, discuss methodological concerns, and show spatial dynamics of avian nucleotide and haplotype diversity across North America. In particular, we focus on discovering how diversity in song and genetics is structured by environmental, demographic, and historical factors. As an exemplar, we highlight one species, the well-studied White-crowned Sparrow (*Zonotrichia leucophrys*), for which we present preliminary results and what insights about the community this taxon can provide.

The influence of pine management on grassland-nesting birds overwintering in central Louisiana, USA

Nancy M. Raginski and Ashley M. Long

Presenting author: **Nancy Raginski**, Louisiana State University, nraginski@gmail.com

In the southeastern U.S. pine forests cover ~28 million ha and are most often used for commercial timber and hunting. Management practices used to reach desired vegetative conditions in these forests (e.g., prescribed fire) may simultaneously influence distributions of overwintering songbirds, including several species of conservation concern that breed in grasslands of the northern U.S. and throughout Canada. From December to February of 2018–2020 and December 2020, we surveyed 26 study sites in longleaf (*Pinus palustris*) and loblolly pine (*P. taeda*) stands to examine the influence of pine management on grassland-nesting birds overwintering in central Louisiana. We used single-season occupancy and N-mixture models to model occupancy and density of grassland-nesting species of conservation concern detected during our surveys. We recorded 9,014 detections of 64 species including six grassland-nesting species. We found Henslow's Sparrow (*Centronyx henslowii*) occupancy increased with increasing vegetation height, Bachman's Sparrow (*Peucaea aestivalis*) occupancy was greatest in longleaf stands, and Sedge Wren (*Cistothorus platensis*) occupancy increased with decreasing percent canopy cover. We found Henslow's Sparrow density decreased with increasing litter depth. Bachman's Sparrow density increased with increasing number of vegetation point contacts between 0 and 10 cm in both stand types. Sedge Wren density increased with increasing percent herbaceous cover. Our results also indicate that overall species richness was greatest in longleaf sites burned within two years of our surveys. Our research will help inform more comprehensive management of grassland-nesting birds overwintering in pine forests of the southeastern U.S.

Natural and anthropogenic effects on Pacific Swallow (*Hirundo tahitica*) populations

Brenda Ramirez, Amanda K. Hund, Amanda Zellmer, and Elizabeth Scordato

Presenting author: **Brenda Ramirez**, California State Polytechnic University, Pomona, brendarosaramirez@gmail.com

Anthropogenic activity has altered ecological communities for thousands of years. Hunter-gatherers during the Pleistocene, and eventually the Agricultural Revolution during the Holocene, reshaped community structures by altering selective pressures and drastically modifying the environment. Despite clear evidence of long-term human landscape modification, we currently have a poor understanding of how this human activity has affected distributions of suitable habitat and evolutionary processes for most species. The Pacific Swallow (*Hirundo tahitica*) is a commensal species found throughout Southeast Asia and the Pacific and is well known for nesting on man-made structures. This commensal relationship makes it an ideal system for studying the effects of human development on species distributions and demographic change over time. We created species distribution models (SDMs) incorporating both climate and human land-use variables and projected models back over 12,000 years to predict the distribution of suitable habitat for swallows during the rise of agricultural practices in Southeast Asia. Our results show that total built-up areas (including towns and cities) and seasonal temperature patterns are the strongest determinants of Pacific Swallow habitat distributions. An increase in human land use over the last several thousand years has likely provided Pacific Swallows with more nesting habitat, which may have led to an increase in population size over time. Including anthropogenic factors in studies of habitat availability and demographic change is not common but is essential for understanding the lasting impacts humans have on ecological communities.

The role of climate in winter range shifts by eastern North American waterbirds

José R. Ramírez-Garofalo, Shannon R. Curley, Lisa L. Manne, and Richard R. Veit

Presenting author: **José Ramírez-Garofalo**, The College of Staten Island, City University of New York, jose.ramirez.garofalo@gmail.com

Climate change is causing distributional shifts in taxa worldwide. In birds, community science projects like the National Audubon Society's Christmas Bird Count (CBC) allow researchers to track these distributional shifts at a large geographic scale. Wintering bird distributions are shown to be constrained by temperature with many species shifting polewards with climate change. However, few studies have specifically focused on distributional changes of coastal birds. In this study, we investigate the role of minimum winter temperature in the distributions of waterbirds wintering in the coastal states and provinces of eastern North America from 1990–2018. We test whether the species' annual winter population centroid has shifted relative to the 0º isotherm between December and January with the expectation that species with centroids that are increasing their annual northward distance from the isotherm have shifted faster with climate change. We also test if the rate of shift between species with winter population centroids that started below the isotherm (southern species) were significantly different from those species with centroids starting above the isotherm (northern species). Overall, we find that 39/118 species shifted significantly northward, 24/118 shifted significantly southward, and 55/118 did not shift their ranges significantly.

Is the passerine superradiation defined by a unique growth hormone gene duplication?

Shauna Rasband, Peri E. Bolton, Qi Fang, Rebecca B. Dikow, Philip L. F. Johnson, and Michael J. Braun
Presenting author: **Shauna Rasband**, University of Maryland, rasbands@si.edu

Passerine songbirds are a true superradiation, comprising more than half of living bird species. However, the reasons driving their diversity and success are unclear. What genetic changes make passerines unique? The growth hormone (GH) gene is duplicated throughout the passerine lineage; analysis of hundreds of avian genomes confirmed that this duplication is the only gene both limited to and found in all passerine lineages (Feng et al. 2020). The ancestral avian GH (GH1) influences critical life history traits such as growth rate, clutch size, and body size, yet little is known of the evolution and basic biology of the new GH paralog (GH2) in passerines. Previously, partial sequence data showed that passerine GHs have evolved more rapidly than those of other birds, indicating an adaptive role for this duplication. With evolutionary analyses of full-length sequences (337 passerine and 160 nonpasserine), we have confirmed accelerated evolution of passerine GHs, with GH2 experiencing positive selection that may functionalize the paralogs for different roles. We have also found that the genomic context of GH genes differs not only between GH paralogs (GH1 on chromosome 27 and GH2 on chromosome 1), but also that the contexts differ between major passerine lineages (oscines vs *Acanthisitta*+suboscines) due to further chromosomal rearrangements. Genomic context may contribute to differing patterns of GH expression we found in a suboscine manakin (*Pipra filicauda*), which has GH2 expression more limited in dosage and tissue location than has been observed in an oscine corvid (*Corvus macrorhynchos*). These findings suggest GH genes may play differing roles in the major passerine lineages.

Higher minimum song frequency of urban Dark-eyed Juncos (*Junco hyemalis*) persists in a common garden experiment

Dustin G. Reichard, Jonathan W. Atwell, Meelyn M. Pandit, Gonçalo C. Cardoso, Trevor D. Price, and Ellen D. Ketterson
Presenting author: **Dustin Reichard**, Ohio Wesleyan University, dgreicha@owu.edu

Urbanization and noise pollution can disrupt acoustic communication. In response, many urban songbirds exhibit vocal behavior that diverges from rural populations such as higher sound frequencies. Whether these frequency shifts in noisy environments are caused by behavioral flexibility, developmental effects of noise exposure, or evolutionary change over multiple generations remains largely unknown. We studied two populations of Dark-eyed Juncos (*Junco hyemalis*), one urban and one rural, and used a common garden experiment to investigate the cause of the higher minimum song frequency observed in urban juncos. We captured juvenile males that were 25-40 days old and raised them in separate but identical aviaries for 3 years before recording their songs. We found that the large frequency difference observed in the field persisted undiminished in the common garden despite the absence of noise. This result indicates that the higher minimum frequency of the urban juncos is not due to behavioral flexibility in response to noise. Instead, this frequency shift appears to be maintained either by genetic evolution or by exposure to noise early in life during song learning before these males were captured. One piece of evidence suggests that early song learning cannot fully explain the persistent frequency difference. Song types that were shared between the common garden and field populations, which were likely memorized before capture, had an identical average minimum frequency to unshared song types that likely developed later in the quiet common garden. This observation is consistent with genetic divergence between the urban and rural populations.

Forest fragmentation in the Amazon reduces the attendance of ant-following birds at army-ant swarms

Patricia F. Rodrigues and Philip C. Stouffer
Presenting author: **Patricia Rodrigues**, Louisiana State University, prodr16@lsu.edu

Neotropical ant-following birds that forage on fleeing arthropods at army ant swarms are consistently identified as one of the most vulnerable avian guilds to anthropogenic disturbance. At the Biological Dynamics of Forest Fragments Project (BDFFP) in central Amazonia, obligate ant-following birds disappeared completely from fragments for up to 5 years following isolation. To examine the long-term effects of fragmentation on the attendance of ant-following birds at army ant swarms, we used 40 years of bird capture data from the BDFFP to retroactively assemble virtual ant-following bird flocks. We then calculated the frequency of attendance at swarms and the proportion of attending to non-attending ant-following birds in fragments before and following isolation. Attendance rates of ant-following birds declined by 45% and 54% in 1ha and 10ha fragments, respectively, following fragmentation. Ant-followers did not resume attending swarms until 8-11 years following isolation, with attendance rates in 10ha fragments returning to pre-isolation rates only after 23 years. Furthermore, the number of attending ant-following birds did not increase with increasing abundance. These results suggest that despite species abundance in fragments increasing as the surrounding forest regenerate, birds may take decades to return to their respective functional roles following disturbance. When measuring the impact of forest fragmentation on birds, researchers should be cautious when using species abundance alone as a metric.

Evaluating the effects of climate change on Yellow Warblers (Setophaga petechia) using telomeres as a biomarker of fitness

Marina D. Rodriguez, Kristen C. Ruegg, and Rachael A. Bay
Presenting author: **Marina Rodriguez**, Colorado State University, mdrod@colostate.edu

The ability of populations to persist when faced with rapidly changing climate conditions depends on their capacity to adapt. Recent work in birds has shown that regions of greatest mismatch between current and future predicted gene-environment relationships, also know of as regions of high 'genomic vulnerability,' are associated with past population declines. While these results are suggestive of the idea that past population declines in some bird species may be due to stress induced by climate change, the results are not conclusive because of the mismatch between the timescale of past declines and the timescale of the modeled future mismatches in gene-environment relationships. A direct link between climate-induced stress and fitness loss is therefore needed to test the role of climate change in recent population declines in birds. Here we use telomere length as biomarker for individual fitness to test the hypothesis that the failure to adapt to changing climate conditions in the wide-ranging Neotropical migratory bird, the Yellow Warbler, can in part explain population declines. To carry out this study, we measure telomere length in Yellow Warbler populations across a gradient in genomic vulnerability throughout the species' breeding range. This work will give insight into the current detrimental effects of climate change across Yellow Warbler populations as well as provide a method for assessing the impact of climate change on species more generally.

Developing aVOICE: An interactive tool for comparative bioacoustics

Carlos Antonio Rodriguez-Saltos, Hans T. Bilger, Chad M. Eliason, and Julia A. Clarke
Presenting author: **Carlos Rodriguez-Saltos**, University of Texas at Austin, carodr@utexas.edu

An emerging goal in comparative bioacoustics is understanding the evolution of acoustic traits related to innovations in sound production. This endeavor is being supported by massive databases of crowd-sourced audio recordings and computational techniques enabling comparative analyses of new depth and rigor. As researchers make use of these opportunities, however, they also find challenges related to working with large acoustic datasets. For example, despite significant progress in automation of acoustic measurements, human supervision is still required. Tools for systematic supervision of large acoustic datasets, however, are limited in capability and scope. Moreover, acoustic measurements are typically transferred to separate programs for downstream analyses, in pipelines that can be tedious to replicate. To begin to address these challenges, we are developing aVOICE, an open-source R-based platform that combines existing tools for acoustic feature extraction and dimension reduction and presents new tools for phylogenetically-informed data visualization. aVOICE will measure acoustic features on sets of vocalizations and

use them to estimate repertoire size using n-dimensional hypervolumes. A graphical user interface will allow calibrating and supervising acoustic measurements and interactively exploring distributions of vocalizations in a multidimensional space. To preview the functionalities of aVOICE, we use it to compare vocalizations in groups of birds and mammals. We filter and segment recordings, supervise automated measurements, estimate hypervolumes, and conduct phylogenetically-informed comparisons. We hope that this tool will contribute to integrating and standardizing comparative bioacoustic analyses.

Birds of many microbes flock together: Genetic and environmental drivers of microbial colonization in a wild sparrow

Sage D. Rohrer, Patricia G. Parker, and Lon M. Chubiz
Presenting author: **Sage Rohrer**, University of Missouri-St. Louis, sdrq5f@umsl.edu

Wild birds are teeming with bacteria, which colonize the various habitats of a host's body and collectively form the 'microbiome.' These microbes impact host health in diverse ways; some long-term residents may aid digestion or provide immune system training, while others at times may induce disease. However, the drivers of microbial colonization are complex and still not fully understood, and wild avian populations are particularly understudied when compared to mammalian or domesticated systems. Here we aim to disentangle genetic and environmental factors driving the composition and function of the gut microbiome of a locally introduced species, the Eurasian Tree Sparrow, focusing on the influence of the major histocompatibility complex (MHC). The MHC is a promising target for host modulation of the gut microbiome due to its known role in facilitating the adaptive immune response to pathogenic invaders, and the MHC has been implicated in other studies as shaping the gut microbiome in laboratory rodents and wild sticklebacks. We captured ~170 tree sparrows using mist nets from sites in Saint Louis County, collected fecal and blood samples, and extracted genomic DNA from both feces and blood. We then used 16S rRNA gene sequencing to characterize the fecal bacteria and targeted amplicon sequencing to genotype sparrows based on a highly polymorphic immune system marker, MHCII exon 2. Results show that the gut microbiome in this species is primarily shaped by location, season, and MHC genotype.

Long-term demography of a reintroduced and isolated population of endangered falcons

Brian W. Rolek, Benjamin Pauli, Alberto Macias-Duarte, Brian Mutch, Paul Juergens, Tim Anderson, Chris Parish, Jeff Johnson, Brian Millsap, and Christopher J. W. McClure
Presenting author: **Brian Rolek**, The Peregrine Fund, rolek.brian@peregrinefund.org

We examined demography of an endangered subspecies, the Northern Aplomado Falcon (*Falco femoralis septentrionalis*), in South Texas, USA. The Peregrine Fund has intensively managed and monitored this population since reintroductions began in 1993. Data spanning 1993–2018 enabled us to build an integrated population model to estimate survival for all life stages, abundance, fecundity, immigration, and emigration. Models revealed that male falcons survived at lower rates than females during their first year; Hurricane Harvey caused a decline in survival rates; and fecundity increased after 2012 coinciding with improvements in management. Both immigration and emigration were negligible for this population indicating an isolated population that probably lacks rescue effects from neighboring populations. Population growth rates were greatest during years having greater numbers of released captive-bred young and greater probabilities of breeder survival. Importantly, breeder survival declined sharply during 2006 to 2008; however, the cause of decline in breeder survival was unknown. Determining the cause of this low breeder survival period could be important for informing the management of populations. Our study greatly improves knowledge and understanding of demographics for a reintroduced, isolated, and intensively managed population of Northern Aplomado Falcons. This modeling framework will enable adaptive management of the South Texas population by providing annual evaluations of vital rates, and will allow a nimble assessment and deployment of management. Lastly, these demographic estimates can be used to inform population viability analyses for evaluation of the relative persistence of populations.

Not singing in the rain: Linking migratory songbird declines with increasing precipitation and brood parasitism vulnerability

Kristen M. Rosamond, Sandra Goded, Alaaeldin Soultan, Rachel H. Kaplan, Alex Glass, Daniel H. Kim, and Nico Arcilla
Presenting author: **Kristen Rosamond**, International Bird Conservation Partnership, kristenrosamond@gmail.com

Few studies have quantified relationships between weather and migratory songbirds, but such research is vital at a time when rapid climate change may disproportionately affect species in temperate grasslands, which are among the most altered and endangered ecosystems globally. We examined the influence of changing weather on the Dickcissel (*Spiza americana*), a migratory songbird of conservation concern and an obligate grassland specialist. Our study area in the North American Great Plains features high historic weather variability, and climate change has been driving higher precipitation and temperatures during the last decade. Brown-headed Cowbirds (*Molothrus ater*), brood parasites that reduce Dickcissel productivity, are also present on these breeding grounds. We used 9 years of capture-recapture data to test whether increasing precipitation on Dickcissels' riparian breeding grounds is associated with abundance declines and increasing vulnerability to cowbird parasitism. We found that Dickcissels declined with increasing June precipitation while cowbirds increased. Dickcissel productivity appeared to be very low, with a 3:1 ratio of breeding male to female Dickcissels likely undermining reproductive success. Our findings suggest that increasing precipitation in this region may drive future declines of Dickcissels and other songbirds. Positive correlations of June-July precipitation, temperature, and time since grazing with Dickcissel productivity did not mitigate Dickcissels' declining trend in this ecosystem. Our findings highlight the importance of empirical research on the effects of precipitation and brood parasitism vulnerability on migratory songbirds to inform adaptive management under climate change.

The impacts of irruption on chickadee social stability

Michael G. Rowley, Christie L. Eldredge, Matt N. Dula, Rebecca D. Garlinger, Breanna L. Bennett, and Robert L. Curry

Presenting author: **Michael Rowley**, Villanova University, mrowley01@gmail.com

Social stability—the consistency of relationships and group structure over time—can be disrupted by changes in ecological context. This study's goal was to determine whether social stability is impacted by irruption. I compared patterns of nonbreeding social stability in resident Carolina Chickadees (*Poecile carolinensis*) between years with and without irruptive Black-capped Chickadees (*P. atricapillus*). I used social network analysis of visitation data from RFID-equipped feeders to assess social stability across three organizational levels. Irruptive Black-capped Chickadees had stronger relationships and greater social involvement over time than did Carolina Chickadees, but irruption did not affect Carolina Chickadee social stability. These patterns suggest that social stability is robust to ecological change but comparing additional modes of social organization could provide more insight.

Solving a nearly 200-year mystery to identify the oldest avian nest specimen in the Natural History Museum London

Douglas G. D. Russell, Tomo Yoshino, Elisa Yang, and Jackie L. Childers

Presenting author: **Tomo Yoshino**, Museum of Vertebrate Zoology, UC Berkeley, yoshinot@berkeley.edu

Nests offer great potential in understanding avian life history, however, they remain relatively understudied in natural history collections. The nests of the weaverbird family (Ploceidae) are especially intriguing as they exhibit elaborate nest design, with many species constructing complex woven structures. The Natural History Museum London (NHMUK) possesses one of the most expansive nest collections globally, with ca. 4500 specimens. One specimen of particular interest is N.178.1/1866.11.17.4, as it stands as the oldest nest specimen in NHMUK and possibly one of the oldest nests in any museum collection. This weaver nest was collected as part of the 1841 Niger Expedition, where a group of British missionaries and naturalists embarked on an expedition to West Africa to oppose the slave trade and promote economic independence among Africans. Although the nest's history and age make it a vital specimen, the weaver species associated with N.178.1 remains unidentified. To identify this unknown specimen, we combined historical information from the expedition with morphological data from 140 nest specimens from several museums. Based on field notes, we hypothesize that the nest was likely collected near coastal Ghana; thus, we looked at nine ploceids that occur in the region. Morphological data were collected for each species, including metrics related to nest size, shape, and material composition. We then performed a linear discriminant analysis (LDA) using these measurements from the candidate species combined with the data collected from N.178.1 to predict its probability of belonging to one of the nine candidates. Our LDA results indicate that the nest most likely belongs to *Ploceus cucullatus* ($p = 0.73$).

Life-history attributes of Arctic-breeding birds may yield uneven responses to environmental variability across different phases of the reproductive cycle

Daniel R. Ruthrauff, Vijay P. Patil, Jerry W. Hupp, and David H. Ward

Presenting author: **Daniel Ruthrauff**, US Geological Survey, druthrauff@usgs.gov

Animals exhibit varied life-history traits that reflect adaptive responses to their environments. For Arctic-breeding birds, traits like foraging guild, egg nutrient allocation, clutch size, and patterns of chick growth are predicted to be under increasing selection pressure due to climate change. We compared the reproductive responses of four migratory birds (Black Brant, Lesser Snow Geese, Semipalmated Sandpipers, and Lapland Longspurs) with varied life histories at an Arctic site in Alaska, USA, from 2011–2018. Semipalmated Sandpipers advanced their site arrival and bred in higher numbers in response to early snow melt and warm temperatures, while Brant and Snow Geese advanced their nest initiation dates and increased their clutch sizes. During chick rearing, longspur chicks were relatively resilient to environmental variation whereas warmer temperatures increased the growth rates of sandpiper chicks but reduced growth rates of Snow Goose goslings. These responses generally aligned with traits along the capital-income spectrum of nutrient allocation and altricial-precocial modes of chick growth. Under a warming climate, the ability to mobilize endogenous reserves likely provides geese with relative flexibility to adjust the timing of breeding and the size of clutches. Warmer temperatures, however, may negatively affect the quality of herbaceous foods and slow gosling growth. Thus, as the Arctic warms, species may possess traits that are beneficial during one phase of the reproductive cycle and others that may be detrimental at another phase, underscoring the need to consider both the nesting and brood rearing periods when assessing the effects of environmental variability on Arctic-breeding birds.

Long-term capture data reveal temporal shifts in activity patterns of Amazonian birds

Cameron L. Rutt, W. Justin Cooper, and David A. Luther

Presenting author: **Cameron Rutt**, George Mason University, cameronrutt@gmail.com

Although the frequency of biological rhythms varies from milliseconds to decades, daily rhythms are especially widespread for individual organisms. These circadian rhythms are synchronized by light-dark cycles but increasing light intensity predictably covaries with microclimatic variables. Despite the fixed nature of daily cycles at low latitudes, little is known about the daily structure of avian activity. Here, we repurposed a long-term banding dataset from primary Amazon rainforest to characterize activity patterns (time of capture) for 65 species of birds in the lowest forest strata (0-2.5 m). Employing ~25,000 unique captures throughout the annual cycle, we found a diversity of species-specific responses. Although activity for most species (71%) peaked within the first two hours after sunrise, others peaked 1-3 hours later. Responses were further organized by guild and strata: terrestrial and near-ground insectivores peaked sharply about an hour after sunrise, while birds from higher strata delayed their arrivals into the lower understory. Our results also reveal a general relationship between timing and length of activity. Early morning species showed a narrow band of peak activity, whereas those most active later in the morning were regularly captured across a wide range of times, suggesting that these species may function as temporal specialists and generalists, respectively. These designations correlated strongly with local abundance trends, indicating that associations with certain microclimates may be contributing to both vulnerable and resilient species. Finally, we offer recommendations to standardize capture effort and encourage cautious interpretation of any data with delays or advances in start times.

Island endemic or recent introduction? Genomic data from historical specimens reveal the complex origin of Cuban bobwhites (*Colinus virginianus cubanensis*)

Jessie F. Salter, Robb T. Brumfield, and Brant C. Faircloth

Presenting author: **Jessie Salter**, Louisiana State University, jsalte5@lsu.edu

The evolutionary history of Cuban bobwhites (*Colinus virginianus cubanensis*) has been a source of controversy among ornithologists for nearly two-hundred years. Since bobwhites were first observed in Cuba in 1839, natural historians have debated whether the birds are island endemics or more recent introductions to Cuba from the southeastern United States. Adding to the confusion, bobwhites from the U.S. have been periodically introduced to Cuba since the late nineteenth century, resulting in birds of intermediate phenotypes. Genetic analyses of a few individuals have also produced conflicting results: a recent study of mtDNA showed no differentiation in haplotypes between Cuban and southeastern U.S. populations of bobwhites, while preliminary data using thousands of UCEs suggest that Cuban bobwhites are most closely related to bobwhites in southern Mexico. To better assess the origin and demographic history of Cuban bobwhites, we collected RAD-seq data from 124 historical bobwhite specimens collected from Cuba and potential source populations in Mexico and the southeastern U.S., including purported hybrids between Cuban and Florida bobwhites, and specimens from Cuban populations with varying histories of recent human involvement. Although we found evidence consistent with recent introductions from Florida, our results suggest that Cuban bobwhites are more closely related to bobwhite populations in Mexico. Furthermore, our data suggest that Cuban bobwhites have been isolated from mainland populations for longer than previously thought, casting doubt on a scenario of recent human introduction.

Avian community structure across an urbanizing county: The effects of noise, light, and landscape composition

Karina A. Sanchez, Cameron Kennedy, and Lauryn Benedict

Presenting author: **Karina Sanchez**, University of Northern Colorado, karina.sanchez@unco.edu

Urban development has drastically altered ecosystems and in turn, we have seen dramatic effects on avian diversity and community structure. Accordingly, there has been a surge of interest in understanding the effects of urbanization on wildlife, but studies have not been conducted in all urban ecosystems. Most studies are conducted in large and established cities, with fewer conducted in areas of current rapid urbanization. While current anthropogenic development may result in similar habitats as development in the past, the pace at which urbanization occurs today is notably faster. Measuring community structure in recently established and growing cities is necessary to understand what species are currently being affected by the process of rapid urbanization. This study investigated the relationship between avian communities and urban characteristics in one of the United States' fastest growing metropolitan areas. I tested the general hypothesis that avian community assemblages will vary with multiple urban characteristics. I measured noise, light, and landscape composition across 20 sites and paired this data with avian species census data. Preliminary results suggest variability within the landscape in noise, light, and land characteristics align with avian community structure. Importantly, this variation does not exist on a linear urban to non-urban gradient, meaning that urbanization can have patchy and unpredictable effects, highlighting the value of measuring urban characteristics separately. Additionally, this study emphasizes how sampling newly developed areas captures the effects of urbanization on species present during the process rather than those who remain or move into urban areas following development.

Does vegetation structure shape the acoustic features of Lincoln's Sparrow songs in Alberta?

Natalie V. Sánchez, Branko Hilje, and Erin M. Bayne

Presenting author: **Natalie V. Sánchez**, University of Alberta, sanchezu@ualberta.ca

Song variation within passerine birds has typically been explained by social interactions or local adaptations to a particular environment. In sparrows, there is evidence of songs adapting to certain vegetation structure even if theirs songs are simple or highly variable. For a less studied sparrow, the Lincoln's Sparrow (*Melospiza lincolnii*), we aimed to describe the variation on its songs' across different ecosystems in Alberta using autonomous recording units. To explain differences in acoustic features along the province, we used geographic location of songs and vegetation structure. For this, we first created a song catalog to classify song types and syllable types. Then, we measured the acoustic structure of songs and unique syllables found for each male using spectrogram and power spectra view. We performed multivariate analysis testing for the effect of space and vegetation on acoustic features. We identified 68 individuals, 69 songs and 127 syllable types. We did not find evidence of geographic structure in terms of song types demonstrating high syllable sharing across Alberta. Birds sang higher-frequency songs in open areas such as grass and shrubs. Finally, unique syllables were lower in frequency in coniferous forest (denser vegetation). Therefore, Lincoln's Sparrow adjusted their songs by vegetation type. This study is a contribution to the understanding of song variation of a common sparrow at a large geographic scale.

Nocturnal roost on South Carolina coast supports nearly half of Atlantic coast population of Hudsonian Whimbrel (*Numenius phaeopus*) during northward migration

Felicia J. Sanders, Maina C. Handmaker, Andrew S. Johnson, and Nathan R. Senner

Presenting author: **Maina Handmaker**, University of South Carolina, maina.handmaker@gmail.com

Hudsonian Whimbrel (*Numenius phaeopus*) are rapidly declining and understanding their use of migratory staging sites is a top research priority. Nocturnal roosts are an essential, yet often overlooked component of staging sites due to their apparent rarity, inaccessibility, and inconspicuousness. The coast of Georgia and South Carolina is one of two known important staging areas for Atlantic coast Whimbrel during spring migration. Within this critical staging area, we discovered the largest known Whimbrel nocturnal roost in the Western Hemisphere at Deveaux Bank, South Carolina. Surveys in 2019 and 2020 during peak spring migration revealed that Deveaux Bank supports at least 19,485 roosting Whimbrel, which represents approximately 49% of the estimated eastern population of Whimbrel and 24% of the entire North American population. We deployed GPS transmitters on Whimbrel at Deveaux Bank to track individuals' daily movements to and from this nocturnal roost and diurnal foraging areas, beginning a longer-term effort to better understand the role this critical roost site plays in the staging ecology of Atlantic flyway Whimbrel.

Drab males, sweet talkers: Larger song repertoires in males with less conspicuous plumage patterns

Luis Sandoval and Diego Ocampo
Presenting author: **Luis Sandoval**, Universidad de Costa Rica, biosandoval@gmail.com

Sexual selection favors the evolution of characters (e.g., morphology or behavior) that increase the individuals' probability of reproduction. Plumage color may play an important role in mate choice and females often select their mates based on such traits. For example, the strong sexual selection often results in sexual dichromatism with males presenting colorful plumages compared to females, in birds such as manakins, cotingas, or hummingbirds. On the other hand, females may use male solo songs as another signal to select males. For example, in canaries and house finches, females prefer males with the longest songs. However, the relationship between color patterns and song repertoires in males is an open question, especially in species where males have very different plumage patterns. Therefore, our objective was to compare the song repertoire from males with different color morphs in Variable Seedeater (*Sporophila corvina*). We counted the number of different song elements (smaller unit of sound) in five songs per male of 41 black, 53 black-and-white, and 10 individuals with hybrid plumages. We found that males with black plumage had song repertoires with >20 or more songs; meanwhile, males with black-and-white and hybrid plumages had repertoire with <20 song types. Additionally, males with black plumages produce more trill elements than black-and-white males and hybrids. In this species, larger repertoires with more trills (an element associated with vocal performance) may compensate for the lack of plumage conspicuousness in female selection.

Changes in bird abundance and phenology in the world's southernmost forest

Erik M. Sandvig, Claudio S. Quilodrán, Juan Rivero de Aguilar, Francisco Aguirre, Omar Barroso, Rodrigo Vásquez, and Ricardo Rozzi
Presenting author: **Erik Sandvig**, Instituto de Ecología y Biodiversidad, Universidad de Chile, chilesummits@gmail.com

Climate change is broadly recognized as one of the most serious threats to global biodiversity. The forests protected by the Cape Horn Biosphere Reserve in southern Patagonia have been described as one of the world's most pristine places, but little is known about the impact of climatic variables on its biodiversity. Here, we report on changes in bird abundance and migration timing from a 20-year capture-recapture monitoring project in the reserve, and its relationship with climatic variables. We found that the relative abundance of all species and the length of stay for migratory species has decreased over the last 20 years. In addition, over this period, precipitation has increased during autumn and winter, while temperature has decreased in winter. These climatic variations have influenced the timing of migratory birds, with increasing precipitation and temperature postponing arrival dates, and decreasing temperature contributing to earlier departures. These results provide evidence of the impacts of climate change on forest birds in even the most pristine landscapes and the importance of long-term bird monitoring programs for identifying these effects. The Cape Horn Biosphere Reserve is showcased as a unique natural laboratory to explore the global impact of climate change in one of the few remaining untouched places of the world.

Modeling breeding phenology from the North American Breeding Bird Survey

John R. Sauer and William A. Link
Presenting author: **John Sauer**, Eastern Environmental Science Center, jrsauer@usgs.gov

Changing climate has modified the phenology of birds and their food resources across North America. We modeled phenology effects for 426 bird species from North American Breeding Bird Survey (BBS) data collected across North America from 1966 – 2019. We modified the hierarchical models used for estimation of population change, adding covariates to model relative counts on routes as a function of yearday and latitude. Modeling phenology effects from BBS data provides information regarding changes in breeding activity, informing our understanding of how changing climate has influenced bird activity across North America and providing critical insights into the validity of BBS protocols and analyses. BBS protocols recommend that surveys be conducted on the same date each year. If phenology changes over time and space are causing shifts in visibility of birds through the breeding season, modeling phenology effects (as indexed by yeardays) allows us to both document and control for bias in estimates of population change. For each species we produced summaries of relative visibility by yearday for selected years and latitudes, documented whether counts varied through the season, and specified timing of peak counts within the acceptable days for counting as defined by BBS protocols. For many species, large differences occurred in visibility within the BBS counting period; overall patterns reflected well-known species patterns of early and late-breeding species. Although many patterns exist in temporal and spatial changes in yearly visibility, it does not appear that peak visibility has been occurring earlier in the survey period for most species.

Integrating data types to quantify multi-species migratory connectivity

Sarah P. Saunders, William V. DeLuca, Timothy D. Meehan, Nicole L. Michel, Jill L. Deppe, Nat Seavy, and Chad B. Wilsey

Presenting author: **Sarah Saunders**, National Audubon Society, sarah.saunders@audubon.org

Migratory birds spend subsequent seasons in different geographical regions, and the connection between breeding and non-breeding areas is defined as migratory connectivity. The quantification of connectivity is important, especially across species groups, as movements between different regions can have important consequences for individuals, as well as for populations. Connectivity is typically investigated using either band re-encounters or observations of tracked animals by remote-sensing technologies (e.g., GPS, geolocators). Here, we quantify migratory connectivity by statistically integrating individual tracking data and band re-encounter data via a joint likelihood within a Bayesian framework. The integration of tracking and band re-encounter data reduces sampling biases and allows for information sharing across migration datasets. We apply this framework to 40 migratory bird species to estimate species-specific migratory connectivity, and then average estimates across four terrestrial species groups (birds breeding in the Canadian Boreal, US Western Lands, US Grasslands, and US Eastern Forests) to approximate multi-species connectivity across the Western Hemisphere. This integrated framework can be used to: (1) fill knowledge gaps for species with limited information on spatial migration patterns; and (2) illustrate full-annual-cycle connections across multiple species that overlap in their breeding ranges. Our findings will be shared with stakeholders via an interactive ArcGIS Online platform such that users will be able to access species-level connectivity results and identify multi-species connections between their regions of interest, advancing conservation planning for migratory bird species in the Americas.

Geolocators reveal diversity of molt and migration strategies within a single population of Lazuli Bunting

Kim Savides and Clark Rushing

Presenting author: **Kim Savides**, Utah State University, kim.savides@gmail.com

Molt migration is a common strategy among Neotropical migrating birds in western North America that is hypothesized to result from birds being 'pushed' off arid breeding grounds and 'pulled' towards more productive areas, causing a suspension in prebasic molts. Molt migration has been documented using specimens and banding captures, however studies directly observing molt during migration are rare. We deployed 25 light-level geolocators on male Lazuli Buntings (*Passerina amoena*) – a species thought to be an obligate stopover molt migrant – in Cache County, Utah, USA to investigate possible molt migration behaviors in this species. Preliminary results show little support for obligate stopover molt migration in the species. Four birds remained in northern Utah for 40 to 60 days after departing the study site, during which they may have molted. The remaining bird migrated south, stopping over in Chihuahua, MX for 40 days. Most individuals wintered along the border between Sinaloa and Sonora, MX, while one individual wintered 500km further south. We additionally found two distinct spring migratory routes, a direct south-north route with several multi-day stopovers, and a longer, looped route through California and Nevada with fewer and shorter stops. Despite differences in spring route, all birds arrived at the breeding grounds on similar dates.

Our research highlights the diversity of molt and migration strategies within a species and emphasizes the importance of integrating information from specimens, banding, and direct tracking to better understand migration.

Mercury in Neotropical birds: A collaborative approach to overcome current challenges

Christopher J. Sayers II, Viviana Ruiz-Gutierrez, David C. Evers, Noe R. Huaraca-Charca, Claudia M. Vega, Jessica Pisconte, Luis E. Fernandez, Oksana P. Lane, Kevin Regan, Evan Adams, Timothy Tear, Wayne Arendt, Marvin Tórrez, Reynold Cal, Wilber Martínez, Stevan Reneau, Mrinalini Erkenswick Watsa, Gideon Erkenswick Watsa, Ari E. Martínez, Jacqueline Gerson, Emily Bernhardt, Victor Sánchez, and Raúl Omar Pérez

Presenting author: **Christopher Sayers**, Biodiversity Research Institute, cjs347@cornell.edu

The monitoring of anthropogenic mercury (Hg) exposure to wildlife has been severely neglected throughout the Neotropics. This lack of prioritization has limited our capacity to assess the impacts of the ongoing degradation of primary forests via illegal gold mining activities, the largest polluting sector of environmental Hg in the world, on neotropical biodiversity. Due to their global abundance and relative ease of detection, capture, and identification compared to other taxa, birds stand apart as the most cost-effective organism for biodiversity and ecotoxicological monitoring in tropical, terrestrial systems. Here, we summarize the largest dataset on neotropical bird Hg concentrations: with over 1700 blood and feather samples from 265 species in 14 countries across Central America, South America, and the Antilles. Our findings align well with those documented in temperate regions, in which there was high spatial variability in Hg exposure, and bird Hg concentrations tended to be highest in species that occupy higher trophic positions — such as piscivores and invertivores. To make future Hg biomonitoring efforts more efficient and comparable, we created an inclusive and equitable data-sharing platform that unites an international network of tropical ornithologists. By standardizing sampling methods among contributing monitoring programs and prioritizing key polluting zones and sentinel species, the Tropical Research for Avian Conservation and Ecotoxicology (TRACE) Initiative seeks to better inform conservation decision making through the understanding of the prevalence, persistence, and distribution of anthropogenic Hg in tropical biomes, and how this ecotoxin impacts both resident and migratory bird populations.

Constraints imposed by migrating warblers on breeding warbler signal space

Joanna M. Sblendorio, Maarten J. Vonhof, and Sharon A. Gill

Presenting author: **Joanna Sblendorio**, Western Michigan University, joanna.sblendorio@wmich.edu

Signals evolve under multiple selective pressures, including conspecifics, heterospecifics, and the environment. Co-existing species may compete for signal space, but typically inhabit well-defined acoustic niches, minimizing signal overlap among species. While partitioning of signal space has been envisioned to result from competition among syntopically breeding species, reports of species singing during migration suggest additional, unexplored constraints on partitioning of signal space. We hypothesized that migrant warblers constrain signal space of breeding warblers and that patterns of niche overlap vary depending on the migrants present in the community. We recorded songs of 11 breeding and 19 migrant warbler species in southwest Michigan, analyzed acoustic niches, and used eBird data to determine temporal co-occurrence among species. Migrant warblers were present for 51 days of the breeding season, with a maximum of 28 species co-occurring over this period. Most species inhabited distinct acoustic niches: only 11% of pairs (n=48 of 435) overlapped. However, the number of overlaps by type (migrant-migrant, migrant-breeding, breeding-breeding) differed over time: migrant-breeding overlaps were most common and peaked when the community was at its fullest. The extent of total niche overlap (range: 0 to 87% of niche volume) was idiosyncratic: some breeding species experienced greater overlap from migrants (avg:9%; range:0-50%), while others were overlapped more by other breeding species (avg:21%; range:0-72%). Our study is the first to explore whether migrants influence partitioning of acoustic space and finds that transient community members may influence both competition for acoustic space and signal evolution.

North American waterfowl migratory connectivity across flyways

Amy L. Scarpignato, Anthony J. Roberts, Allison Huysman, Peter P. Marra, and Emily B. Cohen

Presenting author: **Amy Scarpignato**, Smithsonian Migratory Bird Center, scarpignatoa@si.edu

Flyway designations (Atlantic, Mississippi, Central and Pacific) are used to facilitate management of waterfowl species that migrate between nesting and wintering areas in North America. The strength of migratory connectivity, the co-occurrence of populations throughout the annual cycle, is assumed to be high for waterfowl species managed within flyways between breeding and wintering periods. We used banding and recovery data from 1960-2019, to determine the extent to which waterfowl species remain within flyways between seasons and if these values have changed over the 60 year time period that the data were collected. We further evaluated if movement probabilities vary by age, among species, or by guild for 10 species of dabbling (tribe Anatini) and 5 species of diving (tribe Aythyini) ducks and estimated the strength of migratory connectivity metric (MC) among flyways. We found weaker MC than expected among species and guilds. For example, in the last decade (2010-2019) 35-65% of adult Green-winged Teal (*Anas crecca*) were wintering within the same flyway as they bred. With this mixing of breeding populations among flyways during the wintering period, MC was lower than we expected (0.154 ± 0.06). Though harvest management is done at the flyway scale, managers need to be aware of the level of impact their decisions may have on other flyways, and how connected North American waterfowl populations are.

Degree of habitat heterogeneity correlates with the evolution of plumage colorfulness in both males and females (Cardinalidae)

Benjamin F. Scott, Allison J. Shultz, and Kevin J. Burns

Presenting author: **Benjamin Scott**, San Diego State University, bfscott1906@gmail.com

Habitat has routinely been demonstrated to be an important aspect in the evolution of plumage coloration. However, few studies have attempted to quantify habitat beyond categorical metrics. Habitats are complex, highly dimensional interfaces where selection can vary over both space and time. How do we truly quantify habitat when analyzing the evolution of plumage coloration? Here, we assess how fine-scale differences in ecogeographic variables drive evolutionary changes in male and female coloration in the family Cardinalidae. Using the open-source platform Google Earth Engine, we collected data on percent forest cover, climate, land cover types, and multiple time-series vegetation indices. We additionally compared species distributions models, IUCN range maps, and minimum convex hull polygons to assess how user defined estimates of species ranges impact spatial results on an evolutionary timescale. Using a PGLS framework, and a new phylogeny based on ultra-conserved elements, we find that evolutionary changes in plumage complexity are not correlated with forest cover or land cover. Instead, we find that males in more heterogeneous habitats tend to have more colorful plumage while males in more homogenous habitats tend to have drabber plumage. Interestingly, we find the female color complexity is positively correlated with habitats with higher variation in the visible-red wavelength, but that male plumage complexity is not. These results highlight the importance of incorporating large geospatial databases into the field of color evolution, especially when assessing how alternative selective pressures influence color in a sexually dichromatic family.

A genus at risk: Predicted current and future distribution of all three *Lagopus* species reveal sensitivity to climate change and efficacy of protected areas

Davide Scridel, Mattia Brambilla, Devin de Zwaan, Nick Froese, Scott Wilson, Paolo Pedrini, and Kathy Martin

Presenting author: **Davide Scridel**, University of British Columbia, davidescridel@hotmail.co.uk

Cold-adapted species are considered vulnerable to climate change. However, our understanding of how such sensitivity will influence habitat suitability remains poorly understood, particularly for species at high latitudes or elevations. Using community science observations from 1970–2020, we built distribution models for ptarmigan (*Lagopus* spp.) across British Columbia, a globally unique region harbouring all the species belonging to this genus. White-tailed Ptarmigan (*L. leucura*) and Rock Ptarmigan (*L. muta*) were associated with colder temperatures and tundra-like open habitats, and Willow Ptarmigan (*L. lagopus*) with open, shrub habitats. Future projections based on climate and vegetation scenarios indicated marked losses in suitable habitat by the 2080s (RCP +8.5 W/m^2), with range declines of 85.6% and 79.5% for White-tailed and Rock ptarmigan, respectively, and of 61.3% for Willow Ptarmigan. Predicted current and future suitable habitat occurred primarily outside of current protected areas ('PAs'; 67–82%), yet range size declined at a less pronounced rate within PAs suggesting a capacity to buffer habitat loss. Ptarmigan are predicted to persist at higher elevations and latitudes than currently occupied, with the magnitude of elevation shifts consistent with trends observed elsewhere in the Holarctic. Our spatially explicit assessment of potential current and future distributions of ptarmigan species provides the first comparative evaluation of climate change effects on the distribution of three congeneric, cold-adapted species with different habitat preferences and life-history traits. We also highlight the potential role of PAs in preserving suitable sites for these and other climate-sensitive species in the future.

Elevation and niche divergence in Mexican Yellow Grosbeaks (*Pheucticus chrysopeplus*)

Maeve B. Secor and John E. McCormack

Presenting author: **Maeve Secor**, Moore Laboratory of Zoology, Occidental College, msecor@oxy.edu

Ecology's role in the evolution of species is a fundamental question of evolutionary biology. Some studies have found that the niches of allopatric sister taxa tend to be ecologically similar, while others have found evidence that allopatric speciation is associated with niche divergence. The Mexican Highlands comprise a global biodiversity hotspot where isolated mountain ranges allow for tests of the role of allopatry and ecology in diversification. The Yellow Grosbeak (*Pheucticus chrysopeplus*) is an endemic species of the Mexican foothills and highlands. It is thought to occupy different niches and elevations across its range, presenting an opportunity to test for niche differentiation during the process of speciation. Using univariate and multivariate analysis of environmental variables on rainfall, temperature, and habitat characteristics, we show that there is evidence of niche divergence among the three main lineages of *Pheucticus chrysopeplus*. Niche models suggest that two distinct populations within the established subspecies *P. c. chrysopeplus* occupy substantially divergent niches, with the northern group inhabiting lower elevations with higher temperatures and more rainfall. Lineages split across the Isthmus of Tehuantepec, a major biogeographic barrier in Southern Mexico, also show evidence for niche divergence. Together, results suggest Yellow Grosbeaks have made a dramatic shift in their elevation and environmental niches during divergence across the Mexican Highlands.

Variations in genomic architecture among Horned Larks (*Eremophila alpestris*) along an elevational gradient in western USA

Subir B. Shakya, Cynthia Y. Wang-Claypool, Carla Cicero, Rauri C.K. Bowie, and Nicholas A. Mason

Presenting author: **Subir Shakya**, Louisiana State University Museum of Natural Science, sshaky6@lsu.edu

Structural rearrangements of chromosomes underlie adaptive evolution in many systems and have gained increasing attention as drivers of local adaptation and diversification. Inversions, translocations, and genomic duplications have been observed among and within species and may play a major role in local adaptation. In this study we used RAD-seq and whole genome sequencing to assess variation in genomic structure among Horned Lark (Eremophila alpestris) populations distributed across an elevational gradient from Death Valley (below 0 m a.s.l.) to the top of White Mountain Peak (greater than 3000 m a.s.l.) in western USA. Our comparisons show three distinct patterns: (1) translocations through formation of neo-sex chromosomes, (2) inversions in the Z chromosome, and (3) elevational segregation of loci on some neo-sex scaffolds. In larks, large neo-sex chromosomes have been described previously, but our genomic analyses yield a novel picture of the extent of translocations on Z and W chromosomes and their possible role underlying local adaptation. We also identify potential inversions in the Z chromosome among larks at higher elevations and characterize candidate loci in these regions to look for genomic associations along an elevational transect. Sex chromosomes often play a major role in local adaptation, divergence, and speciation in many avian systems and seems to play a role in local adaptation in larks as well.

A torpor spectrum in hummingbirds: Can metabolism and body temperature be decoupled?

Anusha Shankar, Maren N Vitousek, and Donald R Powers

Presenting author: **Anusha Shankar**, Cornell University, nushiamme@gmail.com

Heterothermic animals are endotherms that can lower their body temperature, metabolic rate, and heart rate, to save energy. They use this strategy called torpor especially under challenging environmental conditions (such as under cold conditions or when food is scarce). Some mammal species, like black bears and many bat species, have been found to decouple heart rate, metabolism, and body temperature in torpor, often maintaining high body temperatures but slow heart rates, or high body temperatures and low metabolic rates. In birds, such decoupling during torpor has not received much attention. We recently found (with thermal imagery) that hummingbirds are able to use torpor to various depths; sometimes they avoid torpor entirely and maintain high surface temperatures (~35°C); or thermoconform and use deep torpor (<20°C); or lower their body temperatures moderately (to ~25-30°C) and use shallow torpor. We will now be using respirometry to measure metabolic rates, while also using thermal imagery to

measure surface temperatures of hummingbirds through the night, to test whether metabolism and body temperatures change together, or if they can be decoupled in hummingbirds. Given their small body sizes, and high surface area to volume ratios, we expect them to be coupled in all states except perhaps in shallow torpor where they might show some decoupling.

Seeking shelter: Winter weather constrains the behavioral flexibility of a winter-adapted bird

Amy A. Shipley and Benjamin Zuckerberg
Presenting author: **Amy Shipley**, University of Wisconsin-Madison, amyashipley@gmail.com

Behavioral flexibility is an important pathway by which animals respond to rapidly changing environmental conditions. Seeking out and accessing microrefugia is an important behavior that can protect animals from inclement weather, predation, and periods of rapid environmental change. During winter, snow serves as a seasonal microrefugium that provides thermal insulation and protects overwintering species from predators. However, snow depth and quality can be highly variable throughout the winter, and it is unclear how species that use snow cover as a microrefugium adjust their behavior with changing climatic conditions and in complex landscapes. We documented roosting behavior of a winter-adapted bird, the Ruffed Grouse (*Bonasa umbellus*), and found significant non-linear relationships between roosting behavior and snow conditions: grouse were more likely to use snow burrows when snow was deep and powdery. Further, grouse experienced warmer temperatures in snow burrows than in other roost types. Contrary to our predictions, cover types did not influence snow roosting behavior, and grouse were not more likely to use snow burrows at colder temperatures, potentially because snow roosting may serve to protect grouse from predators in addition to serving as thermal refugia. However, both the snow conditions necessary for snow roosting, and the occurrence of snow roosting behavior, were relatively rare and declined over the course of our study. Loss of winter microrefugia due to snow cover loss and climate change may severely limit the use of behavioral flexibility for winter-adapted species.

An integrated resource selection model to predict avian habitat use from grassland vegetation structure

Katy M. Silber, Trevor J. Hefley, and W. Alice Boyle
Presenting author: **Katy Silber**, Kansas State University, ksilber@ksu.edu

Grassland birds are highly mobile; many disperse among sites within and between years, yet we know little about how they make post-dispersal settlement decisions. At broad scales, birds often occur in higher densities in areas with heterogenous vegetation, but identifying the vegetation structures that some birds select at the territory level has remained elusive. Grassland vegetation varies in space and time; fire, grazing, and weather variability create heterogeneity in plant communities. Existing methods that quantify resource selection often create spatio-temporal misalignment between habitat and demographic data. To investigate the extent to which vegetation drives grassland bird settlement decisions, we collected point-level data on vegetation height and composition once per month from May-July 2014-2020 at the Konza Prairie Biological Station. Konza is a Long-Term Ecological Research site in NE Kansas consisting of native tallgrass prairie, managed using experimental combinations of fire and grazing. We developed a predictive model for vegetation height and cover at any point in space and time. We integrated these predictions with avian count data using an inhomogenous point process model to evaluate resource selection for Grasshopper Sparrows (*Ammodramus savannarum*), Dickcissels (*Spiza americana*), and Eastern Meadowlarks (*Sturnella magna*). We expected species to select for different vegetation structure and composition based on their life histories and nesting behaviors, and densities would change over time to track changes in vegetation. This study provides a framework for future research in integrated resource selection modeling, which can provide insight into land management for declining grassland birds.

Evolutionary history of the Chotoy Spinetail (*Schoeniophylax phryganophilus*, Aves: Furnariidae): A species with two allopatric populations in seasonally dry forests

Paulo J. V. da Silva-Neto, Layse A. da Silva Lucas, Lays V. de Freitas, Maria W. Pil, and Luciano N. Naka
Presenting author: **Paulo Silva-Neto**, Federal University of Pernambuco, paulonetoserafim2015@gmail.com

Seasonally Dry Forests (SDF) are patchily distributed throughout the Neotropics and hold a number of avian endemics and habitat specialists. Among these, is the Chotoy Spinetail (*Schoeniophylax phryganophilus*), which occurs in eastern South America, including two allopatric populations that inhabit the two largest nuclei of SDFs in South America, the Caatinga and the Gran Chaco. The Pleistocene Arc hypothesis, proposed by Prado and Gibbs in 1993, was developed to explain the existence of allopatric populations in isolated nuclei of SDFs. According to this model, SDFs expanded during glacial periods, and contracted and fragmented during interglacials. The 'Pleistocene Arc' refers to the continuous dry forests that allegedly thrived during glacial periods. To test this hypothesis, we studied the evolutionary history of *S. phryganophilus* and modeled its current and past ecological niche, evaluating the timing of separation. We produced a phylogeny using 10 protein-coding genes of the mitochondrial genome and evaluated the coancestrality of populations using thousands of nuclear loci obtained from 2761 independent SNPs from Ultra Conserved elements (UCEs). Our time-calibrated mitochondrial tree shows that the two populations are reciprocally monophyletic and indicate that their separation dates back to ~150,000 years ago, coinciding with the Last Interglacial, the last time that these forests were connected. These results were consistent with our past niche models, which points to a recent expansion in SDFs during the Last Glacial Maximum, in agreement with the Pleistocene Arc hypothesis. These results add to a growing body of evidence that shows the importance of climatic fluctuations to define current distribution patterns.

A weather surveillance radar view of Alaskan avian migration

Ashwin H. Sivakumar, Daniel Sheldon, Kevin Winner, Carolyn S. Burt, and Kyle G. Horton

Presenting author: **Ashwin Sivakumar**, Flintridge Preparatory School, ahs.birder@gmail.com

Monitoring avian migration within subarctic regions of the globe poses logistical challenges. Populations in these regions often encounter the most rapid effects of changing climates, and these seasonally productive areas are especially important in supporting bird populations—emphasizing the need for monitoring tools and strategies. To this end, we leverage the untapped potential of weather surveillance radar data to quantify active migration through the airspaces of Alaska. We use over 400 000 NEXRAD radar scans from seven stations across the state between 1995 and 2018 (86% of samples derived from 2013 to 2018) to measure spring and fall migration intensity, phenology, and directionality. A large bow-shaped terrestrial migratory system spanning the southern two-thirds of the state was identified, with birds generally moving along a northwest-southeast diagonal axis east of the 150th meridian, and along a northeast-southwest axis west of this meridian. Spring peak migration ranged from May 3rd to May 30th and between August 18th and September 12th during the fall, with timing across stations predicted by longitude, rather than latitude. Across all stations, the intensity of migration was greatest during the fall as compared to spring, highlighting the opportunity to measure seasonal indices of net breeding productivity for this important system as additional years of radar measurements are amassed.

Similar genes underlie the honesty of different ornaments in two populations of a warbler

Nicholas D. Sly, Amberleigh E. Henschen, Corey R. Freeman-Gallant, Linda A. Whittingham, and Peter O. Dunn

Presenting author: **Nicholas Sly**, University of Wisconsin-Milwaukee, nsly@uwm.edu

Ornaments are often thought to signal the genetic quality of males, but the mechanisms that ensure signal honesty remain poorly understood. Common Yellowthroats represent a unique opportunity to investigate the genetic basis of honest plumage signals under divergent sexual selection. Within one widespread subspecies, females in a Wisconsin population prefer males with larger black masks as mates, while females in a New York population prefer males with larger yellow bibs. Despite being produced by different pigments, both ornaments signal similar aspects of male quality in their respective populations (e.g., immune response, body condition, and survival). Here, we combined whole-genome sequencing and transcriptomics to identify genes and pathways associated with mask and bib size in both populations. Size of both ornaments was related to thousands of genes, but the individual genes linked to ornament size were rarely shared between populations or ornaments. In spite of this, the genes related to ornament size in each population had similar functions in immunity, oxidative phosphorylation, and growth, consistent with hypotheses for honest signaling mechanisms. We suggest that although there are different targets of female choice in each population, each ornament is an honest signal of male quality at the molecular level. Thus, female choice can favor convergence in the signaling function of different sexually selected ornaments, even within one subspecies with no known barriers to gene flow.

Modeling the spatial patterns in trends, and covariates of trends, for North American bird populations

Adam C. Smith

Presenting author: **Adam C. Smith**, Canadian Wildlife Service, adam.smith2@canada.ca

The spatial variation in trends of North American bird populations can help understand the factors driving population change. Previously published, spatially explicit models for the North American Breeding Bird Survey (BBS) did not share information on population change (only on abundance); and they were fit at relatively broad scales, not at the level of an individual BBS route. I will describe a new hierarchical Bayesian model that estimates trends at individual BBS routes and shares information on route-level trends and abundance in a spatially explicit way. The model is fit using the Stan probabilistic programming language and uses an intrinsic Conditional Autoregressive structure to estimate the spatial components. I will overview some of the most intriguing spatial patterns in species-specific trends and compare results with those from other BBS trend models. I will also demonstrate one application of the spatial model that includes covariates on the route-level trends to measure the influence of landcover change on changing bird populations. This covariate-version of the model will be useful to researchers seeking to test hypotheses about the causes of bird population change at relatively fine spatial scales. In addition, estimates from the base-model will be useful for visualizing spatial patterns of population change, comparing patterns of change among regions and species, and generating hypotheses related to causes of population change.

Local grassland bird declines were not explained by long-term changes in reproductive output

Dylan J. Smith, Katy M. Silber, Emily J. Williams, Sarah K. Winnicki, Page E. Klug, Karl L. Kosciuch, William E. Jensen, James W. Rivers, Bridget F. Sousa, Brett K. Sandercock, and W. Alice Boyle

Presenting author: **Dylan Smith**, Kansas State University, dylansmith@ksu.edu

North America's grassland birds have declined by over 50% since 1970. While the primary cause for these declines was habitat loss due to agricultural and urban development, other factors have become more important in recent decades. As natural disturbances such as fire were suppressed, woody vegetation has encroached on native prairie, and this may drive declines by increasing rates of predation and Brown-headed Cowbird (Molothrus ater) brood parasitism, thereby reducing reproductive output. As habitat quality is degraded, local populations could decline as birds either choose to stay and potentially suffer reduced reproductive output or leave and seek out new breeding grounds. We used data from 6,000 nests of 48 species from 1971–2020 at Konza Prairie in the Flint Hills of northeastern Kansas to test whether reproductive output has decreased or whether predation or brood parasitism have increased. We then determined whether woody encroachment may be driving these changes by testing if they were correlated with species-level habitat use or reduced disturbance. Overall, reproductive output did not change since 1971 by any metric, although parasitism increased, and parasitism and predation increased for shrub nesting species. Thus, observed population declines at Konza were not driven by reduced reproductive output, but potentially by increased emigration as woody encroachment or other factors displaces grassland specialists. Understanding the drivers of local declines is critical to conserve these imperiled birds, and long-term studies such as ours are integral to that understanding.

A trait-based framework for predicting foodborne pathogen spillover from wild birds

Olivia M. Smith, Elissa M. Olimpi, Kevin A. Cornell, Luke Frishkoff, Nora Navarro-Gonzalez, Tobin Northfield, Tim Bowles, Max Edworthy, Johnna Eilers, Zhen Fu, Karina Garcia, David J. Gonthier, Matthew S. Jones, Christina M. Kennedy, Christopher E. Latimer, Jeb P. Owen, Chika Sato, Joseph M. Taylor, Erin E. Wilson-Rankin, William E. Snyder, and Daniel S. Karp

Presenting author: **Olivia Smith**, Michigan State University, olivia.m.smith@wsu.edu

Recent foodborne illness outbreaks have heightened pressures on growers to deter wildlife from farms, jeopardizing conservation. However, it remains unclear which species, particularly birds, pose the greatest risk to food safety. Using >11,000 pathogen tests and 1,565 bird surveys covering 139 bird species from >350 locations across the western U.S.A., we examined the importance of 11 traits in mediating wild bird risk to food safety. We tested whether traits associated with pathogen exposure (e.g., habitat use, movement, and foraging strategy) and pace-of-life (clutch size and generation length) mediated foodborne pathogen prevalence and proclivities to enter farm fields and defecate on crops. *Campylobacter* spp. were the most prevalent enteric pathogen (8.0%), while *Salmonella* and Shiga-toxin producing *E. coli* (STEC) were rare (0.46% and 0.22% prevalence, respectively). We found that several traits related to pathogen exposure predicted pathogen prevalence. Specifically, *Campylobacter* and STEC-associated virulence genes were more often detected in species associated with cattle feedlots and bird feeders, respectively. *Campylobacter* was also more prevalent in species that consumed plants and had longer generation lengths. Finally, we found that species associated with feedlots were more likely to enter fields and defecate on crops. Our results suggest that separating crop production from livestock farming may be the best way to lower food safety risks from birds. More broadly, our trait-based framework suggests a path forward for co-managing wildlife conservation and food safety risks in farmland by providing a strategy for holistically evaluating the food safety risks of wild animals, including under-studied species.

Accelerating declines of North America's shorebirds signal the need for urgent action

Paul A. Smith, Adam C. Smith, Stephen Brown, Bradford Winn, Julie Paquet, and Christian Friis

Presenting author: **Paul Smith**, Environment and Climate Change Canada, paulallen.smith@canada.ca

Around the globe, shorebirds are declining to a greater extent than many other avian taxa. In North America, shorebirds, along with aerial insectivores and grassland birds, have some of the highest proportions of declining species of any taxonomic group. Here, we apply a new hierarchical Bayesian model to analyze shorebird migration monitoring data from across North America, 1980-2019, and offer the most recent available estimates of trends. This new model better accommodates regional variation in trends and timing of migration, as well as non-linear population trajectories. Precision is improved over previous analyses, but remains a challenge given the transient nature of birds passing through a continental-scale study area, surveyed primarily by volunteers. The results uphold previous findings of widespread declines for a large majority of species. Importantly, we show that the declines have accelerated during the last 3 generations for most species. Arctic-breeding species, also typically the longest-distance migrants, are declining to a greater extent than boreal and temperate breeders. There is some indication of lesser declines at staging sites in the midcontinental United States, and also at sites in Florida for species that winter at temperate latitudes. These declines are worrying, and signal the need for urgent attention. However, among the most important next steps are efforts to improve the certainty of the results through collection and analysis of complementary data, and studies to determine where and when declines are most likely to originate through whole-annual-cycle demographic analyses. This improved information will allow for more targeted efforts to reverse declines through conservation action.

Describing the diet of Eastern Whip-poor-wills and estimating the effect of food availability and landscape composition on their abundance during the breeding season

Ian Souza-Cole, Michael P. Ward, Thomas J. Benson, Jeffrey T. Foster, Rebecca L. Mau, Chris Tonra, and Aaron Skinner

Presenting author: **Ian Souza-Cole**, University of Illinois Urbana-Champaign, iansouzacole@gmail.com

The Eastern Whip-poor-will (*Antrostromus vociferus*) is a species of nightjar native to eastern North America. It is a species of conservation concern, having experienced population declines across much of its range including in the Midwest, U.S.A. Two factors that may be contributing to these declines are landscape alterations and reductions in night-flying insect populations, their sole prey item. To better describe the diet of this species, we assessed the components of whip-poor-will diet using DNA metabarcoding on 145 fecal samples taken from captured birds. We also investigated the role that land cover characteristics and food availability may play as mechanisms underlying the negative trend in whip-poor-will populations by estimating their abundance at twenty-three sites across central Illinois. I conducted nocturnal point counts to estimate avian abundance in 2019 and 2020 and collected nocturnal insects using UV-light traps at these sites to sample available food resources. Metabarcoding results found that Lepidoptera are the primary component of whip-poor-will diet (present in 92% of samples) and that Diptera are also frequently consumed (31%). Results of the abundance modeling determined that the number of large moths has a positive effect on the abundance of whip-poor-wills whereas the proportion of the landscape covered by medium- to high-intensity human development has a negative effect. These results suggest that whip-poor-will populations are particularly sensitive to the prevalence of moths and that human development is a detrimental landscape characteristic.

A comparative species approach to determine gonadal testosterone asymmetry in male birds

Jeremy M. Starkey, Devaleena S. Pradhan, and David J. Delehanty

Presenting author: **Jeremy Starkey**, Idaho State University, starjer2@isu.edu

Many bird species display bilateral asymmetry in their reproductive tracts. In male birds, the trend is for the left testis to be larger in mass and volume than the right testis, although both testes perform steroidogenesis. Gonadal testosterone (T) production is regulated by the hypothalamus-pituitary-gonadal axis. We compared T concentration between left and right testes of male Cinnamon Teal (*Spatula cyanoptera*), Mallards (A*nas platyrhynchos*), European Starlings (*Sturnus vulgaris*), and Eurasian Collared-Doves (*Streptopelia decaocto*) collected from the wild in southeastern Idaho during the 2020-21 breeding seasons. Additionally, we compared T concentration between hypothalamic and testicular tissues. After homogenization, we purified tissue samples using solid phase extraction and quantified T using enzyme immunoassays. We found no difference in T concentrations between the left and right testes within any examined species. Testosterone concentrations were significantly lower within hypothalamic tissue compared to testicular tissue in Cinnamon Teal, Mallards, and European Starlings. Eurasian Collared-Doves had low T concentrations relative to the other species but had equal T concentrations between hypothalamic and testicular tissues. Similar hypothalamic and testicular T concentration of Eurasian Collared-Doves may be related to their long breeding season or an unknown aspect of life history. Conversely, the high T concentrations within the testicular tissue of Cinnamon Teal, Mallards, and European Starlings may facilitate high spermatogenesis for high sperm production and competition for mates.

Rainforest bird communities partially recover in 35-year-old Amazonian secondary forest

Philip C. Stouffer, Cameron L. Rutt, and Claudier F. Vargas

Presenting author: **Philip Stouffer**, Louisiana State University, pstouffer@lsu.edu

How long does it take recovering second growth rainforest to support the bird community found in primary Amazonian forest? We addressed this question at the Biological Dynamics of Forest Fragments Project, near Manaus, Brazil, from spot-map surveys in six 16-ha plots. Three plots were in ~35- year-old secondary forest, each <4 km from one of three primary forest plots embedded in vast rainforest. We detected 30% more individuals in primary forest plots, resulting in 139-154 species/plot compared to 108-110 species/plot in secondary forest. The 57 species detected only in primary forest included both common and rare species, with species from most foraging guilds, from canopy frugivores to midstory flock obligates to terrestrial insectivores. Even so, a large majority of species detected in secondary forest were species whose main habitat association is primary forest. Secondary forest did not support a meaningful component of non-forest species; only eight species detected in secondary forest, representing <2% of detections, were birds whose main habitat association is not primary forest. These results demonstrate that recovering rainforest sheds non-forest species and hosts a large proportion of primary forest species within three decades. Presumably, these secondary forests will support increasingly more individuals and species as they continue to grow, although our data do not reveal the trajectory to complete recovery. These encouraging results represent a best-case scenario, as the secondary forests we studied were recovering from only modest disturbance following deforestation, and were adjacent to undisturbed forest with the full complement of expected species available to colonize.

Validating the performance of citizen science establishes novel evidence base for conservation decision-making

Erica F. Stuber, Orin Robinson, Emily Bjerre, Mark Otto, Brian Millsap, Guthrie Zimmerman, and Viviana Ruiz-Gutierrez

Presenting author: **Erica Stuber**, USGS Utah Cooperative Fish and Wildlife Research Unit, erica.stuber@usu.edu

Methods are being developed to capitalize on the power of volunteer-collected data for biological research and monitoring purposes, but these data are rarely used as part of the established decision-making frameworks of conservation and management agencies. Although data collected within citizen science projects is often perceived to be of lower quality than professional surveys, recent work has highlighted that subsets of these data can be powerful for generating sound scientific inference. Determining when these data can complement professional biological monitoring programs can enable agencies to more optimally allocate limited resources. Here, we demonstrate that carefully filtered volunteer observations can produce ecological predictions equivalent to those based on professional surveys alone. Using a case study, we show how the continuous spatial and temporal coverage attained through citizen science projects can improve estimates of metrics used by the U.S. Fish and Wildlife Service – National Raptor Program in regulatory processes. The data validation presented here enabled partners to scientifically justify complementing professional data collection with citizen science to inform take limits of federally managed species nationwide, and vet citizen science data quality for future management planning goals. These findings illustrate the value of integrating validated, scientific products from citizen science into the current evidence base used to justify, inform, and evaluate conservation decision-making. We demonstrate how agencies can capitalize on a largely untapped, low cost data stream to more efficiently and effectively carry out their mandates to protect wildlife and their habitat for a sustainable future.

Staying stable with fluctuations: How environmental cycles and demography influence a Florida Scrub-Jay population

Jeremy Summers, Reed Bowman, John W. Fitzpatrick, and Nancy Chen

Presenting author: **Jeremy Summers**, University of Rochester, jsummer7@ur.rochester.edu

Identifying the sources of population fluctuations is one of the foundational aims of population biology and is a key concern for the conservation of threatened species. Populations can respond to a host of environmental and demographic factors, and it is challenging to directly connect these influences to the population growth rate. Fluctuations in the population growth rate can also increase the risk of extinction due to stochastic forces. Environmental changes and increased isolation can intensify these fluctuations or lead directly to population decline. Here I show how density dependence, changes in the population stage structure, and an autocorrelated environment create fluctuations in a stable population of the Federally threatened Florida Scrub-Jay (*Aphelocoma coerulescens*). I use highly detailed census data on all individuals within the population across 28 years to parameterize a stage-based matrix population model and connect changes in underlying demographic rates to the population growth rate. This model includes the impacts of a diminishing immigration rate likely caused by the decline of surrounding populations. I find that the population is heavily influenced by density-dependent effects on fecundity and the survival of juveniles as well as changes in the stage distribution. These results show how the apparent stability of this well-preserved population is maintained through small but rapid fluctuations in the population growth rate.

Metapopulation dynamics of adult Northern Great Plains Piping Plovers

Rose J. Swift, Michael J. Anteau, Kristen S. Ellis, Megan M. Ring, Mark H. Sherfy, Dustin L. Toy, and David N. Koons

Presenting author: **Rose Swift**, U.S. Geological Survey – Northern Prairie Wildlife Research Center, rswift@usgs.gov

Metapopulation dynamics are determined not only by within-patch birth and death processes but also by between-patch movements of individuals. For the Northern Great Plains Piping Plover (*Charadrius melodus*), managers have assumed a metapopulation structure with four sub-populations and low, balanced dispersal, which resulted in low extinction risk in a viability study. Here, we evaluated breeding dispersal of adult piping plovers (n = 2,582) between 2014 and 2019 at multiple spatial scales: 1) two assumed sub-populations, 2) four management units within sub-populations, and 3) movements among breeding areas (e.g., a wetland basin or sandbar). Dispersal between the sub-populations was higher than previously assumed and unbalanced (northern Missouri River to U.S. Alkali Wetlands: 0.17 [95% CI 0.15, 0.19]; U.S. Alkali Wetlands to northern Missouri River: 0.04 [0.03, 0.05]). Dispersal probabilities increased following a failed reproductive attempt and when more habitat was available. Dispersal amongst the four management units varied but ranged from very infrequent (0.006) to low (0.07); alternatively, there was a high rate (0.16-0.34) of adults moving among units but not breeding (a transient, non-breeding state) . Roughly 44% of segment dispersal events (n = 4,590) were reciprocal and all segments with centrality measures >0.75 were on the Garrison Reach of the Missouri River. Our results suggest that dispersal by Piping Plovers in the northern Great Plains is influenced by both prior reproduction and habitat availability, and individuals take advantage of dynamic habitats in a broad geographic area suggesting high connectivity of sub-populations leading to potentially increased extinction risk, as previously simulated.

Characterizing genomic patterns of divergence in non-model avian systems: Which sequencing method is best?

Stephanie J. Szarmach, Alan Brelsford, Christopher Witt, and David P. L. Toews

Presenting author: **Stephanie Szarmach**, Pennsylvania State University, sjs7465@psu.edu

Researchers face a number of trade-offs when designing genomic studies for non-model bird species that lack existing genomic resources. Selecting methods with lower marker densities, like restriction site associated DNA sequencing

(RAD-seq) or genotyping by sequencing (GBS) may allow for more individuals to be sequenced at higher depth for a lower overall cost. However, whole genome re-sequencing (WGS) at lower depth can generate a greater number of informative sites that allow researchers to better characterize certain genomic features. To explore how sequencing methods affect the interpretation of divergence across the genome and differ in value per informative site, we applied an identical bioinformatic pipeline to three generations of sequencing data (GBS, ddRAD, and WGS) produced for the Yellow-rumped Warbler species complex (*Setophaga coronata*). We found that while GBS and WGS cost more overall, the cost per informative data site was lower than for ddRAD. When comparing genome-wide patterns of divergence captured by each method, we found that most high-FST peaks were not detected in the ddRAD dataset, and while both GBS and WGS were able to identify the presence of large FST peaks, WGS was superior at a finer scale. In a comparison of Audubon's Warblers (*S. c. auduboni*) with deeply divergent mtDNA resulting from mitochondrial introgression, only WGS allowed us to identify small regions of elevated differentiation, one of which contained the nuclear-encoded mitochondrial gene NDUFAF3. We hope these comparisons demonstrating the benefits of investing in methods with higher marker density will be useful to researchers interested in characterizing genome-wide divergence in avian species lacking genomic information.

Investigating a trade-off between the quality of nest-grown feathers and pace of development in an altricial bird

Conor C. Taff, Brianna A. Johnson, Allison T. Anker, Alyssa M. Rodriguez, Jennifer L. Houtz, Jennifer J. Uehling, and Maren N. Vitousek

Presenting author: **Brianna Johnson**, Cornell University, baj56@cornell.edu

Life history theory provides a framework for understanding how trade-offs generate negative trait associations. While some negative trait associations are observed across biological scales of organization, others are only observed at the intra- or inter-specific level. At the inter-specific level, resource trade-offs may be alleviated by disinvestment in relatively unimportant ephemeral traits, such as nest-grown feathers, that are only retained for a short time. However, direct resource-allocation trade-offs cannot be clearly demonstrated from inter-specific negative trait-associations without complementary intra-specific studies. Here, we asked whether there is evidence for a within-species resource allocation trade-off between nest-grown feather quality and the speed of development in Tree Swallows (*Tachycineta bicolor*). Consistent with the idea that ephemeral traits are deprioritized, nest-grown feathers had lower barb density than adult feathers and cross-fostering revealed that there were both genetic and environmental contributions to variation in nestling feather quality. However, despite substantial variation in fledging age and growth rate among nestlings, there was no evidence for a negative association between developmental pace and feather quality. Furthermore, accounting for potential differences in resource availability by considering parental provisioning rate and an experimental nest predation treatment did not reveal any evidence for a trade-off that was masked by variation in resources. Our results are most consistent with the idea that the inter-specific association between development and feather quality arises from adaptive specialization, rather than from a direct resource allocation trade-off.

Assortative mating for between-patch dispersal status in a wild bird population: Exploring the role of direct and indirect underlying mechanisms

Thibault Tamin and Blandine Doligez

Presenting author: **Thibault Tamin**, LBBE 'Biométrie et Biologie évolutive' UCB Lyon 1, thibault.tamin@univ-lyon1.fr

Previous studies have reported functional integration between dispersal and other phenotypic traits allowing individuals to alleviate dispersal costs, and such associations can affect dispersal evolution in return. In sexually reproducing species, assortative mating according to dispersal can shape the maintenance of such trait associations. Despite the potentially crucial consequences of dispersal in natural populations, assortative mating for dispersal and its underlying mechanisms remain largely unexplored. Here, we assessed assortative mating for between-patch dispersal status in a fragmented population of a small passerine bird, the Collared Flycatcher, and explored whether such assortative mating could result from (i) direct mate choice based on dispersal or dispersal-related behavioural (aggressiveness and boldness) and morphological traits (tarsus and wing length), (ii) biased mating due to spatio-temporal heterogeneity in the distribution of dispersal phenotypes and/or (iii) post-mating adjustment of dispersal phenotype or dispersal-related traits. We found an assortative mating for the current dispersal status but not for natal dispersal status. We also found assortative mating for boldness and age category, and the probability for pair members to be assorted for current dispersal status was higher when both pair members were of similar boldness score and of the same age compared to mixed-age pairs. We thus identified mate choice based on boldness and age as the most likely underlying mechanisms for assortative mating for dispersal status. More work is nevertheless needed to fully assess the evolutionary implications for such a combined age- and behaviour-based assortative mating for dispersal.

Multi-scale landscape effects on breeding scoter (*Melanitta* spp.) and scaup (*Aythya* spp.) occurrence on ponds in the northwestern boreal forest of North America

Moriah S. Tanguay, Kirsty E. B. Gurney, and Eric T. Reed

Presenting author: **Moriah Tanguay**, University of Saskatchewan, moriah.tanguay@usask.ca

North American breeding populations of scoter (*Melanitta* spp.) and scaup (*Aythya* spp.), which breed predominantly in the rapidly changing boreal forest, have declined, yet habitat needs for these duck species remain poorly documented. To help prioritize key habitats for conservation of boreal waterfowl, we applied a multi-scale approach to aerial breeding waterfowl survey data from a key site in Canada's boreal forest. We tested two hypotheses, which predicted (i) that variables describing foraging habitat availability would be the most important in predicting scoter and scaup occurrence and (ii) that scales of greatest effect for landscape variables would correspond with home range size. Consistent with our first prediction, pond size and the number and total area of waterbodies surrounding ponds were the most important variables in predicting scoter and scaup occurrence, though some of the relationships were negative. Further, most of the landscape variables had a characteristic scale of 1960 m (the largest of the four scales considered) for scoter and 210 m (the smallest scale) for scaup, which supports our second prediction, as scaup have smaller home ranges than scoters. Taken together, our results suggest that conservation planning for these species should prioritize complexes of large waterbodies to support breeding scoters and large ponds surrounded by a small amount of waterbody cover to support breeding scaup. The results also showed that the scale of greatest effect varied by species and variable, indicating that future predictive modelling for scoter and scaup conservation in the boreal region should use species-specific, scale-optimized variables to increase predictive performance.

Climate variation influences the timing of the adult pre-basic molt among four passerine species in northern California

D. Julian Tattoni and J. Nicholas Hendershot

Presenting author: **D. Julian Tattoni**, Stanford University, dtattoni@stanford.edu

Annual molts are energy and resource demanding periods in the lives of birds that have important fitness consequences. Little is known on how climate impacts the timing of molt in wild birds and how molting has and may continue to be modified by climate change. To address this gap, we examined over three decades of constant-effort bird banding data from the Coyote Creek Field Station, CA, which included detailed documentation of molt for Bushtits, Chestnut-backed Chickadees, Song Sparrows, and Common Yellowthroats. We hypothesized the adult pre-basic molt advanced in years with higher mean breeding season temperatures and lower growing season precipitation. To test this, we built binomial models in a Bayesian framework to estimate the probability a captured bird was actively molting as a function of Julian day, climate variables, and the interaction between climate and day. For every 100mm increase in growing season precipitation there was a 6.5- and 5.1-day delay in the day of maximum molting probability for Song Sparrows and Common Yellowthroats, respectively. For every 1°C increase in mean breeding season temperature there was 7.0-day advancement in the day of maximum molting probability for Song Sparrows. Our results suggest Song Sparrows and Common Yellowthroats have significant plasticity of molt phenology and are likely responding to local climate conditions, though the exact mechanisms by which this might occur are unknown. The predicted warming and drying over the next century from climate change at our study site may drive long-term delays in molting for Common Yellowthroats, though the impact on Song Sparrows is less clear as temperature and precipitation have opposite effects.

The bird that laid the cosmic egg

Bernie Taylor

Presenting author: **Bernie Taylor**, Community Member, berniejtaylor@aol.com

An Upper Paleolithic panel of images dated to approximately 34,000 years ago in the Spanish Cave of El Castillo include a Great Auk (*Pinguinus impennis*), an Ostrich (Struthionidae) and two Golden Eagles (*Aquila chrysaetos*). The lenses through which Upper Paleolithic cave art has been interpreted are scattered, ranging from art for art's sake, hunting magic, hallucinogenic visions to shamanism. Such lenses do not appear to explain why Upper Paleolithic cave artists depicted these large birds. This study examined the relationship between these large birds and other characters on the panel, as well as a singular depicted egg, through the lenses of animism and the Eurasian cosmic egg myth. The study provides a perspective on why the Upper Paleolithic artist depicted these large birds and which one of them laid the pictured egg in this proposed version of the cosmic egg myth. The study further offers a unique insight as to mankind's prehistoric interest in large birds.

Welfare-conscious approaches to handling and obtaining samples from hummingbirds

Lisa A. Tell

Presenting author: **Lisa Tell**, University of California, Davis, latell@ucdavis.edu

Research on hummingbirds over the decades has provided many scientific insights. Their small size, energy demands, and high metabolic rates are some of the challenges researchers face when obtaining research samples and biological materials from live hummingbirds. This presentation will cover basic methods that scientists could use when handling and obtaining samples from hummingbirds. Based on the authors' experience, best practices for working with live hummingbirds will be presented, including permitting requirements for studying live hummingbirds, trapping and marking, handling techniques, and safe collection techniques for obtaining samples.

Contrasting macroevolutionary trends between mountains and lowlands underlying diversification in Neotropical avian clades

Elkin A. Tenorio and Brian T. Smith

Presenting author: **Elkin Tenorio**, City University of New York, etenorio@amnh.org

Mountains are known for being biodiversity hotspots. Their astonishing diversity is often attributed to factors that have promoted rapid species origination, low extinction events, and a high input of immigrants from lowlands regions. Using geographical and phylogenetic information for several diverse Neotropical bird clades (Trochilidae, Emberizoidea, and Furnariidae), we tested the influence of these processes in the generation of mountain diversity. Here, we hypothesized that mountains have had higher diversification rates than lowlands regions, and that dispersal events from lowlands to mountains have been higher than from mountains to lowlands. Using sister clades that compared montane and lowland lineages and controlled for clade age, we found that montane clades had a higher number of species. Comparisons in diversification rates between mountain and lowland clades did not show differences when using pure birth-death estimations or pulled diversification rates, however, mountains exhibited higher recent speciation rates. Moreover, we found that even though the contribution of lowlands as a source of species has been important, dispersal events from mountains to lowlands regions were moderately higher, at least in the more recent geological time. These results suggest that high species richness in mountains may be driven by a differential contribution of speciation in comparison to lowlands, which could have been promoted toward the present. By integrating the effect of diversification and dispersion in a comparative design, our findings generate new insight in the understanding of the tropical mountain avian diversity evolution.

The range expansion of an invasive avian malaria parasite and its potential impacts on two North American songbird species

Angela N. Theodosopoulos, Kathryn C. Grabenstein, and Scott A. Taylor

Presenting author: **Angela Theodosopoulos**, University of Colorado at Boulder, anha2922@colorado.edu

The impacts of malaria infections on avian populations can range from mild to severe and of conservation concern. Severe symptoms of the disease avian malaria are more commonly reported in birds that lack a coevolutionary relationship with the associated malaria parasite. Recently, I documented that the malaria strain, SGS1, of the highly invasive malaria parasite, *Plasmodium relictum*, has expanded its range to include two songbird species in Colorado– the Black-capped Chickadee (*Poecile atricapillus*) and Mountain Chickadee (*Poecile gambeli*). While SGS1 is widespread in the Eastern Hemisphere there are no previous reports of SGS1 infecting wild birds of western North America. I will discuss SGS1 as a conservation concern, its overall geographic presence, its ecology as it relates to vector transmission and common avian hosts, and I will present data on the presence of SGS1 infections in Colorado chickadees.

Combining genetic, morphometric and ecological-niche modeling methods to assess the evolutionary origins of the Black-throated Gray Warbler (*Setophaga nigrescens*)

Michael A. Tofflemire, John Klicka, and Kevin Epperly
Presenting author: **Michael Tofflemire**, San Diego State University, mtofflemire@sdsu.edu

*Setophaga nigrescen*s is currently split into two subspecies: *S. n. nigrescens* and *S. n. halseii*. This taxonomic classification is based primarily on morphological data sets recorded during the nineteenth and twentieth centuries, and more recently, a handful of restriction fragment length polymorphism sequence studies of only several individuals. Here, we significantly improve our understanding of the phylogeography and evolutionary history of these migratory songbirds by employing a robust analysis that combines genetic, morphometric and ecological-niche modeling methods. Phylogenetic inference of 106 individuals spread throughout their entire breeding range confirms two distinct haplotype clades, with a mean genetic distance of 0.8%, indicating a Late Pleistocene split (~320,000 ybp). Geographic structure between populations west and east of the Cascade Mountain Range and Sierra Nevada was also observed; however, both haplotypes were admixed over a wide range, primarily east of the Sierra Nevada. Furthermore, habitat modification resulting from Late Pleistocene glacial/interglacial cycles is strongly supported from historical distribution models of the last glacial maximum (LGM), as two major refugia were observed from these analyses. From this, we hypothesize that *S. n nigrescens* diverged from *S. n. halseii* following glacial events and eventually adapted to the temperate habitats of the west coast. It's likely that range expansion following the LGM has resulted in secondary contact between both clades, with introgression currently leaking east into the interior clade. Given enough time, both clades may eventually converge, erasing the historical legacy of genetic divergence promoted during the Late Pleistocene.

Geomagnetic disturbance associated with vagrancy in migrating landbirds

Benjamin A. Tonelli, Casey Youngflesh, and Morgan W. Tingley
Presenting author: **Benjamin Tonelli**, University of California, Los Angeles, btonelli@ucla.edu

Rare, out-of-place birds, known as 'accidentals'' or 'vagrants,' have long captivated birdwatchers and puzzled ornithologists. Vagrancy is generally considered to occur due to external weather-related factors, errors in an internal orientation mechanism, or because of a lack of reliable information from navigational cues. One well-known means of navigation in landbirds is through the use of the Earth's magnetic field, sensed using specialized magnetoreceptor structures. Potentially, disruption to either these magnetoreceptors or the magnetic field itself could cause disorientation and vagrancy. Using a dataset of over 7,000,000 banding records comprising captures of 160 species over 60 years, we investigate whether vagrancy is associated with two potential mechanisms that could disrupt orientation: short-term fluctuations in the Earth's magnetic field and oscillating solar radio-frequency emissions during the solar cycle. Our Bayesian hierarchical analysis detected strong effects of the disruption in the Earth's magnetic field, and to a lesser extent the solar cycle, on vagrancy rates. This effect of navigational disruptions on vagrancy was stronger during the fall than spring migration and was stronger for species with longer migratory journeys. Our results provide strong support for a previously unknown interplanetary mechanism underlying avian vagrancy and a potential selection pressure during the often fatal migration season.

Determining bird colors from digital images for high-throughput analyses of color evolution

Whitney L. E. Tsai, Shawn T. Schwartz, Elizabeth A. Karan, Mark S. Juhn, Mackenzie Perillo, Trevor Brokowski, Allison J. Shultz, Thomas B. Smith, and Michael E. Alfaro
Presenting author: **Whitney Tsai**, UCLA, wtsainaka@ucla.edu

Plumage coloration and pattern are essential aspects of the life history of birds that serve a variety of functional roles. They evolve as part of a complex system which includes the visual environment and the visual perception of other organisms the birds interact with. Advances in digital imaging and software tools have provided increasingly accessible datasets and methods for analyzing color evolution. Despite the variety of computational packages available, most rely on manual identification for individual images, a single color class estimation for a large set of images, or an overestimation of color classes. This limits the ability to analyze large datasets of images, decreases accuracy of downstream analyses, and is not representative of biologically relevant color classes. Here, we present charisma, an R tool designed to determine the number and proportions of distinct color classes in an image suitable for large-scale studies. Our toolkit provides a flexible framework to assess color classes. It can be tailored for datasets collected from different sources to yield reproducible results that are designed to work in conjunction with popular

color analyses packages. We find that charisma can classify every pixel in a set of ten high-resolution images in under a minute. We also find that the results are consistent with color classifications made by experts in the field using digital images and spectrophotometry. We apply this method to avian color evolution by investigating how color evolves within a diverse and charismatic group of birds and by matching visual system and color production on a broader scale.

You are what you eat: Connecting foraging and breeding behavior in lekking Greater Sage-Grouse

Eric F. Tymstra, Jennifer Forbey, and Gail L. Patricelli

Presenting author: **Eric Tymstra**, UC Davis, etymstra@gmail.com

Economic models of negotiation provide useful frameworks to understand courtship and mating behavior and the processes that underlie behavior on leks. Mate choice can be viewed as a series of negotiations that occur between buyers and vendors (females and males, respectively) in a marketplace. Males must choose a territory location that maximizes mating opportunities and minimizes predation and competition from other males. In order to afford valuable locations within the marketplace, males must be able to pay 'rent'. Previous work on lek-settlement has focused on using economic models in relation to female home ranges, habitat characteristics, and predation. Yet, we do not know how male display territory placement is affected by the physiological condition (endogenous factor of rent) of territorial males in relation to diet choice. During the lekking season, male Greater Sage-Grouse maintain lek territories, which vary in female visitation rate and thus mating potential. Males engage in aggressive encounters with neighbors, presumably to maintain territory boundaries. Since territories differ in value, males on different parts of the lek pay different costs (i.e. 'rent'). Successful males maybe those who can afford these costs due to higher endogenous energy gained from higher-quality diets (higher income). In this study, I examine how dietary quality relates to territory quality on the lek. I will use biomarkers of diet quality (glucuronic acid) and measurements of diet diversity taken from territories of high and low value across study leks. This will provide data on how habitat quality may influence lek dynamics and will further support the links between foraging, habitat quality, and reproductive behavior.

Management and conservation strategies for the Scarlet Macaw in Reforma Agraria, Chiapas, Mexico

David E. Ucan-Puc, Paula L. Enríquez, Eduardo B. Baltazar, and Vianney J. Cupiche

Presenting author: **David Ucan-Puc**, El Colegio de la Frontera Sur (ECOSUR), davidernestoucan@gmail.com

The populations of the Scarlet Macaw in Mexico have decreased or have become extinct in some regions. Because of this, in Chiapas, Mexico there have been different strategies for its conservation such as the installation of nesting boxes, the establishment of Management Units for the Conservation of Wildlife, Voluntary Conservation Areas, ejido agreements and even ecotourism. The objective of the study was to analyze these strategies and their impact on the abundance of the Scarlet Macaw in the ejido Reforma Agraria, Chiapas. The purpose was to contribute information for macaw management and conservation plans. The methods used were: documentary research on the ejido, conservation strategies, and macaw population conditions. Twenty semi-structured interviews were conducted with ecotourism service providers, members and ejidatarios. Analysis of eBird data and sampling in two 2.5-km line transects and two counts by elevated observation points were also performed. Among the findings, the changes in attitude began in the local people through the ejido organization and the consolidation of the ecotourism center 'Las Guacamayas.' These actors have maintained and strengthened macaw conservation actions for almost 35 years. Ecotourism was identified as a relevant economic activity with 63%, compared to agriculture, cattle ranching and carpentry. In 2020, a total of 81 scarlet macaws were recorded in the line transects, with an average of 7.4 ± 6.3 individuals per sampling.

DNA metabarcoding reveals predictors of diet quality variation in Tree Swallows (*Tachycineta bicolor*)

Jennifer J. Uehling, Conor C. Taff, Jennifer L. Houtz, Paige M. Becker, and Maren N. Vitousek

Presenting author: **Jennifer Uehling**, Cornell University, jju8@cornell.edu

Inter-individual variation in diet can have significant consequences for health and fitness. Historically, it has been challenging to measure the diets of generalist birds on large scales, but this has become increasingly feasible thanks to recent developments in DNA metabarcoding. Here, we use DNA metabarcoding of fecal samples to examine the factors that predict diet quality variation in a declining aerial insectivore, the Tree Swallow (*Tachycineta bicolor*), and to assess whether variation in diet predicts nestling size. For Tree Swallows, aquatic insects are thought to represent higher quality food sources than terrestrial insects because they contain higher levels of important macronutrients, omega-3 long-chain polyunsaturated fatty acids (LC-PUFA). We hypothesized that parents would preferentially feed their young aquatic insects because LC-PUFA may be particularly important during rapid nestling growth. Contrary to our predictions, we found that the diets of nestlings included a lower proportion of aquatic insects than the diets of adult females. There was also no relationship between aquatic insect diet content and nestling mass. Nestling diets were not predicted by their mother's phenotype, but wing length and body mass were associated with aquatic insect content in adult female diets. Our results do not suggest that aquatic insects are particularly limiting for Tree Swallow nestlings, but they do indicate that adult females preferentially consume aquatic insects and that their morphology may affect their own diet quality. Future work may elucidate whether adult morphological variation affects trade-offs associated with foraging behavior.

Raptor foraging ecology and ecosystem services in agricultural landscapes

Olivia J. Utley and Catherine A. Lindell
Presenting author: **Olivia Utley**, Michigan State University, utleyoli@msu.edu

Increasing agricultural productivity while improving sustainability of agricultural landscapes are key challenges facing society. One strategy to help address these two needs is enhancing pest-regulating ecosystem services provided by organisms that reside in these landscapes. In some contexts, raptors provide substantial ecosystem services by reducing damage to crops through consumption and deterrence of pest species. We describe the foraging ecology of raptors in agricultural landscapes and discuss how this information can be used to enhance pest regulation by raptors. Our results show that most studies to date investigate the relationships between land cover types and presence and abundance of raptors. Finer-resolution variables that may influence raptor presence and abundance, and which are less commonly investigated, include vegetation structure, perch characteristics, and distance to a central location. We contend that other response variables warranting investigation include home range size, home range composition, attack rate and success rate, and diet. High attack rates, for example, may increase the number of pest individuals deterred because prey may avoid areas of high predation risk, take refuge longer, or remain vigilant longer. We argue that information on space use and the predation process is critical to enhance ecosystem services provided by raptors. For example, if raptors are known to increase attack rates in shorter vegetation, field margins with tall herbaceous vegetation could be mown regularly or increased in size. We recommend future research to assess additional measures of raptor foraging ecology and their impact on the strength of pest regulation services.

Conspecific attraction for conservation and management of terrestrial breeding birds: Current knowledge and future research directions

Jonathon J. Valente, Christa L. LeGrande-Rolls, James W. Rivers, Anna M. Tucker, Richard A. Fischer, and Matthew G. Betts
Presenting author: **Jonathon Valente**, Oregon State University, jonathon.j.valente@gmail.com

Conspecific attraction during breeding habitat selection has been observed in numerous terrestrial, territorial birds. There is growing interest in using simulated conspecific social cues (e.g., decoys, broadcasted vocalizations) to manage distributions of such species, yet it is unclear when this approach is likely to succeed. We reviewed published studies to evaluate whether the strength of conspecific attraction in terrestrial birds is mediated by characteristics of species (life history traits), simulated cues (e.g., timing and duration), sites (e.g., quality), and how conspecific attraction was measured. We used phylogenetically controlled meta-regression to assess impacts of 19 moderators on settlement across 31 experiments. Simulated social cues generally had a strong, positive influence on settlement decisions, as the odds of site occupancy were 3.12x (95% CI = 0.81, 11.69) greater in treatment sites relative to control sites. Conspecific attraction was also evolutionarily conserved with = 25.5% (CI = 5.1%, 65.4%) of the variance in treatment effects explained by phylogenetic relatedness. However, we found no evidence that any covariates influenced the response to social cues, and we posit this stems from limited research specifically designed to identify the mechanisms mediating conspecific attraction. We therefore developed a research framework for testing mechanistic hypotheses regarding how cue characteristics, species traits, and spatial contexts may mediate attraction to conspecifics. Evaluating these hypotheses will greatly advance the field by helping managers understand how to use simulated social cues to enhance populations of species that are of conservation concern.

Drivers of fatal bird collisions in an urban center

Benjamin M. Van Doren, David Willard, Mary Hennen, Kyle G. Horton, Erica Stuber, Daniel Sheldon, Ashwin Sivakumar, Julia Wang, Andrew Farnsworth, and Benjamin Winger

Presenting author: **Benjamin Van Doren**, Cornell Lab of Ornithology, vandoren@cornell.edu

Millions of nocturnally migrating birds die each year from collisions with built structures, especially brightly illuminated buildings and communications towers. Reducing this source of mortality requires knowledge of important behavioral, meteorological, and anthropogenic factors, yet we lack an understanding of the interacting roles of migration, artificial lighting, and weather conditions in causing fatal bird collisions. Using two decades of collision surveys and concurrent weather and migration measures, we model numbers of collisions occurring at a large urban building in Chicago. We find that the magnitude of nocturnal bird migration, building light output, and wind conditions are the most important predictors of fatal collisions. The greatest mortality occurred when the building was brightly lit during large nocturnal migration events and when winds concentrated birds along the Chicago lakeshore. We estimate that halving lighted window area decreased collision counts by 11x in spring and 6x in fall. Bird mortality could be reduced by ~60% at this site by decreasing lighted window area to minimum levels recorded. Our study shows strong support for a relationship between nocturnal migration magnitude and urban bird mortality, mediated by light pollution and local atmospheric conditions. Although our research focuses on a single site, our findings have global implications for reducing or eliminating a critically important cause of bird mortality.

Harmful algal blooms and Alaska seabirds: Saxitoxin associated with recent die-off events

Caroline Van Hemert, Matthew M. Smith, Robert J. Dusek, Gwen Baluss, Gay Sheffield, John R. Harley, Susan Knowles, Sarah K. Schoen, and Robert Kaler

Presenting author: **Caroline Van Hemert**, USGS Alaska Science Center, cvanhemert@USGS.gov

Harmful algal blooms (HABs) produce biotoxins that can injure or kill fish, wildlife, and humans. These blooms occur naturally but have intensified worldwide due to recent climatic changes, including ocean warming. Such changes are especially pronounced in northern regions, where the effects of HABs on marine wildlife are of growing concern. In Alaska, seabird mortality events have increased in frequency, magnitude, and duration since 2015 alongside anomalously high ocean temperatures. Although starvation related to prey availability has been linked to many bird deaths, HABs have also been identified as possible contributing factors. Here, we present results from two geographically and temporally distinct events: a multispecies die-off in the Bering and Chukchi sea region in 2017 and a localized die-off at a nesting colony of Arctic Terns (*Sterna paradisaea*) in Southeast Alaska in 2019. To investigate possible causes of bird mortalities, we tested seabird tissues for saxitoxin (STX) and domoic acid (DA). Concentrations of STX in tissues collected from Northern Fulmars (*Fulmarus glacialis*) in the Bering and Chukchi seas and Arctic Terns in southeast Alaska were of similar magnitude (maximum of 63.3 and 39.4 µg/100g, respectively) to those reported from other STX-induced die-offs, suggesting that HABs may have played a role in these events. Additionally, elevated STX concentrations from forage fish at Arctic Tern nests provided evidence of direct exposure to STX via their prey. These findings, in combination with other studies in Alaska documenting widespread occurrence of STX in marine taxa, suggest that HABs present a hazard to northern seabirds and should be addressed in future assessments of population health.

Local versus broad-scale drivers: A Bayesian state-space analysis of long-term waterbird colony dynamics

Aimee M. Van Tatenhove and Clark S. Rushing

Presenting author: **Aimee Van Tatenhove**, Utah State University, aimee.van.tatenhove@usu.edu

Environmental conditions play a critical role in avian population dynamics, but interactions between broad-scale and local conditions, which may be opposing or synergistic, are poorly understood for most breeding birds. Broad-scale climate patterns, including the El Niño–Southern Oscillation (ENSO) and the Pacific Decadal Oscillation (PDO) directly and indirectly impact seabird breeding dynamics, but how these processes interact with local conditions has not been well-studied, especially in inland species. As inland-breeding waterbirds, American White Pelican

(*Pelecanus erythrorhynchos*) colony dynamics may be tied to local climate and water levels, but may also fluctuate in response to broad-scale climate. The Great Salt Lake breeding colony is an important source colony for the western metapopulation of white pelicans. Located in the arid Great Basin, this colony is subject to water limitations and extreme drought, but these factors do not fully explain annual variation in colony dynamics, suggesting that large-scale climate patterns may also be important. Using a Bayesian state-space model, we quantified the influence of the Pacific Decadal Oscillation, Southern Oscillation Index, and local water levels and climate variables on 58 years of white pelican colony counts. Despite significant effects on coastal seabirds, broad-scale climate oscillations appear to be less important than local conditions to the inland colony dynamics of Great Salt Lake pelicans. Our findings suggest that the long-term health of the Great Salt Lake may be critical to the future of this colony and the western metapopulation as a whole, and improve our understanding of inland waterbird population dynamics in response to environmental factors.

Flock mates and foraging behavior in mixed-species flocks

Laura N. Vander Meiden, Allison E. Johnson, and Daizaburo Shizuka
Presenting author: **Laura Vander Meiden**, University of Nebraska-Lincoln, l.vandermeiden@huskers.unl.edu

The decision to participate in mixed-species flocks is a balancing act between the costs of competing with foraging partners and the benefits of interspecific grouping. In this study we look at whether a bird's foraging behavior changes based on the presence of other species. Specifically, we assess whether birds adjust their foraging strata when participating in mixed-species flocks and if the identity of flock members influences whether and how they do so. We collected fine-scale foraging and behavioral data on three different flocking species as well as opportunistically collected foraging data on 9 additional species in and out of mixed-species flocks. We found that three of the 12 species adjusted their foraging strata when participating in mixed-species flocks. In addition, we investigated how the composition of each foraging flock affected changes in foraging behavior. Our findings imply that some species facultatively change their foraging behavior when participating in a flock, and that the identity of these flock mates may play a role in the direction of these changes.

Geographical variation and evolution of the vocalizations of the White-throated Magpie-Jay (*Calocitta formosa*)

Paulina Rebeca Vázquez-Calvillo, Luis Antonio Sánchez-González, and J. Roberto Sosa-López
Presenting author: **Paulina Rebeca Vázquez-Calvillo**, UNAM, pauvazquezc@ciencias.unam.mx

Studies of acoustic signals offer opportunities to test the relationship between acoustic divergence and reproductive isolation. Often, studies assessing variation in acoustic signals are centered in taxa with isolated populations; however, less is known about divergence in vocalizations in sympatry. The neotropical White-throated Magpie-Jay (*Calocitta formosa*) inhabits the tropical dry forests from Mexico to Costa Rica. However, unpublished studies on the White-throated Magpie-Jay suggest the existence of three genetically differentiated clades for which geographic/ecological boundaries are not well-known. Here, we analyze the geographic variation of vocalizations within the complex and explore evolutionary factors fostering such divergence. In the first part of the study, we assess the divergence in acoustic signals between the genetic groups, then we compare the acoustic divergence within the complex to the acoustic divergence with two closely-related species (Black-throated Magpie-Jay, *Calocitta colliei*, and the Brown Jay, *Psilorhinus morio*). In the second part, we analyze the relationship between acoustic and genetic divergence to determine whether acoustic variation arose through cultural drift, signals diverge faster than genetic characters, or signals diverge slowly until genetic differences accumulate. This study will shed light into evolutionary mechanisms promoting geographic variation in behavioral traits and their implications in the maintenance of biological diversity in bird species inhabiting tropical dry forests.

Richness, abundance and diversity of birds in the tropical dry forest of the Sierra de Vallejo (Nayarit, Mexico) under different disturbance conditions

B. Yosuki Villegas-Raygoza, M. Esther Quintero-Rivero, and Alejandro Espinosa
Presenting author: **Brenda Yosuki Villegas Raygoza**, Instituto de Ecología, A.C., yokkanvalentine@gmail.com

Tropical ecosystems possess most of the global biological diversity; unfortunately, these ecosystems are gradually being destroyed mainly by anthropic activities that cause habitat loss and modifications. Birds are a group of interest for this type of study due to their ecological importance. The objective of this work was to examine the response of the bird community to the change in vegetation cover, through the analysis of the composition and diversity of species in a tropical forest landscape with a gradient of habitat modification in the Sierra de Vallejo, Nayarit. For that, I conducted bird censuses in 13 sites, through linear transects in two types of coverage (forest and modified areas), in addition to correlating richness and abundance of birds with the characteristics of the environment in which they were surveyed. I recorded a total of 38 species and 214 individuals in the dry tropical forest and 44 species and 450 individuals in human use areas. I did not find differences in the effective number of species at the value q0, but for the values q1 and q2. Although the modified areas registered greater richness and abundance, the results of this study show that tropical forests maintain a lower number of dominant species in the effective number of species contrary to the modified areas, in addition to that half of the species registered in forest they present some category of endemism. I did not find a relationship between the richness and abundance of birds with the percentage of forest cover for each environment.

Evaluating the effectiveness of dispersal barriers in the Negro River Basin for white sand associated passerines

Rachel Wadleigh, Camila C. Ribas, and L. Lacey Knowles

Presenting author: **Rachel Wadleigh**, University of Michigan, wadleigh@umich.edu

The propensity to disperse across barriers varies broadly by taxa and barrier type. All birds face trade-offs between the potential costs of dispersal (e.g. higher predation risk, greater energy expense) and possible rewards of reaching better habitat, but the relative cost and reward varies (Saastamoinen et al 2018). While genetic structure varies significantly across different barrier types, mixed support often exists across taxa for any given barrier indicating a need to better understand their relative strengths for different taxa (Naka and Brumfield 2018, Boubli et al 2014, Nazareno et al 2017). Better understanding these dispersal barriers will help to predict large scale evolutionary and ecological patterns. To understand the role of habitat heterogeneity and barriers in structuring avian populations and constraining movement, multiple barriers need to be evaluated and compared across taxa employing high resolution genomic markers. Here we evaluate the relative effectiveness of barriers across the Negro and Branco Rivers for three passerines associated with Amazonian white sand habitats by examining the genetic structure of populations separated by different rivers and habitat types. A reduced representation genomic library was constructed using double digest RADseq to evaluate the strength of river and habitat barriers, and whether dispersal probabilities differ as a function of species and barrier type. We find that different species, even sharing a similar habitat association, exhibit different relative genetic structure between populations across the same barriers.

How does digestive physiology mediate the relationship between diet and color in New World warblers?

Emily A. Webb and Kevin J. McGraw

Presenting author: **Emily Webb**, Arizona State University, emily.webb.2016@owu.edu

There is extensive evidence to show that diet influences color in birds. Supplementation of carotenoids, which are used to produce reds, oranges, and yellows in feathers and bare parts and cannot be made de novo, in particular has been shown over and over to produce more colorful ornaments on an intraspecific level. However, studies on an interspecific level have only produced weak relationships between diet and color. Since diet does not clearly explain the evolution of carotenoid-based color in birds, we hypothesized that, instead of diet or dietary availability of carotenoids, digestive physiology or ability to absorb and accumulate carotenoids is a better predictor of color. To test this, we collected samples from 11 species of New World warblers (Parulidae) that died by window-strike during migration, and we measured relative expression of a gene known to be important for carotenoid absorption (SCARB1), dietary availability of carotenoids, and extent of carotenoid-based coloration. We found that, when only diet and color were included in the model, there was no relationship between the two. However, when digestive physiology was added to this model, there was a significant positive association between digestive physiology and color. This supported our hypothesis that digestive physiology mediates the relationship between diet and color in birds. It also suggests that more expression of SCARB1 or carotenoid absorption, rather than dietary availability of carotenoids, has facilitated the evolution of greater extent of carotenoid-based coloration. Additionally, this is the first time that SCARB1 expression has been measured in natural, as opposed to artificially-bred, populations of birds.

A call for fully accounting for effects of nest age when quantifying nest survival

Emily L. Weiser

Presenting author: **Emily Weiser**, U.S. Geological Survey, eweiser@usgs.gov

Accurately measuring nest survival is challenging because nests must be discovered to be monitored, but nests are typically not found on the first day of the nesting interval. Samples in nest survival therefore often overrepresent older nests. To account for this, a daily survival rate (DSR) is estimated and used to calculate nest survival to the end of the interval. However, estimates of DSR (and thus nest survival) can still be biased if DSR changes with nest age and nests are not found at age 0. Including nest age as a covariate of DSR and carefully considering the method of estimating nest survival can prevent such biases, but many published studies have not fully accounted for changes in DSR with nest age. I used a simulation study to quantify biases in nest survival estimates resulting from effects of nest age on DSR under a variety of scenarios. I tested four methods of estimating nest survival from the simulated datasets and evaluated the bias and variance of each estimate. Nest survival estimates were often strongly biased when DSR varied with age but the model assumed DSR was constant. Biases were also often strong when the model included age as a covariate but calculated nest survival from DSR at the mean monitored nest age, which is the method typically used in previous studies. In contrast, biases were usually avoided when nest survival was calculated as the product of age-specific estimates of DSR across the full nesting interval. Future field studies can maximize accuracy and precision of nest survival estimates by aiming to find nests at young ages, including age as a covariate in the DSR model, and calculating nest survival as the product of age-specific estimates of DSR when DSR changes with nest age.

The anatomy of a phenological mismatch: Interacting consumer demands and resource availability determine the consequences of mismatching

Luke R. Wilde, Josiah E. Simmons, Rose J. Swift, and Nathan R. Senner

Presenting author: **Luke Wilde**, University of South Carolina, lukewilde95@gmail.com

Climate change has caused shifts in seasonally recurring biological events leading to temporal decoupling of consumer-resource pairs – i.e., phenological mismatching. Although these mismatches often affect individual fitness, they can also affect populations. However, empirical measures of population-level responses remain unclear, making it difficult to assess the risks posed by mismatching. Changes in resource availability and consumer demands could affect a consumer's mismatch differently over time. Nevertheless, most models still adopt the categorical definition of mismatching, in which consumers are 'matched or mismatched'. We analyzed how the effects of mismatching varied over time by studying precocial Hudsonian Godwit (*Limosa haemastica*) chicks and their invertebrate prey from 2009–2019. We developed individual- and population-level models to determine how variation in consumers' energetic demands affects their relationship to resource availability. We found that periods with abundant resources led to higher growth and daily survival of individual godwit chicks, but that throughout development, chick survival was increasingly related to the availability of larger prey. At the population-level, estimates of mismatching using age-structured consumer demand explained 7-30% more variation in annual fledging rates compared to those of previous models. Our study suggests that modeling the effects of mismatching as the disrupted interaction between dynamic consumer demands and the availability of their resources provides a biological mechanism for how mismatching occurs and clarifies when it matters to individuals and populations.

The loss of female vocal complexity and duetting behavior in the ancestors of Carolina Wrens (*Thryothorus ludovicianus*)

Mira Willson and J. Jordan Price

Presenting author: **Mira Willson**, St. Mary's College of Maryland, mtwillson@smcm.edu

Birdsong has historically been approached as a primarily male trait. Emerging research, however, is showing that females of many tropical songbird species are prolific singers and even perform coordinated duets with their mates. In Carolina Wrens (*Thryothorus ludovicianus*), one of the few non-tropical members of the wren family Troglodytidae, females do not sing but rather produce a simple rattling call that often overlaps with the song of their male mate. In my study, I reconstructed the evolutionary history of female vocal behavior in the ancestors of Carolina Wrens using a phylogeny of the family Troglodytidae to investigate how female vocalizations have changed in their complexity and coordination with males. My results showed that the evolutionary ancestors of Carolina Wrens produced female vocalizations that were more acoustically complex and more male-like than the rattle calls of current females,

suggesting past selection against complex female song. Vocal coordination with males, however, has decreased relatively little since the common ancestor of all wrens. My study shows that female Carolina Wrens have lost vocal complexity over time while maintaining coordination with male songs, suggesting that these two aspects of female behavior have evolved independently and perhaps have different functions.

Migration distance is a fundamental axis of the slow-fast continuum of life history in boreal birds

Benjamin M. Winger and Teresa M. Pegan
Presenting author: **Benjamin Winger**, University of Michigan, wingerb@umich.edu

Seasonal migration is a widespread adaptation in environments with predictable periods of resource abundance and scarcity. Migration is frequently associated with high mortality, suggesting that migratory species live on the 'fast' end of the slow-fast continuum of life history. However, few interspecific comparative studies have tested this assumption. We evaluated how migration distance influences the tradeoff between reproduction and survival in 45 species of mostly passerine birds that breed sympatrically in North American boreal forests but migrate to a diversity of environments and latitudes for the northern winter. We find, after accounting for mass and phylogeny, that longer distance migrations to increasingly amenable winter environments are correlated with reduced annual reproductive output, but also result in increased adult survival compared to shorter-distance migrations. These results suggest that long-distance migration imposes selection pressures that both confer and demand high adult survival rates. That is, owing to the reproductive cost of long-distance migration, this strategy can only persist if balanced by high adult survival. Our results reveal migratory distance as a fundamental life history parameter that predicts, and is inextricable from, the balance of survival and reproduction. Our study further provides evolutionary context for understanding the annual cycle demography of migratory species and the strategies long-distance migrants use to maximize survival on their journeys.

Egg-laying order, maternal effects, and embryonic growth in American Robins (*Turdus migratorius*)

Sarah K. Winnicki, Thomas J. Benson, Ryan T. Paitz, and Mark E. Hauber
Presenting author: **Sarah Winnicki**, University of Illinois at Urbana-Champaign, sarahkw2@illinois.edu

Mothers may preferentially allocate embryonic resources to later-produced offspring within the same clutch to offset the costs of competition with older siblings. Alternatively, mothers may bias their investment to favor first-laid and older hatching chicks within the brood's hierarchy. To test these alternative hypotheses, we investigated maternal resource allocation and embryonic development of American Robins. We collected eggs on the day of laying to analyze the relative amounts of egg components, including yolk, albumen, and yolk steroid concentrations. We also artificially incubated eggs to measure heart rate and day 8 embryo size metrics and relate development to known laying order. First-laid eggs were smaller and had higher concentrations of six steroid hormones: DHEA, 17a-hydroxypregnenolone, 17a-hydroxyprogesterone, pregnenolone, androstenedione, and etiocholanolone, but notably not estrone, testosterone, progesterone, pregnanedione, or pregnanolone. All steroids present in the yolk declined in concentration as the embryo developed. There was a consistent effect of laying order on the size of embryos at Day 8 in development, with tarsus length, bill length, and overall embryo size increasing with increasing laying order. Average embryonic heart rate at day 4 and day 8 of development did not vary with laying order. These results support the maternal offset hypothesis as American Robins favor later eggs for increased egg constituent investments.

Dorsal color variation among subspecies of the 'Oregon' Dark-eyed Junco complex

Elisa T. Yang, Philip Unitt, and Nicholas A. Mason
Presenting author: **Elisa Yang**, University of California, Berkeley, chiccadee100@gmail.com

Initial descriptions of avian subspecies were based on expert opinions of geographic variation in phenotypes and are inherently subjective. Reassessing subspecies limits with current, quantitative methods is vital toward refining and improving taxonomic treatments. Plumage coloration is the basis of many subspecies diagnoses but is potentially problematic because of the historical lack of quantitative methods to quantify color. Recently developed methods, such as colorimetry, provide repeatable measurements of color variation that can be used to reassess subspecies limits. In this study, we reassess color variation among subspecies of the Oregon Dark-eyed Junco (*Junco hyemalis* [*oreganus* Group]) complex, in which differences in dorsal and hood color were established as diagnostic characters. We measured back and hood brightness and hue in 206 museum specimens among five Oregon Dark-eyed Junco subspecies using a colorimeter. We then compared mean measurements among subspecies and conducted a discriminant function analysis to assess how well dorsal color predicted subspecies. Our data correctly classified only 67.9% of males and 82.5% of females to their presumed subspecies. Furthermore, no adjacent subspecies pairs passed the '75% rule' due to extensive overlap in plumage characters. Thus, dorsal color alone is not as effective in diagnosing Oregon Dark-eyed Junco subspecies as initially described, suggesting a possible need for taxonomic revision. Specifically, similarity in phenotypic and genetic data suggests that some combination of *J. h. thurberi*, *montanus*, and *shufeldti* may be lumped to recognize broad, clinal variation in dorsal color alongside clinal variation in other phenotypes and extensive gene flow.

A songbird inhibits blinking behavior in flight

Jessica L. Yorzinski

Presenting author: **Jessica Yorzinski**, Texas A&M University, jyorzinski@tamu.edu

Visual attention plays a fundamental role in avian flight but attention is likely limited whenever birds blink. Because blinks are necessary to maintain proper vision, this study tested the hypothesis that birds strategically inhibit their blinks in flight. The blinks of captive Great-tailed Grackles (*Quiscalus mexicanus*) were recorded before, during, and after they flew a short distance in an open environment. The grackles spent the least amount of time blinking in flight (take-off, during flight and landing) and the most amount of time blinking at impact. Their blinking behavior was similar before and after flight. These results suggest that grackles strategically inhibit their blinking behavior in flight, potentially because blinks impose costs to avian flight.

Avian morphological change driven by abiotic variation over time and space

Casey Youngflesh, James F. Saracco, Rodney B. Siegel, and Morgan W. Tingley

Presenting author: **Casey Youngflesh**, University of California, Los Angeles, cyoungflesh@ucla.edu

Abiotic conditions play an integral role in shaping morphological variation in organisms over time and space. Increasing global temperatures are expected to drive shifts towards smaller body sizes, yet attempts to verify this phenomenon have generally been hampered by existing morphological variation across space. Using standardized data from more than 300,000 captures of 111 bird species derived from the Monitoring Avian Productivity and Survivorship program, we assessed intraspecific changes in North American bird morphology over the past 29 years, at locations spanning 40 degrees of latitude and 3 km of elevation. We derived indices of overall bird size and relative wing length based on empirical allometric morphological scaling relationships and used hierarchical Bayesian models to quantify spatiotemporal change in these indices. Across the avifauna, body size declined in association with rising summer temperatures on breeding grounds. This temporal shift was independent of strong ecogeographic variation. In support of Bergmann's rule, birds were generally larger at colder, more northerly locations. Birds at more northerly locations also tended to have longer wings, as did birds captured at higher elevations. Longer wings can increase lift, likely providing benefits to populations that have extended migrations or which live at higher elevations, where air-density is lower. Understanding the role that abiotic factors play in driving large-scale spatiotemporal morphological variation has implications for better understanding differences within and among species and the impacts of rapid climate change on animal morphology.

Impacts of conifer removal on sagebrush songbirds

Elise C. Zarri and Thomas E. Martin

Presenting author: **Elise Zarri**, University of Montana, elise.zarri@umontana.edu

Conifers have encroached into shrubland habitats across the western United States, contributing to the degradation of sagebrush habitat quality. Conifer removal has become a common restoration strategy and is often done to increase habitat quality for Greater Sage-Grouse. Sage-grouse clearly benefit from tree removal through increases in abundance and reproductive success. Other sagebrush associated species are assumed to benefit similarly, but these assumptions are often based on minimal or no data. This study aims to test how conifer removal impacts the abundance and reproductive success of sagebrush songbirds, including sagebrush-obligate, sagebrush-associated, and generalist species. Removal of conifers could result in ecological traps for songbirds due to high spillover nest predation from conifer habitats. I monitored nests and created territory maps of seven species between conifer removal and control areas in montane sagebrush habitat in southwest Montana. Sagebrush-obligate species including Brewer's Sparrow and Sage Thrasher have higher abundance and nest success in conifer removal areas. Sagebrush-associated and generalist species show mixed responses. Vesper Sparrows are more abundant in removal areas, whereas Green-tailed Towhees, Dark-eyed Juncos, Chipping Sparrows, and White-crowned Sparrows are more abundant where conifers remain. Additional data is required to clarify patterns of nest success for these species. However, initial results indicate that conifer removal is beneficial for declining species of sagebrush-obligate songbirds.

Elevational shifts of Great Basin birds over the past two decades

Martha W. Zillig and Erica Fleishman
Presenting author: **Martha Zillig**, University of California, Davis, martha.zillig@gmail.com

Growing evidence suggests that changes in elevational distributions of bird species are occurring globally. Leading theories suggest that the elevational distributions of birds will shift upslope in response to warming temperatures, reflecting an underlying assumption that birds will track spatial changes in temperature. We examined two nearly continuous sets of avian point-count data, spanning 8 and 19 years, respectively, in two regions of the Great Basin. We employed single-species occupancy models to study elevational movement of 32 species at three spatial extents: the full elevational gradient surveyed, the trailing edge of the elevational gradient (lower 25%), and the leading edge of the elevational gradient (upper 25%). We also examined the effects of precipitation, primary productivity, and temperature on occupancy at these three extents. We determined that the elevational ranges of 19 of the 32 species shifted over the past two decades, with substantial species-specific variation in the direction and magnitude of movement. Most of the movement occurred at the leading or trailing edge of the elevational gradient, and only about 50% was upslope. Across the Great Basin, spring precipitation, winter precipitation, and annual temperature have increased over the past two decades. Our results indicated that occupancy of many species was negatively affected by both winter and spring precipitation, and we infer that the distribution of populations may have shifted upslope or downslope in response.

Toward an understanding of the relationship between environment and genetic divergence in White-tailed Ptarmigan

Shawna J. Zimmerman, Cameron L. Aldridge, Kathryn M. Langin, Gregory T. Wann, R. Scott Cornman, and Sara J. Oyler-McCance
Presenting author: **Shawna Zimmerman**, US Geological Survey, szimmerman@usgs.gov

Rapid changes to the alpine resulting from a warming climate will expose alpine-adapted species to novel environmental conditions, forcing one of three responses: shift distribution, acclimate, or adapt genetically to a new climate. Suitable alternative habitat for alpine-specialist species is limited, and the long-term capacity for acclimation will likely be tested, but adaptive genetic variation may provide the raw ingredients for species to adapt to this changing environment. Here, we use a genomic approach to characterize putatively adaptive divergence patterns in an alpine-obligate species, the White-tailed Ptarmigan (*Lagopus leucura*). The species is distributed from Alaska to New Mexico, across an environmentally-variable geographic range. Previous work identified genetic structure and morphological, behavioral, and physiological differences across the species' range; however, those studies were unable to determine the degree to which populations have adapted genetically to local variation in environmental conditions. We used a single nucleotide polymorphism (SNP) dataset generated from 95 White-tailed Ptarmigan distributed throughout the species' range and genotype-environment association analyses to identify candidate adaptive loci. We detected associations between multiple environmental gradients and candidate adaptive loci, suggesting ptarmigan populations may be locally adapted to the plant community composition, local climate, and the seasonality of the environment. Overall, our results suggest there may be groups within the species' range with genetic variation that may be essential for adapting to a changing climate.

Virtual Poster Presentation Abstracts

Listed alphabetically by last name of first author

A draft avian tree of life

Mariem R. Ahmad, OpenWings Consortium, and Gregory Thom
Presenting author: **Mariem Ahmad**, American Museum of Natural History, mariem.ahmad02@gmail.com

Birds make up the most diverse group of land vertebrates in the world with over 10,000 species distributed all across the globe. Understanding the evolution of this extraordinary diversity and ecological variation is contingent on resolving phylogenetic relationships for all birds. The increased application of phylogenomic techniques to different bird clades has clarified evolutionary relationships within and among many groups of birds. This newly available data provides an opportunity to synthesize independent studies to build a draft of the avian tree of life. Here we will discuss our efforts to build a phylogenomic tree of birds using ultraconserved elements, from > 2,700 species, > 1,000 genera, and all families from 47 separate studies. Because these datasets were independently produced, our goal was to explore how variation among datasets, regarding data processing and characteristics impact phylogenetic reconstructions. Our final data set included 5,121 loci with an average of 664bp and 1,590 individuals per loci. Principal Component Analysis of summary statistics revealed that species cluster by study, suggesting that bioinformatics processing leads to a highly heterogeneous distribution of missing sites, parsimony informative sites, singletons, and GC content between studies. We next estimated a phylogeny using a supermatrix analysis that yielded a robust topology. To check for errors in the tree, we assessed whether clades reflected taxonomic relationships and found that 93%, 98%, and 97% of the currently recognized genera, families, and orders were monophyletic, respectively. We conclude by discussing the implications and challenges of estimating phylogenies from large and heterogeneous datasets.

Prioritizing Midwest regional landscapes to conserve habitats for grassland birds

Mohammed A. Al-Saffar, Gregory J. Soulliere, and Kelly R. VanBeek
Presenting author: **Mohammed Al-Saffar**, U.S. Fish and Wildlife Service, mohammed_al-saffar@fws.gov

Breeding populations of grassland birds have been declining in the Midwest region for decades. Although the Upper Mississippi / Great Lakes Joint Venture (JV) lacked sufficient demographic and density data to develop biological models for breeding grassland birds and predict species response to conservation actions, we developed spatial models to target habitat conservation through a landscape change analysis. We used current (2001-2016), back-casted (pre-European settlement and 1970), and future predicted (2100) land cover spatial data, patch size characteristics of grassland bird focal species, and measures of current (2010-2020) recreation and birdwatching activities to generate decision support maps to guide conservation actions. We identify existing core breeding habitats with a focus on patch size (retention) and herbaceous plant composition (enhancement). We also categorize landscapes for grassland restoration based on current restorable areas, their spatial configuration and potential connectedness, land ownership, social values, and potential value to other bird groups. We found that an estimated 13% of grassland area remained in the JV region compared to pre-European settlement, and most of this area was in the southwest and west-central portions of the region. Whereas the greatest grassland restoration opportunity exists in the south half of the JV region, objectives related to people were more prominent near urban centers. Using combinations of spatial data representing above objectives, and weighting those objectives to reflect stakeholder priorities, provided a transparent framework to integrate conservation concerns with a family of large-scale decision support maps.

Morphology, vocalizations, and mitochondrial DNA suggest that the Graceful Prinia is 2 species

Per Alström, Pamela C. Rasmussen, Canwei Xia, Lijun Zhang, Chengyi Liu, Jesper Magnusson, Arya Shafaeipour, and Urban Olsson
Presenting author: **Pamela C. Rasmussen**, Michigan State University Museum, rasmus39@msu.edu

The Graceful Prinia (*Prinia gracilis*), the only prinia species that occurs in the Western Palearctic, is a small, drab, long-tailed species with streaking above and plain pale underparts that has been suggested to fall into 2 groups: the southwestern nominate group (from Egypt to Oman) and the northeastern *lepida* group (from Turkey through India). However, the characters presented to justify this grouping are variable and show a mosaic pattern, and whether genetic and vocal differences exist was unknown. Our integrative taxonomic analysis of morphology, song, and mitochondrial DNA (mtDNA) suggest that 2 species should be recognized in the Graceful Prinia complex. We found consistent between-group song differences, with the nominate group giving consistently longer inter-phrase intervals, whereas the members of the *lepida* group sing an essentially continuous reel. An mtDNA tree suggests a deep split between the nominate and lepida groups, with a coalescence time between these clades of ~2.2 million years ago. Vocal and mtDNA analyses provided evidence that the northeastern Arabian Peninsula taxon *carpenteri* belongs to the *lepida* group. We found that, of all the morphological characters proposed, only proportions and tail barring and spotting relatively consistently distinguish the 2 groups. However, these characters strongly suggest that the eastern Arabian Peninsula is populated by taxa of both the *gracilis* and *lepida* groups, in different areas, but corroborating genetic and bioacoustic data are lacking. Although further study is needed in potential contact zones, we suggest that 2 species should be recognized in the *P. gracilis* complex.

Evaluation of nocturnal birds using acoustic records in the Chirikyacu native community

Lucía X. Alva-Caballero, Víctor E. Sanchez-Cabrera, and José L. Mena-Alvarez

Presenting author: **Lucía Ximena Alva-Caballero**, Universidad Nacional de Trujillo, lucia.alva.caballero@gmail.com

Knowing the population status of the nocturnal birds of the native community of Chirikyacu is fundamental since this community is contiguous to the National Reserve Cordillera Escalera. The most crucial threat to bird populations in Cordillera Escalera is the destruction of habitat due to productive activities (livestock and agriculture), exacerbated by infrastructure projects such as the construction of the Moyobamba-Balsapuerto highway, oil exploration and exploitation, and forestry concessions. Therefore, knowing the species that inhabit this community will allow for the formulation of conservation plans and ensure the sustainable development of Chirikyacu. To achieve this goal, we must use new technologies, such as passive acoustic monitoring (PAM), to improve and expand global monitoring of biodiversity. This project aims to assess the occurrence of nocturnal birds based on PAM at Chirikyacu. To analyze the acoustic records, we used the Arbimon platform. Seven species of nocturnal birds were found. Megascops roraimae napensis was the one most frequently detected. A map with the most frequent sites where each species was found was elaborated. This is among the first experiences using acoustic monitoring to assess the diversity of nocturnal birds in Peru.

Geographic variation in vocalizations and morphology of Cactus Wrens (*Campylorhynchus brunneicapillus*)

Violeta M. Andrade-González, Hernán Vázquez-Miranda, and J. Roberto Sosa-López

Presenting author: **Violeta Andrade**, Instituto de Biología, Universidad Nacional Autónoma de México, mavica1994@gmail.com

The study of ecological processes that influence the geographic variation of characters involved in reproductive isolation are central to explain the biodiversity in our planet. In this study, we evaluate the acoustic and morphological variation in Cactus Wrens (*Campylorhynchus brunneicapillus*) and their association with ecological and geographical factors. Specifically, we test the Acoustic Adaptation Hypothesis (Morton 1975) using vocal traits and Gloger's Rule (1929), Allen's Rule (1876) and Bergmann's Rule (1847) using morphological traits. We analyze the fine structural characteristics of 115 songs belonging to recordings archived at multiple bird sound libraries. For the morphology we will use digital photography of 146 specimens deposited in biological collections in Mexico to assess the color variation in the throat, head, chest, flank and belly. We measure the different spectra of their wavelengths (long, medium and short) and using geometric morphometry we estimate the size and shape of the beak. This study will shed light into the ecological and geographical mechanisms influencing the variation of acoustic and morphological characters in a species of bird that inhabits the deserts of North America. In addition, it will help to clarify the taxonomic status of this species to inform decisions at the level of official protection and strategies for its conservation.

Long-term camera trap monitoring of understory birds in the Peruvian Amazon reveals rarely registered behaviors

Alejandra Arana, Juan F. Esteves, César Arana, Samia Carrillo-Percastegui, George V.N. Powell, Mathias W. Tobler, Alfonso Zúñiga, Mark Bowler, and Letty Salinas

Presenting author: **Alejandra Arana**, Universidad Nacional Mayor de San Marcos, alejandra.arana27@gmail.com

Camera traps are a useful tool to study activity patterns and behavior of terrestrial birds, such as tinamous, as it avoids the disturbance of direct observation. However, long-term studies show that data from a wider variety of birds can be gathered. Here we present new behavioral data from birds in the understory of the Madre de Dios, Peru. We

analyzed data from 10 locations: the biological stations Cocha Cashu and Los Amigos (2 grids), the brazil-nut concessions Alerta and Monterrey, the forest concession Espinoza, the guard post Pakitza, and three locations in the Tambopata National Reserve. The data was gathered from 2005 to 2016 (15 surveys) and corresponds to 34392 days. We installed camera traps at 50 cm from the ground, they were active 24 hours a day and were distributed regularly with 1-3 km of distance between each other. We obtained previous information about microhabitat preference from EltonTraits 1.0 and specialized literature review. We recorded 16 bird species previously considered having a habitat preference to medium strata to aerial, that includes species from the Galbulidae (2), Accipitridae (4), Cracidae (3), Cuculidae (2), Ramphastidae (1), Nyctibiidae (1), Columbidae (1), Tyrannidae (1) and Bucconidae (1) families. We also registered five species of Accipitridae (*Spizaetus ornatus, Spizaetus tyrannus, Rupornis magnirostris, Morphnus guianensis, Pseudastur albicollis*), that present sunning behavior in rainforest clearings, being the first report of this type of behavior for these species. These sightings show camera trap long-term monitoring can be a useful tool to improve our knowledge in bird behavior, even of birds that are not usually registered at understory level.

Patterns of cranial evolution in an adaptive radiation of Malagasy birds (Vangidae)

Anya L. Auerbach and Sushma Reddy

Presenting author: **Anya Auerbach**, University of Minnesota, auerb027@umn.edu

Adaptive radiation involves extreme diversification in both the ecology and morphology of a clade. Of the classic adaptive radiations known in birds, the Malagasy vangas remain particularly poorly known, despite displaying spectacular diversity in ecological niche, shape, and size, to such a degree that several species were until recently placed in different families. In this study we used a dataset of microCT scans of Vangidae in order to better understand how ecologically significant morphological traits evolve in adaptive radiations. Bill shape has been the traditional focus of ecomorphological study in birds, but microCT scanning provides access to the entire skull and high-density, three-dimensional landmarking permits characterization of many important details of shape that traditional linear measurements do not capture. We also examined a mix of skeletal material and skulls preserved in round skins to assess the suitability of the latter for studies of this type, which would drastically increase available sample sizes. These methods enable us to address questions of integration and modularity, or how different anatomical regions evolve relative to one another, which may play a key role in the ability of some clades to undergo dramatic adaptive radiation, as well as evaluate rates of morphological evolution in different regions of the Vangidae tree through time.

Testing the utility of condition indices in nestling swallows: A quantitative magnetic resonance (QMR) approach

Andrew T. Beauchamp, Jackson W. Kusack, Keith A. Hobson, and Christopher G. Guglielmo

Presenting author: **Andrew Beauchamp**, University of Western Ontario, abeauch7@uwo.ca

Nutritional condition is a key factor influencing the survival of migratory birds, and condition indices derived from morphometric measurements are commonly used to assess nutrient and energy stores. However, the performance and utility of condition indices used to examine energetics of growing juvenile birds remain uncertain. Recently, quantitative magnetic resonance (QMR) has been used to provide a non-invasive and non-lethal way to obtain measures of body composition. We calculated three widely used body condition indices using both wing length and tarsus length for nestling Barn Swallows (*Hirundo rustica erythrogaster*) at two ages (Day eight and 15) and compared them to relative fat and lean mass calculated using QMR measurements. Additionally, we used QMR to develop multiple regression formulas to predict nestling fat mass, lean mass, and fat-free lean body mass (LBM) from easily obtainable body metrics. In Day eight birds, variation in both relative fat mass and relative lean mass were adequately explained by total body mass alone, but this relationship was strongest for lean mass. Almost every condition index evaluated failed to explain variation in relative fat or lean mass in Day 15 birds. While our best multiple regression formulas for predicting fat mass and LBM had low predictive power, our formulas for predicting lean mass were precise ($R^2 > 90\%$) in both ages, providing a method to estimate the lean mass of nestlings from more readily obtainable metrics. Estimates of fat mass calculated from LBM and total body mass showed poor precision ($R^2 = 30\%$).

Long-term analysis of the spatial distribution and habitat associations of Purple Martin (*Progne subis*) and Tree Swallow (*Tachycineta bicolor*) roosts in the US Great Lakes

Maria Carolina T. D. Belotti, Yuting Deng, Wenlong Zhao, Zezhou Cheng, Aroma Rodrigues, Elske Tielens, Subhransu Maji, Daniel Sheldon, Jeffrey F. Kelly, and Kyle G. Horton
Presenting author: **Maria Carolina Tiburcio Dias Belotti**, Colorado State University, maria.belotti@colostate.edu

Weather surveillance radar data has become a well-established tool for the tracking, monitoring, and localization of important annual events for migratory birds, particularly at large spatial and temporal scales. While radars do not typically collect species-specific information, communal roost formation of aerial insectivores, species of conservation concern, are distinctly and uniquely identified by the US network of surveillance radars. Here, we specifically examine the roosting behavior of Purple Martins (*Progne subis*) and Tree Swallows (*Tachycineta bicolor*) to quantify consistency in roost spatial distribution and habitat associations. These species are known to form large roosts, often gathering ten to hundreds of thousands of individuals, during different moments of their migratory cycles. From July to December, early morning exodus from roosting sites can be so dense that conspicuous ring-shaped high-reflectivity regions are clearly visible on weather surveillance radar sensors. We use newly developed computer vision techniques to extract roost locations from 12 weather surveillance radar stations in the region surrounding the US Great Lakes from 1998 to 2017, yielding one of the longest time-series for such examinations. With our analysis, we provide new insights into the ability of Purple Martins and Tree Swallows to shift their collective roosting behavior in order to adapt to climate and land cover variation through the years.

Comparison of breeding bird diversity in urban vs. rural areas in an intensive agricultural landscape in Illinois, USA

Leah Bieniak, Rachel Schoenecker, A. P. Capparella, and R. Given Harper
Presenting author: **Leah Bieniak**, Illinois Wesleyan University, leah.bieniak@gmail.com

Many bird species have experienced population declines over the past century due to human development of natural areas. Breeding birds have been forced to rely upon alternative habitats, including urban and agricultural areas. Recent studies have indicated that population increases of some bird species in the Midwestern U.S. have been associated with their use of urban habitat. However, few bird surveys have compared species diversity in urban and agricultural areas in central Illinois. We conducted a two-year breeding bird survey and habitat analysis in Bloomington-Normal, Illinois in 2019 and 2020 via a modified USGS Breeding Bird Survey (BBS) protocol. These data were compared with up to six years of results from the seven rural BBS routes closest to Bloomington-Normal. We observed 79 species in our urban study area, including 16 USGS-designated Species of Greatest Conservation Need (SGCN). In contrast, 93 species and 20 SGCN were observed on the combined BBS routes. When pooled across survey years, the Shannon Diversity Index for Bloomington-Normal was higher than five of seven BBS routes and all BBS routes combined, which is likely explained, in part, by the extensive amount of intensive row-crop agriculture within them (74.97 - 92.05%). The density of urban woodland bird species was significantly higher at sites with taller trees and greater canopy cover. Housing density did not affect the diversity or abundance of birds at urban sites. The results of this study suggest that urban areas can support a greater number of breeding bird species than rural areas dominated by intensive agriculture.

Temporal and spatial patterns of neonicotinoid and butenolide insecticide residues in flowers, hummingbirds and honey bee nectar and honey in the Fraser Valley, BC, Canada (2018, 2019)

Christine A. Bishop, Kristina G. Hick , France Maisonneuve , Alison J. Moran , Julia Common, Heather A. Higo, and John E. Elliott
Presenting author: **Christine Bishop**, Environment and Climate Change Canada, christine.bishop@canada.ca

In 2018 and 2019, 6 systemic insecticides were found in flowers, hummingbirds, honey bee (*Apis mellifera*) nectar, and honey sampled in April through July at 12 sites located 0.16 km to 22.8 km from conventionally sprayed blueberry fields (CSBF) in the Fraser River valley, BC, Canada. We found these wildlife are exposed to chronic and widespread mixtures of these pesticides and that concentrations of some individual compounds are of concern. The spatial and temporal insecticide residue concentrations and number of compounds detected in honey bee nectar and honey significantly declined as distance from CSBFs increased and, in some cases, but not all, increased in concentration throughout the sample period. In cloacal fluid from hummingbirds, residues followed the same spatial and temporal patterns as nectar and honey but only concentrations of flupyradifurone (FPF) showed significantly higher concentrations in sites closest to CSBFs. In flowers, residue concentrations and types varied significantly between years and residues were detected in samples from throughout the valley but were not significantly associated

with proximity to CSBFs. Imidacloprid concentrations detected are associated with sublethal effects in honey bees and hummingbirds. The butenolide, flupyradifurone, was detected at the highest concentrations in the study at 215 ng/g in honey which is four times above the maximum residue levels (MRLs) acceptable for consumption as set by the European Union. There are no MRLs for neonicotinoids or FPF for honey in Canada.

Avian use of agricultural areas as migration stopover sites: A review of crop management practices and ecological correlates

J. David Blount, Joshua J. Horns, Kyle D. Kittelberger, Montague H. C. Neate-Clegg, and Çagan Hakki Sekercioglu

Presenting author: **David Blount**, University of Utah, David.Blount@utah.edu

An estimated 17% of migratory bird species are threatened or near threatened with extinction. This represents an enormous potential loss of biodiversity and cost to human societies due to the economic benefits that birds provide through ecosystem services and ecotourism. Conservation of migratory birds presents many challenges, as these birds rely on multiple geographically distinct habitats, including breeding grounds, nonbreeding grounds, and stopover sites. In particular, stopover habitats are seldom studied relative to breeding and nonbreeding habitats, despite their importance as refueling stations for migratory birds. In this study, we summarize the current research on the use of temporary primary crops by birds during migration and we assess the species characteristics and agricultural practices most often associated with the use of cropland as stopover habitat. First, we conducted a systematic review of the literature to document the effects various farming practices and crop types have on the abundance and diversity of migratory birds using agricultural areas for stopovers. Second, we analyzed the ecological correlates of bird species in the Northern Hemisphere that predict which species may use these areas while migrating. We ran a GLMM to test whether diet, habitat, or realm predicted stopover use of agricultural areas. Our review suggests that particular crop types, as well as farming practices that result in higher non-cultivated plant diversity, encourage the use of agricultural areas by migrating birds. We found that cropland is used as stopover habitat by bird species that can utilize a large breadth of habitats, as well as species with preferences for habitat similar in structure to agricultural areas

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Avian diversity and foraging behavior in a heterogeneous urban-agroecosystem

Rachel E. Bockrath, Eric M. Wood, David W. Still, Erin J. Questad, and Elizabeth S. C. Scordato

Presenting author: **Rachel Bockrath**, California State Polytechnic University, Pomona, rebockrath@cpp.edu

Human landscape modification dramatically alters ecological communities, but some anthropogenic habitats support more biodiversity than others. Many studies have investigated how birds respond to urbanization, but fewer assess diversity and habitat use in agricultural lands, despite agriculture being the dominant form of human land use. To better target conservation efforts and mitigate biodiversity loss, it is important to understand how birds use agricultural landscapes. Here, I investigate species diversity and foraging activity in a complex agroecosystem comprising five main habitat types (scrub, riparian, orchards, suburban, urban) in the Santa Clara River Valley of California. I use point counts to compare community structure across the landscape and observe foraging behavior to determine the key dietary niches each habitat type supports. By comparing several types of human-modified landscapes, my study will elucidate how habitat structure and food resources drive variation in avian community structure across a heterogeneous landscape.

Spatial relationship between avian host communal roosts and West Nile virus infected mosquitos in Maricopa County, Arizona

Skyler Bol, Pete Motyka, and Crystal Hepp

Presenting author: **Skyler Bol**, Northern Arizona University, stb226@nau.edu

The most common mosquito-borne disease in the continental United States is West Nile virus (WNV). Zoonotic events of WNV occur when mosquitos transfer the disease to humans after being infected from avian hosts. Maricopa County, Arizona is an epicenter for WNV in the Southwest and two species of bird, the Great-tailed Grackle (*Quiscalus mexicanus*) and the House Sparrow (*Passer domesticus*), have been identified as primary amplifying host for the disease. WNV vector mosquito densities are greater around the large communal roost sites for both bird species. It was expected that research into the spatial distribution of roost location and infected mosquitos would show a direct relationship between host and infected vector presence. eBird data was filtered to identify large communal roosts of the two species and mosquito trap data was used to show locations where mosquitos had tested positive for WNV in the years 2015, 2016, 2017, 2019, and 2020. The data sets were put into presence-absence maps for each year using rasters in R programming to quantify spatial distribution. Chi-square tests on the presence absence data suggest a direct relationship between both Great-tailed Grackle and House Sparrow communal roosts with mosquitos infected with WNV. Elucidating the relationship between host-vector interaction has potential to reduce human cases as well as effectively manage outbreaks of the disease.

Factors affecting breeding productivity of Common Nighthawks nesting on south Louisiana beaches

Sarah M. Bolinger, Erik I. Johnson, and Paul L. Leberg

Presenting author: **Sarah Bolinger**, University of Louisiana - Lafayette, sarah.bolinger@gmail.com

Restoration projects, storms, and cattle grazing on the Louisiana coast create sparsely vegetated habitat in various stages of succession favored by multiple ground-nesting species, including Common Nighthawks (*Chordeiles minor*). Although nighthawks are not generally thought of as beach-nesting birds, on Louisiana beaches they nest near other beach-nesters at densities of up to 8-10 pairs per linear mile in the southwest of the state. It is unclear, however, whether this habitat in Louisiana (much of which is in cattle pasture or highly subsided areas that flood during every large storm) is leading to favorable population outcomes or is creating an ecological trap, in which fitness is lower in attractive nesting habitat. To begin assessing population dynamics of coastal Louisiana nighthawks, I studied factors affecting their breeding productivity. In coastal Louisiana, nighthawks nest on and near beaches that exhibit varying levels of predation and disturbance, as well as differences in vegetation cover, type of vegetation, elevation, and available nesting substrate. These beaches are also located near varying habitat types and land use classifications. In this study, I sought to discover the effect of habitat variables on nest survival and nesting density during the 2017-2020 breeding seasons. In addition, I used measurements of individual nighthawk chicks from 2017-2020 to create growth curves and evaluate the effects of these same factors on chick growth and survival.

Recent history the Ecuadorian Hillstar: An example of divergence with gene flow?

Elisa Bonaccorso, Carlos A. Rodríguez-Saltos, Juan F. Freile, Nicolás Peñafiel, Laura Rosado-Llerena, and Nora H. Oleas

Presenting author: **Elisa Bonaccorso**, Universidad San Francisco de Quito, elisabonaccorso@gmail.com

Studying young lineages is among the most promising approaches for unveiling the processes behind speciation. Here, we examined the evolutionary history of the Ecuadorian Hillstar (*Oreotrochilus chimborazo*), a high Andean species of hummingbird that might have experienced rapid diversification in the recent past. To do that, we generated a dataset of ten microsatellite markers and complementary data on morphometrics, plumage variation, and ecological niches. Using these data, we explored the genetic structure and the history of lineage differentiation within the species, as well as the signatures of current and historical gene flow between populations. We found that *O. chimborazo* comprises three genetic groups: one corresponding to subspecies *O. c. chimborazo*, from Chimborazo volcano and surroundings, and two corresponding to the northern and southern ranges of subspecies *O. c. jamesonii*, found from the extreme south of Colombia to southern Ecuador. We inferred modest levels of both contemporary and historical gene flow between these three populations, which suggest a history of differentiation with gene flow, and found a pattern of isolation by distance. We also proposed the location of the potential contact zone between these populations. Finally, our coalescent-based analyses supported a rapid split among these three lineages during the mid-to-late Holocene. We discuss our results in the light of past and present potential distributions of the species, in addition to evolutionary trends seen in other Andean hummingbirds.

Exploring over-wintering avian diversity and parasite prevalence in a private working forest

Rebecca D. Bracken, Daniel U. Greene, Darren A. Miller, and Scott A. Rush

Presenting author: **Rebecca Bracken**, Mississippi State University, r_bracken1@hotmail.com

Through certification standards for sustainable forest management and other forest management goals, working forests exist in a mosaic of forest patches of varying stand ages and stages. For birds, research on habitat use within working forests has primarily focused on breeding season surveys, while over-wintering bird communities remain understudied. Therefore, our objectives were to evaluate how: 1) varying forest stage classes influence winter bird communities, and 2) birds respond to food resources and forest structure during winter. To date, we have banded winter birds during 8 sessions from November-March, 2019-2021. We placed mist nets in young open canopy, unthinned, and thinned loblolly pine stands (4, 10, and 24 years since planting, respectively). We banded each captured bird and collected a blood sample to evaluate dietary origins of nutrients assimilated and parasite prevalence. We banded 87 individuals of 15 species. Captures among bird species were highest in the young stand (43%) and decreased as the stand aged. 47% of recaptures occurred in the mid-age stand. Species commonly classified as mature or interior forest birds, including Ruby-crowned Kinglet, were captured most often in the young and mid-age stands during our study, while overall species diversity increased across all stands during the second winter. Multiple species were found to contain ecto- and bloodborne parasites. Our high capture success in mid-aged, unthinned stands, a stage often associated with poorest habitat quality during the breeding season, illustrates the importance in maintaining stands of varying ages, as habitat use in wintering and breeding bird communities differs based on food availability and different environmental conditions.

Physiological condition of migrating thrushes at a Great Lakes stopover site

Alexandra Bros, Rachael Hoh, and Susan S. Pagano

Presenting author: **Alexandra Bros**, Rochester Institute of Technology, ajb5545@rit.edu

Habitats near the Lake Ontario shoreline serve as important stopover sites for migrating landbirds as they rest and refuel during their long-distance journeys. Landscape and stopover habitat in this region have likely changed over recent years by means of anthropogenic factors, including introduction of invasive species and urbanization, which may degrade the quality of stopover sites and ultimately impact the resources required by these birds for refueling. This study seeks to examine the physiological condition of three species of thrushes stopping over at the Braddock Bay Bird Observatory (BBBO) during fall migration, and to examine patterns in refueling and health metrics over time. Birds were captured, banded, and blood samples were collected over multiple fall seasons in order to assess variation in several indices of physiological state. Heterophils/lymphocytes were evaluated using blood smears from sampled birds as a measure of chronic stress levels. Plasma samples were analyzed to measure variation in triglyceride (fat deposition), uric acid (protein utilization), and glucose (carbohydrate nutrition). Changes in these indices over time may correlate with a change in the quality of habitats used by these birds, which can impact the migrants' ability to refuel and continue migration. The results obtained may be important for managing a healthy environment for these passerines in order to preserve their populations during a stressful period of their annual cycle.

Do nice jays finish last: Diagnosing the causes of undermatching in a synanthropic species

Kristin M. Brunk, Elena H. West, Anna M. Pidgeon, and M. Zachariah Peery

Presenting author: **Kristin Brunk**, University of Wisconsin-Madison, kbrunk@wisc.edu

Ecological theory predicts that the distribution of individuals in heterogeneous landscapes is a function of habitat selection strategies mediated by social system. Under an Ideal Despotic Distribution (IDD), avian populations are expected to undermatch available resources because dominant individuals exclude subordinates, forcing them into lower quality habitats. However, IDD can collapse in resource-rich, high-quality habitats due to agonistic interactions and breakdown of territoriality, which instead promote resource matching where mean fitness is similar between habitats. We studied a population of Steller's Jays in coastal California to elucidate how undermatching can be maintained despite behavioral mechanisms that should theoretically lead to the breakdown of IDD. Jays in this area are undermatched to locally abundant human food subsidies, despite a high degree of territorial overlap and frequent agonistic interactions. We studied the maintenance of undermatching by examining the distribution of fitness among individual jays. We used behavior trials to classify individuals into dominance classes, and we compared fitness metrics, including core area size, body condition, human food consumption, and annual fecundity, between dominance classes. We found no striking differences in fitness patterns between dominance classes, indicating that undermatching is likely maintained by incomplete exclusion of subordinate birds. This resulted in "many winners" with fitness equally distributed among them. This work helps elucidate how individual behavioral strategies mediate population-level responses to resource availability and habitat quality when habitats are highly altered by anthropogenic subsidies.

Metabolic health and physical development of Barn Swallow (*Hirundo rustica*) chicks under natural photoperiod and artificial light at night

Murry L. Burgess, Caren B. Cooper, and Margaret A. Voss
Presenting author: **Murry Burgess**, North Carolina State University, mburges5@ncsu.edu

Artificial light at night (ALAN) disrupts circadian rhythm, increasing the metabolic demand of growing chicks. Therefore, glucose must be converted from other sources, such as lipids and proteins, to sustain the demand. This shift in metabolism affects developing anatomy and inhibits chick growth. In this case, we might see a shift in phenotype, such as delayed growth, as chicks exchange protein for glucose. In addition, gluconeogenic pathways can maintain high plasma glucose concentrations even though the cells themselves are not metabolizing glucose. Therefore, ALAN may also increase blood glucose concentrations thus affecting physical development and metabolic health and potentially lead to metabolic disease, such as avian diabetes. Through field experimentation on wild, free-ranging Barn Swallows, I investigated multiple research questions about natural photoperiod and artificial light at night on chick health and development: RQ1. Does chick development vary with natural latitudinal photoperiods? RQ2. How is chick development altered by ALAN? Based on data analysis results, chick growth and development are impeded by ALAN and also affected by location. There was a statistically significant difference in Barn Swallow conditions between latitudes and treatments. All body measurements and glucose levels were greater in chicks from higher latitudes, while head size, wing chord, and mass were affected by the treatment. With standardized photos, I documented striking visual differences between chicks in each treatment.

Physiological condition during molt differs between songbirds with contrasting molt strategies

Luke K. Butler, Sydney F. Hope, Frank A. Stabile, Alexandra Immerso, and Sriya Revankar
Presenting author: **Luke Butler**, The College of New Jersey, lbutler@tcnj.edu

Small birds double their metabolic rate during the post-breeding molt, when flight also becomes especially costly due to missing feathers and the risk of damage to active follicles. We explored molt-related changes in three measures of energetic state in songbirds with contrasting molt strategies and molt-related flight costs: Ovenbirds (*Seiurus auricopilla*) molt rapidly and replace many feathers simultaneously, and they cease territorial behavior soon after molt begins, whereas Carolina Chickadees (*Poecile carolinensis*) molt slowly and behave territorially throughout the molt. Ovenbirds and chickadees each showed slight declines in hematocrit and little change in body mass near the onset of molt. By contrast, Ovenbirds gained substantial subcutaneous fat at the onset of molt, but chickadees only gained fat slightly during the study, and not until the end of molt. Fat stored by Ovenbirds early in the molt may be used as an energy source during the subsequent period of intensive, rapid feather replacement, when flight capabilities may be severely limited, whereas chickadees may not benefit from storing fat because they can fly and forage relatively efficiently throughout their slower molt. Alternatively, fat gain in Ovenbirds may reflect pre-migratory fattening that precedes movement away from the breeding grounds to complete the molt elsewhere. This study shows species-level differences in how songbirds adjust their energetic state in relation to molt intensity, reflecting different physiological adaptations to the least-understood life history stage in birds.

Major histocompatibility complex (MHC) variation among boreal breeding passerines that differ in migration distance

Susanna K. Campbell, Liliana Cortés-Ortiz, and Benjamin M. Winger
Presenting author: **Susanna Campbell**, University of Michigan, susannak@umich.edu

Seasonal migration has several trade-offs that impact the immune system, including exposure to a diversity of pathogens and high susceptibility to infection during migration. Pathogen exposure can drive sequence evolution in immune genes, such as the major histocompatibility complex (MHC). MHC genes have high nucleotide diversity and high copy numbers which facilitate diverse antigen recognition for pathogen defense. However, it is unknown if or how differential selection imposed by seasonal migration selects for differences observed in MHC genetic diversity. To address this, we compare MHC Class 1 exon 3 genetic diversity among closely related passerines with sympatric breeding ranges in boreal North America, but variable migration distances and wintering latitudes. To reduce phylogenetic signal, we restrict comparisons to within genera for the following groups: *Setophaga*, *Catharus*, *Vireo*, *Regulus*. If long-distance seasonal migration increases pathogen risk, then we expect greater allelic diversity among MHC class 1 exon 3 sequences in long-distance migrants compared to sympatric congeners with shorter migration distances. However, if wintering habitat drives MHC sequence evolution then MHC allelic variation may not be correlated with migration distance and may be better predicted by wintering climate, such as temperature and precipitation, which is expected to drive pathogen distributions. The results of this study will contribute insight into the selection pressures influencing MHC molecular evolution and the tradeoffs of seasonal migration.

Two new records of the Tufted Flycatcher (*Mitrephanes phaeocercus*) in the coast of Veracruz, Mexico

Adrián Ciprés-Chávez, Enya A. Córdoba-Cuevas, and Jordi Toto-Cobix
Presenting author: **Adrián Ciprés**, Universidad Veracruzana, adriancipreschavez@outlook.com

The Tufted Flycatcher (*Mitrephanes phaeocercus*) is a Tyranid widely distributed in the mountainous regions of Mexico and Central America. Although it resides primarily in pine-oak and cloud forests, it is known to make altitudinal migrations to lower elevation tropical forests during the non-breeding season in northwestern Pacific Mexico. We describe two records of the Tufted Flycatcher on the Gulf of Mexico coast during the non-breeding season (January and February 2021), particularly in a fragment of mangrove forest in the "Arroyo Moreno" Protected Natural Area, Veracruz, Mexico. We consider these records to be indications of altitudinal migratory movements in the non-breeding season on the Gulf Mexico coast.

Potential effects of climate and land cover change on forest songbirds of the Appalachian Mountains

Hannah L. Clipp, Christopher T. Rota, and Petra B. Wood
Presenting author: **Hannah Clipp**, West Virginia University, hlclipp@mix.wvu.edu

Climate is a key factor shaping avian biogeography, and altered temperature and precipitation trends associated with global climate change are predicted to result in long-term changes in bird distributions, populations, and communities. Shifting patterns of land use also affect avian occupancy and abundance. Thus, recent assessments of avian responses to global climate change are beginning to increasingly incorporate landscape change as an additional and synergistic factor. Here, we combine climate and land cover metrics with North American Breeding Bird Survey data to focus on long-term changes in the relative abundance of forest songbird species within the Appalachian Mountains region. Specifically, we use negative binomial models with random site effects to determine the relative influence of temperature, precipitation, and proportion of land cover covariates on route-level total counts of 15 species between 1997–2017. We then project future changes based on multiple emission scenarios representing varying levels of climate change and land cover change. Data analyses are ongoing, but we will report the effects of climate and land use on species counts, as well as spatial differences between projected historical and future distributions. Ultimately, a greater understanding of how avian distributions, populations, and communities in the Appalachian Mountains may change over time will inform conservation and management efforts in this region.

Birds' eggshell colors conform to Bogert's rule

Sela H. Cooper and Daniel Hanley
Presenting author: **Sela Cooper**, George Mason University, scoope@masonlive.gmu.edu

Bogert's rule states that darker coloration provides a thermal advantage for animals inhabiting colder regions. Avian eggshell coloration appears to follow this rule because darker eggs are found in the coldest regions on Earth. These patterns suggest that eggshell color enhances the ability for eggs to absorb solar energy, which is vital to hatching success in cold environments. However, as temperatures rise due to climate change, darker colors in colder regions may disadvantage species that have adapted dark eggs in response to historically cold climates. These species must survive in warmer climates with eggshell traits poorly suited to warmer temperatures and parents constrained by their own metabolic demands. Previous research has documented how eggshell pigmentation varies with latitude at the level of avian communities, but the inter- and intra-specific patterns remain relatively unclear. However, we must understand such patterns to predict how species and genera (particularly those of concern) might respond to climate change in these cooler regions. To address this, we quantified avian perceived colors from photographs of more than 380 clutches of Charadriiform eggs. These data support the patterns from the community-level dataset and show a negative correlation between egg brightness and latitude; birds within cooler northern regions have darker egg coloration than birds from southern regions. Here, we discuss other potential factors necessary to maintain egg temperature including egg size, clutch size, nest structure, and parental behavior. Finally, using these data, we interpret whether avian communities in general, or whether certain specific species, are at thermal risk due to climate change.

Are ecosystem engineers keystone habitat providers for secondary cavity nesters in temperate forests of South America?

Cecilia Cuatianquiz-Lima, Tomás A. Altamirano, Fernando Novoa, and José Tomás Ibarra

Presenting author: **Cecilia Cuatianquiz-Lima**, Pontificia Universidad Católica de Chile, cecilia.cuatianquiz@uc.cl

Ecosystem engineers influence resource availability for other organisms, and thus they play important roles as drivers of community assembly. We investigated the relationship between nest occurrence of secondary cavity nesters (SCNs: Thorn-tailed Rayadito, Chilean Swallow, and Southern House Wren) and their selection of cavities supplied by five ecosystem engineers (Magellanic Woodpecker, Chilean Flicker, Striped Woodpecker, White-throated Treerunner and rot fungi/insects) in a Global Biodiversity Hotspot, southern Chile. Further, we quantified the reproductive success of SCNs as a function of the characteristics of cavities (internal volume, entrance size and height) supplied by ecosystem engineers. We searched for nests during 10 breeding seasons and monitored each nest to determine cavity origin, nest fate and quantified cavity characteristics. We found 842 nests for our three SCNs. Most nests (>80%) of rayaditos and house wrens were placed in cavities supplied by rot fungi/insects with relatively small volumes (1976 ± 121.7 and 1857 ± 185.6 cm3, respectively) but with different entrance sizes and heights. Swallow nests were placed in high cavities (8.2 ± 0.42 m) with small-sized entrances (3.4 ± 0.11 cm), and chiefly supplied by White-throated Treerunners (56%). Reproductive success of SCNs varied between 50-65%, but the cavity characteristics showed no influence on the reproductive success of any species. Rot fungi/insects play a major role as ecosystem engineers for SCNs, but some ecosystem engineers may be functionally similar. The conservation of populations of SCNs may require the development of different management actions for each key ecosystem engineer in temperate forests of South America.

Effects of habitat alteration due to logging on migratory songbird abundance in Canadian boreal forest

Vianney J. Cupiche and Brian McLaren

Presenting author: **Vianney Cupiche**, Lakehead University, vcupiche@lakeheadu.ca

Most studies of habitat loss and fragmentation effects on biodiversity have been in tropical and temperate ecosystems, with less attention to boreal forest. The boreal forest has been considered naturally altered and patchy, but if logging becomes an increasingly common disturbance there will be important changes to species abundance. Long-distance migratory songbirds that nest on the ground have been identified as the most sensitive to fragmentation in temperate forest. Our objective is to identify the effects of habitat alteration on migratory songbird abundance in relation to anthropogenic disturbance due to logging in the boreal forest of Canada. To evaluate the effects on migratory songbird abundance, we conducted a literature search and a meta-analysis. We compared changes to species abundance among different types of logging (clearcutting, partial retention, salvage), succession after harvest, and reference old-growth forest. We also evaluated the response among nest guilds and habitat preferences (young forest, mature-old forest and generalist). Based on 13 studies and 608 responses of 20 species, the general pattern was decline of abundance in the areas affected by logging. Species abundance was less affected by partial retention logging than by clearcutting and salvage logging. Patch isolation and connectivity did not affect this pattern. Long-distance migrants were affected more than short-distance migrants, but in relation to nest guilds, those nesting in the canopy had lowest abundances in the disturbed areas. Species that prefer mature forest had lowest abundance in disturbed areas, while generalist species' abundance increased and there was no significant difference in young forest species.

Have North American birds been shrinking over time? A test of Bergmann's rule in the context of climate change

Caitlin R. De Bellis, Steven P. Campbell, Frederic Beaudry, Claire Stuyck, Julie A. Heath, Jackie Speicher, Samuel H. DeMent, Lawrence K. Fischer, and Virginie Rolland

Presenting author: **Caitlin De Bellis**, Arkansas State University, caitlin.debellis@smail.astate.edu

Bergmann's rule is a biogeographic rule describing the relationship between spatial patterns and physical characteristics of endothermic species. According to that rule, in cooler climates individuals within a species are larger bodied, whereas in warmer climates individuals have, on average, a smaller size. Our aim was to assess whether Bergmann's rule applies temporally to North American birds with global warming. We asked 1) is there a relationship between avian morphology (i.e., wing chord, mass) and time in North American birds? and 2) do detected relationships follow Bergmann's rule? We used banding data collected by 73 contributors across North America, from 1968 to 2020, for 14 species of five orders. We adjusted data for latitude and elevation differences, and treated seasons (breeding, non-breeding, fall and spring migration) separately. Linear mixed models (after controlling for age and sex) indicated species- and season-specific temporal trends. Overall, of 12 species that presented a trend in at least one morphological parameter, we detected a decrease for 11 species and an increase for five species. However, within a given season, only four species at most experienced a decline in mass or wing chord, which is less than expected (i.e., >50%) for Bergmann's rule to be validated as an effect of climate change. Implications of these results and future directions will be discussed.

Characterization of Hermit Thrush (*Catharus guttatus*) song overlapping during simulated territorial intrusions and natural countersinging

Kendra DeMerchant, Jillian Jessulat, and Sean P. Roach

Presenting author: **Kendra DeMerchant**, University of New Brunswick Saint John, kdemerc1@unb.ca

Researchers have long explored how male songbirds use their songs to defend territories and convey aggression. While signals like soft song are well established as aggressive signals, the possible role of song overlapping is controversial. While often proposed as an aggressive signal, recent findings across several species, including our work with Hermit Thrush (*Catharus guttatus*), show that males actively avoid overlapping during aggressive interactions. Such avoidance suggests that, even in the context of active territorial defense, timing of song can be best explained through the acoustic interference hypothesis, wherein songbirds adapt their singing behaviour to avoid interference by other biotic and abiotic sound sources. The present study will build on our recent finding that hermit thrush males overlap playback songs at below-chance levels during simulated territorial intrusion by determining whether overlapping is associated with magnitude of aggressive response (e.g., more overlapping by more aggressive males). In addition, overlapping in response to playback will be compared to overlapping in natural countersinging interactions between neighbouring males recorded using autonomous recorders. It is hypothesized that overlapping in response to playback will not be significantly associated with physical aggression and that similar avoidance of overlapping will be observed in countersinging males, in line with the acoustic adaptation hypothesis. This unique approach, combining assessment in aggressive and non-aggressive contexts, will add to our understanding of both overlapping and the avoidance of acoustic interference.

Investigating the genetic mechanisms of bill color plasticity and its environmental drivers across time and space

Amelia-Juliette C. Demery, Jennifer Houtz, Irby J. Lovette, and Jennifer Walsh

Presenting author: **Amelia-Juliette Demery**, Cornell University, ajdemery93@gmail.com

Avian bare-parts — beaks, ceres, feet, and leg integument — exhibit a dynamic plasticity in color deposition. These traits' plasticity — defined as intra-individual variation in response to environmental signals — can change colors in response to multiple signals. Beak color in particular demonstrates an exceptional level of inter- and intraspecific variability, and is an ideal trait to leverage advancements in color analysis and genomic methodologies to investigate multiple drivers within the network of pathways that together shape avian color evolution. The European Starling (*Sturnus vulgaris*) is a songbird whose beak changes from black to yellow as it shifts into its breeding phenotype. This shift — which we refer to as beak color plasticity — corresponds with seasonal photoperiodic changes, where increasing daylength induces a change in starlings' beak color. In 2019 and 2020, I experimentally induced beak color plasticity of *S. vulgaris*, manipulating environmental cues that trigger beak color plasticity in wild-caught starlings while in captivity. In this poster, I present my preliminary results that suggest that beak color plasticity operates under an endogenous clock, decoupled from direct photoperiodic stimuli as seen in physiological pathways associated with sexual maturity. These results build upon the next step of my dissertation, which is to investigate observed patterns of differential expression throughout the starlings' plastic shift, shedding light on an under-studied aspect of avian biology and describing the phenotypic network of color production and regulation within vertebrate systems.

Phenology shift of Purple Martin roosting behaviors in the Great Lakes region

Yuting Deng, Maria Carolina T. D. Belotti, Wenlong Zhao, Zezhou Cheng, Aroma Rodrigues, Elske Tielens, Subhransu Maji, Daniel Sheldon, Jeffrey F. Kelly, and Kyle G. Horton

Presenting author: **Yuting Deng**, Colorado State University, hermione.deng@colostate.edu

In response to climate change, organisms may shift life history phenologies to adjust to changes in the timing of primary productivity or changes in other resources. For migratory organisms, this can be especially important, yet quantifying such events at macroscales that capture population dynamics is particularly challenging. To this end, we use the US weather surveillance radar (WSR) network to uniquely collect data on the communal roosts of Purple Martins (*Progne subis*). Annually, nocturnal roosts form shortly after the breeding season and disperse as migrants head south during fall migration. The discrete nightly roosting behaviors of this aerial insectivore are captured by radar during the morning exodus from the roosting locations — to which we measure the start, peak, and end of seasonal roosting behavior. Using a novel machine learning detector, we identified roost locations from radar scans 30 minutes before sunrise and 60 minutes after sunrise across the Great Lakes region from June 1 to Oct 31. We use 20 years of remote sensing data collected by 12 WSR to quantify the change in timing of roosting phenology of Purple Martins and their correspondence with seasonal temperature and normalized difference vegetation index (NDVI). This study represents one of the longest-term examinations of macroscale aerial insectivore phenology. We expect our findings will provide a stepping stone for examining the phenology of aerial insectivores across the scale of the continental US WSR network.

The effects of variation in temperature and parental behavior on embryonic period length, chick body size and telomere length in House Sparrows (*Passer domesticus*)

Abigail J. Dennis, Rebecca C. Young, Anuj Ghimire, Theo K. Nguyen, Sydney E. Warcup, Kori J. Rutkowski, and Britt J. Heidinger

Presenting author: **Abigail Dennis**, North Dakota State University, abigail.dennis@ndsu.edu

Exposure to higher than optimal temperatures during embryonic development can have long-lasting phenotypic consequences and possible fitness effects, including more rapid development, smaller body size and shorter telomeres. In birds, parents exert some control over the embryonic environment through incubation behavior. The link between environmental temperature and phenotypic consequences has been explored. However, the degree to which developmental outcomes are shaped by the interaction between natural variation in environmental temperature and parental incubation behavior is less clear, particularly in species exhibiting high rates of developmental plasticity. To address this gap in knowledge, we examined how parental incubation attentiveness influenced embryonic period length, body size, and telomere length and loss in the presence of naturally varying environmental temperatures in developing House Sparrows (*Passer domesticus*). House Sparrows are found throughout North America across a range of environments, and therefore have an enormous potential for developmental plasticity. Variation in nest temperature was quantified using iButton temperature loggers and parental behavior was measured using video recordings. We predicted that embryos developing under warmer conditions would hatch earlier, be smaller at hatching, and have shorter telomeres than embryos that develop under cooler conditions, but that these effects would be less prevalent at nests where parents increase incubation attentiveness. This study will shed light on the influence of developmental temperature and parental behavior on phenotypic outcomes in a highly plastic, geographically widespread species.

Geographic variation in morphology of Northern Cardinals (*Cardinalis cardinalis*): Possible application of Bergmann's rule?

M. Susan DeVries, Meg Waraczynski, Daniel T. Baldassarre, Morgan Slevin, Rindy Anderson, and Jodie M. Jawor

Presenting author: **Susan DeVries**, University of Wisconsin-Whitewater, devriesm@uww.edu

Geographic variation in morphological characteristics of a species can be influenced by environmental conditions. Bergmann's rule states that endotherms inhabiting colder climates at higher latitudes are predicted to have larger body sizes to conserve heat. However, application of Bergmann's rule to songbirds has yielded mixed results. Our study examines whether geographic variation in morphology exists in the Northern Cardinal (*Cardinalis cardinalis*), a resident songbird with a broad distribution range extending from Central America to Canada. Measures of body size (mass, wing chord, tarsus length) and ornamentation (tail, crest length) were compared in populations of cardinals near the northern (Ohio, New York; USA) and southern (Mississippi, Florida; USA) extremes of the species' North American distribution range. Cardinal populations in Florida and Mississippi demonstrated significantly smaller body size than populations in Ohio and New York, as southern birds weighed significantly less than northern birds and had significantly shorter tarsus and wing chord lengths. Further analyses suggested a primary discriminant function comprised of a linear combination of mass, wing chord length, and tarsus length made a clear discrimination between cardinal populations at higher latitudes and populations in lower latitudes. Ornamentation length appears to be less discriminatory between northern and southern populations. Our findings suggest that Bergmann's rule could apply to the Northern Cardinal and environmental factors potentially influencing the observed morphological variation in this species are discussed.

Inferring successful breeding of a precocial bird with tracking data

Matthew Duggan, Luke R. Wilde, Mo A. Verhoeven, Theunis Piersma, and Nathan R. Senner
Presenting author: **Matthew Duggan**, University of South Carolina, mtduggan@email.sc.edu

Reproductive success plays a major role in the regulation of animal populations. In shorebirds, assessing breeding success usually requires large-scale field efforts to detect and monitor fledgling survival due to the inaccessibility and low density of preferred nesting sites, as well as the mobility of young birds. Following the recent surge of data from miniaturized animal-borne sensors, machine learning tools may help investigators to infer behavior in a wide variety of taxa. While tools based from revisitation patterns to a probable nest site can produce accurate estimates of reproductive success in birds with altricial (i.e., dependent) young, these can be less accurate for species with precocial (i.e., independent) young, such as shorebirds. In this study, we used GPS tracks from 28 individual Black-tailed Godwits (*Limosa limosa*) during the breeding season to construct both a hidden Markov model (HMM) and random forest algorithm (RF). Both models used sliding window variance in velocity and turning angle, and step length to predict four behavioral states from adult movements: incubation, foraging, chick-tending, and migration, as well as detect mortalities. Preliminary tests of the RF achieved greater than 90% accuracy while the HMM performed slightly worse. After further tuning, the annotated tracks predicted by our models will enter survival models to assess the probability of detection and survival of young during the nesting and chick-tending phase. Ultimately, we will combine methods in a single R package that may prove useful for monitoring population processes in similar species from remote data alone.

Worth the risk? Female House Wrens (*Troglodytes aedon aedon*) defend similarly against two simulated nest predators

Ross C. Eggleston, Kyle M. Davis, and Dustin G. Reichard
Presenting author: **Ross Eggleston**, Ohio Wesleyan University, rceggles@owu.edu

Offspring predation is one of the greatest obstacles to an organism's reproductive success, but parents vary in the strength of their response to potential predators. One explanation for this variable investment is that defending current offspring has the potential to lower future reproductive success if the predator is capable of injuring or killing the parent as well as the nestlings. House Wrens (*Troglodytes aedon aedon*) are small, cavity-nesting songbirds that defend against multiple species of nest predators including rodents, birds of prey, and snakes. Here, we used two different predator decoys, an eastern chipmunk (*Tamias striatus*) and a black rat snake (*Pantherophis alleghaniensis*), to elicit nest defense behavior and test whether females are consistent in their anti-predator response and whether that response predicts fitness. We found that anti-predator behaviors were not significantly different between the two predatory species. However, there was a significant weak negative correlation between time spent within five meters of the decoy and the number of offspring produced, which contradicted our prediction. The two simulated predators likely posed similar threats to the females as neither species frequently captures adult wrens, which may explain the consistent response. Measuring anti-predator responses to a higher threat such as a bird of prey is critical to assess whether females adjust their nest defense according to risk level.

Decline of North American avian populations as a function of land use, land cover and migration period

Nicholas A. Faraco-Hadlock, Colleen R. Miller, and Maren N. Vitousek

Presenting author: **Nicholas Faraco-Hadlock**, Cornell University, naf42@cornell.edu

Avian populations have decreased at an alarming rate over the past 50 years, but the causes of these declines, particularly for migratory birds, are debated. Evidence from temperate regions in the Palearctic suggests that bird populations are most severely decreasing in their wintering grounds, especially when those wintering grounds have been converted to agricultural use. However, the details of population declines for migratory birds in North American temperate regions are less well understood. This study explores two guiding questions: 1) How are bird population declines related to agricultural land use and 2) during which stage of the migratory cycle are bird populations declining the most? Our analyses address these questions by comparing avian population trends at regional and local spatial scales based on migratory status and land cover, respectively. We expected that migratory species in North America suffer the greatest population losses in their wintering grounds and in areas with the most agricultural land use. A preliminary analysis of population trends in Western Meadowlarks revealed that their numbers have decreased more severely in areas with high proportions of agriculture. We intend to delve deeper into these trends by comparing population trends of at least 10 common agricultural species across the annual cycle. This will help to discern at which stage of the migratory cycle Western Meadowlarks' and other species' population trends have the strongest relationship with agriculture. This study will be valuable to determine which bird species are most severely impacted by modern agricultural landscapes and help to pinpoint the differential declines during different stages of the annual migratory cycle.

Tail shape classification of *Tyrannus* species based on geometric morphometrics

Martín N. Fasanelli, Pablo S. Milla Carmona, Ignacio M. Soto, and Diego T. Tuero
Presenting author: **Martin Fasanelli**, Instituto de Ecología, Genética y Evolución de Buenos Aires, fasanellimartin@gmail.com

Tail morphologies of birds are driven by natural and sexual selection affecting flight performance, foraging strategies and even communication. These evolutionary processes fueled tail diversity but, until now, no study proposed a sound criterion to quantify and interpret such phenotypical variation. *Tyrannus* (Tyrannidae) is a New World group which includes 13 species with a wide range of tail morphologies, classically categorized into five shapes (round, square, notch, shallow fork and deep fork) based on the rectrices' length proportions. Although descriptive, we think this linear (and arbitrary) approach may not be enough to grasp forms and their conformational aspects. Our aim was to describe and quantify tail shapes of all the species in *Tyrannus* – via geometric morphometrics – in order to assess the clustering structure of the sample and the correspondence to their traditional categorizations. Tail shape of non-deep forked species (i.e., previously grouped with round, square, notch or shallow-fork tail) failed to display any clustering structure matching the traditional categorization, while deep-forked species were subdivided into two (morpho)groups. When model-based clustering was applied to the entire specimens' distribution, eight different groups were detected, while combining and disengaging traditional tail categories. Our results showed that classic categories cannot be retrieved as consistent morphogroups. This lack of descriptive resolution indicates that the whole variability of *Tyrannus'* tail phenotypes could be not only underestimated but misinterpreted if preset categorizations are forcefully applied.

Genomic differentiation between three subspecies of Orange-crowned Warblers

Finola Fogarty, Kenny Askelson, Quinn McCallum, Andrew Huang, Ellen Nikelski, and Darren Irwin
Presenting author: **Finola Fogarty**, University of British Columbia, fogartyfinola@gmail.com

Genomic analysis of subspecies is a modern and effective method for examining early population divergence, and allows for the identification of genomic regions which may be involved in local adaptations. Three morphologically distinct subspecies of Orange-crowned Warblers (*Leiothlypis celata*) inhabit different ranges which are separated by the Coastal and Rocky Mountain ranges of North America. Here, we use a genotyping-by-sequencing approach to assess the degree of genomic divergence between these three subspecies and identify regions of the genome which may be resistant to gene flow. Using more than 36,000 Single Nucleotide Polymorphisms, we find low levels of relative genomic differentiation (FST) across the genome for each subspecies comparison. Furthermore, levels of mean within-group nucleotide variation are almost as high as between-group nucleotide divergence, suggesting recent population differentiation and/or continued gene flow between the subspecies. Mean relative differentiation is greatest between the two most geographically distant subspecies. We have identified narrow peaks of high relative differentiation, and are currently investigating them for potential implications in local adaptations. These findings of low relative differentiation across the genome with few narrow peaks of divergence add to our understanding of genomic patterns that arise in the earliest stages of speciation.

What can the ejection of foreign objects from Eastern Bluebird nests reveal about selection on bluebirds to eject the parasitic eggs of Brown-headed Cowbirds?

Adam W. Gelman, Eleanor Diamant, and Mark Stanback

Presenting author: **Adam Gelman**, Davidson College, adgelman@davidson.edu

The ejection of foreign objects in nest-cleaning behavior has been proposed as a potential precursor to the ejection of parasitic eggs. We used foam earplugs and model Brown-headed Cowbird (*Molothrus ater*) eggs to test several aspects of parasitic egg ejection by Eastern Bluebirds (*Sialia sialis*). In our first experiment, we placed Brown-headed Cowbird eggs into the nests of bluebirds during laying. One week later we returned, assessed the fate of the model cowbird egg (removing it if still present), and added an orange foam earplug into the nest. We returned after an additional week to assess its fate. We found that the vast majority of bluebirds ejected earplugs, but those that ejected model cowbird eggs specifically were significantly more likely to also eject earplugs. This suggests that individual bluebirds differ in their propensity to remove objects from their nests. In 2020 we conducted an additional experiment in which we placed either blue or orange earplugs into the nests of bluebirds during laying. Bluebirds did not eject blue (egg-colored) earplugs at a lower rate, suggesting that color may not significantly influence the response of *S. sialis* to foreign objects.

Assessing breeding origin and migratory pathways in a declining aerial insectivore (Tree Swallow)

Rachel M. Gingras, Audrey R. Taylor, and Douglas Causey

Presenting author: **Rachel Gingras**, University of Alaska, Anchorage, rmgingras@alaska.edu

Pinpointing breeding origins and wintering locations of migratory birds is critical for understanding migratory connectivity and population dynamics in order to address the declining status of many migratory bird species. Using migratory Tree Swallows (*Tachycineta bicolor*; TRES) as a model avian organism, our study aims to use stable isotope ecology techniques to better understand interannual variation in breeding origin, migratory catchment, and dispersal for Tree Swallows breeding in southcentral Alaska. This project will infer breeding and wintering origins derived from feather samples collected from a local population of Tree Swallows during the 2017-2019 breeding seasons, and compare these data to migratory pathways determined from analysis of geolocator data from the same population. A standard precipitation isoscape will be converted to a feather isoscape specific to songbirds through implementation of a transfer function previously derived for North American passerine species. Assignments will also be derived from a TRES-specific model calibrated using known origin tissues from this breeding population in addition to a more generalized model approach that encompasses multiple species, such as the feather hydrogen isoscape for all North American passerines using the IsoriX package in R. Taken together, the stable isotope and geolocator data will provide information on the overall migration patterns for Tree Swallows breeding in Anchorage. This will illuminate the degree of connectivity that exists between this breeding population and specific wintering and stopover regions, and inform our understanding of breeding site fidelity and non-breeding season risks for this declining songbird species.

Conserving Alberta Greater Sage-Grouse (*Centrocercus urophasianus*) populations: An assessment of translocation recovery using genetic markers

Brendan A. Graham, Joel Nicholson, Mecah Klem, Eric Spilker, Sara J. Oyler-McCance, and Theresa M. Burg

Presenting author: **Brendan Graham**, University of Lethbridge, b.graham001@gmail.com

Since 2011, the Greater Sage-grouse (*Centrocercus urophasianus*) recovery project has translocated 118 individuals (3 males, 115 females) from Montana to southern Alberta to augment declining local populations. Although survival of translocated individuals is comparable to local birds, recruitment may be lower because of nest site selection and anthropogenic disturbances. In this study we quantify the impact of translocated birds on genetic diversity for local Alberta populations. We collected samples over a ten-year period (2010 to 2020) and genotyped 450 individuals at 14 variable microsatellite loci and the mitochondrial control region and compared contemporary genetic patterns to genetic patterns from pre-2005. We found that although some measures of genetic diversity (allelic richness) have decreased in the AB populations, others (both observed and expected heterozygosity, and haplotype diversity) are comparable to historic levels. Analyses based on mtDNA markers indicate that mtDNA haplotype frequencies have changed from pre-2005 levels, and we detected several new haplotypes in AB that were previously found in MT showing the translocated birds successfully reproduced. Our study suggests the current recovery techniques, such as translocations, are having a positive impact on the native sage-grouse population. Further analyses will provide greater insights into the genetic makeup of wild Alberta sage-grouse populations and assist with the recovery across their former range.

Are early successional birds declining because of lack of early successional forests or loss of fire-dependent open forests in the eastern United States?

Brice B. Hanberry and Frank R. Thompson

Presenting author: **Brice Hanberry**, USDA Forest Service, brice.hanberry@usda.gov

Early successional bird species are declining in the eastern United States, but this is regardless of the amount of early successional forests available by region. The successional bird guild is declining in regions with 25% young forest. Indeed, only the tallgrass prairie region has a positive trend for the successional bird guild. One reason for continued decline may be that successional species relied on oak and pine savannas and woodlands, which were kept open by fire, rather than ephemeral successional vegetation. Historical forests predominantly were open forests, whereas early successional forests covered 1–13% of forestlands in the eastern United States prior to Euro-American settlement. Early successional songbirds reach great densities in open forests and potentially greater numbers in landscapes with historical amounts of open forest than in present-day landscapes and those under intensive even-aged forest management. Restoration and management of open forests have not been prioritized or well-articulated for management of early successional birds and other species, but open forests provide an alternative option to consider for supporting early successional bird species.

Hosts select for the eggshell color of the Brown-headed Cowbird

Daniel Hanley, Samantha Rutledge, and Beheshteh Moghaddame-Jafari

Presenting author: **Beheshteh Moghaddame-Jafari**, George Mason University, bmoghad@gmu.edu

The exquisite eggshell mimicry that can result from co-evolutionary arms races between Common Cuckoos (*Cuculus canorus*) and their hosts is well-known. However, unlike these specialist brood parasites, many brood parasites are generalists that exploit a range of host species. The evolutionary mechanisms that select for their eggshell phenotypes are unclear. For example, the Brown-headed Cowbird is a brood parasite that produces a generic egg that is passably similar to the eggs of some of its hosts but noticeably unlike those produced by the majority of its diverse host community (a Jack-of-all-trades strategy). We propose that the cowbird's eggshell phenotypes have evolved via diffuse coevolution. Under diffuse coevolution, the cowbird's entire host community, with their varying eggshell phenotypes and recognition abilities, would select for a cowbird eggshell phenotype intermediate to that of its host community. Since only rejecter species select against cowbird eggs, we expect that cowbird eggshell colors can be more accurately estimated by both the phenotypes and rejection abilities of these hosts rather than those that accept cowbird eggs. Using eggshell reflectance data from 84 host species we demonstrate that the cowbird eggshell phenotypes are better predicted by rejecter hosts than accepter hosts. These findings suggest that diffuse coevolution could explain the generic eggs of cowbirds and other generalist brood parasites that employ a Jack-of-all-trades strategy. Importantly, this research provides insight into the underlying evolutionary processes that explains observed phenotypic variation and provides a framework for studying the phenotypes of parasites that range in specificity: generalists to specialists.

Nest box occupancy by four local species prior to anthropogenic modification

Jordan A. Harris, Royia J. Hope, and Dawn E. Drumtra

Presenting author: **Jordan Harris**, University of North Georgia, jaharr3301@ung.edu

Anthropogenic activities have the potential to pose a threat to surrounding wildlife by forcing wildlife to compromise their daily actions. This can be detrimental to these animals' lives due to them having to work around human activity (D'Acunto, 2018). Gagne, Bates, and Bierregaard (2015) found that Barred Owl fatalities increased in densely human-dominated areas when compared to areas with lower speed limits and less traffic (as implied by road width). In that study, human structures resulted in a negative impact on Barred Owls. On the other hand, Gagne et al. (2016) found

that Wood Duck populations suffered no major effects due to construction of a harbor and railroad within 300m of their habitat. We are interested in examining the impact of construction activities and a new apartment complex on populations of owls and ducks in a forested area adjacent to the University of North Georgia's Gainesville campus, Tumbling Creek Woods (TCW). Recently, a portion of TCW was sold for the construction of a student apartment complex (Leonard, 2020). Construction is expected to begin in July 2021 and students are expected to move in as early as August 2022. Many avian species use this forest for nesting including our species of interest: Barred Owls, Eastern Screech Owls, Wood Ducks, and Hooded Mergansers. We placed 9 nesting boxes out in TCW for these birds in 2016. Nest box monitoring was intermittent between 2016-2020. Starting in January 2021, however, we continuously collected nest box usage information by using trail cameras attached to a nearby tree. The 2021 breeding season is expected to end in late April through early May at which time we will be able to conclude this year's investigation.

Nest success and nest site characterization in Gray Catbirds: How does the prevalence of invasive shrubs impact their nest success and breeding biology?

Bethany E. Hollenbush and Lucas J. Redmond
Presenting author: **Bethany Hollenbush**, Penn State Schuylkill, beh5250@psu.edu

Nest predation is an important selective pressure on nesting habits of birds. Nest site characteristics like height and concealment can influence the likelihood of nest predation and should be related to nest success. We studied nest success and nest site selection in Gray Catbirds during the breeding seasons of 2016 to 2019 in southeastern Pennsylvania on the Penn State Schuylkill campus. Catbirds began arriving at our study site in early May and began nesting by early June. After catbirds arrived, we conducted daily surveys to locate breeding pairs and nests. Once found, nests were checked every 3 to 4 days until they were either successful or failed. Following fate determination, we measured nest height, concealment, and orientation. For shrubs in which nests were placed, we measured their height, diameter at breast height, and canopy area. We used program MARK to estimate daily survival rates and understand how nest success varied. Across the period of this study, ~47% of catbirds nests were successful. MARK analysis indicated that daily survival rates of nests varied yearly and tended to decline as the breeding season progressed. Our nest site characterization indicated that catbirds primarily used three species of invasive shrubs: multiflora rose, tatarian honeysuckle, and privet. Nest height exhibited differences among the plant species and was higher in privet than rose. We found no other consistent differences in nest placement among the three species of shrub used. Future analyses will incorporate nest site characteristics into the MARK analysis to examine the influence of nest site characteristics on nest success in this species.

An open-source tool for data fusion of GPS tracking and geomagnetic data: A case study of bird migration

Aranya Iyer, Fernando Benitez-Paez, Vanessa Brum-Bastos, Urška Demšar, and Jed A. Long
Presenting author: **Aranya Iyer**, University of Western Ontario, aranya6776@gmail.com

Long-distance migrants like birds may use the Earth's magnetic field as a navigation cue during migration. It has previously been a challenge to explore this hypothesis at global scales due to the inaccessibility of global geomagnetic datasets. We have recently developed a new algorithm (titled MagGeo) to address this concern by fusing wildlife tracking data with a spatial-temporal interpolation of the European Space Agency's SWARM satellite data. We performed a comprehensive, global error analysis for MagGeo to test if it can reliably predict geomagnetic data for any location on the Earth's surface. To demonstrate a possible application, we used MagGeo to combine geomagnetic data with the migratory movement track of a Semipalmated Sandpiper individual available on the open-source platform, MoveBank. We used a step-selection function to demonstrate how geomagnetic information can be used to study movement behaviour responses. Preliminary error analyses show a high level of agreement between MagGeo and other sources of geomagnetic data thus verifying that the spatial-temporal interpolation algorithm we used is a reliable method for linking geomagnetic data with wildlife tracking datasets. Results of the step-selection analysis provide weak support for migratory bird movement based solely on geomagnetic information. Incorporating other quantifiable navigation cues is likely necessary to build a more realistic representation of migratory bird navigation. We believe that MagGeo's validation and application highlights its potential for helping bridge the gap between geophysics, geospatial data, and movement ecology to explore fundamental and novel hypotheses in the field of animal behaviour.

Seasonal song variation in Carolina Wrens (*Thryothorus ludovicianus*)

Holly R. Keating and Dustin G. Reichard

Presenting author: **Holly Keating**, Ohio Wesleyan University, hrkeatin@owu.edu

Birdsong's primary function is attracting and stimulating mates and repelling rivals during the breeding season. However, many species also sing during the nonbreeding season, which raises questions about the function of nonbreeding song and the proximate mechanisms underlying its production. In this study, we compared spectral and temporal measurements from a large sample of breeding (N = 267) and nonbreeding songs (N = 283) of Carolina Wrens (*Thryothorus ludovicianus*), a nonmigratory, temperate species that sings year round. We found that breeding songs were longer than nonbreeding songs and had more syllables within each song. Trill rate, the number of notes per syllable, minimum and maximum frequency and frequency bandwidth did not differ detectably between the two seasons. This study is the first to examine seasonal song differences in Carolina Wrens and provides a basis for future investigations into the drivers behind this seasonal variation.

Sex ratios and the city: Investment in offspring sex ratios and parental care in urban versus rural European Starlings

Denyelle Kilgour, Todd Pierson, Rebecca Carey, and Sarah Guindre-Parker

Presenting author: **Denyelle Kilgour**, Kennesaw State University, dkilgour@students.kennesaw.edu

According to the Trivers-Willard Hypothesis, mothers should adjust the sex ratio of their brood according to their own condition and their current environmental conditions. Under poor conditions, mothers should invest in the less costly sex, typically daughters. Urbanization alters many environmental characteristics; however, the effect of these anthropogenic changes on maternal condition remains unclear, and the downstream impacts on offspring sex ratio have not been explored. We will be comparing secondary sex ratios of urban and rural European Starlings (*Sturnus vulgaris*) to test the Trivers-Willard Hypothesis under urban environments. Furthermore, we will be exploring correlations between parental care and sex ratio adjustment. We predict that urban starlings will have female-biased sex ratios due to poor conditions associated with urban environments. We also predict that regardless of habitat, there will be a negative correlation between parental care and the proportion of daughters produced. This study provides needed insight into how urbanization may shape investment in offspring sex ratios and offspring care.

First satellite-tracked migration of an Eurasian Thick-knee (*Burhinus oedicnemus*) in the Middle East ends in human-caused mortality

Kyle D. Kittelberger, Evan R. Buechley, Michael Ford, Kayahan Agirkaya, and Çagan H. Sekercioglu

Presenting author: **Kyle Kittelberger**, University of Utah, kyle.kittelberger@utah.edu

Eurasian Thick-knee (*Burhinus oedicnemus*) is a widespread wading bird that occurs throughout much of Europe, the Middle East, and northern Africa. We captured a juvenile specimen at the Aras River Ornithological Research Station, Turkey in October 2019, fitted it with a GPS-GSM transmitter, and tracked its migration. The bird migrated from Turkey in late October, made an eight-day stopover in northern Iraq, and then flew southwest to the Red Sea coast of Saudi Arabia. The bird was killed in early November by a falcon being flown for falconry near Yanbu Al Sinaiyah, Saudi Arabia. The thick-knee migrated more than 2100 km in 36 days between tagging and death. This study provides the first description of Eurasian Thick-knee migration in the Middle East, as well as the first description of autumn migration of this species from satellite-tracking data.

A review and guide for describing the vocal behavior in birds

Wiliam Ku-Peralta, Luis Sandoval, Edna González-Bernal, Antonio Santos-Moreno, and J. Roberto Sosa-López

Presenting author: **Wiliam Ku-Peralta**, Instituto Politécnico Nacional, kuperw23@gmail.com

Birds' acoustic behaviors are among the most complex and diverse forms of communication in the animal kingdom. Such complexity and diversity can be evaluated in different contexts and levels of organization: from repertoire sizes, the forms in which songs are delivered – solos, duets, or choruses – and how elements within signals are arranged to patterns of daily and seasonal vocal output, and patterns of song sharing. However, comparisons across signal types are inherently challenging for evolutionary biologists. Further, there are relatively few purely quantitative descriptions of vocal behavior in the literature – specially for tropical birds – with many studies lacking standardization in the terms and methods used to assess vocal traits, which often imposes difficulties for comparisons between populations and species, slowing down the progress towards our understanding of the evolution of bird vocalizations. Here we review the literature, and (1) document the more common used variables for describing birds' vocal behaviors, (2) analyze pros and cons of the different recording techniques used during the description of vocal behavior, and (3) review the tendencies in the field by analyzing the number of studies describing vocal behaviors in birds by latitudinal zone (tropical or temperate), taxonomic group (oscines, sub-oscines, and non-oscines), and sex. We also provide a practical guide for describing vocal behaviors, whose main goal is to support researchers with little or no experience in the field and standardize vocal variables definitions.

Habitat characteristics of breeding Black Rails in vulnerable coastal locations

Matthew Larson and Christopher Butler

Presenting author: **Matthew Larson**, University of Central Oklahoma, mlarson4@uco.edu

The Black Rail (*Laterallus jamaicensis*) is a species most affected by wetland loss. In October 2020 the US Fish & Wildlife Service listed the Black Rail as a Threatened species. The Black Rail inhabits relatively shallow wetlands where vegetative composition preference varies locally but occupancy is strongly affected by the structure of these vegetative communities. The most prevailing threat to Black Rail persistence is habitat destruction and degradation. The two predominant drivers causing the ruination of Black Rail habitat are losses associated with impinging land-use practices and rising sea levels. Current survey protocols yield low detection probabilities which require visiting sites multiple times to confirm the presence of Black Rails. Due to the threatened status of the Black Rail there is an urgent need to modify the existing protocol to more efficiently survey Black Rails in both data deficient areas and areas that are susceptible to rising sea levels. Identification of the specific habitat variables associated with the presence of Black Rails will aid in the conservation of this species. Identifying vulnerable areas in addition to understanding how occupancy and these habitat variables change over time following disturbance is also important to land managers tasked with managing habitats for a variety of species. The goals of this project are to explore whether alternative methods of surveying for Black Rails (Autonomous Recording Units and camera traps) will more efficiently detect rails than conventional call-playback surveys, classify vegetative characteristics associated with occupancy by Black Rails, and to create a species distribution model to identify areas susceptible to rising sea levels.

Global patterns of phenotypic macroevolution in parrots

Elliot Lee, Jon T. Merwin, Ryan Terrill, Leo Joseph, and Brian Tilston Smith

Presenting author: **Elliot Lee**, Bergen County Academies, elliot.h.lee@gmail.com

One of the most pressing problems in macroevolution is untangling whether diversification is driven by rapid bursts of diversification or slow accumulation of variation over time. We examined these dynamics in the Parrots (Order: Psittaciformes), whose vast diversity in shape, size, and color varies across their pan-tropical distribution. To test whether quickly evolving clades exhibit more phenotypic variation or if clades with greater phenotypic variation have experienced steady accumulation of variation over time, we compared diversification rates and phenotypic evolution across all and each continental radiation. To characterize and model phenotypic evolution, we quantified plumage and morphometric variation in parrots. We sampled museum specimens of over 95% of parrot species, and quantified plumage color and pattern using an automated pipeline. We compared the morphological space occupied by different clades of parrots to test if increasing regional phylogenetic diversity was correlated with phenotypic diversity. We also compared phylogenetic and phenotypic diversification rates between clades to test if faster evolving lineages accumulated phenotypic diversity more quickly. Overall, we found most parrot clades occupied a large amount of morphological space, that closely and distantly related genera occupied similar color space, and that unique colors were rare. We also found that phenotypic diversification rates were correlated with speciation rates across the phylogeny. Our data suggest Parrots have likely become so morphologically diverse in order to adapt to environments across individual continents, but shared adaptive strategies may have led to morphological convergence at a global phylogenetic scale.

Linking climate change to foraging effort in a pagophilic seabird, the Mandt's Black Guillemot

Thomas J. Leicester, Kyle H. Elliott, and George J. Divoky

Presenting author: **Thomas Leicester**, McGill University, tommyleicester@gmail.com

Climate change is leading to pronounced and rapid declines in Arctic summer ice cover in the Beaufort Sea. Northward range shifts and population declines have been observed for many upper trophic level predators, possibly linked to increased foraging costs as temperature-sensitive prey disappear. For example, Mandt's Black Guillemot rely on ice-associated Arctic Cod, switching to alternative prey when ocean temperatures exceed 3.5 degrees Celsius. As a result, we might expect increased foraging effort to compensate for the loss of Arctic Cod. To test whether pagophilic birds (Mandt's Black Guillemots) alter their foraging behavior as ocean temperatures warmed, leading to a loss of Arctic Cod, we used time-depth records to measure dives per day and time spent underwater per day in incubating and chick-rearing Black Guillemots from 2011-2018. Time spent underwater did not vary with light levels (time of day) until the sun first set in early August, with a six-hour gap of reduced foraging at night by late August. Within and across seasons there was a remarkably strong correlation between sea surface temperatures and both dives per day and time spent underwater. In conclusion, in years when ice leaves early and Arctic Cod are no longer available, guillemots spend more time diving for their rapidly disappearing prey or less nutritious alternative prey—while also having less time available to forage by late August. By linking this study to research on prey behavior in the context of climate change and studies on dive behavior and colony health, these data help understand species' resilience to environmental change.

Monitoreo de aves en dos fincas agrícolas de café y cacao de sombra considerando la distancia entre disturbios antropogénicos y bosques naturales

Gabriel León Morales

Presenting author: **Gabriel León Morales**, University of Puerto Rico Utuado Campus, gabriel.leon@upr.edu

In the last 50 years, human activity has modified ecosystems more rapidly and extensively than in any equivalent period in history, largely to meet the demand for food and fresh water. Considering the relationship between the magnitude of disturbance and the type of practices carried out, the focus on ecological conservation in agriculture is important, highlighting the multiple benefits it offers to the farmer and vice versa. With this objective, I document the diversity and abundance of birds integrated to cocoa and coffee agroforestry systems with different forest densities in two farms located in the municipality of Utuado, Puerto Rico. We conducted bird counts in a systematic way in transects with two (2) fixed points in each plot and a duration of six (6) minutes of monitoring at each point. We compared the abundance of species in the cocoa, coffee, and forest plots. In my hypothesis I indicated that plots with higher forest density will host a greater number of birds than plots with low forest density. Abundance was also compared between plots near anthropogenic disturbances of infrastructure surrounding the study sites, time, temperature, wind, and precipitation as environmental factors for the presence of birds. A total of 11 endemic bird species, 23 resident species and two migratory species were found for a total of more than 40 bird species. The UPR farm in Utuado had an average of 20.9 and the Del Carmen farm had an average of 11.4. A T-test was performed that showed a significant difference between plots ($P = 0.05$), which affirmed the hypothesis. With the findings, it is recommended to manage agroforestry farms with a focus on conservation of natural areas for the benefit of birds.

Linking species distribution models to landscape simulation scenarios and conservation planning approaches to support the identification of critical habitat for Species At Risk: Wood Thrush (*Hylocichla mustelina*)

Lionel Leston, Yan Boulanger, John Brett, Sylvain Giguere, Karl Heide, David Hope, Audrey Robillard, Kathy St. Laurent, Junior A. Tremblay, and Russ Weeber

Presenting author: **Lionel Leston**, University of Alberta, leston@ualberta.ca

The Wood Thrush (*Hylocichla mustelina*) is a declining Neotropical migrant breeding in eastern Canada. We are using this species to test a four-part critical habitat identification framework for Species at Risk in Canada. Initially we reviewed known life history and ecological characteristics of this species. Second, we identified whether Wood Thrush exhibited different responses to environmental features in different parts of its range, in which case we would develop separate regional models. Third, finding no evidence justifying more than a single management region across eastern Canada, we are currently running boosted regression tree models predicting abundance and distribution across eastern Canada. Initial results suggest Wood Thrush is most abundant where there is more deciduous forest within 1-2 km, more swamp within 150 m-2 km, and away from roadsides (>150 m). Separately, we are running future land use scenarios that account for forest succession, harvest, and other footprint, and simulated natural

disturbances under present and future climate (RCP 4.5 and 8.5 scenarios). We will use outputs from these scenarios to predict Wood Thrush abundance and distribution over time under different possible futures to assess population risk. Finally, using current and future distribution of Wood Thrush, we will use conservation planning software to identify low to high-risk options to support Wood Thrush critical habitat identification. Our work builds upon previous, nearly completed applications of the critical habitat identification framework.

Nutrition of non-native fruits for migratory songbirds in the Northeastern U.S.

Cynthia Loi, Victoria Kwasinski, Jenifer Rosete, Todd Pagano, and Susan Smith Pagano
Presenting author: **Cynthia Loi**, Rochester Institute of Technology, chl5182@rit.edu

Migratory songbirds must acquire proper nutrition at stopover sites to sustain them throughout migration. Wild fruits available at fall stopover sites in the Northeast are important for birds to refuel, so fruits must comprise adequate amounts of energy and nutrients to support them during their journey. The goal of this study was to analyze the nutritional content of local non-native fruits and compare them to the nutritional content of common native fruits at an important stopover site in New York State. Ripe fruits were collected at peak migration times over several seasons. The fruits were freeze dried and energy density, % crude fat, % ADF, and Brix-TC were measured to quantify key nutrients available to birds. This study also aimed to analyze chemical components in non-native fruits that may be relevant for migratory bird nutrition and health. To do this we quantified the anthraquinone emodin in ripe *Rhamnus cathartica* (Common Buckthorn) berries. We also conducted a preliminary captive songbird experiment to gain insight into the physiological effects of a buckthorn diet.

Differential community response to threat: Using a novel soundscape approach to understand community signaling changes

Parks T. Marion and Sharon A. Gill
Presenting author: **Parks Marion**, Western Michigan University, parks.marion@gmail.com

What happens to collective signaling when communities confront threats to survival and reproduction? Bird communities experience avian predators and nest parasites as threats, provoking changes in individual acoustic signaling. These responses transmit complex and unique information, which other individuals in a community can interpret and act on, leading to community level responses that have significant spatial impact. Community interactions are difficult to detect and few studies investigate responses to threat at this scale. We adopted a soundscape approach to investigate the impact of simulated predation and brood parasitism on acoustic signaling at the community level. We presented models and playbacks of Cooper's Hawk, Brown-headed Cowbird, and control Fox Sparrow in forests and grasslands, and recorded community signaling where the stimuli was presented and at 45 m. We divided recordings into three time periods ("before", "during", and "after" stimuli), analyzed these using acoustic indices, and compared them using linear mixed modeling. Preliminary analyses revealed differences between the before period and the during/after period. We also found differences between stimuli treatments. Together these indicate a pattern of change in response to stimuli. Habitat effects differed in index measurements and interacted with treatment effects. Thus, community patterns in signaling response to threat exist, as revealed by application of acoustic indices. Future work is planned to describe these patterns and better understand habitat effects. Detecting community level acoustic events has the potential to inform our understanding of threat response by communities and expand our ability to utilize acoustic monitoring data.

Assessing changes in population size through time in California Gnatcatcher

Camila Martínez-Avila and Hernán Vázquez Miranda
Presenting author: **Camila Martínez-Avila**, Institute of Biology, UNAM, camila_martinez@ciencias.unam.mx

What we see today in biological populations is determined by past and present environmental, ecological and demographic conditions. Knowing how populations changed in the past can help us understand how they could change in the future under certain circumstances, and what evolutionary forces led to those fluctuations. An approach for doing so is historical demography, which uses coalescent theory to determine when a population passed through a bottleneck decreasing effective size, or an expansion increasing population size. Using genomics and tools like the Pairwise Sequentially Markovian Coalescent model (PSMC), we can recognize changes in population size and correlate them with specific phenomena, such as the formation of barriers or glaciations, to infer how these changes influenced species evolution. While speciation in continents and islands is a frequently explored question, evolution

in peninsulas is a less well-known issue relevant to ecologists and evolutionary biologists. It is unknown whether there are unique mechanisms behind peninsular patterns of speciation. The Baja California peninsula is considered a natural laboratory since it has a complex geological history and environmental landscape. Moreover, the North American deserts are an ideal system to study the role of the Quaternary glaciations in shaping biodiversity. We will use California Gnatcatcher (*Polioptila californica*) genomic data to study the relevance of the Last Glacial Maximum on the historical demography of peninsular populations using PSMC. This will shed light on which conservation strategies could best help us protect peninsular species given the demographic changes and ecological traits of desert populations.

Occupancy and detection probability for resident tropical birds in a working landscape in Nicaragua

Conor P. McGowan

Presenting author: **Conor McGowan**, US Geological Survey, conor.mcgowan@ufl.edu

Significant effort has been allocated to research on presence/absence surveys and occupancy studies for neotropical migrant birds in central American (e.g. MoSI), but limited effort has been invested in studying resident species using survey and statistical approaches that account for detection. In this study, I conducted 58 fixed radius point count surveys for four Neotropical resident bird species on the Island of Ometepe, in Nicaragua. Surveys were done as 15-minute visits broken into three, independently surveyed, 5-minute periods and the detection or non-detection was recorded for Great Kiskadee, Inca Dove, Banded Wren, and White-throated Magpie-Jay. Further, during the visit, I recorded the number of vehicles, pedestrians, cats and dogs that were present and wind, canopy closure, and later used Google Earth to measure distance to the nearest buildings from the point count. Occupancy rates varied by species with jays exhibiting 0.72 occupancy and Inca doves exhibiting the lowest rate of 0.23. Detection probability varied but was generally high for all 4 species (>0.55). Human activity and human development (i.e., buildings) did not affect occupancy or detection of wrens, but may have impacted presence and detection of White-throated Magpie-Jays, Great Kiskadees and Inca Doves. Presences of domestic cats and dogs had no measurable effects on the 4 species, though, species co-occurrence modeling may be more informative in the future. Nicaragua is an impoverished nation and lowland terrestrial animals, such as iguanas, are very rare in human populated areas compared to neighboring Costa Rica, however my results suggest that perceived pattern has not extended to these four resident bird species.

To mixed flock or not to mixed flock: Foraging ecology of the Brown-headed Nuthatch (*Sitta pusilla*)

Noah C. McNeill and Jeffrey R. Walters

Presenting author: **Noah McNeill**, Virginia Tech, nmcneill@vt.edu

Temperate mixed species bird flocks are of particular interest to ornithologists, both for their driving mechanisms and the community-wide impacts that mixed flocks generate. The Brown-headed Nuthatch (*Sitta pusilla*) depends heavily on pine seeds when available and readily joins nonbreeding season mixed flocks, presumably driven by foraging efficiency or predation threat. Prior research on this species has demonstrated potential links between mixed flock recruitment and pine seed depression, while the impact of predation threat on nuthatch mixed flocks remains largely unstudied. I have systematically recorded mixed flock composition at two divergent sites, the North Carolina Sandhills Gamelands and Marine Corps Base Camp Lejeune, as well as Brown-headed Nuthatch pine seed foraging and predator vigilance rates in and out of mixed flocks. In this manner, I determine that pine seed availability primarily drives variation in mixed flocking behavior, while generalized predation threat may drive background levels of mixed flock recruitment, based on decreased vigilance rates in larger flocks. My work also suggests that Brown-headed Nuthatches modify their pine species foraging rates according to seasonal and annual variation in longleaf pine (*Pinus palustris*) and loblolly pine (*Pinus taeda*) seed production, as well as intersite variation in pine species abundance. These findings form a clearer picture of the mixed flock drivers for a sedentary foraging specialist, and demonstrate the impact of food resource variation on mixed flock diversity and recruitment.

Divergent trophic responses of sympatric penguin species to shared historic environmental change

Chantel I. Michelson, Michael J. Polito, and Kelton W. McMahon
Presenting author: **Chantel Michelson**, Louisiana State University, cmichelson@alaska.edu

The Southern Ocean ecosystem is undergoing rapid environmental change due to ongoing and historic anthropogenic impacts such as climate change and marine mammal harvesting. Taken together, these climatic and ecosystem shifts may impact the structure and function of the ecosystem and register as behavioral responses in higher trophic organisms, such as penguins. We examined the trophic responses of sympatric Gentoo (*Pygoscelis papua*), Chinstrap (*P. antarcticus*), and Adelie (*P. adeliae*) penguins to 100 years of shared environmental change in the Antarctic Peninsula region using compound-specific stable isotope analyses of museum specimens. We also compared the trophic responses of Adelie Penguins between two regions that experienced different levels of environmental change. Over the last 40 years Gentoo Penguin trophic position increased a full trophic level as krill densities declined in response to recent climate change, the development of a krill fishery, and marine mammal population recovery. Alternatively, Chinstrap and Adelie penguins' trophic position remained stable in the Antarctic Peninsula over the last century despite variability in krill densities. While the Antarctic Peninsula experienced greater historical marine mammal harvesting, recent warming, and larger krill declines than the Ross Sea, Adelie Penguins in both regions showed no trophic response since the 1840s. The specialized foraging of Chinstrap and Adelie penguins identifies their vulnerability to further declines in krill densities. Over the next century, similarly divergent trophic responses are likely to occur among Antarctic krill predators if climate change and other anthropogenic impacts continue to favor generalist over specialist species.

Hybridization and speciation of an Amazonian manakin

Else K. Mikkelsen and Jason T. Weir
Presenting author: **Else Mikkelsen**, University of Toronto, else.mikkelsen@mail.utoronto.ca

Hybridization between species has a complex role in the speciation process. When widespread, hybridization can prevent species divergence, or lead to the collapse of two lineages into a hybrid swarm. Alternatively, hybridization can be a creative process, facilitating adaptive introgression of alleles between species. At its most extreme, hybridization can lead to the formation of new species from hybrid swarms, combining adaptive variation from two species while potentially requiring the resolution of genetic incompatibilities. In this study, we investigate the genome evolution of the Golden-crowned Manakin (*Lepidothrix vilasboasi*), an Amazonian passerine species of putative hybrid origin, proposed to have arisen via the admixture of the Opal-crowned Manakin (*Lepidothrix iris*) and the Snow-capped Manakin (*Lepidothrix nattereri*). We assembled high quality de novo genomes for all three species using linked-read sequencing technology, combined with whole genome resequencing of several individuals per species. Using this whole-genome dataset, we test for introgression between the three species, and evaluate the signature of hybrid speciation across the genome of *L. vilasboasi*. If *L. vilasboasi* is confirmed to be of hybrid origin, this dataset will allow us to observe the long-term genomic outcome of hybrid speciation in a relatively old hybrid species. We investigate patterns of introgression across the genome to search for a mosaic pattern of inheritance, and test for signatures of positive selection during the diversification of this manakin trio.

Combining population genomics and demographic modeling to inform conservation of a threatened migratory bird, the Canada Warbler (*Cardellina canadensis*)

Caitlin V. Miller, Christen M. Bossu, Samuel Haché, Richard B. Chandler, David P.L. Toews, Junior A. Tremblay, Amélie Roberto-Charron, Clark S. Rushing, and Kristen C. Ruegg
Presenting author: **Caitlin Miller**, Colorado State University, caitlin.miller@colostate.edu

The broad geographic ranges of many species of migratory birds often pose challenges for the development of coherent conservation and management strategies. Adding to this complexity is the challenge of defining units of conservation that reflect the best available information on demographic and genetic population boundaries. Species can be subdivided in several ways and each method may have benefits depending on the conservation objective. Evolutionarily significant units (ESU) define broad groups with distinct evolutionary histories, adaptive units (AU) identify groups that share similar adaptive traits, and management units (MU) define demographically independent populations nested within the ESU and AU. While genetic information is often one of the most important sources of data for the designation of ESUs and AUs, methods for defining MUs vary more broadly by species. In migratory birds, which often demonstrate low levels of population structure and high rates of dispersal, genetic tools often fall short in their utility for MU designation. An alternative method for defining MUs in migratory birds is to use Breeding

Bird Survey data to define populations that share demographic rates. Here I combine this demographically based method for defining MUs with population genomic designations of ESUs and AUs in the threatened Canada Warbler (*Cardellina canadensis*). I hypothesize that genomic analyses alone will not resolve MUs, but by integrating demographic data I will be able to delineate MUs across the species range. The overall goal of this work is to provide conservation managers of migratory bird species an alternate technique to determine ecologically relevant units for management within a broad species range.

Female song is acoustically similar to male song in a temperate species with delayed plumage maturation

Michelle J. Moyer, Kevin E. Omland, D'Juan A. Moreland, Aiman Raza, and Bernard S. Lohr

Presenting author: **Michelle Moyer**, University of Maryland, Baltimore County, mmoyer1@umbc.edu

Female birds in many temperate species are thought to sing reduced or quieter songs and appear to sing less often than their male counterparts. Therefore, female song may be easily overlooked. Increasingly, researchers are recording female song in well-studied species in which females were generally not thought to sing. Our previous work documented extensive use of female song in Orchard Orioles (*Icterus spurius*), a species previously assumed to have little or no female song. We performed detailed acoustic analyses comparing male and female song structure, and we investigated the rates at which each sex sings throughout the breeding season. Though females sang significantly less often than males, female and male songs were statistically equivalent for five of the seven variables investigated, indicating that the two sexes sing acoustically similar songs. Females also sang more often than initially assumed, suggesting that researchers may be missing female song in other species if they are not directly searching for it, particularly in species with delayed plumage maturation. Therefore, this study highlights the need to re-explore well-studied systems. We are currently conducting song playback experiments to investigate if and how female song may function in this species. The response of male and female orioles to male and female song will help us to develop better hypotheses for how Orchard Orioles use song.

The not-so-Common Eider (*Somateria mollissima*): Using demographic data synthesis, meta-analysis and matrix population modelling to reveal a mismatch between data availability and needs for seaducks

Alex Nicol-Harper, C. Patrick Doncaster, Geoff M. Hilton, Kevin A. Wood, and Thomas H.G. Ezard

Presenting author: **Alex Nicol-Harper**, University of Southampton, a.nicol-harper@soton.ac.uk

Seaducks are a group of high conservation concern, with many species in decline – but there is substantial uncertainty in forecasts. Even the best-studied, the Common Eider (*Somateria mollissima*), has an 'Unknown' global population trend. The abundance of demographic datasets available for this species motivated our data synthesis, with the aim of providing a life history parameterisation as a reference standard for the less-studied seaducks. We collated estimates of the vital rates determining survival and reproduction from >100 studies across the scientific and grey literature. New collaborators additionally contributed three previously unavailable clutch size datasets in response to a call for data through the IUCN Species Survival Commission's Duck Specialist Group. The resulting database forms the basis for a meta-analysis determining mean vital rates for our matrix population models exploring the demographic consequences of different breeding assumptions. This combination of data synthesis and population modelling exposed a striking mismatch between data availability and analysis needs. Perturbation analysis of our matrices revealed that transitions between breeding and non-breeding states (together contributing approx. 1/3 of population growth rate) had a strong influence, secondary only to continued breeding, and much greater than fertilities (<5%). However, the number of studies documenting components of fertility (n=79) greatly exceeded those quantifying adult survival (n=34) or breeding propensity (n=6). Such a disconnect between data collection by researchers and the information needs of conservation biologists and wildlife managers necessitates better stakeholder collaboration for improved decision-making.

What factors influence the light environment in burrows of Atlantic Puffins?

Noah O'Brien and Pierre-Paul Bitton

Presenting author: **Noah O'Brien**, Memorial University of Newfoundland, nnobrien@mun.ca

In seabird breeding colonies close to urbanized areas, fledglings seem attracted and/or disoriented by anthropomorphic light pollution. This often leads to land stranding and death of the young birds. Fledgling attraction to light, though well documented, is not yet fully understood. One hypothesis suggests that the rearing of young in deep burrows may lead to an underdeveloped visual system. To determine the plausibility of this hypothesis, it is first important to quantify and understand which factors affect the light environment in seabird burrows. To address this question, we investigated the burrows of Atlantic Puffins on Gull Island, Witless Bay Ecological Reserve, Newfoundland, Canada. We hypothesized that the size of the burrow entrance, its tortuosity, grass coverage, and opening orientation in relation to the sun would affect the interior chamber light environment. In the field, we characterized the burrows, and collected irradiance measurements using a light sensing probe. Our analyses determined that light intensity in the interior chamber averaged only 0.7 % that of the ambient external light. On a sunny day, the young puffin would be bathed in light no stronger than a night lit by a full moon. These results suggest that the chick's light environment may constrain visual development. We also show that the presence of covering grass dramatically decreased the light entering the burrow; all other measured characteristics could not explain the variation in irradiance. We discuss these findings in the context of visual development, and future studies.

Genetic basis for the population differentiation and local adaptation of White-crowned Sparrow (*Zonotrichia leucophrys*) to different forest habitats

Bukola G. Oguntuase-Osagie and Theresa M. Burg

Presenting author: **Bukola Oguntuase-Osagie**, University of Lethbridge, b.oguntuaseosagie@uleth.ca

Variables such as temperature, rainfall, topography, and elevation that define a bird's habitat are associated with the evolution of traits and adaptation. Our study seeks to combine high-throughput genomic data with available environmental data to assess the genomic differences and adaptation of White-crowned Sparrow to coniferous and deciduous forest habitats in North America. The distribution, seasonal range, and morphological and behavioral variation make it an ideal species to study local adaptation. Previous research using microsatellite markers has suggested White-crowned Sparrows from different forest types (alpine coniferous and riparian deciduous) may be genetically distinct. For this study, we will examine non-neutral markers to identify genes corresponding to differences in these populations. Morphological data and blood/feather samples will be collected for genetic analyses from different forest types. This study will test the hypotheses that Isolation by Environment (IBE) may be occurring between populations of White-crowned Sparrows, and different genetic backgrounds may be associated with the adaptation of these populations to their local habitats. Successful adaptation of each population to its habitat type will be measured through evaluation of genetic diversity within and among the populations and identifying loci under selection through Fst outlier analyses and environmental association.

Variation in two types of *Setophaga townsendi* song and a test of association with mtDNA phylogeography

Madelyn J. Ore, Silu Wang, and Darren E. Irwin

Presenting author: **Madelyn Ore**, Cornell University, Mjo234@cornell.edu

Learned bird song is shaped by both genetic and cultural processes, presenting a particularly tractable system for understanding how communication and reproductive barriers can interact to drive or inhibit diversification. Song dialects—or differences in song structure across geographic space—can act as signposts of cultural differences between populations, which may also indicate genetic differences in the population. The Townsend's Warbler (*Setophaga townsendi*) is a species with geographic structure in mitochondrial genetic signatures, raising the possibility of similar geographic structure in phenotypic traits, especially those involved in mate choice. We investigate if concordant variation occurs in song, by describing and quantifying geographic variation of song at the macrogeographic scale across Townsend's Warbler range. We demonstrate there is extensive macrogeographic variability in Type I song, whereas Type II song is more consistent across the range. There is little distinct grouping that coincides between song and the isolation-by-distance pattern in the nuclear DNA. A mismatch between song and genetic patterns suggests that song divergence is not predicted solely by genotype. By characterizing the within-species variation in song and genetic structure, we can expand our understanding of the dynamic interplay between cultural traits and population structuring.

A high prevalence of malaria parasites in Great-tailed Grackles (*Quiscalus mexicanus*) in Arizona, USA

M. Andreína Pacheco, Francisco C. Ferreira, Corina J. Logan, Carolyn Rowney, Luisa M. Bergeron, Kelsey B. McCune, and Ananias A. Escalante

Presenting author: **M. Andreína Pacheco**, Temple University, tug00270@temple.edu

Great-tailed Grackles (*Quiscalus mexicanus*) are a social, polygamous species whose populations are rapidly expanding their geographic range across North America over the past century. Before 1865, their populations were only documented in Central America, Mexico, and southern Texas. Here, 87 grackle blood samples from Arizona (a more recent population in the middle of the northern expansion front) were screened for haemosporidian parasites using microscopy and a PCR protocol that targets the parasite mitochondrial cytochrome b gene. Grackles were caught in the wild from January 2018 until February 2020. Overall, haemosporidian parasite prevalence was 64.4% (56/87). A high prevalence of *Plasmodium* parasites was found (98.2%, 55/56), and only one grackle was infected with *Haemoproteus* (*Parahaemoproteus*) sp. (lineage SIAMEX01). Twenty-two grackles were infected with *P. cathemerium*, fifteen with *P. homopolare*, four with *P. relictum* (strain GRW04), and fourteen with different *Plasmodium* spp. including two new parasites that have not been reported before. Furthermore, grackles were infected with the haplotype of *P. homopolare* that is circulating in other local bird species. This is the first report of Haemosporidian parasites infecting grackles from Arizona. Our results contrast with a recent study in Texas where *Haemoproteus* species were more prevalent than *Plasmodium*, and *P. cathemerium* infected only one individual. Based on those local differences, we hypothesize that grackles, as a species expanding its geographic range, affect the local parasite diversity as a new susceptible host that changes the transmission of local parasites rather than introducing new parasites into the local species pool.

Testing the acoustic adaptation hypothesis in songs of *Artisornis* tailorbirds

Shelby Palmer, Jay McEntee, Tricia Blankenship, Gabriel Jamie, Sam Jones, Elia Mulungu, and Norbert Cordeiro

Presenting author: **Shelby Palmer**, Missouri State University, Palmer904@live.missouristate.edu

Under the acoustic adaptation hypothesis (hereafter AAH), the design of acoustic signals is shaped by environmental constraints on transmission. This hypothesis has led to specific predictions for the evolution of song at different forest strata – e.g. understory and canopy – based on the contrasting vegetation densities across strata. Previous authors have suggested that understory species should evolve songs with lower frequency, narrower frequency bandwidth, and with slower delivery than mid-canopy birds. We tested these predictions in the male-female duets of the understory-dwelling African Tailorbird (*Artisornis metopias*) and the mid-canopy Long-billed Tailorbird (*Artisornis moreaui*), recently diverged Cisticolidae warblers that live in sympatry in different strata of eastern African forests. For frequency and frequency bandwidth, our findings were strongly opposite predictions based on vegetation density considerations, in both males and females. However, divergence in note length in both males and females may be consistent with the prediction stemming from considering vegetation density. We conclude that, if *Artisornis* songs have evolved by acoustic adaptation for maximal transmission, then there is a factor more important than vegetation density in their transmission. Alternatively, maximizing acoustic transmission has not been a driver of song divergence in *Artisornis* tailorbirds.

Use of Data Mule UAS to remotely download camera trap data to support bird species monitoring on military lands

Jean J. Pan, David A. Delaney, Zane Mountcastle, Martin Ruane, and Aaron Alvidrez

Presenting author: **Jean Pan**, Naval Facilities Engineering and Expeditionary Warfare Center, jean.pan@navy.mil

Camera traps are often placed in inaccessible or remote areas to collect important data on sensitive species that can inform management decisions on military installations and other land management agencies. Data are often collected manually (i.e. by vehicle, by foot) which is time consuming, costly, and can risk personnel safety (e.g., unexploded ordnance, rugged terrain). Moreover, access to field equipment can be restricted due to military training, inhospitable weather, or to reduce disturbance to sensitive species and during sensitive periods (i.e. breeding season). This can delay data acquisition and lead to missed opportunities to make informed management decisions. There is a need for technology that can improve access to ground-based sensor data. We demonstrated the use of a Data Mule UAS to remotely collect camera trap data at two military installations. Camera traps were placed in the habitat and within

nesting colonies of different sensitive bird species. The Data Mule UAS autonomously flew to and circled over each ground-based sensor and wirelessly uploaded data from the sensor to the UAS communications payload. The UAS then returned home loaded with sensor data, which was offloaded by the flight crew upon landing. We successfully conducted flights to multiple field sites and conducted missions where multiple ground sensors were visited and data downloaded in a single flight. We found that the Data Mule UAS could fly to and visit ground sensors without disturbing birds. The results of this project show that the Data Mule UAS is a cost-effective alternative for collecting data from camera traps and other remote ground-based sensors.

Using Unmanned Aircraft Systems (UAS) to monitor endangered California Least Terns

Jean J. Pan, Alan Jaeger, Todd van Epps, Lucas A. Overbey, Jamie R. Lyle, Ryan Jaeger, and Martin Ruane
Presenting author: **Jean Pan**, Naval Facilities Engineering and Expeditionary Warfare Center, jean.pan@navy.mil

The endangered California Least Tern nests along beaches from Baja California to the San Francisco Bay Area and is an important species of management concern for many military installations along the California coast. California Least Tern nests are typically monitored by field crews walking through the nesting colony or remotely with binoculars. Walking through the colony can lead to both bird and environmental disturbance (i.e., trampling). Remote monitoring can result in parts of the survey area being missed, because some sections are out of sight of field personnel; this is especially problematic for nesting colonies that are spread over large areas. We evaluated the use of unmanned aircraft systems (UAS) for monitoring nesting colonies of California Least Terns. We were able to successfully establish flight parameters that did not disturb the nesting birds, even when different UAS were used. Using a camera, we were able to identify multiple life stages of Least Terns in the UAS imagery, including eggs, fledglings, and adults. We also evaluated an infrared (IR) sensor to see if we could identify terns from their heat signature, but did not find IR sensors useful for finding terns because of background noise. Manual review of imagery was slow and time-consuming, especially since the number of images collected of the survey area was high. We investigated the use of machine learning for automated target identification in imagery, focusing on adult terns. The best algorithm was able to identify approximately 80% of the adult birds and had a false positive rate of around 30%. We found that UAS are a promising method for monitoring California Least Terns.

Use of stopover sites by four raptor species and assessment of their migratory connectivity

Adelaida Pérez-Cadavid and Ernesto Ruelas-Inzunza
Presenting author: **Adelaida Pérez Cadavid**, Universidad Veracruzana, apcadavid88@gmail.com

Despite migratory raptors being a well-studied group, little is known about their habitat requirements during migration. Satellite tracking has been a useful tool that has enabled the study of the migratory movements of birds and answers ecological questions beyond those of their breeding ranges. Our objective is to understand from existing satellite telemetry data the Spatio-temporal patterns of habitat use at stopover sites by four migratory raptor species (*Buteo platypterus*, *Buteo swainsoni*, *Cathartes aura*, and *Pandion haliaetus*) across the Americas. From the data analysis, we plan to create a map of stopover sites, which will be characterized in detail using Geographic Information Systems (GIS). We plan to visit and ground-truth some of these stopovers. Concurrently, we plan to assess the migratory connectivity between breeding, stopover, and wintering sites to understand how spatio-temporal patterns are linked throughout the annual cycle. Finally, we plan to describe the movements and the length of time that an individual spends on each site and its relationship with site variables. This work will allow us to infer the role that each stopover site plays in providing resting or refueling habitat, as well as determine the habitat requirements, that each of the evaluated species has during migration.

Effects of a hematophagous ectoparasite on nestling European Starlings (*Sturnus vulgaris*)

Jessica C. Poirier and Colleen A. Barber
Presenting author: **Jessica Poirier**, Saint Mary's University, jessica.poirier06@hotmail.ca

Studies have shown that ectoparasites on nestlings cause poor condition, reduced hematocrit levels, increased heterophil/lymphocyte (H/L) ratios, decreased parental investment, and reduced fledging success. *Carnus hemapterus* is a common ectoparasite that impacts cavity-nesting birds, one of which is European Starlings (*Sturnus vulgaris*). *Carnus* leave red-brown spots on eggs in infested nests; eggs become more spotted over the incubation period. Some studies found a positive correlation between egg spot density and *Carnus* abundance; our results from 2019 found that nests with heavier egg spotting tended to have a higher *Carnus* presence than nests with fewer spots. We studied

Carnus effects on 13 early broods (63 nestlings) in 2018 and 54 broods (191 nestlings) in 2019. We predicted that nestlings from nests with more egg spots would be in poorer condition, have lower hematocrit, a reduced number of parental provisioning visits, and lower fledging success than nestlings from nests with fewer egg spots. We found no significant differences in nestling condition, hematocrit, male parental investment, or fledging success in 2018 between nests with and without *Carnus*. However, in 2019, the number of egg spots (representing *Carnus* abundance) was negatively correlated with hematocrit, male provisioning efforts, and fledging success, but not nestling condition. Condition may have been unaffected as females provisioned offspring from spotted-egg nests more often than did those from nests with fewer egg spots. *Carnus* adversely affected nestling European Starlings in our population in one of the two years of study.

Turning induced plasticity into refined adaptations during range expansion

Ahva L. Potticary, Erin S. Morrison, and Alexander V. Badyaev

Presenting author: **Ahva Potticary**, University of Arizona, apotticary@email.arizona.edu

Robustness against environmental fluctuations within an adaptive state should preclude exploration of new adaptive states when the environment changes. Here, we study transitions between adaptive associations of feather structure and carotenoid uptake to understand how robustness and evolvability can be reconciled. We show that feather modifications induced by unfamiliar carotenoids during the House Finch range expansion are repeatedly converted into precise coadaptations of feather development and carotenoid accommodation as populations persist in a region. We find that this conversion is underlain by a uniform and coordinated increase in the sensitivity of feather development to local carotenoid uptake, indicative of co-option and modification of the homeostatic mechanism that buffers feather growth in the evolution of new adaptations. Stress-buffering mechanisms are well placed to alternate between robustness and evolvability and we suggest that this is particularly evident in adaptations that require close integration between widely fluctuating external inputs and intricate internal structures.

Distribution and abundance of Neotropical migrant swallows in Western Cuba during the winter period 2020-2021

Alejandro Rodríguez-Ochoa, Daniela Ventura del Puerto, Lourdes Mugica Valdés, Elio Armando Fontes, Rodolfo Castro, Ana María Suárez, Yuniel Machado, Karen Aguilar Mugica, Keith Hobson, and Kevin Kardynal

Presenting author: **Alejandro Rodríguez-Ochoa**, University of Havana, Cuba, lmugica@fbio.uh.cu

The Cuban archipelago is an important stopover and non-breeding site for migratory birds. However, little information is available on occupancy and habitat use during these periods by aerial insectivores with declining populations. The objective of this work was to determine the distribution and abundance of Nearctic-Neotropical migrant swallows in western Cuba during the non-breeding period in 2020-2021. Surveys were conducted on five routes, consisting of 10 point-count stations, in three sampling periods: Early (December 1st – January 7), Mid (January 7 – February 15), and Late (February 16 – March 22). In addition, some isolated records of Neotropical migrant swallows not included in the monitoring protocol during the migratory and winter season (August 2020- March 2021) were compiled. Two species of swallow listed on the Canadian Species at Risk Act, *Hirundo rustica* and *Riparia riparia*, and four declining migratory swallow species, *Progne subis, Stelgidopteryx serripennis, Tachycineta bicolor,* and *Petrochelidon pyrrhonota*, were detected during surveys. *Tachycineta bicolor* exhibited the highest abundance across the three survey periods, with more than 6000 individuals on a single route, followed by *Hirundo rustica* and *Progne subis*. All three survey periods had a high abundance but the late period had the highest occurrence of species. The wetlands of the south of Pinar del Río had the greatest richness and abundance of migrant swallows, and rice paddies and swamp marsh grasslands were the most used habitats. Survey results and incidental observations highlight the importance of Cuba as non-breeding habitat for multiple swallow species and as a stopover site for *Hirundo rustica*.

Natural behavior in a songbird shows accurate interval timing with no increase in error

Carlos A. Rodriguez-Saltos, Fernanda G. Duque, and Julia A. Clarke

Presenting author: **Carlos Rodriguez-Saltos**, University of Texas at Austin, carodr@utexas.edu

Animals, including humans, have a sense of time that allows them to anticipate events or produce behaviors at predictable intervals. The accuracy with which intervals are estimated tends to decrease in proportion to the duration of the interval. This pattern has been shown mostly by animals in laboratory studies of food or stimulus anticipation. Here, we report an exception, which we found on a natural, vocal behavior. The song of the Scaly-breasted Wren (*Microcerculus marginatus*) consists of whistles separated by intervals that increase in duration from less than 1 s to more than 10 s. We found that in nearly half of the songs, the accuracy for timing whistles did not change with interval duration. Moreover, at the longest intervals, the wren's accuracy is rivalled only by humans who count as a timing aid.

Do Eastern Bluebirds guard nest boxes during the fall and winter?

Maxwell Rollfinke, Faith Kipnis, Julia Barnfield, Tifani Panek, Tiffany Haydt, and Mark Stanback

Presenting author: **Maxwell Rollfinke**, Davidson College, marollfinke@davidson.edu

Eastern Bluebirds quickly occupy nest boxes installed at the onset of the breeding season, and it is often assumed that this is when nest sites are chosen. However, because of intense competition for cavity nest sites, one might expect that non-migratory bluebirds would guard prospective nest sites for months ahead of time. Our anecdotal data suggest that when nest boxes are available to bluebirds during the winter, bluebirds exclude smaller species. To test whether fall and winter access to nest boxes increases the probability of spring occupancy by bluebirds, we made 40% of 350 nest boxes unavailable to bluebirds from mid-August to mid-February. We found that bluebird occupancy did not vary between the two treatment groups (Fisher Exact P = 0.636); 71% of "winter available" boxes were occupied by bluebirds in spring and 69% of "winter unavailable" boxes were subsequently occupied by bluebirds. Additionally, we compared clutch size and first egg date in both treatment groups to determine whether the eventual occupants of "winter available" boxes were higher quality individuals.

The effects of environmental conditions on eggshell thickness of Western Bluebirds and Ash-throated Flycatchers

Alicia T. Romero, Andrew W. Bartlow, Charles D. Hathcock, and Jeanne M. Fair

Presenting author: **Alicia Romero**, Los Alamos National Laboratory, atrom@lanl.gov

Hatchability is a critical component of individual reproductive success and is directly associated with eggshell thickness. The thickness of eggshells can be affected by contaminants such as DDT and other organochlorines, which can cause population declines. Dehydration can also lessen the structural stability and negatively affect eggshell thickness and hatchability. However, the natural variation in eggshell thickness is unclear, especially in relation to environmental conditions. We aimed to determine how eggshell thickness changes over time, and if it is influenced by nesting elevation, drought (PDSI), temperature, and precipitation. Here, we collected unhatched eggs from Western Bluebird (*Sialia mexicana*; n = 384) and Ash-throated flycatcher (*Myiarchus cinerascens*; n = 128) nests from 1997 to 2014 on the Pajarito Plateau in northern New Mexico. We measured the thickness of eggshells and tested for correlations between environmental variables. For both species, we found that eggshell thickness significantly increased over time. Nesting elevation was not significantly correlated with eggshell thickness for either species. Bluebird eggshell thickness was not correlated with any environmental variables, while flycatchers showed a negative correlation with drought, with thicker eggshells in drier conditions. These results show that the eggshells of both species have increased over time and that environmental variables examined here have negligible effects on eggshell thickness. Future work will help to uncover why thicker eggshells were found in drier conditions in flycatchers.

Ejection of Brown-headed Cowbird (*Molothrus ater*) eggs by Eastern Bluebirds (*Sialia sialis*) influenced by timing of parasitism in relation to bluebird laying

Maxwell W. Saucier, Cameron M. Dove, Antoinette Cozier, Eleanor S. Diamant, and Mark T. Stanback

Presenting author: **Maxwell Saucier**, Davidson College, maxwellsaucier@gmail.com

Avian brood parasites such as the Brown-headed Cowbird (*Molothrus ater*) lay their eggs in the nests of other birds, offloading incubation and rearing costs. This puts great selective pressure on potential hosts to reject parasitic eggs placed in their nests. One of the most successful and widespread methods of rejection is egg ejection, wherein host birds physically remove parasitic eggs from their nest. While most host species are seen as being either 'acceptors' or 'rejectors' of parasite eggs, some species like the Eastern Bluebird (*Sialia sialis*) show more variable rejection behavior. This variable nature may be used to test how specific factors influence the likelihood of egg ejection. We sought to determine whether the stage of bluebird laying could be one such factor. We placed model Brown-headed Cowbird eggs into nests of Eastern Bluebirds containing between 0 and 4 bluebird eggs and recorded the rates of model egg ejection. Nests containing 0 or 3-4 bluebird eggs had the highest rates of rejection at ~70%, while nests containing a single bluebird egg had the lowest rate of ejection at 49%. Nests containing 2 bluebird eggs had an intermediate rate of ejection at 56%. These results suggest that it is disadvantageous for a cowbird to parasitize a nest either before or late into the laying period, and that parasitizing a nest containing a single host egg provides the minimum likelihood of ejection.

Relating song to morphology, ecology, and phylogeny in the genus *Vireo*

Linnea N. Schaefer, Carla Cicero, Phred M. Benham, Lauryn Benedict, and Rauri C. K. Bowie

Presenting author: **Linnea Schaefer**, University of California, Berkeley, linneanoelle@berkeley.edu

Evolutionary relationships and adaptive radiation within the avian family Vireonidae have intrigued ornithologists for decades. Studies using molecular data have investigated phylogenetic relationships and song evolution, but questions remain about vireo diversification in the context of phylogeny, behavior (including song), and ecology. We present a new vireonid phylogeny based on multilocus DNA sequences and examine trait evolution with a focus on the genus Vireo. In agreement with prior data, we found Vireo to be split into three clades that conform to phenotypic traits. We also found the genus *Hylophilus* to be polyphyletic, with "canopy" *Hylophilus* nested weakly within *Vireo*. We used this phylogenetic framework to explore song variation among 28 of the 33 Vireo species and to study the effects of morphological and ecological traits on song. Song has been hypothesized to vary in frequency, length, and complexity based on habitat, and has been correlated to body size across vireonids and other groups as an indicator of sexual selection. We found a negative correlation between mean body mass and song low frequency and center frequency, and a significant association between habitat and song minimum frequency that has not been documented previously in *Vireo*. Species that occupy scrub (open) habitats, regardless of whether it's exclusively or in addition to forests, have lower minimum frequencies than species that occupy only closed habitats. These findings contradict the acoustic adaptation hypothesis, which predicts lower frequency songs in closed habitats, but fit with research suggesting that evolutionary history, body size, and sexual selection have stronger effects than habitat on song.

Migration genomics of Golden-crowned Kinglets (*Regulus satrapa*) and Red-breasted Nuthatches (*Sitta canadensis*)

Danika J. Schramm, Theresa M. Burg, Garth M. Spellman, and Vicki L. Friesen

Presenting author: **Danika Schramm**, University of Lethbridge, schramm@uleth.ca

Every year, thousands of bird species migrate great distances to make use of fluctuating resources. Birds make these migratory trips with alarming accuracy, often returning to the same places each season. There is incredible diversity in migratory behaviour in birds such as the direction of migration, distance, and the propensity to migrate at all. In certain species, only some populations migrate while others are year-round residents. Unfortunately, birds have been forced to alter their migration behaviour due to human interference including habitat loss and climate change. It is critical to study migratory habits in birds to develop appropriate conservation efforts. While migration has been studied for decades, much less is known about the genetic processes that cause birds to migrate each year. Previous studies have investigated the genetics of migration; however, the results are not consistent. For example, genes related to migration are often different between species. Understanding the genetics of migration is critical to shed light on whether birds can alter their migratory behaviour to adapt. This study will focus on Golden-crowned Kinglets and Red-breasted Nuthatches. Both are forest dwelling birds with migratory and resident populations. To do this, we will use next-generation sequencing to evaluate the potential differences between resident and migratory populations. We will also be able to examine gene flow between resident and migratory populations to explore their population connectivity. The results will allow us to further investigate if there is a shared mechanism to migration between species.

A resolved phylogeny of Cardinalidae based on ultraconserved elements

Benjamin F. Scott and Kevin J. Burns

Presenting author: **Benjamin Scott**, San Diego State University, bfscott1906@gmail.com

The cardinals, buntings, and grosbeaks (Cardinalidae) are a charismatic clade distributed across the Americas, renowned for their iconic coloration, songs, natural history strategies, breeding behaviors, and habitat preferences. However, to date no phylogeny has been generated for the cardinals using whole-genome sequencing, and certain taxonomic relationships remain unresolved. In this study, we used ultra-conserved elements to delimit the topological relationships among species within Cardinalidae. We sequenced 62 recognized species and subspecies, recovering 4,201 loci in our concatenated alignment. Using both concatenated and multi-species coalescent-based approaches, we confirm many previously estimated phylogenetic relationships and identify novel topological relationships. Our findings show that *Habia* is not sister to *Chlorothraupis*, but rather *Piranga*. Additionally, we find that *Amaurospiza* is not embedded within *Cyanoloxia*, but instead is sister to *Passerina*.

Assessing Black Tern colony occurrence and habitat associations in the Canadian prairie pothole region using aerial imagery

Nicholas Shephard, Ann McKellar, and Matthew Reudink

Presenting author: **Nicholas Shephard**, University of Saskatchewan, ngs285@usask.ca

The Black Tern is an obligate marsh-breeding colonial waterbird. Black Terns in the prairies are predicted to lose up to 97% of suitable nesting sites by 2100 due to habitat degradation. Habitat association studies have noted important relationships between Black Terns and specific wetland characteristics, including both small scale factors such as vegetation type, and large scale factors such as wetland density. Recent studies in the Great Lakes region have shown a greater decline in the number of Black Tern colony sites rather than population size, suggesting limited breeding habitat is a major threat for populations. However, similar studies have yet to be conducted in the Canadian prairies, the core of the species range. We examined wetlands using aerial imagery to assess habitat, land use, and geographic distribution metrics. We then analyzed relationships between these covariates and Black Tern colony occurrence/abundance. Similar to previous studies, we found that colony occurrence was positively associated with the extent of emergent aquatic vegetation present at a wetland, but no other habitat or land use covariates were associated with Black Tern occurrence/abundance. Interestingly, we found a strong non-linear effect of latitude, whereby colony occurrence and abundance were highest at mid-latitudes in Saskatchewan, but lower at higher and lower latitudes. This spatial trend may begin to inform how Black Terns disperse on breeding grounds. It is possible that individuals may be returning to general natal areas and dispersing latitudinally to select nesting grounds. These results are a first step towards determining habitat associations and may begin to inform our understanding of Black Tern breeding dispersal.

Maternal adjustment of offspring sex allocation in Greater Sage-Grouse

Katie L. Smith, Eric F. Tymstra, Steven R. Mathews, Peter S. Coates, and Gail L. Patricelli

Presenting author: **Katie Smith**, University of California, Davis, kalsmith@ucdavis.edu

Greater Sage-Grouse (*Centrocercus urophasianus*) is a species of conservation concern that is widely used as a model for lek breeding. Females of lekking species may invest asymmetrically in male and female offspring in favor of the sex that is predicted to have the highest reproductive potential. This is typically achieved by either producing more offspring of one sex or adjusting the distribution of resources and parental care. Though the physiological mechanisms underlying offspring sex biasing have been examined in other taxa, they have yet to be studied in Greater Sage-Grouse. I measured stress endocrinology, morphometrics, and age of female sage-grouse to determine the predictive power that maternal condition and experience have over biases in offspring sex ratio. Quantifying this relationship will elucidate the strategies of brood demographics and through this understanding, the population implications of anthropogenic stressors.

The influence of local conditions on the arrival-breeding interval in a long-distance migrant

Lakesha H. N. Smith and Kevin C. Fraser

Presenting author: **Lakesha Smith**, University of Manitoba, smithl6@myumanitoba.ca

Exploring the factors that influence the timing of arrival and breeding has become an increasingly critical area of study for determining whether species can keep up with the pace of climate change. Previous research has focused primarily on how spring arrival and first-egg lay dates may respond to environmental conditions. Yet, few studies have focused on how local conditions and other factors may influence or constrain the length of time between spring arrival and first-egg dates (arrival-breeding interval). Therefore, the two aims of this study are: (i) to determine how temperature, precipitation, and latitude affect the length of the arrival-breeding interval in a long-distance migratory songbird, Purple Martin (*Progne subis*); and (ii) does the length of the interval affect breeding success. Light-level geolocators deployed across their breeding range in 2007, 2009-2016 were used to estimate arrival dates and corresponding nesting data was collected for 63 females and 61 males. We predict that the arrival-breeding interval will be shorter with warmer spring temperatures, medium levels of precipitation, and at more northern latitudes. We anticipate our results will improve our understanding of the degree to which breeding phenology is plastic to changing climate conditions.

Nest placement decisions in Grey Fantails (*Rhipidura albiscapa*) relative to neighboring conspecific nest proximity and stage

Nadya M. Sotnychuk, Janet W. Ng, and Christa Beckmann

Presenting author: **Nadya Sotnychuk**, Western Sydney Unversity, nadya.sotnychuk.2016@owu.edu

Numerous factors can impact breeding success and nest predation is considered the greatest contributor to nest failure in passerines. Due to this strong selection pressure, birds likely use tactics to reduce nest predation risk. The importance of nest placement on breeding success has been studied, however, studies on nest placement and abandonment strategies relative to predation risk and nest placement relative to the proximity of neighbors' nests has not yet been studied. The Grey Fantail (*Rhipidura albiscapa*) has high nest predation and abandonment rates; therefore, pairs have many renesting attempts per breeding season. We examined whether proximity to conspecific nests, and nest stage of conspecific neighbor nest influenced nest placement within a home range. We assessed the influence of neighboring conspecific nest proximity and nest stage by contrasting nest locations and random points within the territory. Distance to neighbor nests did not vary from the random points in either analysis ($P = 0.86$). However, the neighbor's nest stage did influence nest placement distances ($P < 0.01$), where nests were placed an average of 147 m, 208 m, 154 m, and 182 m from neighbors that were at the stages of building, egg-laying, incubation, and chick-rearing, respectively. Our results suggest that placement near neighbors might not be dependent on how long the neighbor nest has been established and avoided predation, but rather on the activities during the various nest stages of the neighbors'. Including the potential of placing nests further away from egg-laying neighbors to avoid the risk of extra-pair paternity as well as placing the nest closer to buildings pairs limiting the need to search for resources.

The effect of moonlight on the diel activity patterns and reproduction of a crepuscular bird

Ian Souza-Cole, Michael P. Ward, and Thomas J. Benson

Presenting author: **Ian Souza-Cole**, University of Illinois Urbana-Champaign, iansouzacole@gmail.com

The Eastern Whip-poor-will *(Antrostromus vociferus*) is a species of nightjar, a group of aerially insectivorous bird that exhibit unique adaptations to take advantage of crepuscular and nocturnal periods when few other birds are principally active. I investigated Eastern Whip-poor-wills to better understand the constraints placed on them by their crepuscular/nocturnal habits and the degree to which they match their activity to the lunar cycle. To do this, I tagged 43 adult birds with VHF telemetry tags in 2019 and 2020 and monitored them using an automated radio telemetry system to quantify their rates of activity. I found that both male and female whip-poor-wills increase their rates of activity when there is more moonlight available at night. I also show that whip-poor-wills were much less active than diurnal birds over the course of a 24-hour period. Furthermore, I found some evidence to suggest that chicks were more likely to survive if their pre-fledging period coincided with nights of greater moonlight availability.

Nature versus nurture: Structural equation modeling indicates that parental care does not mitigate consequences of poor environmental conditions

Madeline Sudnick, Bekka S. Brodie, and Kelly Williams

Presenting author: **Madeline Sudnick**, Ohio University, ms224916@ohio.edu

Offspring growth and condition are positively correlated with fledging success, recruitment, adult aerobic capacity, and flight performance, and are affected by environmental conditions and parental care behavior. Offspring may face tradeoffs between growth and condition when adverse environmental conditions such as low food availability and parasites are present; however, parents may increase care behaviors to mitigate the impacts of poor environmental conditions. We monitored 69 Eastern Bluebird nests over two years in Athens County, Ohio to determine how environmental conditions including food availability and parasites influence parental care behaviors and nestling condition. We used general linear mixed models to investigate direct effects of environmental conditions and parental care on offspring growth and hematocrit. We also used piecewise structural equation modeling (SEM) to evaluate the direct effects of the environment on offspring and indirect effects of the environment on offspring via parental care behaviors. Nestlings in areas with lower food availability had lower hematocrit. The presence of bird blow flies (*Protocalliphora* spp.) was associated with reduced nestling growth rates. However, parental care behaviors had no relationship to hematocrit or growth rate. Our piecewise SEM indicated that parents had greater provisioning and nest attendance in habitats with greater arthropod biomass and larger amounts of small prey items but did not alter behavior in response to parasitism by blow flies. Parental care behaviors were not correlated with offspring condition, thus behavioral responses did not override the direct effects of environmental conditions on offspring growth and hematocrit.

Effects of oil well drilling noise on breeding behavior of Chestnut-collared Longspurs (*Calcarius ornatus*)

Lee A. Sutcliffe

Presenting author: **Lee Sutcliffe**, University of Manitoba, sutclifl@myumanitoba.ca

Chestnut-collared Longspurs (*Calcarius ornatus*) are obligate grassland songbirds with populations in steady decline. Noise from oil development contributes to grassland habitat loss and can lead to changes in avian behavior. Sex-specific decreases in parental care of longspurs near operating wells suggest that drilling noise may also impact the conservation of this species-at-risk, especially given that drilling noise is unpredictable and at a higher amplitude than operating noise. In 2019, we set up 3 experimental treatments with 3 sites each of playback drilling noise with associated infrastructure, infrastructure and no noise, and no infrastructure or noise. We found 79 longspur nests, placed cameras on 31 nests with nestlings, and reviewed 400 hours of video footage (3 hours/day). Within each hour, we recorded number of visits, sex of the adult, and length of time at the nest. We observed trends that may suggest both drilling noise and infrastructure have an impact on parental care. The number of visits of females per hour may increase in the presence of drilling noise as compared to silent infrastructure, while the total visit time of females per hour decreases. Also, female average visit time per hour may increase in the presence of silent and drilling infrastructure as compared to control sites. These preliminary results suggest longspur adults may misallocate their time in the presence of drilling noise and infrastructure. Since the drilling stage of oil extraction is temporary, management opportunities include erecting provisional sound barriers to reduce the amplitude at which the sound is perceived. Additional research should focus on policy recommendations, linking avian research with management suggestions.

Investigating the plasticity of migration timing to environmental variability in a songbird

Christophe Turcotte-van de Rydt, Saman Muthukumarana, and Kevin Fraser

Presenting author: **Christophe Turcotte-van de Rydt**, University of Manitoba, turcott5@myumanitoba.ca

Rapidly changing environments impact the timing of crucial resource availability for breeding birds. Long-distance migrants are particularly threatened, as they must rely on their phenotypic plasticity in migration timing on a greater scale than other migrants. One such neotropical migrant, the Purple Martin (*Progne subis*), a colonial aerial insectivore, exhibits a high intraspecific variation in migration strategies. Whether this variation and plasticity in timing will remain synchronised with advancing springs is largely unknown. Environmental factors such as weather variability and stage of spring phenology are known to influence bird timing but have rarely been investigated for their impact across entire migration routes. Using about 350 individual migration tracks of purple martins derived from the deployment of light-level geolocators at breeding colonies across their range, this study is investigating how environmental factors encountered en-route (e.g., daylength, vegetation phenology) influences migration timing and pace. Understanding the environmental factors influencing migration timing will allow us to better predict responses to environmental change.

Are House Wrens responsible for the decline of Bewick's Wrens? Using models to assess the impacts of interspecific competition over space and time

Zach H. Vickers and Jay P. McEntee

Presenting author: **Zach Vickers**, Missouri State University, zv93s@missouristate.edu

Bewick's Wrens (*Thryomanes bewickii*) are widely distributed across Mexico and the western United States. Previously occurring across most of the entire U.S., this species has since become extirpated from most eastern states over the past several decades, and now occurs in low numbers in states such as Kansas and Missouri. Some evidence suggests that this decline is at least partly attributable to interference competition with House Wrens (*Troglodytes aedon*). Our research has two primary aims: 1) to model the abundance of Bewick's Wrens across the U.S. over time by integrating several sources of longitudinal data, and 2) to test the hypothesis that increases in House Wren abundance correspond spatio-temporally with declines of Bewick's Wrens. A key component of these models will be the count data provided by the Breeding Bird Survey, which has been conducted annually since 1966. Because these surveys include many "absence" data points (i.e., "zeros"), we will employ Zero-Inflated Poisson and Zero-Inflated Negative Binomial regression to model local abundances. We will incorporate bioclimatic data, vegetation indices, and detection probabilities calculated from replicate counts into the models. To test whether House Wrens negatively affect Bewick's Wren abundances, we will compare models of Bewick's Wren abundance with and without House Wren abundance as a predictor variable. In summary, this research aims to model the distribution, abundance, and potential reasons for population declines of the Bewick's Wren.

High-efficiency genomic typing of historic oriole specimens

Vicens Vila-Coury, Shawn M. Billerman, Vanya G. Rohwer, Bronwyn G. Butcher, Irby J. Lovette, and Jen Walsh

Presenting author: **Vicens Vila-Coury**, Cornell University, vv253@cornell.edu

Genomic information from specimens collected many decades ago can add historical insight to the study of contemporary hybrid zones. However, obtaining sequence data from older specimens is complicated by their degraded DNA, making whole genome or reduced representation approaches less efficient. The Bullock's-Baltimore Oriole hybrid zone has a long history in ornithological literature and thousands of associated specimens, both historical and modern. Here we leverage sequence data from modern specimens to target twenty-three 100 bp amplicons that are known to contain SNPs diagnostic to each species. Using next generation sequencing of multiplex PCR-based libraries (amplicon sequencing), we successfully amplityped 90 individuals (45 modern and 45 historic), representing a mixture of pure and admixed orioles, at high coverage. Historic DNA was extracted from the toe pads of specimens collected over half a century ago. These methods performed similarly well between contemporary and historical samples, recovering 90% of the targeted SNPs and providing a rapid method of typing historic specimens at these informative locations in their genome. Wider deployment of these methods to the full complement of historic samples will add to the knowledge of the hybrid zone's evolutionary history and its changes over time.

Insights into the nest site characteristics of pueo (Hawaiian Short-eared Owl; *Asio flammeus sandwichensis*) on Oʻahu

Olivia Wang, Chad J. Wilhite, Marie-Sophie Garcia Heras, Wade H. Naguwa, Kicah P. H. Acoba, Julen Torrens-Baile, Kaleiheana-a-Pohaku Stormcrow, Corrina J. Carnes, and Melissa R. Price

Presenting author: **Olivia Wang**, University of Hawaiʻi at Manoa, owang@hawaii.edu

Short-eared Owls (Asio flammeus) are an appropriate model species for understanding intraspecific variations in life-history traits due to their global distribution across continental and island systems at a variety of latitudes. However, more regional studies outside of their range in North America and Europe are necessary to draw comparisons. Here, we investigated the nest-site characteristics of Hawaiian Short-eared Owls (*Asio flammeus sandwichensis*), or Pueo, the only endemic raptor species known to breed across all the main Hawaiian Islands; it is currently listed as endangered on Oʻahu. We predicted that Pueo select nest sites with taller and denser vegetation than the surrounding area. We searched for nests during the 2020-2021 breeding seasons and collected nest-site characteristics, including visual obstruction readings (VOR), maximum vegetation height, and percent cover at Pueo nest sites and at four randomly selected points within 100 m of the nest sites. Nest data were collected at eight active nests across Oʻahu. Seven nests were found in managed buffelgrass (*Cenchrus ciliaris*)–dominated grassland, and one nest was found in a wetland dominated by pickleweed (*Batis maritima*). Using a logistic regression model, we found that VOR was the most important predictor of use of the site for nesting and is positively correlated with the relative probability of use. This is the first study investigating Short-eared Owl nesting ecology in Hawaiʻi, and our initial results suggest that greater vegetation height and densities are important habitat characteristics to manage for in order to optimize Pueo occupancy and nesting.

Neither sex appears to benefit from divorce within migratory Northern Flickers consistent with accidental loss and bet-hedging

Karen L. Wiebe

Presenting author: **Karen Wiebe**, University of Saskatchewan, karen.wiebe@usask.ca

Divorce is widespread in birds and may either be an adaptive strategy to secure a better mate or territory or be a non-adaptive result of a failure to maintain the pairbond. I examined causes and consequences for divorce in the Northern Flicker (*Colaptes auratus*), a migratory woodpecker with a high annual mortality rate. In a long-term population study of 1793 breeding pairs over 17 years, the within-season divorce rate was 4.6% and the between-season divorce rate was 15.5%. Faithful pairs within a season initiated their renest 5 days faster than divorced birds, suggesting that within-season divorce was making the best of a bad job with severe time constraints. Poor performance in the year prior to divorce was not a trigger for it and analysis of multiple breeding stages revealed that divorcing individuals subsequently had later laying dates, smaller clutches and fewer fledglings than faithful pairs but had equivalent performance to widowed individuals. Separate analyses by sex showed that neither males nor females benefitted reproductively from divorce, thus there is a reproductive cost linked to finding a new partner per se. New mates after divorce were usually not older (not higher quality) than previous mates, so intrasexual competition was probably not driving partnership splits. The most plausible explanation seems to be a "bet-hedging" hypothesis in which birds re-pair rapidly in spring if their previous mate does not quickly arrive during spring migration. Divorce in Northern Flickers does not appear to be intentional and future studies on arrival and interactions of individuals in spring will elucidate proximate constraints on relocating the previous partner.

3D morphometrics on shorebird skulls suggest semi-independent evolution of beak and braincase

Xiaoni Xu and Rossy Natale

Presenting author: **Xiaoni Xu**, University of Chicago, xiaoni@uchicago.edu

Morphological structures pose questions on the pattern of macroevolutionary that lead to diverse physiological traits, and the avian skull (beak and braincase) is one of the areas of research that focuses on the evolutionary modularity of how the correlation pattern of morphology change within the various bones of the skull. Using 3-D, geometric morphometric data of over 270 species of Charadriiformes (shorebirds, gulls, and allies), we tested 9 different hypotheses of modularity using recently developed statistical tests that use the covariance ratio between landmarks to determine the relative support for different hypotheses of modularity. The result of our tests and analyses demonstrated strong modular signals in the skull and suggested that the beak and braincase have evolved semi-independently from one another. We also found that the modular signal in suborders Lari (gulls and allies), Charadrii (plovers and allies), and Scolopaci (sandpipers and allies) differ in strength when comparing the covariance ratio across s groups, introducing the potential for further research on the development of anatomical traits in subgroups of shorebirds. Our work has implications for our understanding of the evolutionary history of shorebirds, specifically for the development of sections of skulls across shorebird species.

Did the Flint Water Crisis impact urban wildlife? A look at bird blood lead levels

Dorothy L. Zahor, Kenneth J. Glynn, and Jamie M. Cornelius

Presenting author: **Dorothy Zahor**, Eastern Michigan University, dzahor@emich.edu

The Flint, Michigan Drinking Water Crisis occurred when some neighborhoods experienced lead contamination of their tap water. Watering of lawns may have provided a potential pathway for lead to enter urban ecosystems and reside in soils, given that human consumption was advised against but irrigation practices were not. Background levels of lead persist in urban soils sourcing from historical gasoline, paint, and industrial emissions, and irrigation with leaded water may have elevated urban soil lead levels further. Lead is a neurotoxin, and urban soils pose a threat to local humans, pets, and wildlife. American Robins (*Turdus migratorius*), which consume large amounts of soil during their consumption of earthworms, may be at high risk of exposure to soil contaminants. We will discuss blood lead levels of robins captured in irrigated and unirrigated sites of Flint and nearby reference sites, and compare these levels to soil lead levels. Robins may have the potential to serve as a bioindicator species for urban soil lead risks to local communities.

Sources of geographic variation in songs within the genus *Patagioenas*, and an assessment of reproductive character displacement between two closely related species

Dan Zapata

Presenting author: **Dan Zapata**, Missouri State University, dz33s@missouristate.edu

Geographic variation in phenotypic traits is thought to have a central role in speciation. Differences among spatially segregated populations are believed to represent a first step of divergence. In principle, geographic variation studies seek to understand how variation is distributed in space, what correlates with the variation, and what causes the variation. This is particularly highlighted for species-specific traits important for mate selection. In birds, species-specific songs are thought to play a crucial role in this regard, as they are believed to be an important isolating mechanism among species. Furthermore, songs can be shaped by the interaction between two closely related species via reproductive character displacement (RCD), a phenomenon in which related lineages exhibit greater divergence in a sexual trait in sympatric rather than allopatric areas. Very few studies of geographic variation and the effect of RCD in song have been done in the tropical region, and most of them have been in passerine birds, leaving a gap of knowledge in regard to the sources of song variation for non-passerine taxa in a biologically diverse region. Here, I aim to assess the relative contribution of the subspecies rank, the climatic distance, and the geographic distance to the song variation in two largely sympatric and closely related neotropical pigeons in the genus *Patagioenas*: *P. subvinacea* and *P. plumbea*. Additionally, I aim to evaluate if interspecific differences species are more pronounced in sympatric than in allopatric areas, as RCD predicts. This study aims to increase our understanding of the sources of geographic variation in vocal signals in non-passerine taxa of the neotropics.