101ST ANNUAL MEETING
OF THE
AMERICAN SOCIETY OF MAMMALOGISTS
17 – 21 JUNE 2022

WESTIN LA PALOMA RESORT & SPA
-TUCSON, ARIZONA-

ASBSTRACT BOOK

The logo for the 101st Annual Meeting of the American Society of Mammalogists was designed by Danielle Forte. It features a coyote (*Canis latrans*) in the Sonoran Desert.

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AMERICAN SOCIETY OF MAMMALOGISTS (ASM)

The American Society of Mammalogists (ASM) was established in 1919 for the purpose of promoting interest in the study of mammals.

An Overview

In addition to being among the most charismatic of animals, mammals are important in many disciplines from paleontology to ecology and evolution. We, of course, are mammals and thus are in the interesting position of studying ourselves in quest of a greater understanding of the role of mammals in the natural world.

The ASM is currently composed of thousands of members, many of whom are professional scientists. Members of the Society have always had a strong interest in the public good, and this is reflected in their involvement in providing information for public policy, resources management, conservation, and education.

The Society hosts annual meetings and maintains several publications. The flagship publication is the *Journal of Mammalogy*, a journal produced six times per year that accepts submissions on all aspects of mammalogy. The ASM also publishes *Mammalian Species* (accounts of individual species) and *Special Publications* (books that pertain to specific taxa or topics), and we maintain a mammal images library that contains many exceptional photographs of mammals.

We encourage you to peruse the ASM web site (www.mammalogy.org) for information about mammals and the American Society of Mammalogists. Check out our interesting history by clicking on the Our History tab on the Archives Committee page. We hope it will stimulate your interest in mammals and further your appreciation of their importance.

ASM Leadership

The ASM is led by a group of scientists who are elected by the membership.

ASM Committees

Much of the work that the ASM does is accomplished through a large number of volunteer committees. These committees work to further the aims of the Society and the science of mammalogy as a whole.

ASM Endorses Human Diversity

The ASM is dedicated to ensuring the opportunity for active, equal participation in all ASM functions by all members, regardless of gender, race, ethnic background, age, physical disabilities, or sexual orientation.

http://www.mammalsociety.org/

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WELCOME

Dear friends, colleagues, and fellow mammalogists:

I am pleased to extend you a warm welcome to the 101st Annual Meeting of the American Society of Mammalogists. To encourage participation under challenging circumstances, these are hybrid meetings, with options for both in person and virtual attendance. I am very happy to report that registrations are above 540 attendees, including more than 380 in person and 160 virtual, from a total of 25 different countries across the globe.

I sincerely hope you take full advantage of the opportunities provided by the meetings to profit from an impressive array of talks, contributed posters, plenary presentations, and informal exchanges during our social events and beyond. The meetings also provide opportunities to highlight some of the most exciting work in mammalogy. We will hear from both student and senior award recipients during the corresponding plenary sessions. Also, our closing awards ceremony will allow us to learn about the recipients of this year's awards, from Grants-in-Aid and five named research awards for students to the Shadle and ASM Fellowships, as well as the Leopold, Jackson, Grinnell, and Merriam Awards for established colleagues. To this already stellar roster of awards, the Society will proudly announce the inaugural recipients of the Black and Indigenous Scholars in Mammalogy Award and the J. Mary Taylor Award.

Keep in mind that, as ASM members, you will have an opportunity to nominate and vote new members to the Board of Directors, the governing body of our Society during our member's meetings. The importance of a rich and diverse representation of society members cannot be overemphasized. One of the society's strengths is offering numerous opportunities to join a committee to contribute to their important service to our society and science. Don't hesitate to approach committee chairs and representatives, as well as society Officers, if you are considering joining a committee. Finally, our dedicated Ombudspersons and Meeting Allies are ready to assist you if you have any questions or concerns regarding the expected adherence to our Code of Conduct during the meetings (both virtual and in person).

Sincerely,

Enrique Lessa
President, American Society of Mammalogists

PROFESSIONAL CODE OF CONDUCT

Statement of Inclusion

The American Society of Mammalogists (the Society) prohibits discrimination, harassment, and bullying against any member because of ancestry, color, national origin, marital status, veteran status, gender identity or expression, sexual orientation, race, ethnicity, religion, age, disability, political affiliation or any other characteristic protected by law. The Society expects its employees, volunteers, members and other constituents, when and wherever they are conducting Society business or participating in Society events or activities, to maintain an environment free of discrimination, harassment, bullying, or retaliation.

Discrimination is defined as treating individuals differently – either preferentially or with adverse impact – because they have similar characteristics or because they are from specific groups, unless differential treatment is reasonable, essential, and directly related to conducting Society business or when serving as an official representative of the Society.

Code of Conduct

Professional conduct is expected of all participants in ASM sponsored activities, including the annual meetings, and of any individual representing the ASM. ASM is dedicated to ensuring the opportunity for active, equal participation in all ASM functions by all members, regardless of gender, race, national origin, ethnicity, age, physical appearance, disability, or sexual orientation. Discrimination and harassment are prohibited by the ASM; no individual should feel harassed, threatened, or unsafe at any ASM sponsored activity. The full text of ASM's Statement on Inclusion is above and available here. Concerns or allegations of misconduct or harassment should be directed the Office of the Ombudsperson or reported online here. Course of action for alleged misconduct may be found here. We note that ASM policies for professional conduct will evolve over time. The most recent version of these policies will be posted on the ASM Ombudspersons webpages and notifications of updates to the policy will be emailed to all ASM members. All ASM members and participants in ASM sponsored activities are expected to follow the most recent version of ASM Professional Conduct policies.

General Guidelines

1. Unprofessional conduct by any ASM member or meeting attendant will not be tolerated and is subject to disciplinary action. Unacceptable behavior includes, but is not limited to, unwanted verbal attention, unwanted touching, intimidation, stalking, shaming or bullying in person or through social media outlets (see additional definitions above). If you experience such behavior, depending on the context and if you feel comfortable, you should let the offender know and tell him/her to stop and/or seek help from bystanders. Participants asked to stop any harassing behavior are expected to comply immediately. Concerns can also be presented to the Ombudspersons in person (contact information above) or reported online here. Note that persistent offensive or unwelcome behavior may constitute harassment and that harassment presented in a joking manner is still harassment and both would be subject to disciplinary action.
2. Scientific presentations are expected to adhere to ASM standards of professional conduct and should not include inappropriate and/or graphic images or language that include (but are not limited to) pornography, demeaning or degrading images or language, or depictions of violence.
3. Established professionals and all ASM leaders should recognize that they hold positions of power, formal or informal, over students and aspiring professionals. These individuals are expected to lead by example regarding our high standards of professional and personal conduct.
4. All ASM members are potential bystanders to unprofessional or unwelcome behavior. Bystander intervention can prevent, divert, or mitigate harassment. Do not look the other way. See the Resources page for additional information about bystander intervention and training.

Reporting Misconduct

Concerns or allegations of misconduct or harassment should be directed the Office of the Ombudsperson (Erika Barthelmemss [barthelmess@stlawu.edu]; Jessica Light [jlight2@tamu.edu], Marjorie Matocq [mmatocq@cabnr.unr.edu], and Morty Ortega [morty.ortega@uconn.edu]) or reported anonymously online (http://www.mammalogy.org/alleged-misconduct-report-form).

ACKNOWLEDGEMENTS

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ABSTRACTS

-Please note all abstracts listed with a prefix (V-) are virtual presentations-
-Numbers 15-30 were inadvertently **not** used-

001: Gut check: exploring gastrointestinal morphology as a continuous functional trait in Appalachian small mammal communities

Olivia S. Chapman[1], Bryan S. McLean[2]
[1]University of North Carolina at Greensboro, Greensboro, NC, [2]University of North Carolina Greensboro, Greensboro, NC

Functional traits are critical parameters that help explain how species persist in varied environments. In mammals, functional traits derived from skeletal tissues are extensively utilized, but there has been a lesser focus on continuous functional measurements of soft tissues. This is true for the digestive system, which plays a major role in the dietary ecology of species. To guide the utilization of gastrointestinal (GI) morphology as a functional trait, we examined GI morphology within a population of deer mice (*Peromyscus maniculatus*) throughout 2021 in western North Carolina, USA, providing insight into how this trait varies over time. We then applied this underutilized trait to small mammal communities across the Appalachians, to assess the effectiveness of GI morphology as a continuous functional trait versus already established craniodental traits, and to ask whether GI morphology can explain small mammal community structure. We found that season and reproduction have a significant effect on GI morphology, with GI tracts being longer in the winter and in reproductively active females. We also found that GI traits are comparable to more commonly used craniodental traits in their effectiveness, and more seasonal communities at higher latitudes show longer mean GI tract lengths. We show that GI traits have implications for understanding community assembly in small mammal populations, as well as resulting in a new database of a rarely utilized soft tissue trait.

002: Ancient bears provide insights into Pleistocene ice age refugia in southeast Alaska

Flavio Augusto da Silva Coelho[1], Stephanie Gill, Timothy Heaton, Sandra L. Talbot[4], Charlotte Lindqvist
[1]University at Buffalo, Buffalo, NY, [2]Department of Biological Sciences, University at Buffalo, Buffalo, NY 14260, USA, [3]Department of Earth Sciences, University of South Dakota, Vermillion, SD 57069, USA, [4]Far Northwestern Institute of Art and Science, Anchorage, AK

During the Late Pleistocene, major parts of North America were periodically covered by ice sheets. However, there are still open questions whether ice-free refugia were present in the Alexander Archipelago along the southeast Alaska coast during the Last Glacial Maximum (LGM). Numerous subfossils spanning the last 50,000 years were recovered from caves in southeast Alaska, including American black (*Ursus americanus*) and brown (*U. arctos*) bears that today are found in the Alexander Archipelago but are genetically distinct from other bear populations. Hence, these bear species offer an ideal system to investigate long-term occupation and refugial survival. We present genetic analyses based on complete mitochondrial genomes from ancient bear remains. Black bears form two southeast Alaskan subclades, one preglacial and a postglacial, the split time of which is >100,000 years ago. All postglacial brown bears are closely related to modern bears in the archipelago, while a single preglacial brown bear is found in a distantly related clade. A hiatus in the bear subfossil record around the LGM and the deep split of their pre- and post-glacial subclades suggest that southeast Alaska bears did not survive in LGM refugia. Our results are consistent with an absence of refugia along the southeast Alaska coast but support a short-lived LGM peak and that vegetation quickly expanded after deglaciation, allowing bears to recolonize the area.

003: Density-dependent effects of personality on survival in fluctuating small mammal populations

Allison M. Brehm[1], Alessio Mortelliti
[1]University of Maine, Orono, ME, [2]University of Maine

Theories explaining the maintenance of among-individual differences in behavior (personalities) predict that “risky” (bold, active, and aggressive) individuals should offset increased resource acquisition and reproduction for higher mortality. However, field studies show that these individuals often do not suffer greater mortality, but the reason for this is unclear. We suggest that whether risky traits increase mortality depends on the riskiness of the environment (i.e., refuge and competition). We posit that the relationship

between risky traits and survival should differ among (1) forests with varying structure and (2) periods of high and low rodent density. In a large-scale manipulative experiment, we trapped deer mice (*Peromyscus maniculatus*) and southern red-backed voles (*Myodes gapperi*) in five years across forest stands with varying refuge availability. We used robust design models to estimate apparent survival while incorporating the probabilities of detection, recapture, and emigration. Similar to previous empirical studies, aggressive mice had higher survival than docile conspecifics regardless of context. However, personality traits associated with stress coping and de-arousal had a density-dependent effect—increasing survival at high density and decreasing survival at low density. We propose that behaviors associated with stress coping and de-arousal be further examined and incorporated into theory. These findings suggest that current discrepancies between theory and empirical evidence may arise due to context-dependence in the relationship between personality and survival.

004: Disruption of an ant-plant mutualism alters predator-prey dynamics in an african savanna

Douglas Kamaru[1], Alfred K. Kibungei[2], Michael Ong'ayo[3]

[1]University of Wyoming, Laramie, WY, [2]Ol Pejeta Conservancy, Nyahururu, Rift Valley, Kenya, [3]Conservation Department, Ol Pejeta Conservancy, Nanyuki, North-Eastern Kaskazini Mashariki, Kenya

Biological invasions have ecological consequences that reverberate across ecosystems. Over the past two decades, invasion of the big-headed ant (*Pheidole megacephala*) in Laikipia, Kenya, has disrupted a foundational mutualism between the monodominant whistling-thorn tree (*Acacia drepanolobium*) and their symbiotic bodyguards, ants in the genus *Crematogaster*. In exchange for food and shelter, *Crematogaster* ants protect trees from lethal herbivory by elephants. Big-headed ants kill and displace these native mutualists, rendering trees defenseless against elephants, which transform bushland savannas into open grasslands by breaking and killing adult trees. Using a combination of GPS telemetry, large-scale exclusion experiments, and structural equation modeling, I tested the hypotheses that open grasslands created by big-headed ant invasion would (1) be selected by plains zebra (*Equus quagga*) relative to uninvaded areas; and (2) confer increased safety from predation by lions (*Panthera leo*). Both hypotheses were supported. Invasion by the big-headed ant made whistling-thorn trees more palatable to elephants, reducing tree biomass by >40% in invaded areas relative to uninvaded areas. The reduction of tree biomass increased visibility, which was correlated with selection by (and thus densities of) plains zebra. Predation risk by lions decreased in invaded areas, even though zebra densities were higher in invaded areas. My results demonstrate that the disruption of a foundational mutualism reorganized predator-prey dynamics through spatial shifts in predation risk manifesting across an entire landscape.

005: Cascading effects of eavesdropping: predator sociality mediates foraging behavior and multiple plant-consumer interactions

Savannah L. Bartel[1], John Kilgo[2], John Orrock
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A mammal's social environment can affect individual foraging decisions by providing information about the frequency or outcome of competitive intraspecific interactions. Social predators use social cues (e.g., vocalizations or scent marking) to communicate with conspecifics, and prey may use these cues as indicators of predation risk to inform their own foraging decisions. Using multiple field experiments, we explore the strength of socially mediated foraging, the role of social cues in modifying predator-prey interactions, and the downstream effects of social cues on plant-consumer interactions. We found that coyotes (*Canis latrans*) were less likely to consume resources in patches that were visited by other individuals, indicating that the social environment shapes foraging decisions. We also found evidence that coyote social cues (i.e., vocalizations and feces) affect several trophic interactions. Experimental manipulation of coyote vocalization cues revealed that white-tailed deer (*Odocoileus virginianus*) respond to these cues through increased vigilance while foraging, but these effects were contingent on habitat context. Spatial variation in deer responses to coyote cues reflected spatial variation in the effects of deer herbivory on plant communities. We also found that seed dispersal within coyote feces improved post-dispersal seed survival since rodent granivores were deterred by this cue of risk. Taken together, our findings suggest that coyote sociality not only affects individual foraging decisions but can have cascading effects on plant communities through multiple trophic pathways.

006: Community ecology of North American migratory bats

Dana Green, Erin Baerwald, Mark Brigham
[1]*University of Regina*

The evolution of long-distance migration has occurred independently in a variety of taxa, and two North American migratory bats are the hoary (*Lasiurus cinereus*) and silver-haired bat (*Lasionycteris noctivagans*). While both species can migrate long distances (>1000 km), they are not closely related and exhibit differences in wing morphologies indicative of foraging behaviour. In the Cypress Hills of Saskatchewan, both species co-occur during the summer pupping season, and we catch them in abundance. We have collected data on wing morphometrics, nitrogen and carbon isotopic signatures, and Glucocorticoid levels to explore if migratory bats separate dietary niches and if it potential competition influences physiology.

007: Biodiversity informatics of mammals: identifying the next big breakthroughs

Robert P. Anderson[1], Eileen Lacey[2]
[1]*City College of New York, City University of New York, New York, NY,* [2]*University of California, Berkeley, CA*

Biodiversity informatics portals offer copious information about natural history collections, but advances in data quality and accessibility are needed to address key questions in basic and applied research (e.g., zoonotic diseases, invasive and threatened species, environmental change). This talk introduces the symposium “Transforming the Digital Frontiers of Mammalogy,” which aims to identify the next leaps forward for collections-based informatics. Mammalogy has long played a major role in this arena, beginning with the first efforts to digitize specimen data and later including georeferenced localities and associated spatial uncertainties. This foundation allows mammals to play a central role in future digital innovations. Major outstanding challenges include: 1) characterizing the uncertainty of taxonomic identifications; 2) integrating diverse data sets (e.g., parasites, DNA sequences) associated with the same physical samples; and 3) incorporating data from behavioral and demographic studies. The next five talks in this symposium outline new research possibilities related to parasites/pathogens, genomes, isotopes, microbiomes, and morphology; each describes associated data challenges and potential solutions. The symposium concludes with two more synthetic talks, one focused on linking across different data domains and the other highlighting parallel developments in ornithology. Through these talks and ensuing discussions, we hope to catalyze coordinated efforts to secure the funding needed to increase online availability of diverse, high-quality collections-based data for uses of importance to society.

008: Pitfalls and prospects for parasites and pathogens in the digital museum era

Kelly Speer[1], Kayce C. Bell[2]
[1]*National Museum of Natural History, Washington, DC,* [2]*Natural History Museum of Los Angeles County, Los Angeles, CA*

Wildlife are a significant source of emerging pathogens in humans. Our ability to prevent and prepare for the next pandemic is dependent on building foundational knowledge of pathogen transmission in wildlife prior to spillover. Natural history collections have the power to track the transmission of parasites and pathogens through space and time, yet are often underutilized in researching and detecting parasites and pathogens. Digitized host, parasite, and pathogen data are central to our ability to detect and monitor outbreaks and facilitate cross-disciplinary communication. Parasites and pathogens belong to diverse taxonomic groups and standards for depositing parasite and pathogen vouchers, and databasing those vouchers vary by research field. This hampers our ability to build collective knowledge of parasite and pathogen biodiversity, host associations, and responses to global change. Here, we present 1) best practices for connecting host vouchers to parasite and pathogen data, 2) examples of the uses of parasite and pathogen data derived from existing specimens, and 3) recommendations for improving databasing and accessibility of parasite and pathogen data from future collecting efforts. Our goal is to highlight the importance and underdevelopment of databases that account for hierarchical interactions, like those between hosts, parasites, and pathogens, and provide possible solutions.

009: Harnessing the power of museum specimens: generation and public-sourcing of molecular data

Jocelyn P. Colella[1], Diego Alvarado-Serrano
[1]University of Kansas BIodiversity Institute, Lawrence, KS, [2]Ohio University

The ability to sequence the genomic material of individuals has revolutionized the life sciences, however, genomic research into non-model mammals has been slow due to large genome sizes and financial and computational limits. Rapid improvement in sequencing technologies and bioinformatic tools, along with plummeting sequencing costs, have expanded our ability to probe the genomes of a greater breadth of mammals (and their symbionts). This has given rise to consortia, like the DNAzoo and Vertebrate Genome Project, which have facilitated generation and public sharing of genomic data through online web-portals. These genomic data resources valuably serve as a foundation for comparative and population genomic investigations, and for newer data-mining and machine learning applications, but legal and ethical considerations surrounding access and benefits sharing of genetic sequence data remain under negotiation internationally. Automated, standard archival of genomic sequence data remains a major challenge. For example, more than half of all sequence data in GenBank is not associated with a voucher specimen, and thus cannot be validated, reproduced, or extended. Further, the current dissociation of genomic data from other relevant biological and environmental data severely limits the utility of genomic data, especially in cases of taxonomic change or uncertainty. As a best practice, we recommend digitally linking all types of genomic data to a physical voucher specimen, using stable Darwin Core unique identifiers.

010: Evaluating the past and present ecology of mammals: stable isotope analysis of biological collections

Emma Elliott Smith[1], Phil Manlick

[1]Smithsonian Institution - National Museum of Natural History, Washington, DC, [2]University of New Mexico

Patterns of resource use within animal communities influence biological processes from community to ecosystem scales. Our ability to characterize these patterns has been revolutionized by stable isotope analysis, which can provide critical information on mammalian foraging ecology and trophic interactions in modern, historical, and paleo contexts. Although traditional measurements of whole ('bulk') tissues such as fur, whiskers, or muscle have yielded important insights, recent advances in molecular isotopic analyses, such as measurements of individual amino acids, allow characterization of mammalian ecology and physiology at finer scales. As part of the "*Transforming the Digital Frontiers of Mammalogy*" symposium, we explore the ecological insights that can be gained from isotopic analysis of individual compounds, and the application of these techniques to museum specimens through two case studies. In the first, we explore the relative contribution of production from plant-based ("green") versus detrital-based ("brown") energy channels to small mammal communities in North America, and the implications for local food web structure and stability. In the second study, we explore the applications of stable isotope analysis for specimens from archaeolgical contexts and collections. We focus on remains of an endangered marine mammal, the sea otter (*Enhydra lutris*), and use bulk tissue and compound-specific isotope anlaysis to characterize the historical trophic niche and habitat use of the species from the mid-Holocene to the present day.

011: Microbiomes from biorepositories: intestinal bacterial community characterization from museum archived samples of shrews

Stephen E. Greiman[1], Schuyler Liphardt[2], Joseph Cook[3]
[1]Georgia Southern University, Statesboro, GA, [2]University of Montana, Missoula, MT, [3]University of New Mexico, Albuquerque, NM

Biorepositories are critical resources for basic and applied research, including pathogen discovery. Technological advances in DNA sequencing have increased the usability of these repositories for examining the symbiotic communities on and within larger organisms. The mammalian gut microbiome is extremely complex and has been shown to be essential to host fitness and health, assisting in both nutrient acquisition from diet, as well as protection from pathogens. This community of microorganisms: bacteria, viruses, fungi, and even multicellular parasites, can all interact with each other and their host. Natural history collections that include gastrointestinal tracts, either preserved within the mammal, or as a separate part in ethanol or frozen can be used to increase our understanding of both spatial and temporal variation in the

gut microbiome. In this study we employ both complete and partial 16S rDNA amplicon sequencing to characterize the bacterial community within two North American shrew species, Sorex monticola and Sorex cinereus from New Mexico and Southeast Alaska. These samples vary in age (1968 to 2013) and preservation method (Liquid Nitrogen, -20C frozen, and 70% ethanol at room temperature) allowing for examination of the feasibility of obtaining accurate microbial community composition data from museum archived samples.

012: Transforming the Digital Frontiers of Mammalogy: Morphology

Noé de la Sancha, Stephanie Smith[2], Meghan Balk[3], Cody Thompson[4]
[1]Chicago State University, [2]Field Museum of Natural History, Chicago, IL, [3]BIO5 Institute, University of Arizona, Tucson, Arizona, [4]American Society of Mammalogists, Ann Arbor, MI

Morphology is one of the primary approaches used to understand evolutionary, ecological, and biogeographical questions in mammalogy. Our aim is to identify the next major leaps forward for collections-based informatics in mammalian morphology. We examine two different approaches. First, we explore the use of combined datasets made findable, accessible, interoperable, and reusable (FAIR) through the FuTRES data store (i.e., 'big data'). Previously, trait data was hiding in unsearchable fields or not standardized across datasets. We discuss challenges with standardizing trait terms and datasets in terms of FAIR. Second, we explore the use of 3D scanning techniques (x-ray CT, surface scanning) to develop shareable, citable 3D models of museum specimens, and address the limitations for researchers. We also discuss the future of modern morphological inquiry as related to mammalian species concepts, intraspecific trait variation, and trait quantification as well as applications to ‘big data’ bioinformatics, including artificial intelligence (AI) and machine learning. New applications of CT technology provide opportunities to quantify novel characters and standardize geometric morphometrics between datasets, such as traits for skeletal anatomy and soft tissues. These datasets have the potential to increase access to natural history collections, but also to widen the technological divide and inequities in biological science.

013: Realizing the specimen nexus: links across data types

Jessica Light[1], Joseph Cook[1]
[1]Texas A&M University, College Station, TX

As described in this symposium, massive amounts and types of data have been collected from specimens held in natural history collections over the last several decades. However, our ability to link these data to voucher specimens has lagged behind rates of data acquisition. The lack of data linkage and specimen attribution can be immensely disruptive to the scientific process and the ongoing effort to recognize the importance of natural history collections. To remedy this, collection data management systems (e.g., Arctos) and protocols must continue to develop and improve the capability to link data to voucher specimens, wherever those data may be stored (e.g., GenBank, MorphoBank). Data aggregators and portals such as GBIF and iDigBio need to ensure that these new specimen-to-data linkages are easily discoverable. Lastly, investigators using specimens and collecting novel, linkable data, need to ensure that their newly derived data are properly linked to individual voucher specimens and used to generate their research products. In turn, the scientific community (e.g., reviewers and editors) must continue to hold researchers accountable for reporting specimen use and ensure proper data linkages. Database capacity building as well as protocols shared among natural history collections worldwide to link specimens to their data are necessary to make specimen-to-data linkages easily discoverable. These advancements will be immensely beneficial for the future of specimen-based research.

014: Museums, biodiversity, and the digital data revolution: An ornithological perspective

John M. Bates[1], Carla Cicero[2], A. Townsend Peterson[3]

[1]Field Museum, Chicago, IL, [2]Unviersity of California, Berkeley, CA, [3]University of Kansas, Lawrence, KS

Like mammalogy, ornithology has catapulted into the digital age. Ornithology has an advantage in the ease of encountering many species such that citizen science databases (e.g., eBird, iNaturalist) have revolutionized gathering sighting data often accompanied by additional details (e.g. photos and/or recordings). Also, the extended specimen concept (ESC), has argued for the expanded value of traditional specimens to embrace new technologies. While collection databases have existed in our fields for more than three decades and data portals make accessing data from multiple institutions possible in a single search, the ornithological collections community has recently worked to make databases more searchable through a workshop on terminology standardization for important data fields (e.g., sex, life stage, body part, and preservation method). Realizing the ESC requires better integration of growing associated data types (e.g., parasites, DNA sequences, CT scans) and presents both opportunities and challenges. We need greater capacity to link additional types of extended data such as that from behavioral, ecological, and demographic research. Ornithology needs to explore these extensions to integrate long-term studies of behavioral ecology. Extended specimen networks require database capabilities that connect different components through an organism ID or other shared identifier. The ESC applies to mammology and all other aspects of biodiversity and we need to continue to grow common capacity to more rapidly adopt best practices across research fields.

031: Local scale habitat structure mediates interactions between coyotes and lagomorphs

Gabriela Palomo[1], Ty Werdel[1], Colleen Piper[1], Mason Fidino[2], Adam Ahlers[1]
[1]Kansas State University, Manhattan, KS, [2]Urban Wildlife Institute, Lincoln Park Zoo, Chicago, IL

Conversion of grasslands to agriculture is pervasive across the Great Plains and has potential to mediate species interactions. Coyotes (*Canis latrans*) are a predator of eastern cottontail rabbits (*Sylvilagus floridanus*) and black-tailed jackrabbits (*Lepus californicus*) and all are sympatric in these human-modified landscapes. It remains unclear, however, how local habitat composition in these novel landscapes influences spatiotemporal interactions among coyotes and their prey. We investigated environmental drivers of site occupancy by lagomorphs, and how coyotes influence lagomorph habitat use, using three years (2018-2020) of presence/absence data from camera traps sites (n = 381) distributed across western Kansas, USA. We used Bayesian multispecies occupancy models to test if coyotes influenced site occupancy by both lagomorph species and if local-scale habitat structure affected their interactions. Site occupancy was dynamic across years for coyotes (naïve occupancy range = 0.55-0.66), eastern cottontail rabbits (naïve occupancy range = 0.17-0.24), and black-tailed jackrabbits (naïve occupancy range = 0.15-0.33). Temporal activity patterns at sites were similar for coyotes and lagomorphs where all species remained nocturnal and did not vary across local scale landcover types. We found evidence that local vegetation structure may mediate spatial interactions between coyotes and both lagomorph species though more research is needed to uncover mechanistic explanations for these effects. Understanding how landscape change influences species interactions will be important for informing future conservation efforts.

032: Modeling eighteen years of community science data reveals extensive recolonization of bobcat in Illinois, USA

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Many terrestrial mammals have undergone substantial distribution changes in recent decades; yet collecting broad-scale occurrence data for carnivores is difficult due to their low densities and cryptic behaviors. Carnivore observations from community (i.e., citizen) science programs can be a potentially valuable approach for understanding changes in carnivore distributions over long time periods. We used 18 years of bobcat (*Lynx rufus*) observations collected by archery deer hunters (participants) across Illinois, USA, to estimate spatiotemporal patterns in occurrence using a Bayesian spatial multi-scale dynamic occupancy model. We estimated model parameters as a function of county-level landscape covariates while accounting for county-level spatial dependence in colonization. Our spatial occupancy model had greater predictive and more ecologically realistic performance than a non-spatial occupancy model we ran for comparison. Mean annual statewide county-level occupancy increased substantially from approximately 0.30 to 0.81 while participant-level occupancy also increased but remained low (≤ 0.12). Bobcat were primarily restricted to southern Illinois during the early 2000s but by 2018 occurred throughout western and southern Illinois. Landscape covariates had relatively weak effects on model parameters. Our study illustrates how community science observations analyzed with hierarchical occupancy models can be used to model spatiotemporal changes in species distributions. Bobcat have recolonized much of Illinois, but this colonization appears not strongly mediated by county-level landscape features.

033: Counting bats with computer vision to see if Kasanka is the world?s largest colony.

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Estimating animal populations is essential for conservation. Censusing large congregations is especially important since these are priorities for protection, but efficiently counting hundreds of thousands of moving animals remains a challenge. We developed a deep learning-based system using consumer cameras that not only count but also record behavioral information for large numbers of flying animals in a range of lighting conditions including near darkness. We built a robust training set without human labeling by leveraging data augmentation and background subtraction. We demonstrate this approach by estimating the size of a straw-colored fruit bat (*Eidolon helvum*) colony in Kasanka National Park, Zambia with cameras encircling the colony to record evening emergence. Human counters had previously estimated this colony to be between 5-10 million bats. Detection of bats was robust to deteriorating lighting conditions and changing backgrounds. Combined over five days, our population estimates ranged between 750,000 and 976,000 bats with a mean of 857,233. This is smaller than some large cave bat aggregations. In addition to counts, we extracted wingbeat frequency, flight altitude, and local group polarity for 639,414 individuals. This open access method is an inexpensive but powerful approach that, in addition to radial emergences from central locations, can also be applied to unidirectional movements of flying groups, such as migratory streams of birds or bats.

034: Improving occupancy estimation for inconspicuous species using multiple sign types: a case study of American pika

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Occupancy models have emerged as one of the most powerful tools to investigate regional population trends and dynamics, range shifts and habitat association. A key issue in occupancy surveys is the possibility of failing to detect a species when it is present or falsely detecting a species when it is not present. Using 10-year survey data for American pika (Ochotona princeps) collected at five national parks in the Pacific Northwest, we use multiple direct and indirect indicators of pika presence including fresh scat, fresh haypiles, pika calls and pika sightings ("multi-sign occupancy model") to investigate pika occupancy trends and the environmental drivers of both occupancy and detection processes. We investigate the sensitivity of these estimates to four increasingly realistic methods of modeling the pika observation process: (1) perfect detection (many previous attempts to model pika occupancy have assumed no observation errors), (2) standard occupancy model (single observation process), (3) multi-sign occupancy model with no false detections, and (4) full multi-sign occupancy model. Our findings indicate pika are less detectable than previously thought and provide inference for management on important drivers of both occupancy and detection processes of multiple sign types in an inconspicuous species.

035: Variation in resource selection by a large herbivore: effects of reproductive status and interspecific competition

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Periodic declines in mule deer (*Odocoileus hemionus*) populations across much of their range in recent decades, garnered much interest from federal and state wildlife agencies. Effective management of mule deer requires an understanding of how they interact with their environment. Our objectives were to quantify resource use by adult female mule deer during late gestation, provisioning of offspring, and following the loss of offspring. We conducted our study on the Starkey Experimental Forest and Range in northeastern Oregon. We evaluated resource selection by mule deer using a Random Forest machine-learning approach. We assessed temporal variation in resource selection across three time periods: third trimester of pregnancy, 30 days post-parturition, and following the loss of offspring. Mule deer selected for further

distances to roads during late stage pregnancy and after the loss of offspring. In contrast, mule deer selected for distances closer to roads during the 30 days post-parturition. We observed higher selection for distances closer to water while rearing young than the other two time periods. Our analysis also incorporated space use by elk (*Cervus canadensis*). Mule deer showed avoidance for areas with high probability of elk use across all time periods.

036: Mammalian foraging and fate of seeds in an oak forest

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The size of seed dispersers and their specialized hoarding behaviors can influence seed fate in many plant species. We examined whether members of a rodent community differed in their effectiveness as seed dispersers and how this relationship may be altered by seed species and predator presence. Northern red oak acorns and silver maple seeds were marked with aluminum tags and placed in size-selective rodent exclosures: (1) *Peromyscus leucopus* only, (2) *Peromyscus* and *Tamias striatus* access, (3) exclusion of all vertebrates and (4) open access for all vertebrates. A split-plot design with half the seed stations exposed to coyote urine was used to examine the effects of predator presence on seed fates. Maple seeds were removed at a significantly greater rate than the acorns. This may be attributed to the all access and *Tamias* access treatments and chipmunks placing seeds in their check pouches. The vast majority of the acorns were consumed in two days on the open treatment. *Peromyscus* cached acorns at almost twice the rate of larder hording; *Tamias* cached at about the same rate as larder hording**.** By day seven the rate of return was low enough that consumption rate asymptoted. The predator treatment did not have a significant effect. Cameras found that omnivores such as raccoons, opossums, and skunks, but not deer or turkeys, consumed a large number of seeds.

037: Selection of resources by pronghorn near large-scale disturbance

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Pronghorn (*Antelocapra americana*) are a native species in the Great Basin that occupy open habitats, such as sagebrush steppe and grasslands. Resource selection and movements of pronghorn are likely driven, in part, by water sources and open terrain that allows for escape from coursing predators. Large-scale mineral extraction such as open-pit mining, causes large-scale disturbance of landscapes occupied by pronghorn. The Cortez Mountains in the central region of Nevada are impacted by an active open pit mine located at the base of the mountain; an area used extensively by a resident population of pronghorn. Our objective was to evaluate how open-pit gold mining affected movement patterns and selection of resources by pronghorn. We captured 12 female pronghorn in the Cortez Range in January 2018. Each animal was fitted with a Vectronic GPS collar that collected six location points per day. We recorded 35,000 locations over two years, with an average distance from the mining boundary of 4,653 meters and 42% of the locations fell within the boundary. Pronghorn do not appear to avoid habitat near the mine, suggesting they may have adapted to living in a high-disturbance environment.

038: Flipping the scales of allometrics with early-life conditions

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In cervids, life-history tradeoffs associated with reproductive success and survival may be reflected in variation of resource allocation towards antlers and body mass. The growth of ornamental weaponry is energetically costly but can lead to greater reproductive success. Conversely, animals can invest energetic reserves towards body mass which is often associated with greater survival. This trade-off, termed allometric scaling, is when characteristics of organisms vary with body size. The effects of early-life conditions of white-tailed deer (*Oidocoileus virginianus*) were evaluated for allometric scaling between antler and body mass utilizing a 14-year dataset containing annual antler size and body weight measurements for 471 known-age white-tailed deer. These individuals were born in one of two 445-hectare, high-fenced pastures or a 2.5-hectare pen. Within the pen, movement was limited, predators did not occur, and sires were selected for large antler sizes. All deer had access to ad libitum food and water. Deer born in pens were released to the larger pasture at approximately 4 months of age. Offspring born in pens had predictably larger antlers but surprisingly smaller body sizes compared to pasture-born deer. Our results suggest early-life conditions permanently influence the allocation of energetic reserves towards either antler development or body mass in mature white-tailed deer. These findings of allometric scaling highlight the importance of early-life conditions and their influence on lifelong morphometrics and fitness.

039: Climatic refugia and anthropogenic threats: Impacts on mammals of conservation concern within the Appalachian ecoregion

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The Appalachian ecoregion of the United States encompasses the greatest diversity of mammalian species in the eastern Nearctic. Having served as a refugium during past glaciation events, the Appalachians will likely provide a different type of refugium in the face of anthropogenic climate change. In this study, I used ecological niche modeling to examine possible geographic range shifts due to climate change for 58 mammalian species of concern in the Appalachians. I created predictive ranges under future climatic conditions (2021-2040) for all species, and analyzed the model outputs in the context of suitable land cover and overlap with existing protected areas to determine which taxa were most threatened by climate change and limited by land use. I overlaid these models to identify areas with the highest number of priority species overlap. Models predicted suitable climate would persist into the future for the majority of examined species; however, urbanization and resource extraction in the region pose additional threats to crucial refugial areas, resulting in fragmentation and lack of landscape connectivity. Ultimately, due to the high amount of suitable climate predicted outside of currently protected areas, much of the conservation effort will lie in the hands of private landowners, creating a need for us to engage with both local conservation agencies and private citizens to preserve our species of greatest conservation need in the near future.

040: Umbrella effect of monitoring protocols for mammals in the Northeast US

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Developing cost-effective monitoring protocols is a priority for wildlife conservation agencies worldwide. In particular, developing protocols that cover a wide range of species is highly desirable. Here we applied the ‘umbrella species’ concept to the context of ecological monitoring; specifically testing the hypothesis that protocols developed for the American marten would contextually allow detecting occupancy trends for 13 other mammalian species (i.e., an umbrella effect). We conducted a large-scale four-year camera trapping survey across a gradient of forest disturbance in Maine, USA. We sampled 197 sites using a total of 591 cameras and collected over 800,000 photographs to generate detection histories for the most common terrestrial species. By combining multi-season occupancy modelling and power analyses, we estimated the required sampling effort to detect 10%, 25% and 50% declines in the fourteen species. By conducting a spatially explicit comparison of sampling effort, we found evidence that monitoring protocols for American marten would provide an umbrella effect for up to 11 other mammal species. The capacity of the umbrella effect varied among species, with fisher, snowshoe hare, red squirrel, and black bear consistently covered under several scenarios. Our results support the application of the umbrella species concept to monitoring (here defined as ‘umbrella monitoring species’), providing empirical evidence for its use by management agencies.

041: Mountain lion predation in a multi-prey system on private lands in Texas

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Prey selection and diet by large carnivores can have impacts on food webs and wildlife management. Mountain lions (*Puma concolor*) are large, apex predators that are commonly controlled for livestock depredation and ungulate population management. We assessed predatory behavior on privately owned lands in the Davis Mountains, Texas using GPS data from 16 collared mountain lions and inspections of 200 kill sites. Trail camera data were used to assess relative prey abundance. We assessed food selection using Ivlev's electivity index, *E*, to compare prey availability and use. A variety of native and non-native prey species were available within the study site. The top prey species (80% of diet) were deer (*Odocoileus* spp.), elk (*Cervus canadensis*), feral hog (*Sus scrofa*), and javelina (*Pecari tajacu*). While mule deer (*Odocoileus hemionus*) were the most common prey species, elk made up the largest percentage of biomass consumed. Females significantly avoided hogs (E = -0.46) and males significantly selected deer (E = 0.14) and javelina (E = 0.38) based on 95% confidence intervals. Mountain lions in the Davis Mountains specialized in preying on deer with use always greater than availability. Importantly, livestock were available in the study area, however, these species were never preyed upon. Our results on mountain lion diet and prey selection can provide important ecological information for predator and prey management.

042: Do African wild dog populations benefit from reduced lion density if prey is depleted?

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African wild dogs (*Lycaon pictus*) are limited by dominant competitors, particularly lions (*Panthera leo*). We measured wild dog demographics in the Kafue Ecosystem, Zambia. The Kafue is affected by prey depletion, particularly of large herbivores, and thus the density of lions is significantly lower than ecologically comparable ecosystems. Counter to expectations from mesopredator release theory, wild dog density in Kafue was far lower than comparable ecosystems with higher lion and prey densities. Annual survival rates were comparable to large and stable populations but average pack size was small and home-ranges were among the largest ever recorded. Our results show that low lion density did not competitively release the Kafue wild dog population and we infer that the low density of wild dogs was caused by low prey density. Wild dogs likely reduce in parallel with dominant competitors in prey depleted systems. Because wild dogs naturally occur at lower densities than their dominant counterparts, prey depletion may drive wild dog populations to local extinction thresholds sooner than their dominant competitors. Our results suggest that there is an optimal ratio of prey and competitors at which wild dogs achieve their highest densities. This finding has immediate implications for the conservation of the endangered African wild dog, and broad implications for the conservation of subordinate species affected by resource depletion and intraguild competition.

043: Fantastic pygmy rabbits and where to find them: investigating long distance movements with GPS collars

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Pygmy rabbits (*Brachylagus idahoensis*) are sagebrush obligates and a species of special concern due to continual degradation and fragmentation of suitable habitat. Many populations or colonies are thought to be declining, but recent evidence suggests that some colonies may be moving across the landscape over time. We aim to follow pygmy rabbit movement over time to understand how and why colonies may be moving. We GPS collared 23 rabbits at sites in the Great Basin near Jiggs and Austin, Nevada from July 2021 to April 2022. Individual rabbits were collared 4 days - 6+ months, collars were set to take a fix every 3.5 hrs, and individuals had 21 – 709 reliable fixes. We documented rabbits at both sites that traveled as far as 1.5-km in 3.5 hrs. All rabbits returned to their previous range at least once following long-distance movements indicating that adult rabbits may not be dispersing but rather, may be exploring new areas for access to a larger suite of potential mates or less saturated habitat. Although this study is ongoing, our data have already revealed much larger exploratory movements by adult pygmy rabbits than previously documented. These data not only provide insight into pygmy rabbit behavior but also illuminate connectivity between colonies and habitat characteristics that allow for these long-distance movements to guide conservation efforts for this species of special concern.

044: Tough to track: developing cost-effective monitoring protocols for track-surveys using a 16-year *Lynx canadensis* dataset

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Population monitoring is crucial in wildlife conservation, however, protocols for elusive mammals are difficult to develop because of the low detection rates and fieldwork costs. A key knowledge gap concerns how spatio-temporal dynamics in species occupancy and detection rates alter the cost-effectiveness of sampling protocols. Here, we used a 16-year dataset on Canada lynx (*Lynx canadensis*) snow track surveys conducted in Maine, USA and developed optimal monitoring protocols that empirically assess the cost-effectiveness of these protocols under different scenarios. We surveyed in 61 townships and detected 723 track intercepts which were converted to detection histories under a spatially replicated occupancy design. By combining occupancy modelling and power analyses, we estimated the sampling effort required to detect a suite of declines in occupancy ranging from 10 to 50%. After calculating the monetary cost of protocols under these scenarios we found that detecting subtle changes in occupancy (<10%) is very expensive even for high suitability habitats and may be an unrealistic management option in many circumstances. However, protocols that detected medium (25%) to large (50%) declines required similar budgets and were in line with the observed shifts in lynx occupancy (32%) during our survey period, suggesting that a modest budget increase would pay large dividends in population assessment. Our results provide important guidelines on how to allocate conservation funds to monitor elusive mammals using snow track surveys.

045: The value of dry riverbeds as corridors and habitat in Tucson, AZ

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Like many cities around the globe, Tucson has experienced rapid population growth and urban expansion in the past 20 years, reducing Sonoran Desert habitat that wildlife rely upon. Whereas some species are extirpated from urban areas and require undisturbed fragments of the Sonoran Desert, others have adapted or learned how to survive in the new urban environment. Riparian corridors may be a valuable resource for both sensitive and flexible species to cope with urban development. Intermittent rivers and ephemeral streams (IRES) in Tucson create important corridors that coyotes and javelina are known to use for travel through the city and cover to avoid extreme sun exposure and heat. Our preliminary results show that urban washes are also used by a variety of other mammals, and that the biodiversity benefits provided by IRES may be maintained in low to medium levels of impervious surface when preserved. Native mammal diversity drops substantially where impervious surface levels are high, especially where streambeds are paved over. Our results highlight the value of preserving intermittent streams for limiting the effects of habitat loss and fragmentation as urban centers expand.

046: Genomic variability is consistent with the history(s) of fragmentation of a southwestern riparian mammal

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Persistently low population sizes contribute to low genomic variation via genomic erosion, and when coupled with reduced connectivity can impede the long-term viability of species in fragmented landscapes. During the last century, riparian habitats across the American Southwest have deteriorated due to the synergistic effects of livestock grazing and other anthropogenic impacts making local populations less demographically stable and susceptible to the negative impacts of drift. Furthermore, due to heterogeneous environments and the intersection of multiple biomes in the region, genomic variation is also potentially adapted to local conditions. We evaluated genomic variation within and across geographic areas (*i.e.,* mountain ranges and river systems) to determine the relative contribution of drift and selection in structuring the federally endangered New Mexico meadow jumping mouse (*Zapus luteus luteus*). We further evaluated whether 1) historical allopatric divergence, 2) recent anthropogenic fragmentation, or 3) both influenced observed genomic variation. We sampled 145 specimens, obtained over 8,800 single nucleotide polymorphisms, and found that nine geographic areas reflect individual lineages that are significantly differentiated from one another, have exceptionally low genomic variability, and low effective population sizes (often fewer than 50 effective individuals). Additionally, each lineage has genomic variation consistent with adaptation to local conditions. Combined, these results suggest that there may be insufficient genomic variation to sustain viable populations without thoughtful management efforts.

047: Impacts of periodical cicada outbreaks on *Peromyscus leucopus*

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Small mammal populations have evolved to respond rapidly to changes in potential food resources. Many potential prey species have evolved long periods of reduced or no reproduction followed by mass eruption as a form of predator swamping. One such group of prey species is the periodical cicada, specifically the Brood X 17-year cicada group. In Berks County, PA, Brood X emerged in 2004 and again in 2021 in Nolde Forest. We compared white-footed mouse (*Peromyscus leucopus*) population size, survival rates, age and sex distributions, reproductive activity, and individual mass in pre-emergence years (2003 and 2020) to emergence years (2004 and 2021). While in the 2004 emergence year the population size was considerably higher than in 2003, the population size in 2021 was lower than in 2020 indicating that cicada abundance does not necessarily correlate with an increase in population size. Additionally, survivorship during the summer trapping season was not different in emergence years and non-emergence years. Although the age structure was similar across all years, the proportion of reproductively active individuals did increase during emergence years. Finally, the mass of individuals showed a complex relationship between year, reproductive status, and sex, but reproductive individuals were consistently heavier during outbreak years. Overall, white-footed mice show a complex response to periodical cicada emergence that depends on many factors yet to be explored.

048: Monitoring little brown bat (*Myotis lucifugus*) movements using passive integrated transponders (PIT tags)

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Technological improvements and collaboration push the envelope of science and lead to new innovations. A collaboration between bat and salmon researchers in Cypress Hills, Saskatchewan is facilitating advancement by using passive integrated transponders (PIT tags), which have been used to monitor salmon and livestock movements, to monitor bat movement. We capture bats in mist nets set along Battle Creek, a known foraging corridor, and inject PIT tags subcutaneously. PIT tags have unique identification codes and can last for the life of the bat. Large antenna arrays are suspended across Battle Creek (~10 m) and read the unique PIT tag ID codes as implanted bats pass through the antenna. Antennas are located in areas of “open” and “cluttered” vegetation to allow us to access when and where bats are moving in foraging areas. To our knowledge, this type of system is a novel method for studying bat movements. We aim to obtain fine-scale movement data and identify key migratory corridors and foraging locations for populations of endangered little brown bat (*Myotis lucifugus*) not yet affected by White-nose syndrome, as well as two migratory species, silver-haired (*Lasionycteris noctivagens*) and hoary (*Lasiurus cinereus*) bats.

049: Development of a custom mobile app for community monitoring of American pikas (*O. princeps*)

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Expanding citizen science to larger and more diverse communities is often hampered by high barriers to entry for volunteers, such as in-person trainings. Such barriers were particularly salient during the COVID-19 pandemic, when large gatherings were limited. Mobile apps offer a potential solution to broaden participation, particularly if they incorporate volunteer training, data collection/submission, and project branding. Here, we present a custom mobile app (“Pika Patrol”) for volunteers to record observations of American pikas (*Ochotona princeps*), climate-sensitive lagomorphs that are ideal for citizen science because they are charismatic and easily identified. Pika Patrol allows users to collect and submit data, including sound recordings and photographs, and view offline training materials for pika identification. This

year, we successfully engaged over 40 volunteers in beta testing Pika Patrol on iOS/Android platforms. However, we also encountered several unexpected challenges, including complex legal agreements and technical issues, which required significant staff time. Because the source code is freely available on GitHub, we hope that this app can serve as a template for other mammal citizen science projects seeking to streamline data collection and engage broader audiences. Specifically, this platform may offer additional options for projects interested in focusing volunteer effort on a single project/species, recording sound, and using apps to engage users in taking conservation actions beyond submitting data (e.g., participating in restoration projects or carbon-offset efforts, etc.).

050: Patterns of stress and survival in an isolated population of American pikas (*Ochotona princeps*)

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Climate change is affecting ecosystems globally, particularly mountain ecosystems. American pikas (*Ochotona princeps*) are alpine lagomorphs that have suffered recent declines linked to climate change, particularly in isolated mountain ranges. We evaluated the effects of territory-level habitat quality on survival and stress of individual pikas in the La Sal mountains of southern Utah, a unique, highly isolated, and understudied pika population predicted to be vulnerable to climate change. Pikas were live-trapped and marked with colored ear tags, and their territories were revisited annually to determine survivorship and estimate haypile size. We assessed habitat quality by estimating vegetation cover in each pika's territory, including relative cover of graminoids/forbs. We also placed temperature sensors near the haypile of each marked pika, which we used to calculate metrics of thermal stress from previous studies. Finally, we collected scat samples to measure fecal glucocorticoid metabolites. Territories of surviving pikas had significantly cooler summer temperatures than those of non-survivors, suggesting that summer heat stress is an important determinant of pika survival. In addition, average summer temperature was marginally negatively correlated with haypile size, which may represent the first empirical evidence that warming summers cause pikas to restrict their foraging, leading to smaller winter food caches. Such studies are important for monitoring this species under continued climate change and for developing effective conservation and management plans.

051: Keep on Survivin?: The search for plague survival alleles in Gunnison?s Prairie Dog (*Cynomys gunnisoni)*

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Identifying genes underlying adaptation is a fundamental goal of modern biology. Genome-wide association studies (GWAS) represent a critical first step in identifying the genetic basis of a phenotype in question. In this study, I conduct a GWAS on the non-model Gunnison's prairie dog, *Cynomys gunnisoni* – a semi-fossorial rodent native to the Four Corners region of the American West. Eradication campaigns and recreational shooting have contributed to the continuing decline of this taxon, though infection by *Yersinia pestis*, the bacterium responsible for sylvatic plague, is likely the primary contemporary threat to the persistence of *C. gunnisoni.* Recent reports, however, of evolving resistance to plague in natural prairie dog populations have begun to arise. The Aubrey Valley colony complex in northwestern Arizona has been largely spared from plague epizootics despite neighboring colonies experiencing extirpations from plague. Differential mortality rates from experimental infections of animals trapped in this region support the hypothesis of developing resistance heterogeneity. Despite its importance for the persistence of prairie dogs and dependent species, the genetic mechanism underlying this adaptation is unknown. Using an established bioinformatics pipeline, I identify SNPs associated with survival from plague to test my hypothesis that adaptive variation affects survivorship. The candidate alleles unveiled in this GWAS will be used to design a genotyping assay to explore the evolution of resistance over space and time.

052: Security at multiple scales: concealment and visibility both influence selection of habitat by a leporid

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Mammals at risk of predation select habitats that provide security from predators in addition to meeting other resource needs. Properties of habitat related to security include concealment (i.e., how well habitat structure hides an individual from visual detection by others) and visibility (i.e., the visual information accessible to an individual as a function of habitat structure). Although often negatively correlated, visibility is not the inverse of concealment, which allows animals to select for both properties, particularly across spatial scales. We investigated habitat selection by pygmy rabbits (*Brachylagus idahoensis*), which are subject to heavy predation, to test the hypothesis that individuals select for both increased visibility and concealment at two spatial scales. We evaluated selection at the patch and micro-site scale by adults fitted with telemetry collars. We estimated visibility using terrestrial lidar data, and concealment using photographic analyses, at three randomly selected locations within paired used and unused patches. Within used patches, we also estimated fecal pellet density to index use of micro-sites. Selected patches conferred higher concealment and lower visibility than unselected patches, however, the patterns differed when segmented into terrestrial and aerial perspectives. Variation in sightline lengths at micro-sites may be important in allowing individuals to select sites with concealment and also visibility. These analyses help disentangle functional properties of habitat structure to understand how prey species select secure habitat.

053: Using CT scanning to identify a potential new *Sorex* species in Colorado

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Robust research in ecology and wildlife management relies on accurate species identifications. Identifying small mammals, particularly shrews, can be inaccurate based on external morphology. In the San Juan Mountains of southwestern Colorado, seven shrews were captured by Dr. Christy McCain during a field collection in 2012. These specimens were distinct from the six *Sorex* species verified in Colorado based on skull and teeth characteristics and cytochrome-b molecular data. We assess the utility of Computerized Tomography (CT) scanning as a morphological tool for comparing external and internal skull morphology traits across Colorado *Sorex* species and potential species (e.g., *S. preblei*, *S. haydenii*, *S. sp. SW*) using fifty-seven scans. We use geometric morphometric analyses to identify which internal and external skull features (e.g., braincase volume, dental composition) provide reliable and distinctive measurements. We conduct discriminate function analyses of all the variables to reliably identify the unknown specimens to known *Sorex* species or show they are quantitatively morphologically distinct. Preliminary results suggest that the shrews of interest have distinct characteristics from the *Sorex* species confirmed in Colorado and may be most closely aligned with *S. preblei*. The latter occurs in southwestern Colorado based on a single specimen, but its identity is contested. These analyses may offer additional morphological characteristics, external and internal, and publicly available CT scans to improve species identification keys for other *Sorex* species.

054: Rangewide phylogeography of *Sorex monticola*

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Pleistocene ice sheets, once thought to have hampered speciation of high latitude faunas by periodically shifting the ranges of northern populations, are now known to have generated population substructure and even endemic species through a series of isolation in ice-free refugia punctuated by population expansion and secondary contact. Using whole genomes, I have examined signatures of demographic change throughout the Pleistocene from throughout the range of the montane shrew, *Sorex monticola,* and six closely related species, which together make up the *Sorex vagrans* complex. These signatures provide a lens to examine the detailed timing of how climatic fluctuations impacted geographic isolation and colonization events throughout the Late Pleistocene. Recent phylogeographic studies of *S. monticola* identified three lineages – coastal, northern continental, and southern continental – whose divergence may have been driven by isolation and secondary contact resulting from glacial cycles. Deep investigations of nuclear genomes and comparisons of autosomal and mitochondrial genomic data will shed light on the extent to which reticulate evolution (past and/or ongoing hybridization) has shaped current patterns of diversity in this species complex, providing a test of biogeographic, phylogenetic, and demographic hypotheses that have been outlined in previous studies, based on one or a few genes.

055: A taxonomic catalog of mammals described exclusively from Texas

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Of the 417 terrestrial vertebrates described from Texas, the Class Mammalia has the largest number of taxa, constituting almost 35% of the total number (143 types described from specimens and type localities in Texas). The taxa represented by these types encompass 8 orders, 22 families, and 53 genera of mammals, with the largest numbers coming from Order Rodentia (95 taxa), Order Carnivora (22 taxa), and Order Lagomorpha (10 taxa). Of the 143 mammals described exclusively from Texas, 50 (35%) originally were described as species and 93 (65%) as subspecies; 48 (34%) are now in synonymy and no longer tenable; 88 (61%) lack topotypes or near topotype specimens; and only 46 of those with topotypes or near topotypes (32%) are represented by genetic tissues. Mammals described exclusively from Texas are known from 94 localities in 47 of the 254 Texas counties, and 66 (46%) are from localities in counties that border Mexico. The period of greatest activity in terms of published descriptions was from 1876 to 1925, when 81 taxa (57%) were described; another 36 taxa (25%) were described from 1926 to 1950. The special importance of type localities and topotype specimens relative to resolving taxonomic problems and conservation issues is discussed, and a Type Locality Project designed to collect voucher specimens and genomic-grade samples from type localities in the state is proposed.

056: Utilizing museum collections and community collaborations to study the establishment of fox squirrels in Utah

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The fox squirrel (*Sciurus niger*) is natively distributed east of the Rocky Mountains in North America, but has become naturalized in urban environments after multiple introductions across the west coast of the United States. Most recently, they appeared in Salt Lake City, Utah in 2011 and their population continues to expand across northern Utah. While the source of this population remains unknown, it is evident they have become naturalized in Utah's urban environments, which might displace populations of two native species, the red squirrel (*Tamiasciurus hudsonicus*) and the rock squirrel (*Otospermophilus variegatus*). To examine the distribution of fox squirrels and their impact on native fauna, the Natural History Museum of Utah (NHMU) is using citizen science to track fox squirrel across Utah. This collaboration has resulted in ~2500 observations by community members, which we are using to map the distribution of fox squirrels across the valley over the past 10 years, documenting their behavior and interactions with native squirrels. Observational data are supplemented with specimens at NHMU, unlocking the potential for additional areas of research, like examining population genetics or morphological features that could reveal the source of the Utah population. Citizen science is a powerful tool to engage the local community and supplement traditional specimens to rapidly build a large dataset to study the establishment of non-native species and potential impacts on urban ecosystems.

057: Then and now: Documenting the squirrels of Southern California with collections and community science

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Specimens archived in museum collections are the gold standard for documenting species occurrences in time and across the landscape. However, specimens cannot capture all possible occurrences for a species and community science observations can supplement specimen occurrence data. We use natural history collections data and observations to examine changes in occurrence records through time in Southern Californian sciurids. We find that natural history specimens documented a broader geographic area and go farther back in time, but numbers of observations tended to be dramatically higher than specimen occurrences in the last 20 years. Some species, such as the California ground squirrel, have many more observational records than specimen records. There was an increase in observations correlated with the launch of the Southern California Squirrel Survey iNaturalist project in 2013, suggesting that focused projects can increase community scientist observations. However, this project appears to have had the biggest impact on observations of urban-adapted species that tend to be ubiquitous in human-dominated areas. Our findings suggest that encouraging community scientists to make observations for less common and sensitive species will improve our understanding of these species' distributions, particularly in urbanized areas. This initial project lays the groundwork for further investigating how squirrels in southern California have responded to urbanization and identify the habitats that allow the species to persist in densely populated regions.

058: Mesopredator occupancy and songbird richness along an urbanization gradient in central coastal California

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Habitat is increasingly being developed for anthropogenic uses such as housing or agriculture, fragmenting remaining habitat and imperiling wildlife. As available habitat decreases, some patches grow too small or isolated to support apex predators, which may allow mesopredator populations to flourish in the absence of predation and competition pressure. Where mesopredator occupancy is high, increased predation pressure may be placed on mesopredator prey species such as songbirds, which already suffer population declines from anthropogenic-caused habitat degradation and destruction. We evaluate the occupancy of one apex predator (coyotes) and three mesopredators (bobcats, gray foxes, and domestic cats) along an urbanization gradient in California's Salinas Valley and the relationship between these occupancy rates and local songbird richness. We used wildlife cameras at 35 sites along the gradient to collect data on mammal occupancy. Additionally, we conducted avian point counts to collect data on songbird richness at all 35 cameras sites as well as 35 nearby secondary sites. Preliminary findings show higher mesopredator occupancy, particularly for gray foxes, at sites without coyotes regardless of placement along the urbanization gradient. Preliminary results also show higher mesopredator occupancy correlates with lower songbird richness, although passerine richness is likely influenced more by habitat heterogeneity. Understanding how interspecific interactions interplay with anthropogenic land use patterns to shape community structure is critical for evaluating and predicting species distributions.

059: Hyena morphology after occupying an urban environment

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Humans have dramatically altered nature by means of urbanization and agricultural expansion. These anthropogenic changes to the environment can exert strong selective forces on residing animals, especially large carnivores. This study looks at morphological changes in spotted hyenas (Crocuta crocuta) due to life in urban environments. Physical morphology can change on both evolutionary and developmental time scales and previous studies have found morphological changes in animals after occupying increasingly urban environments. We investigated whether shoulder and limb morphology changed in spotted hyenas as a result of urbanization. We tested this hypothesis by analyzing limb and shoulder lengths of adult female spotted hyenas living in urban or natural environments. We used the photogrammetry software ImageJ on still captures of spotted hyenas to measure seven different body parts. We tested the validity of these measures using data from females immobilized in the field and tested the reliability of still captures using repeated measures of stills and subjects. Our results showed that only one measurement, lower leg length was both reliable and valid. This measure also differed significantly between urban and non-urban hyenas: urban hyenas were found to have shorter lower leg lengths. One possible explanation is the switch from

primarily hunting to primarily scavenging in urban environments. It will be important to further evaluate how animals adapt to increased anthropogenic change to better protect nature and ourselves.

060: Swamp rabbit (*Sylvilagus aquaticus*) occupancy across a flood prone landscape in Missouri

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Swamp rabbits (*Sylvilagus aquaticus*) persist in Southeastern Missouri along the northern edge of their range where fragmented bottomland hardwood forests help sustain a metapopulation. Due to vulnerability from habitat loss and other factors, swamp rabbits are designated as a species of conservation concern in Missouri (State Rank- S2: Imperiled). Within their Missouri range along the Mississippi River, much of the flood prone landscape is designated as a Priority Geography (River Bends Priority Geography), one of only nine areas that hold the highest conservation value for the state. Major flood events have negatively impacted swamp rabbit occupancy in the short term (1-5 years), but longer-term data (25+ years) suggest that the most frequently flooded regions may sustain higher occupancy. We investigated swamp rabbit occupancy in relation to flood risk, habitat patch size, as well as other landscape covariates. Suitable swamp rabbit habitat was modeled using MaxEnt software. Survey sites were then selected using a stratified-random design based on flood risk categories: batture side (highest risk), floodway, and ditched/leveed (lowest risk). Latrine surveys were conducted between November 2021- March 2022. Sites were revisited to account for potential seasonal detection variation. Analyses will be completed using a Bayesian occupancy framework. Results from this study will provide science-based information to guide appropriate management actions within the River Bends Priority Geography.

061: Using museum specimens to study geographic expansion of Lyme disease in the southeastern United States

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Lyme disease (caused by *Borrelia burgdorferi*) is the most frequently reported vector-borne disease of humans in North America. *Borrelia burgdorferi* is transmitted primarily by the black-legged tick, *Ixodes scapularis*. The white-footed deermouse, *Peromyscus leucopus*, is commonly parasitized by *I. scapularis* and is a highly competent reservoir for *B. burgdorferi.* Case numbers of Lyme disease have increased rapidly in western Virginia and North Carolina since 2000. To better understand the factors related to this increase, we tested the hypothesis that *B. burgdorferi* was present in *P. leucopus* populations living in this region prior to the recent emergence of Lyme disease. Specifically, we examined archived *P. leucopus* museum specimens for *B. burgdorferi* DNA. We used custom COXI primers to confirm DNA viability in 344 tissue samples (skin clips from ears) of *P. leucopus* study skins collected between 1945 and 2000 in 19 Virginia counties and 17 North Carolina counties. Ten mice, all collected in eastern Virginia in 1989, tested positive for presence of *B. burgdorferi* at two loci (oligopeptide permease periplasmic A2 and outer surface protein A). Our results suggest that *B. burgdorferi* was not historically present in western Virginia and North Carolina. Rather, the emergence of Lyme disease in this region is likely to have been driven by the relatively recent arrival of widespread *B. burgdorferi* infection in ticks and reservoir hosts.

062: Diversification of Philippine murid rodents: Mating system disparity suggests the involvement of sexual selection

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The Philippine archipelago supports a highly diverse murid rodent fauna including the old endemic clades Phloeomyini and Chrotomyini characterized by substantial morphological disparity, and morphologically

conservative members of the tribe Rattini derived from more recent colonization events. Given the species richness and rapid tempo of *in situ* diversification of all three clades, we assess differences among species in traits that are shaped by sexual selection to elucidate the role of that process in diversification of Philippine murids. Within all three tribes, there is significant male-biased sexual size dimorphism in some species indicating direct male-male competition, whereas other species are statistically monomorphic. Likewise, there are substantial differences in relative testis size among species within each tribe reflecting variable likelihood of sperm competition. Male-biased size dimorphism and relative testis size are independent features influenced by sexual selection operating at different stages of the mating cycle. Together, they reveal disparity in underlying mating systems, ranging from apparent monogamy to promiscuity. Differences among closely related species, including putative sister-taxa, indicate that speciation has involved shifts in mating system that may reinforce species boundaries in situations where closely related species are sympatric. Results suggest that sexual selection has played an important, but not universal, role in the diversification of Philippine murids.

063: Parasites of spotted skunks (*Spilogale* sp.) in the eastern and central United States

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To date, few studies exist on the extent of the parasitic fauna found on and within spotted skunks (*Spilogale* sp.). Most research has focused either on skunks from a portion of their range, or on a specific parasite group, creating a bias towards heterogeneous sampling efforts and incomplete sampling. As such, the goal of this project is to report on the parasite community of spotted skunks collected across their ranges. Skunks collected represent eight states and were obtained from vehicle-killed animals, mortalities from previous research projects, donations from natural history collections, and legally harvested animals by fur trappers. We performed fifty total necropsies on spotted skunks: eight western spotted skunks (*S. gracilis*) and forty-two eastern spotted skunks (*S. putorius*). When possible, both an internal and external evaluationa were performed. Endoparasites (acanthocephalans, cestodes, and nematodes) were found in thirty-five hosts and ectoparasites (fleas, lice, mites, and ticks) were found on fifteen hosts. Additional ectoparasites were obtained from a radio collar project in Harris County, Texas. Identification based on morphological keys of the collected parasites is ongoing.

064: Spatial factors influencing wildlife use of crossing structures on the Central Arizona Project canal

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Anthropogenic linear corridors (ALCs), including roads, railways, and canals, can reduce landscape connectivity for wildlife. Crossing structures along ALCs can facilitate animal movement across landscapes and maintain connectivity among populations. Spatial factors, including environmental attributes of the surrounding landscape and crossing structure features, can influence whether animals use crossing structures. Compared to roads, little research has evaluated how factors at multiple spatial scales influence wildlife use of overpass crossing structures on major canals. Our objective was to evaluate wildlife use of overpass crossing structures across structural and environmental factors at broad and fine scales. Forty-three wildlife cameras were deployed at overpass crossing structures on the Central Arizona Project (CAP) canal. We used Royal-Nichols models to evaluate relative use of overpasses across a suite of structural (e.g., openness) and environmental factors (e.g., vegetation cover at fine scales and plant productivity, topography, and human development at broad scales) for one season (e.g. May-June). We detected 15 wildlife species using overpasses to cross the canal, and report results for four focal species (e.g., bobcat, coyote, mule deer, collared peccary). Relative use of overpasses varied among species, and animals exhibited species-specific responses to structural and environmental factors. Future analyses will occur across multiple seasons, and for additional species. Results from this study can be used to inform the long-term management and conservation for wildlife associated with major canals.

065: Discovery of novel viruses within urban coyotes of the Phoenix metropolitan area

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Coyotes (*Canis latrans*) are often the top predator in urban ecosystems, particularly in the southwestern states of the United States. Despite how common coyotes are across the country, we know very little about the viruses associated with coyotes and their viral dynamics. During the spring/summer (March - June 2021) and fall/winter (October 2021 - January 2022) seasons, coyote scats were collected along 43 transects along the Salt River wildlife corridor in the Phoenix metropolitan area. A pilot study using a subset of the scats collected to identify viruses using a viral metagenomic approach. Our initial investigations reveal a diverse range of novel viruses, including a novel circovirus that is most closely related to canine circovirus. Based on the pilot work, the study is being expanded to analyze a larger number of the scat collected during fall/winter season. We aim to study the prevalence and distribution of the coyotes-associated novel viruses in urban coyotes of the Phoenix metropolitan area. The viral species identified can help bolster our understanding of the diversity and viral dynamics of coyotes and the urban desert they occupy.

066: Surveying LA's backyard bats: A community effort

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Collecting biodiversity data from urban areas is extremely challenging because the mosaic of private properties limits access. Most bat species are considered intolerant of urbanization, though 16 known bat species persist in Los Angeles County. Previous local studies focused on large urban wildernesses, and little is known about bat habitat use in the urban core. In 2016, we began the Backyard Bat Survey, an acoustic community science survey, to conduct the first large-scale study of habitat usage by bats in urban and suburban habitats of Southern California. A total of 72 sites were surveyed between 2016-2021 and 12 bat species were detected, including four California Species of Special Concern. Some urban adapted species that are common throughout North America are surprisingly scarce, whereas some foliage roosting specialists are more common than expected and more widely distributed compared to what is represented in museum collections. Our preliminary results suggest certain species are more adaptable or sensitive to urban settings than previously thought. Further investigations into urban bat habitats can guide urban planning for the benefit of bat conservation, especially when supplemented by bat roost emergence counts. Community science roost surveys were initiated in 2021 and conducted at 11 sites, indicating that Los Angeles County bats utilize a variety of urban bat structures but more research is needed to identify species-specific preferences, especially for more sensitive species.

067: Examination of prion disease signature in Suborder Caniformia and Order Chiroptera reveals susceptibility and resistance

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Transmissible spongiform encephalopathies (TSE) are fatal neurogenerative diseases caused by the misfolding of a prion protein gene in the exon 3 region. Various prion amino acid polymorphisms are associated with three categories of TSEs: 1) familial, where deleterious alleles are inherited, 2) sporadic, in which mutations occur spontaneously, and 3) transmissible, where the prion disease is infectious among mammalian species. Recent investigations of protein misfolding cyclic amplification indicated that Canids (dogs and relatives) and some Chiropterans (bats) display a low susceptibility to TSE due to a specific nonsynonymous substitution (N163D/E) in the prion protein that may result in a protective role in prion replication. Therefore, the goal of this study is to compare the distribution of the N163D/E substitution across mammalian orders to determine the possible correlation between presence of substitution and susceptibility. Methodology for this research includes the collection of samples, followed by PCR of the

prion protein gene (PRNP) exon 3 and sequencing of the substitution region. Subsequent downstream analyses determines the presence of an amino acid substitution. The entire PRNP gene was examined in four genera of Canids and nine genera of Chiropterans. Although current findings suggest no susceptibility/resistance pattern relating to diet or geographic location, PRNP protein sequences of several members within Canidae, Mustelidae, and Vespertilionidae displayed the unique amino acid substitution that confers resistance.

068: Variation of prion protein genotypes among Kansas deer with implications for chronic wasting disease susceptibility

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Chronic wasting disease (CWD) is a prion disease affecting cervid species that is rapidly spreading across North America. Relative susceptibility to CWD has been linked to genotypic variation of the prion protein gene (*PRNP*). The recent emergence and spread of CWD across the state of Kansas has highlighted the need to investigate *PRNP* gene diversity in both white-tailed deer (*Odocoileus virginianus*) and mule deer (*Odocoileus hemionus*). This study was designed to understand the spatial distribution of CWD resistance across Kansas, particularly considering ongoing decline of mule deer coupled with expansion of white-tailed deer. We extracted genomic DNA of hunter-harvested white-tailed deer (n=100) and mule deer (n=80) and sequenced 771bp of exon 3 of the PRNP gene. We provide the first information on both *PRNP* genotypes, coupled with infection status from immune-histocompatibility testing for CWD within Kansas. Our results identify spatial heterogeneity in the prevalence of 'reduced susceptibility' genotypes and identify variants previously reported elsewhere that are consistent with high susceptibility within Kansas. Sustained surveillance of herd susceptibility to CWD across cervid species is increasingly applicable with modern molecular methods for guiding applied wildlife management. This is especially important for CWD infected regions where multiple deer species interact, coupled with high hunting pressure and associated risks for human pathogen transmission.

069: Updating IUCN Red List status through a novel neighborhood approach to post-processing species distribution models

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Masking range maps to remove areas currently lacking appropriate vegetation can support conservation assessments. Two metrics used by the International Union for the Conservation of Nature (IUCN) in Red Listing can be calculated from these refined maps: Extent of occurrence (EOO) and Area of occupancy (AOO). However, coordinate uncertainty from occurrence records and disparities in data resolutions can lead to under- or overestimates, especially for AOO. We present a novel methodological approach to resolve these discrepancies and implement it for *Handleyomys chapmani*, a montane rodent endemic to Mexico considered threatened by the IUCN. We built an optimized Maxent model and then defined deforestation tolerance thresholds (the lowest value of forest cover where the species has been observed) using two approaches: 1) extracting the exact pixel value where an occurrence record fell; and 2) using an aggregate measure of that and surrounding pixels (the "neighborhood" likely within the radius of actual sampling). We applied these thresholds to the respective annual forest data to mask the suitability prediction, then calculated EOO and AOO. The neighborhood approach indicated less tolerance to deforestation, leading to a smaller area indicated as suitable and still containing sufficient habitat. Despite this, we found the species falls into a less threatened category than currently listed. This approach should prove useful for many species and highlights the importance of accurate georeferencing in the field.

070: Invasive oryx and encroaching shrubs: implications for landscape change in the Chihuahuan Desert

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Landscape change and invasive species are two drivers of biodiversity decline and altered ecosystem services. The expansion of invasive African oryx (*Oryx gazella*) across northern Chihuahuan Desert landscapes historically dominated by black grama (*Bouteloua eriopoda*) may be acting synergistically with encroaching honey mesquite (*Prosopis glandulosa*) shrublands. We sought to elucidate how landscape use and diurnal activity of oryx interacts with ongoing shrub encroachment. From 2014-2018, we conducted camera trap surveys at 24 sites established across an extensive shrub encroachment gradient in the Jornada Basin, New Mexico. We hypothesized that oryx would prefer remnant grassland habitats, which could accelerate shrub encroachment processes. Because oryx are adapted to the Kalahari Desert, we hypothesized their diel activity would follow a crepuscular pattern, whereby foraging could be balanced with thermoregulation and predator surveillance. We found that oryx prefer grasslands, especially during dry years, when grasslands are most at risk to shrub encroachment. Oryx displayed crepuscular diel activity, which was consistent across the shrub encroachment gradient. Our current focus is on disentangling the relative roles of herbivory by oryx, native rodents and lagomorphs, and domestic cattle in triggering and reinforcing shrubland states through long-term (25-year) experimental exclosures and grass seedling survival trials. We anticipate the collective preference of this novel herbivore assemblage for perennial grasses can reduce grassland biotic resistance to shrub encroachment.

071: Biodiversity benefits of ecosystem engineers are negated by invasive predators and anthropogenic disturbance

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Ecosystem engineers play vital roles in community assembly by modifying the environment to create novel habitats. Woodrats (*Neotoma* sp.) all build and maintain intricate stick-nests that stockpile organic materials and create habitat for other small species. The Key Largo woodrat (*Neotoma floridana smalli*) is an insular endangered subspecies endemic to Key Largo, Florida, USA, that has undergone substantial declines due to habitat loss and exotic predators. We leveraged data from a distribution-wide camera trap monitoring grid to survey the migratory and resident bird community visiting supplemental woodrat nest structures in their last remaining habitat. We evaluated the role of woodrat nest use and woodrat stick-nest building on bird abundance using generalized linear models. We predicted that woodrat occurrence and stick-nest building would positively correlate with bird diversity and abundance due to the habitat structure that supports prey for birds. We compared the relative support of woodrats to other external environmental, anthropogenic, and exotic predator factors. Bird relative abundance was positively associated with woodrat supplemental nest use and stick-nest building. However, these positive associations were negated by the presence of domestic cats (*Felis catus*), an exotic predator, and by proximity to human development. Therefore, we provide evidence that woodrats are supplying an ecosystem service in creating foraging grounds for resident and migratory birds, but this positive relationship is overridden by domestic cats and people.

072: How much data is needed? Testing an island biogeography model in a sky island system.

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Island biogeography has become a prominent research subject since its first treatment in 1967, but there is limited understanding of the historical and dynamic contribution of species' traits toward biogeographic distributions among islands. The Constraint-based Dynamic Model of Island Biogeography (C-DIB) is a systematic attempt to discern the drivers underlying such complexity. Central to the C-DIB model is how an island system's historical and contemporary habitat suitability, island connectivity, and island size affect present species distributions on islands. By evaluating this model in a natural system, we can quantify how ecologically relevant traits interact with environmental constraints over history to produce island biodiversity. We curated 2,367 occurrence records for 12 small mammal species from the Global Biodiversity Information Facility (GBIF) to identify sampling gaps for 12 "sky islands" in the southern Appalachians. Our study revealed significant data deficiencies in high elevation sites along the archipelago based on a quantitative summary of geographic and taxonomic biases. Large islands have been well-sampled, however smaller islands show community composition discrepancies between museum occurrence data and community science data. Inconsistencies indicate the need for more data collection along the spruce-fir archipelago to test the C-DIB model. We conclude with future directions to fill data gaps with field survey methods and museum data.

073: Correlation between 17-year periodical cicada numbers and mammal activity

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Optimal foraging theory predicts that animals will minimize time and energy to obtain the maximum amount of food. 17-year cicadas (*Magicicada cassini*, *M. septendecula*, *M. septendecim*) represented a large pulse of easily accessible but temporarily available food in ecosystems in the Midwest and Eastern United States in the summer of 2021. After emergence, adult cicadas serve as food for many mammalian species, which can shift their diets to consume high number of cicadas during periodic emergences. However, little research has investigated the impacts of periodical cicada emergence on mammal activity patterns. We predicted that carnivores and omnivores, but not herbivores, would increase activity levels during periodical cicada emergence. To evaluate mammalian activity patterns before, during, and after Brood X cicada emergence, we surveyed cicada numbers and mammal activity using trail cameras and acoustic recorders from 18 May – 20 June 2021 in northwestern Indiana. We determined that as cicada numbers increased, the activity levels of mammalian carnivores and omnivores also increased, whereas the activity levels of herbivorous mammals remained consistent. Thus, potential cicada predators increased their activity levels in response to the influx of easily attainable prey, supporting predictions from the optimal foraging theory.

074: 50 years of warming at an American pika study site

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Climate change in mountain regions has exposed high-elevation species to rapidly changing temperatures. The American pika (*Ochotona princeps*) often inhabits high elevations, and is considered climate-sensitive. Pikas thermoregulate by taking refuge in subsurface microclimates found in taluses and other rocky habitats, where daily thermal fluctuations are attenuated and somewhat decoupled from free-air temperatures. Although climate exposure can be reduced in microclimates, the quality of microclimatic refugia may degrade with climate change and reduce the efficacy of this behavioral thermoregulation. This study compares recent (2009-2021) subsurface temperatures at a long-term pika study site with a rare instance of historical (1963-1964) data from the same location. We place historical and recent microclimates in context using long-term data on free-air temperatures from the same area. Recent free-air temperatures were often warmer than historical records, while subsurface temperatures exhibited even stronger warming between periods, especially at the deeper of two talus sensor placements in this study. Winter months showed the greatest changes in both talus and free-air temperatures. Differences between historical and recent microclimates were not explained by the precise placement of sensors, as indicated by other recent subsurface sensors and similar temporal changes in free air measured by nearby weather stations. Together, these results suggest that subsurface microclimates important for pika thermoregulation have changed over the past few decades, perhaps even faster than observed changes in free-air temperatures.

075: Population genetic analysis of the Humboldt?s flying squirrel using high-throughput sequencing

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The San Bernardino flying squirrel (*Glaucomys oregonensis californicus*) is thought to be the southernmost population of the Humboldt’s flying squirrel (*G. oregonensis*) and is restricted to the San Bernardino and San Jacinto Mountains in California. However, recent surveys indicate they have been extirpated from the latter locality. In this study, we characterized the intraspecific genetic structure and diversity of *G. oregonensis*. We amplified and sequenced at least 300 bp of the mitochondrial cytochrome-*b* gene and 11 nuclear microsatellites, investigated *G. oregonensis* genetic structure with a focus on Californian subspecies, and evaluated genetic diversity within *G. o. californicus*. Population and phylogenetic analyses were performed on a total of 147 samples (tissue, hair, and museum specimen) using the Illumina high-

throughput sequencing (HTS) platform, thereby bioinformatically coding microsatellite alleles using established pipelines. Our results indicate reduced genetic diversity in *G. o. californicus* and highlight genetic distinctiveness of the San Jacinto population. Additionally, the differences in genetic diversity between the mitochondrial and nuclear markers suggest sex-biased dispersal and historic separation of the species in multiple refugia followed by more recent gene flow among northern California subpopulations. This study contributes valuable information toward understanding the genetic variation within *G. oregonensis*, provides information for future conservation decisions for *G. o. californicus*, and has novel implications for HTS genotyping-by-sequencing.

076: Recovering threatened and endangered mammals in California: Recovery plans and the California Endangered Species Act

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The California Endangered Species Act (CESA) is a useful tool to protect threatened and endangered mammals in California. The California Department of Fish and Wildlife (CDFW) is charged with conducting scientific reviews of species petitioned for listing, administering permitting programs to authorize take, and conducting periodic reviews to determine if conditions that led to the listing are still present. While CESA provides protection for listed/candidate species, to date, CDFW has had neither the funding nor the authority to write recovery plans that provide a roadmap for recovery and delisting. This situation changed in 2019 when a state law gave CDFW authority to develop recovery plans and in 2021 when the legislature approved funding for 31 positions dedicated to conservation of CESA species—several of which focus on creating recovery plans. These plans will provide essential frameworks for the recovery of the 21 species of mammals listed under CESA, several of which are not listed under the federal Endangered Species Act and thus have no federal recovery plan upon which to rely (e.g., Mohave ground squirrel, Sierra Nevada red fox, wolverine), or the federal plan is outdated or not yet available (e.g., gray wolf, Humboldt marten, Pacific fisher, San Bernardino kangaroo rat). This poster will provide information on CESA while soliciting recommendations from those with experience on recovery planning as CDFW begins producing these plans.

077: Characterizing coyote urine as a social olfactory signal distinct from non-social odors

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Urine is a common mode of chemical communication among carnivores. Coyote (*Canis latrans*) urine is regularly used to elicit anti-predator responses in laboratory rodents and to attract or repel wild animals in the field. Further investigation is needed to understand what information is contained in coyote urine as an olfactory signal and how it drives behavior within coyotes. Since June 2021, we have collected and catalogued urine from captive coyotes at the USDA Millville Predator Research Facility to use as odorant stimuli in behavioral tests. We have collected 822 samples from 40 individuals, including males and females, pups to adults, throughout breeding and non-breeding seasons. Exposing coyotes to urine from conspecifics will reveal the range of behaviors that coyotes exhibit in response to social odors. This will allow us to analyze the influence of variables like sex and relatedness of the stimulus donor on the test subject's behavior. A subset of urine samples will be analyzed for chemical composition. Pilot testing was designed to demonstrate that coyotes can discriminate the scent of urine from an odorless control (water) and to determine whether behavioral responses to a social odor (urine) differ from behavioral responses to a non-social odor (tea). This research will shed light on the mechanisms of olfactory social communication in carnivores and inform the use of coyote urine in wildlife management and laboratory research.

078: Differentiation of species distribution patterns between sympatric *Eulemur* spp. in Ankarafantsikan National Park, NW Madagascar

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The persistence of endangered species in disturbed landscapes partly depends on their capacity to occupy a wide breadth of habitat conditions across their home range. Little is known about the landscape ecology of the critically endangered mongoose lemur (*Eulemur mongoz*). In comparison to its sympatric congener, the near-threatened common brown lemur (*E. fulvus*), population densities of *E. mongoz* have severely declined over the past 30 years across their geographic range in northwestern Madagascar. Despite the severe conservation issues *E. mongoz* is currently facing, this species has received considerably little attention. We modeled the distribution patterns of these two sympatric lemurs using MaxEnt (v3.4.3) across Ankarafantsika National Park (ANP). We hypothesized that due to its current conservation status, *E. mongoz* will exhibit a smaller distribution pattern than *E. fulvus*, marked by a narrower selection of effective habitat conditions. The results from our species distribution models support our hypothesis. Across ANP, *E. mongoz* exhibits a smaller probability of occurrence than *E. fulvus*, based on the presence of rare habitat conditions like tall hardwood forests located near freshwater that are only found in a handful of river valleys. In contrast, *E. fulvus* exhibits a broad distribution pattern, limited by forest area. Our research shows that in the immediate future, river valleys stand as the best stronghold for the survival of this Critically Endangered species in ANP.

079: Comparing methods for recording fine-scale temporal fluctuations in social behavior in free-living mammals

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Social variables constitute a highly dynamic aspect of an animal's environment, because one individual's behavior may affect others in complex and nuanced ways. The ability to detect social information and modify behavior accordingly may allow animals to identify social challenges, avoid costly conflicts, and navigate their environment to maximize fitness. However, many animals are difficult to directly observe in their natural environments, making it challenging to discern important aspects of their social behavior. Prairie voles (*Microtus ochrogaster*) are one such model species; they are important for understanding the development of social behaviors such as pair bonding but difficult to observe in their natural grassland habitat. We therefore compared the efficacy of several methods for measuring fine-scale fluctuations in pairwise social behavior over time, including traditional live trapping, radio-frequency identification (RFID), and Bluetooth Low Energy (BLE) proximity loggers. We manipulated the social environment of established semi-natural populations and used social network analyses generated from these three data sources to determine the strengths and limitations of each method for measuring temporal changes in social behavior. Preliminary results suggest that proximity loggers provide the highest level of detail on social association, and we discuss future directions for improving methods of measuring fine-scale social behavior in free-living mammals with higher resolution.

080: Behavioral mechanisms underlying sound transmission of semi-arboreal pinyon mouse (*Peromyscus truei*) vocalizations

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Many animals produce long-distance acoustic signals to mediate a variety of social interactions, and the efficacy of transmission depends in part on attenuation caused by the environment. In other taxa, advertising from positions that optimize transmission is one key solution to minimizing attenuation. In this study, we assessed if transmission of advertisement vocalizations produced by pinyon mice (*Peromyscus truei*) varied based on the position of senders and receivers. Pinyon mice are semi-arboreal due to their dependence on trees for food and nest sites, and like other congeners produce sustained vocalizations for social communication. Synthesized signals derived from a population average of fundamental frequency, duration, and amplitude were broadcast and recorded at different heights (0, 1, and 2 m) and distances (1, 2, 4, and 8 m) in a full factorial design to mimic hypothetical senders and receivers. Preliminary findings from experiments in a semi-anechoic chamber indicate that vocalizations showed less attenuation when emitted from an elevation compared to the ground if the signal was received at least 2 m from the sender. Additionally, less attenuation occurred when both senders and receivers were elevated. Our findings indicate that signaling from heights confers benefits for sound transmission, thereby extending the taxonomic scope of this behavioral mechanism and contributing to the unique ecology of the species.

081: Mitonuclear discordance in the five-toed jerboas (Genus *Orientallactaga*) of the Gobi Desert

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Inferring the history of lineages is difficult when there is phylogenetic conflict among gene trees. Asymmetric introgression, for example, can lead to mitonuclear incongruence that complicates analyses if we fail to accommodate such uncertainty. We estimate phylogenetic relationships across the five-toed jerboas (Genus *Orientallactaga*), which is a clade that centers on the Gobi Desert in Asia, using fifteen nuclear genes and a more densely sampled (ca. 300 samples) phylogeographic mitochondrial cytochrome *b* (cyt*b*) dataset. We apply a fossil-calibrated, multilocus, multispecies coalescent model (MSCM) and coalescent simulations to reconstruct evolutionary relationships and test for mitonuclear discordance. By placing the evolution of these jerboas within the context of the Gobi Desert's dynamic climates and heterogeneous landscapes, we suspect that the mitonuclear discordance in this system is consistent with the complexity of interspecies interactions across time. More broadly, these results could highlight the value of independent assessments of nuclear DNA and mitochondrial DNA, which will improve our understanding of historical demographic processes, species limits, and phylogeny in systems with episodic gene flow.

082: Social sleepers: Sleeping positions as contestable resources

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Social status among group-living mammals can impact access to resources (e.g., water, food), mating opportunities, and social support. This differential access to resources can have consequences on fitness and health. Here, we propose that social status may impact an animal's access to sleep opportunities, as social status may predict when and where an animal sleeps, who they sleep with, and how well they sleep. This review of terrestrial mammals examines how sleep architecture and intensity may be impacted by an animal's sleeping conditions. Sleeping positions vary in thermoregulatory properties, protection from predators, and exposure to parasites. Thus, high-quality sleeping positions are limited resources that are subject to intragroup competition. Individuals of high social status likely benefit from priority of access to these positions, which may lead to differential energy expenditure and sleep quality between social strata. While sleeping positions are often mentioned as important resources, there is little empirical research examining both direct and indirect intragroup competition for these resources among mammals.

083: Influence of face masks on flight responses of North American wildlife during the COVID-19 pandemic

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COVID-19 caused a rapid shift in human behavior with the widespread use of masks to limit pathogen spread. This shift provides a unique opportunity to understand wildlife responses to changes in human behavior. Flight initiation distance (FID), or the distance at which a behavioral escape is initiated, indicates risk perception, with longer FIDs indicating higher risk sensitivity. A study conducted in China found that Eurasian tree sparrows shorten FID in response to mask-wearing, whereas another study in Europe found FID of 32 bird species was not associated with mask-wearing. In 2020-2021, student groups associated with Squirrel-Net used a standardized protocol to measure FID in five North American wildlife groups (ground squirrels, tree squirrels, gulls, deer, and songbirds), along with multiple habitat covariates. Using these data, we tested competing hypotheses about the relative importance of masks vs habitat factors on animal risk perception with generalized linear mixed models. Across all five taxonomic groups, our models highlighted the importance of measured habitat covariates, such as time of day and presence/absence of conspecifics, while consistently showing little support for models that included mask-wearing. Our results indicate that for these North American taxa, anti-predatory escape behavior is not influenced by mask-

wearing, but rather by environmental factors and life history traits. Therefore, as mask mandates are eased, unmasking should not influence perceived risk of predation in our study groups.

084: Life history trade-offs in Columbian ground squirrels: insights gained from new technology and targeted manipulations.

Jeffrey Lane, University of Saskatchewan, Saskatoon, SK

Classical life history evolution theory posits that energy invested in one trait is not available for, and is thus traded off against, others. This is assumed to produce negative relationships among the traits. If individuals differ in the energy that they have available to them, however, those with greater access can increase their allocations to full suites of traits more than their competitors. This can produce positive correlations among life history traits, across individuals. Well established theoretically, the resource-dependency of life histories can be difficult to test empirically, due to the logistical challenges of quantifying and manipulating resources available to individuals. We overcame these challenges by precisely measuring the energy stores (as masses of fat and lean tissue) of individual wild Columbian ground squirrels using a minimally invasive, field portable technology: quantitative magnetic resonance analysis. We also directly manipulated the resources available to individuals through PIT-tag activated feeders. Fed females emerged from hibernation with more fat than controls, and weaned both individual pups and full litters with higher masses. They also carried more fat into hibernation, and both the female and her pups had higher survival. These results indicate that available resources influence the energy that can be acquired by females, which directly influences core life history traits. In so doing, they provide empirical support to the resource-dependency hypothesis of life histories.

085: The evolution of seasonal camouflage in white-tailed jackrabbits in response to past and future climates

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Adaptation from standing genetic variation is a critical component of evolutionary responses to rapid environmental change. However, the difficulty of identifying the genetic basis of fitness-relevant traits in natural populations has limited the direct incorporation of genotype-to-phenotype information into conservation efforts. We studied the evolution of adaptive winter color variation in the white-tailed jackrabbit (*Lepus townsendii*), a North American species undergoing population declines. Using extensive museum records, we show that winter pelage color closely tracks dynamics of snow cover across the range of white-tailed jackrabbits, suggesting that geographic variation for the trait is maintained by strong selection. Using whole genomes of specimens collected during winter, we show that seasonal camouflage variation was primarily determined by additive genetic variation at three pigmentation genes. Using ecological and genetic modeling and forecasted environmental parameters, we predict that future declines in snow cover will strongly favor darker winter phenotypes across much of the white-tailed jackrabbit distribution. We also predict that low levels of standing adaptive variation should enable severely mismatched populations to adapt to this shift in snow cover conditions. However, adaptation to future snow cover may be impeded by ongoing population declines that appear to differentially threaten adaptive standing genetic variation. Our study illustrates how evolutionary genomics can be used to identify functional genetic variation of critical importance for climate change adaptation.

086: Foraging strategies influence lifetime fitness in a long-lived mammal

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Our understanding of climate impacts is fundamentally limited by the complexity and context-dependence of animal life history traits including survival and reproductive success. We combined mark-recapture techniques and biologging technologies on northern elephant seals *Mirounga angustirostris* to better characterize fitness consequences of foraging strategies. We found that lifetime reproductive success increased with mass gain during the 8-month foraging trip, which in turn varied with depth but not migration route or timing. However, 87% of the variation in LRS was explained by lifespan, and survival was most strongly determined by mass gain. A 100kg increase in mass gain from 225 to 325 kg increased survival by 6.3% each year. Seals that gained more mass also produced significantly heavier pups, which is known to increase the physiological development and subsequent survival of offspring. However, a large proportion of the variation in lifetime fitness remained unexplained, suggesting that predation and other causes of mortality may be driven by chance and only weakly influenced by the behavioral strategies we measured. These findings contribute to a growing body of work demonstrating the importance of stochastic variation in lifetime reproductive success as well as the evolution of underlying behavioral strategies.

087: Possibilities and limitations of using community-sourced photographs to investigate ecological patterns and processes

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We previously leveraged existing citizen science portals, especially iNaturalist, to rapidly amass photographs of mountain goats *(Oreamnos americanus*) over a large spatial scale (nearly 700 photos spanning 4,500km between latitudes 37.6°N and 61.1°N from 0m to 4333m elevation). Photographs were also sourced from professional photographers, researchers, and protected area staff and visitors; people readily shared photographs with us. Rather than omitting photographs associated with incomplete information (e.g., animal sex, presence of offspring), our statistical analysis inferred likely states of animals when not known. We combined data extracted from these community-sourced, spatially-explicit photos with findings from 2018 fieldwork in the Yukon, Canada, to evaluate mountain goat winter coat molt patterns and phenology. Tracking molt in known individuals allowed us to see whether the community-sourced data would lead to similar conclusions about factors influencing molt. Limitations in our data included bias towards recent photographs and variation in how animals were oriented in the photos. To deal with this latter added uncertainty, we used 25 equal-sized shedding bins or categories, each representing 4% of a goat's coat. Despite data limitations, we were still able to detect effects of goat sex, presence of offspring, elevation and latitude on molt. Both the community science component and our focal study of mountain goats provided consistent predictions.

088: Assembling individual-level trait-bases for small mammal phenology research

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Effects of global climate change on population persistence are often mediated by life history traits of individuals, especially the timing of somatic growth, reproductive development, and reproduction itself. Currently, however, the trait data necessary for reconstructing breeding behavior and use of breeding cues at rangewide scale in most mammal species remains sparse. This talk maps the current landscape of reproductive trait data available for small mammals, focusing on observations that are digital, open, and linked to individual occurrence records (museum specimens or census efforts). We provide an example workflow by which such data can be assembled and analyzed, focusing on an especially well-sampled species (the North American deer mouse; *Peromyscus maniculatus*), and use the data to reconstruct breeding phenology and its drivers both among ecosystems and between the sexes. Developing reproductive trait-bases for virtually all small mammal species will demand harmonization across a broad base of digital data resources, but can expose drivers of phenological variation within and among species and inform predictions of small mammal phenological shifts under future global change scenarios.

089: Back to the FuTRES: New informatics platforms, tools and research applications for individual-level trait measurements.

Robert P. Guralnick, Florida Museum of Natural History, Gainesville, FL

Traits are the measurable morphological, physiological, behavioral, and life-history characteristics of organisms that directly interact with the environment. Trait-based approaches in ecology have been ascendant, leading to novel insights about linkages between traits and niche overlap at population and community levels, as well as the importance of traits in structuring composition of assemblages. Traits also are central in time-extended, evolutionary approaches, given that trait evolutionary rates often condition processes of species diversification and determine ability of populations to respond to past and present environmental change. Despite the central role traits play in linking across disciplines, current mammal life-history trait compilations are both incomplete and focus on species-level averages or ranges. The basis for these species-level reports are individual measurements of specimens, but these are rarely ever reported, ultimately limiting use of current compendia. Here I present informatics efforts to enable best use of specimen-level trait data, focusing on our work to create FuTRES, a semantic-based data store for trait measurements of individuals. I discuss the vision and architecture of FuTRES and showcase the use of FuTRES in enabling new research. Finally, I discuss next steps for FuTRES and how it can connect dots to community science and 3D landmarking.

090: Population genetic structure of bobcats in South Dakota: using harvested samples to inform management

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An important component of wildlife management is identification of management units. The bobcat (*Lynx rufus*) is an ecologically and economically important furbearer. Population genetic structure can delineate demographically independent populations, which can inform management. We sampled bobcats harvested in South Dakota (2014–2019) to infer population genetic structure. We used 17 microsatellite loci, calculated measures of genetic diversity, assigned individuals to genetic clusters (K) using spatial and non-spatial Bayesian clustering algorithms, and quantified differentiation (F_{ST} and G''_{ST}) among clusters. Across loci, mean allelic richness was 10.8 (range: 7–19) and mean expected heterozygosity (0.80) exceeded mean observed heterozygosity (0.74). We found support for structure at $K = 2$ and $K = 4$, and evidence of finer-scale structure. At $K = 2$, pairwise F_{ST} (0.012–0.014) and G''_{ST} (0.105–0.119) values indicated weak to moderate differentiation, respectively. Estimates of differentiation were lower for $K = 4$ (F_{ST}: 0.009–0.018; G''_{ST}: 0.073–0.153), but still suggested weak–moderate differentiation. For $K = 2$, eastern and western clusters aligned closely with historical bobcat management units in South Dakota, but our results suggest that shifting the boundary of these units slightly west in the southern half of the state would better align units with population boundaries. Genetic divergence observed at $K = 4$ may be associated with environmental gradients, which may be important to consider for conserving genetic diversity.

091: Genetic structure and diversity in bobcat (*Lynx rufus*) populations in Oklahoma

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Bobcats (*Lynx rufus*) have been recorded in a majority of counties within the state of Oklahoma and are regularly harvested for their pelts statewide. There have been a limited number of studies on bobcats in Oklahoma, and due to annual hunting seasons, human alterations to the environment, and regular long-distance dispersals of male bobcats, questions have been raised regarding the genetic diversity, structure, and health of the population in the state. To better understand the current genetic makeup of Oklahoma's bobcats, tongue samples from harvested individuals were collected by the Oklahoma Department of Wildlife Conservation (ODWC) and deposited at the University of Central Oklahoma and Oklahoma State University. We extracted DNA from tissue samples collected across 22 counties and performed fragment analyses using 10 microsatellite loci, plus a sex-determining locus. This allowed us to assess the current genetic structure of bobcats within the state, as well as levels of genetic diversity. Preliminary data suggests the presence of two distinct genetic clusters, with the possibility of additional structure, as well as high levels of heterozygosity across the state. Additional assessments of genetic structure will be performed to determine if clusters can be associated with geographic and habitat boundaries, or if they are the result of collections bias and isolation by distance.

092: Context and diversity of the endangered *Abrocoma boliviensis* (Rodentia: Abrocomidae)

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The family Abrocomidae belongs to a lineage of South American rodents that have inhabited the continent since the Eocene (i.e., Caviomorphs). Members of this family are well adapted to rocky environments of the central Andes and include no less than seven extinct and two extant genera: *Abrocoma* and *Cuscomys*. One species, *A. boliviensis*, is endemic to Bolivia and considered Critically Endangered by the IUCN. With the procurement of unique samples, we reconstructed the phylogenetic relationships within the family and assessed the genetic diversity of *A. boliviensis*. Results from the analyses of mitochondrial and nuclear markers support a close phylogenetic relationship between *A. boliviensis*, *A. cinerea* and *Cuscomys* spp. with *A. bennettii* as the sister taxon. These results call for a taxonomic review of the family. In addition, mitochondrial data from 11 individuals of *A. boliviensis* revealed high levels of genetic distance when compared with other closely related taxa. Possible explanations for these results include: 1) *A. boliviensis* is a species complex and further revision is required, 2) sex-biased dispersal is promoting divergence within the mitochondrial genome, or 3) *A. boliviensis* might require further partitioning into subspecies. Preliminary results point to the second hypothesis as the most likely scenario. Given the conservation status and limited distribution of *A. boliviensis*, understanding how its genetic diversity is apportioned will better inform any potential conservation efforts.

093: Host genetics and social environment shape Yellowstone wolf microbiomes

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In humans and model systems, the host-associated microbiome has emerged as an important player in diverse immune and physiological processes. Similar studies conducted in wildlife support these patterns, and further suggest that commensal microbes function in the ecology and evolution of their hosts. Yet our understanding of the factors shaping microbiomes remains incomplete, particularly in wildlife sampled *in situ*. We bridged this knowledge gap in a wild population of gray wolves (*Canis lupus*) inhabiting Yellowstone National Park in Wyoming, USA. By contextualizing 16S rRNA microbiome data within decades of observational and host genetic data, we characterized the host-associated microbiome at six distinct body sites and identified which variables primarily shape microbial communities. We found that the gray wolf microbiome closely mirrors other mammal and canid species, with body site specific microbes exhibiting functions relevant to local physiological processes and microenvironmental conditions. We further identified genetic relatedness and social environment (*i.e.,* pack) as the two factors most strongly associated with microbial community composition across body sites. We additionally reported preliminary evidence for coat color and body condition influencing skin and gut microbiomes, respectively. The Yellowstone wolf system provided the unique opportunity to examine wildlife microbiomes and their underlying factors *in situ*. Results provide important baseline information for this reintroduced population, while also illuminating the relationship between wildlife microbiomes and the ecology and evolution of their hosts.

094: The effect of 60 years of translocations on populations of Texas desert bighorn sheep

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In Texas, desert bighorn sheep (DBS, Ovis canadensis) historically occupied 16 mountain ranges in the Trans-Pecos Region. Described as O. c. texianus in 1912, this subspecies of DBS was extirpated in the 1960s due to overharvesting, competition, and diseases. Historical restocking efforts have depended on translocating O. c. nelsoni and O. c. mexicana from Nevada, Utah, and Arizona, and Mexico and from in-state locations. These efforts reestablished populations from <14 to >1,500 individuals across 11 mountain ranges by 2018. The effects of these inter- and intrastate translocations on the genetic and genomic composition of contemporary populations are unknown. Mitochondrial markers (Cytochrome b, Cytb; Displacement loop) and restriction site-associated DNA sequencing (RADSeq) was used to determine the subspecific status of known pre-extirpated individuals and population structure, genetic variation, and connectivity in contemporary populations, respectively. To date, the Cytb gene has been successfully sequenced from 11 of 23 pre-1960 bone samples, suggesting pre-extirpated DBS represent a 'desert-like' subspecies rather than the Rocky Mountain subspecies. Preliminary RADSeq analyses indicate that DBS west of 104° (Sierra Diablo, Beach, Baylor, and Van Horn Mountains) are similar in the nuclear genome to populations in Arizona whereas DBS east of 104° (Elephant, Black Gap, Dove, and Bassey Mountains) are similar to populations in Nevada. Consequently, reintroduction efforts from multiple out-of-state sources were successful with evidence of detectable contributions to the nuclear genome.

095: Epigenetic signatures of male infertility across testes, sperm, and blood in captive-reared black-footed ferrets

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The black-footed ferret (*Mustela nigripes*; BFF) is a highly endangered mustelid that has been the focus of intensive captive breeding efforts since its rediscovery from near extinction in 1981. Ongoing conservation efforts to bolster BFF population sizes and genetic diversity have focused on breeding individuals of known ancestry in captivity and reintroducing them to protected natural areas. Despite the success of these efforts, captive BFFs exhibit reproductive problems (such as poor sperm quality), likely due to inbreeding depression and artificial settings encountered in captivity. Notably, sperm quality improves in wild-born progeny descended from reintroduced captive individuals. This suggests that environmentally induced regulatory changes alter reproductive pathways in captivity. We investigated the epigenetic underpinnings of this emergent condition using biobanked testes, sperm, and blood samples from captive BFFs bred since this species' recent population recovery. Our findings show expected tissue-type specificity in DNA methylation across the BFF genome, with differentially methylated sites identified in genomic regions enriched for various developmental processes and anatomical morphogenesis. We further linked patterns of methylation variation within gene networks to changes in relevant reproductive phenotypes, including testes morphology and average litter size. Results will inform the conservation management of this iconic North American mammal, while also providing insights to gene regulatory processes that influence the successful conservation of other rare, ex situ managed species.

096: DNA and RNA extraction optimization from mammalian museum specimens

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Museum specimens are being used more than ever as sources of DNA despite the degradation of these samples. To evaluate which methods perform the best on these degraded samples we repeated DNA extractions incorporating various methods of nucleic acid isolation (spin-columns, magnetic beads and phenol/chloroform). We tested extractions from adherent osteological tissues, bone, skin clips, baleen, and teeth as they are commonly requested for destructive sampling. We also compared an ancient DNA protocol to determine if it improves the quality and quantity of DNA yields from museum samples. Phenol/chloroform recovered the highest DNA concentrations, and generally, if a sample was successful in one protocol, it was in all, but fragment length distribution varied. A cost comparison was done to identify which protocols were the most efficient in terms of nucleic acid recovery and cost. Finally, we conducted a preliminary analysis of RNA extraction from formalin-fixed fluid specimens with the downstream goal of pathogen screening from museum holdings. RNA was recovered from frozen tissues and formalin-fixed specimens but not from specimens which predate the use of formalin. The addition of Proteinase K increased RNA yield and we also tested the efficiency of RNA recovery following single and multiple rounds of bead-beating during extraction. Shotgun sequencing was performed on both DNA and RNA extraction protocols to also evaluate the proportion of exogenous to endogenous sequences recovered.

097: Genetic structure and persisting genetic-environmental associations for a fossorial rodent (*Geomys bursarius*)

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Genetic structures of a species are influenced by large scale colonization histories as well as fine scale gene flow processes. Species with low dispersal, such as the plains pocket gopher (*Geomys bursarius*), are ideal for understanding these multi-scale genetic spatial structures. The plains pocket gopher has expanded northward since the Wisconsonian Glaciation, even crossing the Mississippi River eastward into Illinois. In Illinois, gophers have persisted in highly altered and converted landscapes. Here, we describe range wide and Illinois genetic structure, and then estimate gene flow based on soil characteristics. First, we use 7 microsatellites from museum specimens (1941-1981) and live-trapping samples (2018-2019) with STRUCTURE and Moran Eigenvector Maps (MEMs) to describe genetic clustering and clinal genetic structure. Second, we estimate associations of soil color and sand percentage with gene flow using an Isolation by Environment framework. We found that Illinois represents a unique genetic cluster, but that clinal genetic signatures show a south-north gradient both across the range and within Illinois. Illinois predominantly had clinal genetic structures. Furthermore, despite persisting in a highly altered landscape, we identified surface soil color and sand percentage still impacts gene flow. In addition to determining genetic structure, we show that isolation by environment can identify persisting environmental-gene flow associations.

098: Do muskrats influence water chemistry in Great Lakes coastal wetlands?

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It is important to understand the role muskrats (*Ondatra zibethicus*) play as potential ecosystem engineers in wetland systems, especially as muskrat populations decline across North America. By consuming cattails (*Typha* spp.) as a primary source of food and use of cattails for building houses, muskrats create perforations within otherwise contiguous stands of vegetation. While the chemical and physical properties of water determine the foundational abiotic environment in coastal wetlands, it is unknown if muskrat activity directly influences water quality attributes. Our objective was to investigate the direct influence of muskrats on water chemistry around muskrat houses. We sampled paired sites, a muskrat house site, and a non-house site within 20 m of one another, in coastal wetlands during summer 2021. At each site, we used a YSI Multiparameter Water Quality Sonde to measure water quality variables to determine the magnitude of effect muskrats have on water quality. Principal component analysis (PCA) was used to analyze the data, along with multiple response permutation procedure (MRPP). The PCAs that were performed on each site separately showed potentially different patterns, which are still being investigated. Preliminary results have

shown that the effects muskrats may have on water quality is dependent on the type and various attributes of the wetland.

099: Spatial structure of North American mammal paleocommunities is unique during early Cenozoic mammal radiation

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Taxonomic beta diversity has been widely used to examine the spatial structure of mammalian communities. More recently, functional beta diversity, a taxon-free approach, uses traits to more directly evaluate how ecosystem functioning varies across space. Taxonomic and functional beta diversity are often decoupled at local scales in the modern, but not consistently. Furthermore, ecological mechanisms driving spatial structure is not well understood. The North American fossil record of mammals over the last 65 million years encompasses several major environmental and ecological events making it an ideal system to evaluate functional beta diversity of mammals on a geologic timescale. We compiled 264 mammal paleocommunities spanning the Cenozoic. Functional diversity was calculated using four traits that are reflected in morphology: locomotion, body mass, life habit and diet. Paleocommunities were binned into 5-million-year intervals to calculate functional and taxonomic beta diversity using a pairwise approach. To determine if the results were driven by the arbitrarily chosen bins, we employed a sliding window approach and adjusted bins by 1-million years. We find that functional and taxonomic beta diversity are highly correlated throughout the Cenozoic apart from the Paleocene. The Paleocene has high functional diversity and low taxonomic diversity, suggesting this period has unique ecological dynamics in play. This study provides important information on how abiotic and biotic factors can influence mammal paleocommunity spatial structure on evolutionary timescales.

100: Northern long-eared bat summer roosts and population structure along the Eastern Seaboard

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The northern long-eared bat (*Myotis septentrionalis*) has been heavily impacted by white-nose syndrome (WNS), with population declines (>90%) throughout much of its range. Nonetheless, some remnant populations persist with evidence of multi-year survivors and successful reproduction, particularly along the Atlantic Coast. From 2014–2020, we monitored populations from coastal Massachusetts to eastern North Carolina. Day-roosts in trees and snags used by northern long-eared bats, primarily in cavities and, to a lesser extent, exfoliating bark, varied by location and local forest composition. Use of anthropogenic structures was greater in the Northeast than the mid-Atlantic whereas use of taller roosts was greater in the mid-Atlantic. At most locations, successful reproduction was noted. Restriction-site associated DNA sequencing suggested that coastal populations and adjacent Appalachian populations remain fairly panmictic with some inter-population gene flow, similar to conditions prior to WNS. Overall, lower heterozygosity than expected was observed, perhaps indicating increased inbreeding due to colony collapse following WNS. Northern long-eared bats on Martha’s Vineyard were the most distinct clade whereas the bats from Marine Corps Base-Quantico in northeastern Virginia were more genetically connected to eastern North Carolina than to closer populations in the Appalachians. Whether WNS impacts are occurring more slowly in coastal populations as compared to traditional cave-hibernating populations,

or if unique overwintering conditions are allowing northern long-eared bats to persist on the coast is unknown and merits future work.

101: Abundance-occupancy relationships in small mammals: why are widespread species common and restricted species rare?

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Positive interspecific abundance-occupancy relationships (AOR) are nearly universal patterns in ecology. Widely distributed species tend to be locally abundant, while those with restricted distributions tend to be locally rare. This pattern has been attributed to differences in resource-use flexibility among species, such that those species that thrive on a broader range of resources should both occupy more sites and should be relatively common where they occur. We quantified an interspecific abundance-occupancy relationship in a Kenyan small mammal community, using DNA metabarcoding to quantify diet composition of five species along the AOR spectrum. We tested two predictions: (1) populations of common, widespread species should exhibit the greatest dietary diversity (a prediction of the resource breadth hypothesis); and (2) common, widespread species should exhibit the greatest variability in diet among individuals (a prediction of the niche variation hypothesis). Abundant, widespread species exhibited the greatest dietary diversity, as well as greatest variation among diets of individuals. Our results provide support for the resource breadth and the niche variation hypotheses. Ongoing efforts are testing the complementary role of source-sink dynamics in maintaining this AOR.

102: Forest structural diversity as a potential predictor of mammal species occupancy

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Wildlife studies increasingly incorporate more structural characteristics into studies of habitat. However, most still collect habitat data primarily from field measurements, which are limited in extent and force researchers to extrapolate from small-scale, ground-based measures. Light detection and ranging (LiDAR) can objectively measure habitat features across landscape extents. We measured forest canopy structural diversity at 182 Indiana plots at three (25 m, 50 m, 100 m) radii to explore forest heterogeneity across space, utilizing new aerial LiDAR in tandem with camera traps. We aimed to quantify the relationship between occupancy of six mammal species and habitat structural characteristics, specifically predicting species presence as a function of LiDAR metrics. We found that measures of vertical complexity were the best predictors for raccoon (*Procyon lotor*) and coyote (*Canis latrans*). Models for eastern cottontail (*Sylvilagus floridanus*) incorporating vegetation area indices (VAI), Gini diversity, and percentage of canopy gaps demonstrated significance and low error. Generalists, such as white-tailed deer (*Odocoileus virginianus*) and Virginia opossum (*Didelphis virginiana*) did not select for structural metrics and were best predicted by the null model. Ultimately these results indicate that LiDAR is a promising potential tool for measuring ecologically meaningful variables at large scales. Metrics of structural diversity have the capacity to act as proxies for broader environmental attributes, quantifying aspects of habitat that defy traditional measurement.

103: Mammalian host segregation alters ectoparasite infestation in a desert ecosystem

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Community ecology has much to offer to the study of multi-host, multi-parasite systems. Specialist and generalist parasites respond differently to changes in host community structure. At the Portal long-term research site in the Chihuahuan Desert of southeastern Arizona, we experimentally segregated key mammalian hosts (kangaroo rats, *Dipodomys* spp. and black-tailed jackrabbits, *Lepus californicus*) of two groups of ectoparasites: a specialist tick species (*Dermacentor parumapertus*) and a generalist flea community. As expected, specialist ticks were absent when their primary host was removed. Furthermore,

habitat partitioning between kangaroo rat and jackrabbit hosts resulted in lower levels of tick infestation. We found that the removal of kangaroo rat hosts did not affect the degree of generalist flea infestation on the rodent community level, but that individual rodent host species differed in host competence. Taken together, these results indicate that mammalian host segregation can alter ectoparasite infestation, with differential effects as a function of the degree of specialization. As changes in host communities are pervasive due to anthropogenic impacts, our study emphasizes how altering host community structure can differentially affect specialist and generalist parasites.

104: Mammals? diversity and habitat use in the US-Mexico western borderlands

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The international border between Arizona and Mexico traverses a vast landscape of extreme biodiversity. Habitat degradation, fragmentation and loss of functional connectivity are potential consequences of increased border-related disturbances and physical barriers. Few studies have directly monitored space use by mammals to understand how wildlife use natural corridors and respond to border-related disturbances and barriers. Our aim was to determine how the diversity and habitat use of terrestrial mammals and bats changes across major features in the landscape: the Cajon Bonito stream which is the only superficial water source, the border wall and the most transited highway in the area. We installed 100 camera traps for two years, trapped bats using 20 infrasonic recorders in dry and wet seasons and surveyed environmental DNA along 10 sites in the stream. In total, we found 52 species of wild mammals belonging to 17 families. We also found two different jaguar individuals and other cryptic species in the region such as the ocelot and beavers. We found that the Cajon Bonito stream is a hub for biodiversity in the region and the areas close to the highway and the border have less diversity. Our results highlight the need to keep bi-national connectivity for mammal populations that use the mountain corridor in the Continental Divide and prioritize sites to mitigate the impacts of the highway and the border wall.

105: Rodent community responses to urbanization in southern California

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Through habitat loss and fragmentation, the effects of human development can alter community composition and interactions. Where some species become less abundant, others take advantage and exploit these changes. The effects are not only experienced within communities of similar species (rodents, mammalian carnivores) but also altering the interactions between these groups. Here we assess rodent community composition across sites with varying degrees of urbanization, describing the response of rodent richness and abundance. We also investigate how the presence of mammalian carnivores serve as a predictor for the rodent community. Rodent trapping was conducted at 12 sites for four months a year. A camera trap was deployed at each trapping site to detect mammalian carnivores. Preliminary findings suggest there are significant effects on the rodent community based on site and season effects, where rodent detection is lower in Summer compared to other months. There is evidence that woodrats (genus *Neotoma*) and pocket mice (genus *Chaetodipus*) are associated with rural and semi-urban sites with greater shrub/scrub cover. Deer mice (genus *Peromyscus*) and harvest mice (genus *Reithrodontomys*) appear more often at sites with increased grass cover and development. Understanding interactions between the rodent community, predation, and habitat across an urbanization matrix is important as rodents often an indicator of habitat quality, serving as a mechanism for plant dispersal and a prey base for many species.

106: When the tap runs dry: The physiological effects of acute experimental dehydration in *Peromyscus eremicus*

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Availability of essential resources is one of the most important drivers of survival and to persist in changing environments, animals must either relocate or adapt in place. Physiology often represents one of the first lines of defenses against changing environments, as physiology is dynamic, reversible, and often happens in real-time. Animals living in desert environments are hypothesized to be physiologically adapted to extreme temperatures and aridity, and therefore represent an interesting natural experimental model to examine processes important to adaptation. High ambient temperatures and lack of extrinsic water challenge mammalian survival, as most mammals rely on total evaporative water loss for cooling. Historically, metabolism was studied under constant environmental conditions with snapshot measurements, but new methods of continuous metabolic phenotyping offer a window into organismal responses to dynamic environments, enabling the identification of abiotic controls and the timing of physiological responses relative to environmental transitions. We use indirect calorimetry to characterize metabolic responses of the desert-adapted cactus mouse (*Peromyscus eremicus*) to examine the role water access has in whole-organism performance. We contrast metabolic responses for animals consuming water ad libitum to animals experiencing acute experimental dehydration to investigate circadian patterns of metabolism across time, sex, and water treatment with a specific interest in the hydration status, organismal water economies, physiological, and biochemical changes.

107: Physiological resistance of moose calves to flies: cortisol and environmental stressors

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Young animals are particularly vulnerable to environmental stressors that can impair growth and compromise survival. Moose (*Alces alces*) face threats from predators and infectious diseases from birth. We used salivary cortisol, a glucocorticosteroid hormone, to characterize the stress response of moose calves in relation to age, time of day, ambient air temperature, and the abundance and type of flies. We measured salivary cortisol in 5 calves up to 4 times a day on 25 days through the summer with corresponding samples of on-host fly collections by sweep nets. Of the 2,618 flies sampled on the animals, 68% were moose flies, 13% were coprophagous flies, and 9% were mosquitoes. Salivary cortisol levels were low (<0.2 mg×dL^{-1}) from 25 to 89 d of age at ambient temperatures of 13 to 34 ºC from June through August. Cortisol did not increase with ambient air temperature or with counts of flies. A low-stress response to flies is consistent with low avoidance of flies by female adult moose and the calves that must follow their mothers. Moose calves apparently rely on their coat and their immune system to resist fly bites and pathogens associated with wounds or bites. Recruitment and recovery of moose populations may be sensitive to increases in vector borne pathogens associated with a warming climate because calves appear to rely on physiological resistance to flies.

108: How to determine reproductive stage in free-ranging bats: a refined method using vaginal cytology

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Many species of bats mate in the fall, but delay conception until spring by maintaining spermatozoa within the female's reproductive tract. Current methods to identify female sperm storage (FSS) rely on dissection and microscopy to detect the presence of sperm. However, detection of FSS while a bat is alive is essential for longitudinal studies. To determine if we could identify reproductive stage and FSS in female bats, we tested the use of vaginal lavages, a non-invasive cytological assessment of vaginal cells. Here we present data from a modified vaginal lavage method. We collected samples from 10 female pallid bats (*Antrozous pallidus*). Using a modified Papanicolaou's (Pap) stain, we identified the presence and relative abundance of nucleated epithelial cells, cornified squamous epithelial cells and leukocytes. From changes in cell typology, the reproductive stages of proestrus, estrus and metestrus were determined. FSS, however, could not be determined using this method. We present our modified protocol as well as discuss uterine microscopy in sperm storing bats. A female's reproductive stage has important effects on many aspects of an animal's biology, including immunology and bioenergetics, as well as clear implications in behaviour and sexual selection. Being able to identify reproductive stage, such as described here, is essential to begin factoring reproduction into future research. We anticipate the methods we present could be applied to many additional taxa.

109: A comparison of accelerometer and global positioning system estimates of energetic expenditures in brown bears

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Within optimal foraging theory, animals should maximize their net energy gain while minimizing energetic costs. Energetic expenditure in wild animals is therefore a key component to measure proxies of fitness. Accelerometers (ACC) offer an effective tool to study wild animal energetics but retrieval of the device is usually required and often difficult. Measuring energetic expenditures using a global positioning system (GPS) approach may provide an alternative method. We compared ACC and GPS methods to estimate energetic expenditures in brown bears (*Ursus arctos*) on the Kodiak Archipelago. We then used the GPS method to examine intrinsic and extrinsic factors influencing brown bear daily energetic expenditures (DEE). We found that while the two energetic measurements were significantly different, they were strongly positively correlated. The GPS approach on average provided 1.6 times higher energy estimates than did ACC. Brown bears had lower DEE during periods of high food abundance, supporting optimal foraging theory. Reproductive status and age did not influence DEE, however movement rates had a positive linear relationship with DEE. Energetic ecology is important for understanding drivers of animal movements. We suggest a GPS-derived estimate of determining energetic expenditure is suitable when ACC is unavailable. Brown bear energetic expenditure was influenced by intrinsic and extrinsic factors, which highlighted the importance of access to prime foraging sites to enhance energetic efficiency.

110: Temporal contrast sensitivity of white-tailed deer

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Prey species rely on information from their sensory systems to successfully navigate heterogenous landscapes of risk and reward. For ungulates, vision plays an important role in the identification of immediate risk (i.e., predatory attacks) and execution of escape behaviors. However, the physiological capabilities of ungulate visual systems are not fully explained, particularly in relation to their ecology. To better understand what signals and cues ungulate prey species can detect, we investigated white-tailed deer (*Odocoileus virginianus*) temporal contrast sensitivity using electrophysiological experiments. We recorded electroretinograms from 17 deer (0.5 to 12+ years of age) in response to achromatic stimuli of varying luminance (0.003 to 1500 cd m^{-2}), contrast, and frequency (4 to 100 Hz) levels. The electroretinogram responses of deer frequently remained in phase with flickering stimuli of 100 Hz, even at relatively low luminance and contrast levels. These preliminary results indicate deer possess a visual system capable of high temporal resolution under a wide range of lighting conditions. The apparent ability of white-tailed deer to detect rapid changes within their visual field during nocturnal, crepuscular, and diurnal activity periods likely represents an important visual specialization for ungulate prey species.

111: Using indirect metrics to evaluate how environmental stressors shape physiological condition in New England Cottontails

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We assessed the use of fecal glucocorticoid metabolites (FGMs) as indirect metrics of physiological condition to determine how invasive competitors (eastern cottontail, *Sylvilagus floridanus*) and invasive plant species (Japanese barberry, *Barberis thunbergii*) impact the physiological health of New England cottontails (*Sylvilagus transitionalis*). We tested the hypothesis that fecal glucocorticoid metabolites provide an accurate measure of physiological condition in different environments and correlate negatively with survival. We leveraged existing fecal pellet samples collected from sites in Hudson Valley, NY (2014-2017 and stored frozen) with corresponding habitat and survival data for FGM analysis by comparing FGM concentrations to habitat features, presence of eastern cottontail, and survival. FGM concentrations of NEC

were higher in sites with higher eastern cottontail prevalence except in preferred, mid-successional shrublands, where FGMs were unaffected by eastern cottontail prevalence. NEC typically occupy mid-successional shrublands, as these habitats contain abundant preferred resources such as available forage and intermediate canopy closure, thereby ameliorating any effects of resource competition with eastern cottontails. Our findings are supported by existing literature proposing the use of FGMs as a non-invasive tool to quantify how environment shapes physiological health and that competitive stress can be ameliorated in preferred habitats.

112: The role of pre-hibernation body condition in hibernation expression in Canadian black-tailed prairie dogs

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During hibernation, individuals enter recurring bouts of multiday torpor where metabolism and body temperature (Tb) decrease below euthermic levels. In between bouts of torpor, individuals enter arousal bouts where metabolism and Tb return to their euthermic levels. While torpor use offers energetic benefits, its use is associated with physiological costs. As a result, hibernation expression is thought to be influenced by an individual's energetic state prior to hibernation ('hibernation optimization hypothesis'). We tested the hibernation optimization hypothesis in adult Canadian black-tailed prairie dogs (*Cynomys ludovicianus)* by investigating the role of pre-hibernation body condition (BC) on hibernation expression. Across three hibernation years, we measured prairie dog BC prior to the onset of hibernation and surgically implanted temperature-sensitive data loggers to quantify hibernation expression over winter. In one hibernation year, we experimentally expanded variation in pre-hibernation BC by supplementally feeding a subset of prairie dogs. Results indicate that prairie dogs in better pre-hibernation BC spend proportionally less time in torpor and utilize longer periods of arousal but do not adjust the number of torpor bouts used or the duration of the hibernation season. Identifying factors that influence hibernation expression can inform our understanding of if and how hibernators will respond to changing environmental conditions. More specifically, investigating the role of body condition can inform our predictions of how species will be affected by changes in resource abundance.

113: Allometry, ecology, and distribution in western North American chipmunks

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The speciose clade of western North American chipmunks (*Neotamias* spp.) is noted for many species pairs having parapatric distributions, with aggressive, interspecific territorial conflicts defining the contact zones. Many aspects of a species' ecology scale to body size, and similarity of ecological niche may prevent sympatry between species within a guild. Therefore, body-size similarity should be greater than expected by chance in parapatric species pairs, and body-size dissimilarity should be greater than expected by chance in sympatric pairs. We used body lengths from 3086 museum specimens representing 44 taxa (21 species and 23 additional subspecies of 5 polytypic species) of *Neotamias* to test these hypotheses. We constructed a null set by randomly sampling from the 1007 mean body-length differences between possible interspecific pairs of taxa. The 33 interspecific pairs that were parapatric were highly significantly more similar in body length than expected by chance, whereas the 32 pairs that were sympatric were marginally significantly more different in body length than expected by chance. Strong support of the parapatry-allometry hypothesis confirms the likely importance of competitive exclusion. Weaker support of the sympatry-allometry hypothesis may be due to finer scale division of heterogeneous niche space—including microhabitat and dietary niche, and three-dimensional partitioning of habitat space—by chipmunk species that are to a degree allotopic while being broadly sympatric.

114: Distribution and disease surveys of nine-banded armadillo in Tennessee using roadkill and community science data

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Nine-banded armadillo (*Dasypus novemcinctus*) sightings continue to increase in quantity and range throughout middle and east Tennessee. We are using community science data collected from 2008 - 2021 to learn more about this adaptable, semi-fossorial mammal. These data plus recent roadkill surveys are being assessed in various geospatial models that integrate soil types, land use, and climate data to determine which environmental factors may most strongly influence armadillo presence and distribution. Specifically, we are creating Species Distribution Models (SDM) that incorporate climate patterns to better understand how this aligns with the expanding range of the nine-banded armadillo in Tennessee over time. We predict that climate patterns involving less-harsh winters will be one of the main factors allowing nine-banded armadillos to expand their range. Supplemental data from camera traps, used for monitoring the behavior of armadillos at active burrow sites throughout the winter, are also being used to evaluate the effect of temperatures on armadillo activity. As part of our roadkill surveys to monitor for the presence of armadillos, blood samples from deceased armadillos are being collected and tested for Hansen's disease (leprosy). No seropositive individuals have been detected in middle or east Tennessee so far (n = 25), but in order to have stronger results we plan on gathering at least thirty more samples from a broader range of sites in 2022.

115: Can niche overlap help select chipmunk hosts as predictors of pinworm and lice distribution models?

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The number of methods for integrating biotic interactions into species distribution models (SDMs) has grown following increased recognition of the role these interactions play in shaping species distributions. Yet, for parasites, whose survival, reproduction, and dispersal are strongly dependent on host species, such interactions are rarely considered. Moreover, frameworks to select which host species could serve as biotic predictors in parasite SDMs do not currently exist. We assessed if parasite-host niche overlap metrics can inform which host species could be used as predictor variables, along with climatic data, in parasite distribution models. We focused on two parasite species associated with western North American chipmunks (*Neotamias*), *Heteroxynema cucullatum* (pinworm) and *Hopolopleura arboricola* (sucking louse) and the five host species most frequently parasitized by each parasite. Parasites were obtained from recently collected chipmunks, with additional louse records gathered from museum specimens. We evaluated niche similarity and equivalency in environmental space for every parasite-host pair. Additionally, we estimated distributional overlap between parasite-host pairs based on Maxent models. Preliminary findings suggest that the distributions of these parasite species may be largely shaped by a few widely distributed hosts with niches that are similar to their own. Furthermore, distributional patterns indicate potential changes in host associations across the parasites' ranges. Future directions include determining the role of host diversity and identity in shaping parasite distributions.

116: Discovering diversity: a new center of mammalian endemism on Mindanao Island, Philippines

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The current upsurge in the number of mammal species recognized is taking place in substantial part due to discovery of previously unknown species, often resulting from focused, conceptually-driven field surveys. For example, forty-one previously unknown species of mammals have been described from the Philippines since 2002, the majority as a result of biogeographically targeted field surveys on Luzon Island, where each isolated mountain range has a set of locally endemic montane species. Mindanao Island is similar to Luzon in area (ca. 98,000 km^2), topography (up to 3,000 m), and geological history, but political unrest, isolation, and limited field surveys kept our knowledge of the native non-volant mammals mostly restricted to a few mountains in central Mindanao. Our recent studies have now identified the mountains of southeastern Mindanao (Mts. Hamiguitan and Kampalili) as a previously unknown center of mammalian endemism, with at least four new locally endemic species. Data on degree of isolation and maximum elevation lead us to predict that additional new species will be found on those mountains, and we identify eight additional mountains on Mindanao where we predict many additional locally endemic species will be found.

117: Patterns of genetic and phenotypic divergence across the Isthmus of Kra

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Sundaland and Indochina are two biodiversity hotspots and biogeographic subregions separated by a transition from rainforest to more seasonal forest along the Thai-Malay peninsula, near the Isthmus of Kra (IOK). This biogeographic break has been defined based on the distributional limits of many taxa. However, some species do not follow such general patterns and are distributed both north and south of IOK. In this study, we combine molecular and morphological evidence collected from museum specimens to assess if the pattern observed in species distributions (turnover at the IOK) is mirrored within the genetic and phenotypic structure of three species of squirrels (*Callosciurus caniceps*, *Dremomys rufigenis* and *Tamiops mcclellandii*) and one gymnure (*Hylomys suillus*) that are distributed across this biogeographic break and have different ecological requirements. The four species showed genetic structure and phenotypic variation geographically consistent with IOK. These findings suggest that the pattern observed in the distributions of so many species are mirrored in others at the intraspecific level, or that some of these widespread species might represent multiple species with distribution boundaries in IOK. Finally, high levels of genetic and phenotypic divergence were also confirmed within Indochina in *Dremomys rufigenis* and *Tamiops mcclellandii*, and in Sundaland in *Hylomys suillus*.

118: History of small mammal community assembly and diversification across the Great Plains suture zone

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The Great Plains, encompassing the middle third of North America generally lacks physical barriers and supports mammal faunas from both western and eastern communities at the peripheries of their ranges. Diverse species origins and a lack of geographic complexity in this region presents a novel system for diagnosing both evolutionary histories and community assembly of Great Plains mammals. We couple comparative phylogeography with ecological niche models to investigate the evolutionary history of ten small mammal species that are currently co-distributed across the Great Plains. We assess (1) intraspecific diversification across the Great Plains, (2) congruence of species histories considering western versus eastern origins, and (3) the location of regional biodiversity hotspots for both historic and emerging eco-evolutionary interactions. Bayesian phylogenies were estimated from mitochondrial DNA, and Last Glacial Maximum (LGM) niche models were estimated using bioclimatic layers. Intra-specific phylogeographic breaks based on current distributions showed broad-scale clustering in the southern Great Plains for both eastern and western species. LGM niche models showed that Great Plains small mammals occupied either distinct southeast or southwest refugia, but with a region of contact between eastern and western assemblages maintained in the southern Great Plains. The combined evidence strongly suggests that the southern Great Plains is a suture-zone and hotspot for both diversification within species, and long-term interactions among distinct communities, despite a lack of distinct geographic barriers.

119: Interstate 40 as the northern limit of Mexican wolf recovery

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Wildlife are commonly managed within administrative boundaries. Recovery of a controversial carnivore on a human-dominated landscape cannot happen without geographic limits and those limits are likely to be roads or other well-defined boundaries. The northern boundary of Mexican wolf recovery has been repeatedly expanded northward from their historical range. Defining I-40 as the northern boundary was yet another extension to include the historical overlap with larger northern wolves. Ecological niche models identified environmental conditions consistent with those under which Mexican wolves naturally existed and found very little similar habitat north of I-40. Assertions that I-40 is an arbitrary line drawn through the middle of Mexican wolf habitat, or that habitat north of I-40 is necessary for recovery, are completely lacking in scientific support. The state-of-the-art peer-reviewed habitat analysis in the recovery plan showed Mexico has more than 64,000 km^2 of high-quality wolf habitat. Rules associated with 10(j) populations prohibit recovering Mexican wolves north of historical range unless habitat in Mexico is unsuitable. The real question is not whether wolves can live north of I-40, it is whether that area is needed for recovery. It is not. Recovery north of I-40 is not only prohibited, but unnecessary and would be inconsistent with the ESA because we would have to ignore a significant (90%) portion of their historical range in Mexico.

120: A multivariate approach to assessing landscape structure effects on wildlife crossing use

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Globally, wildlife crossing structures (WCS) are constructed to help improve connectivity and reduce wildlife-road mortality. The use of WCS may be affected by the 3D structure of vegetation in the surrounding landscape. We computed seven metrics of horizontal woody cover structure (percent land cover, patch density, edge density, mean patch area, largest patch index, aggregation index, and Euclidean nearest neighbor distance) from a classified 1-m resolution aerial image in 1-km buffers around 14 wildlife crossing structures in Cameron County and 14 random locations in nearby habitat. We estimated vegetation density at five different heights above the ground from classified light detection and ranging (LiDAR) point clouds within each buffer. We then used permutational multivariate analysis of variance to compare the vegetation structure around wildlife crossings to the surrounding landscape. To assess how landscape structure affects wildlife crossing use, we used camera traps to identify bobcat (*Lynx rufus*) presence at each WCS location. We used a generalized linear mixed model to assess how bobcat detections were related to landscape structure and internal vegetation structure. The landscape structure at WCS did not differ from the surrounding landscape and bobcat use of WCS increased with increasing dense woody cover in the surrounding landscape. We show that by combining landscape metrics into a measure of landscape structure, we can more effectively assess how landcover patterns impact wildlife.

121: Ecology and conservation genetics of the Galapagos bats

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Globally, bats face many conservation challenges including habitat destruction, invasive species, and climate change. Island species face additional challenges including smaller population sizes, lower genetic diversity, and a highly stochastic environment. Despite being located in a charismatic and heavily-studied system, the two bat species found in the Galapagos Islands—the red bat (*Lasiurus blossevillii brachyotis*) and hoary bat (*L. villosissimus*)—have rarely been studied. Currently, we know little about the colonization history, taxonomic status, population trends, distribution, or genetic health of the Galapagos bat populations. First, we are using Sanger sequences of one mitochondrial and one nuclear gene to generate preliminary data about taxonomic relationships, genetic diversity, and gene flow of the Galapagos bat populations. Second, we are using acoustic monitoring data and an occupancy modeling framework to evaluate whether factors such as season, elevation, and habitat type influence bat distribution on Santa Cruz island, Galapagos. Our preliminary results from genetic data suggest Galapagos bat populations may be genetically distinct enough to be considered separate species. Preliminary data from captures and acoustic monitoring suggest that hoary bats are more broadly distributed than red bats. This project will generate baseline data about the taxonomic status, habitat use, distribution, and genetic health of the Galapagos bat populations. We will use this information to create a data-informed bat monitoring and management plan in collaboration with Galapagos National Park.

122: Wildlife Insights as a platform to manage threatened species in Palawan, Philippines.

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The Philippines, as one of the 17 megadiverse countries in the world, is characterized by high species richness and endemism in flora and fauna. It is also a hotspot for the illegal wildlife trade, being a source, transit point, and end destination for illegally traded species. Palawan, an island once connected to Borneo and still containing large tracts of native forest, contains unique mammal assemblages. In 2019, we conducted a series of workshops in Puerto Princesa, Palawan to train park guards and community conservation representatives, with the goal of building local capacity to measure and monitor species in three protected areas; Puerto Princesa Subterranean River National Park, El Nido-Taytay Managed Resource Protected Area, and Mt. Mantalingahan Protected Landscape. Camera traps were deployed sequentially across three target protected areas between December 2019 and August 2020. During this project, 12 species of birds (one domestic), 13 species of mammals (two domestic), and one large reptile species (common water monitor) were recorded, with at least one new mammal record. Considering the challenges faced logistically and due to COVID-19 restrictions, this project has been incredibly effective at documenting the rare and unique fauna of Palawan Island. The results of this project demonstrate both how diverse the islands fauna still is and how international collaborations can benefit local knowledge and capacity to conduct research and monitor wildlife.

123: The shot heard round the forest: revolutionizing jaguar protection via gunshot detection in Costa Rica

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Poaching is one of the largest threats facing remaining jaguar (*Panthera onca*) in Costa Rica. Whether it is for trophy, the illegal trade of jaguar parts, retaliatory killing, or optimistic hunting, poaching is especially problematic in La Amistad International Peace Park in southeastern Costa Rica. La Amistad contains some of the only contiguous primary and secondary forest in the region and supports very high levels of biodiversity. Managers often detail the difficulties of (a) being informed of illegal hunting, (b) determining where the gunshots originated from, and (c) deploying park officials to the location fast enough. To support park officials in their fight against illegal take, we have developed an acoustic network to detect gunshots and immediately report this information back to park headquarters. In May 2022, we tested version 2 of our gunshot detection program with four gateways and 20 nodes along the south-western park border. The nodes are solar powered and listen for the subsonic frequency gunshots emit. Once detected, it sends a signal via LoRa technology back to the gateway. The gateway then communicates with the Internet of Things (IoT) to alert park officials of the location the gunshot was fired. Future applications for this technology include acoustic identification of specific species, adding camera technology onto the LoRa network to identify wildlife and potentially poachers, and expanding the network to different landscapes.

124: Islands as Breeding Colonies for Conserving a Threatened Small Mammal

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Lagomorphs have a long history of being translocated to islands by people, usually for hunting and consumption. More rarely, islands have been used to help conserve species by establishing insurance populations. The New England cottontail (NEC, *Sylvilagus transitionalis*) is a species of conservation concern in the Northeastern United States and the focus of a large-scale collaborative research program. Since 2012, state and federal biologists have translocated animals to establish two NEC populations: on Patience Island (PI), Rhode Island and on Nomans Land Island (NLI), Massachusetts. We have used VHF/GPS radio collars and genetic analyses to estimate their survival, population size, gender ratio, and genetic diversity over time. Preliminary findings suggest a slightly reduced survival post translocation and relatively stable population sizes with minimal decrease in genetic diversity over time. The PI population has been intensively monitored over the past decade and has already served as a source population to seed mainland release sites. Our goal is to maximize the number of NEC translocated from PI without causing a detrimental decline in their population size or genetic diversity. The NLI population is still in the early stage of population establishment, but hopefully will serve as a source population for mainland sites in the future. Islands have played a critical role and will continue to serve as an essential component in helping to conserve New England cottontail.

125: Convergent evolution of *Peromyscus* mice in response to hypoxia

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Understanding the mechanisms of adaptation to novel environments is a crucial step towards predicting how species will respond to climate change. In particular, studies of convergence, the independent evolution of similar traits, can help to explain the extent of repeatability and predictability of evolution when facing novel challenges. However, quantification of convergence has been difficult due to the complexity of intersecting genetic and physiological pathways. Here, we combined transcriptomic analyses with whole organism performance of six species of laboratory raised Peromyscus mice, whose elevational range spans nearly all of North America. Our goal was to examine convergent solutions to the problem of low O2 availability (hypoxia) at extreme elevations. To do this, we acclimated mice to hypobaric hypoxia (1,000, 3,000 and 4,500 m above sea level) for six weeks, after which we measured maximal oxygen consumption (VO2max) during cold exposure, and sequenced skeletal muscle transcriptomes, as skeletal muscles play a well-defined role in aerobic performance at altitude. In a phylogenetically informed framework, we compared gene expression profiles across species and acclimation treatments. Differentially expressed genes could be categorized broadly as: (1) those with highly conserved acclimation effects, but no evolved differences; (2) those constitutively differentiated between highland vs. lowland natives; or (3) those showing species-by-acclimation interactions. Our data yield insight into the molecular and physiological mechanisms that allow mammals to repeatedly colonize extreme, high-altitude environments.

126: The mystery of mouse graveyards on the summits of >6000 m Andean volcanoes

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Understanding the factors that influence range limits of animal species is a longstanding goal in evolution and ecology, and has added significance in the context of global climate change. In the most mountainous regions of the planet – where potential elevational range limits are the highest – the upper limits of species' ranges are often poorly demarcated due to a paucity of survey data. During the past two years we have conducted mountaineering mammal surveys in the Central Andes that have yielded live-trapping records of mice (*Phyllotis* and *Abrothrix*) at extraordinarily high elevations (5800-6740 m [=~19,000-22,100']), far exceeding all previous specimen-based records for mammals. In addition to live-trapping records, we have also discovered mouse graveyards (collections of desiccated cadavers and skeletal remains) on the summits of several >6000 m volcanoes in the Puna de Atacama (Chile-Argentina). Here we report an investigation into this mysterious phenomenon using genomic analysis and radiocarbon dating of high-elevation mouse 'mummies'.

127: Revisiting the invasion conundrum with genomic simulations: hippopotami invasion to Colombia as a case study

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Commonly introduced with few individuals, invasive species are expected to face a loss of genetic variation, inbreeding depression, and reduced evolutionary potential. Nevertheless, they are often able to establish and thrive in their new location. This conundrum has captivated researchers for decades, with several explanations advanced to explain it. These explanations include both demographic processes (e.g., genetic rescue by recurrent introductions) and selective forces (e.g., selection against homozygous individuals). However, empirical support for either of these processes that increase the population viability during the establishment period has been elusive. Using the relatively recent introduction of hippos into Colombia as a model system, here we test the hypothesis of whether balancing selection in the introduced range could maintain relevant genetic variation associated with traits of ecological importance. Specifically, we generate synthetic population genomics data using the software SLiM3 to test if genetic diversity at loci under varying degrees of balancing selection can be maintained despite overall heterozygosity loss elsewhere in the genome. We carry out our simulations mimicking the known introduction history of Colombian hippos under three alternative evolutionary scenarios: neutrality (no selection), overdominance (heterozygotes at selected loci have higher fitness than homozygotes), and negative frequency-dependent selection (rare variants at selected loci.

128: Experimental diet manipulation reveals differential gene expression in two species of woodrat

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Revealing the genetic basis of herbivore tolerance to plant toxins has implications for our understanding of antagonistic coevolution, community ecology, and herbivore conservation. Throughout their range, woodrats (genus *Neotoma*) are known to consume a variety of plants and harbor unique mechanisms for the metabolism of toxic plant secondary compounds (PSCs). We studied two species of woodrats that are ecologically segregated and maintain distinct diets, but hybridize, across a sharp ecotone. *Neotoma bryanti* (Bryant's woodrat) consumes *Frangula californica* (California coffeeberry) and *N. lepida* (desert woodrat) consumes *Prunus fasciculata* (desert almond); both plants are known to produce toxic PSCs. We prepared experimental diets with extract from either plant, and measured woodrat response to their native and non-native diets. To quantify metabolic response to these diets, we measured differential gene expression in liver tissue. Of the nearly 1600 differentially expressed genes, 16 exhibited a diet effect and were associated with loci involved in detoxification. Four genes exhibited a significant species by diet effect, including a sulfurtransferase known to be involved in cyanide metabolism in other mammalian species. These findings highlight possible differential dietary adaptations that may play a role in shaping hybrid zone dynamics between these two woodrat species. Furthermore, such dietary adaptations may be critical to the persistence of mammalian herbivore populations as they respond to environmental change.

129: Body size within fossil and extant Ailurinae (red pandas): Herbivory does not equal small size

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Fossil red pandas (Ailuridae: Carnivora) are larger than the extant *Ailurus fulgens*. However, the body size transition has not been investigated phylogenetically, through time, or based on diet. Therefore, using standard methods/equations for fossil carnivorans, body mass was estimated for the subfamily Ailurinae (and one basal Ailurid, *Simocyon*), and mapped on phylogeny. Results suggest that smaller body size is not positively correlated with time or a more herbivorous diet; some more derived taxa (exhibiting more complex teeth for processing vegetation) being larger in body size than basal (teeth less derived = retaining a carnivorous/omnivorous diet) forms. Specifically, within the tribe Pristinailurini, tooth complexity and body size actually increase through time. Additionally, the two North American taxa are smaller than their Old

World counterparts (yet all larger than extant *Ailurus*). Within the tribe Ailurini, increased tooth complexity and body size are inversely correlated through time; with extant *Ailurus* representing the smallest member of the subfamily. Several Pleistocene forms (reported as *Ailurus fulgens*) are larger than extant *Ailurus*; supporting the body size decrease within Ailurini. Results reported here, coupled with recent reconstructions of the best-known fossil ailurine, *Pristinailurus bristoli*, as a puma-like omnivore (similar to the larger carnivorous *Simocyon*), suggest that the small size and arboreal body proportions of the extant *Ailurus* are likely not coupled to its herbivorous diet, but instead unique to the taxon.

130: Metagenomic surveillance of zoonoses and their wildlife hosts in the south-central United States

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Typically little is known about the zoonotic load of most ecosystems. Information is often gathered about a particular zoonotic agent as it emerges and poses a risk to humans. However, in most cases, we have a paucity of data concerning the number of potential pathogens that occupy a specific locality or region, or are associated with a variety of host species. To better predict and evaluate zoonotic outbreaks that may adversely impact wildlife populations, we developed a comprehensive multi-level surveillance approach to sample mammal host species from a variety of ecosystems across the south-central United States. Here, we identified multiple, novel zoonotic agents from a metagenomic analysis of samples from *Peromyscus attwateri* collected from the Junction, Texas area between 1994 and 2019. Thus far, we detected novel variants of the viral Family Herpesviridae, Poxviridae, Coronaviridae, and Mammarenaviridae. Though preliminary, this study represents a research model that can be developed into an “early-warning” system for staying one step ahead of zoonotic outbreaks.

131: Field work, field stations, and the accessible field experience

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For many biologists, geologists, and environmental scientists, field work is an integral component of their professional and personal lives. Despite the proven value of nature-based experiences, there are many barriers to field work. Access to the field has been increasingly curtailed during COVID times—on-line classes, travel restrictions, and a drastic loss of revenues and personnel support to field stations. Innovative responses include NSF-funded programs such as The Virtual Field of OBFS (Organization of Biological Field Stations) and OCELOTS (Online Content for Experiential Learning Of Tropical Systems), as well as academic arrangements through OTS (Organization for Tropical Studies) to pair interns virtually with scientists in Costa Rica and South Africa. As courses and researchers return to field sites and field stations, it is critical to ensure that access to the field experience embodies principles of diversity, equity, inclusivity, and justice in the US and internationally more than previously. The full range of options includes community science, international collaborations, fellowships for underrepresented students, and the use of urban green spaces, zoos, and museums. The value of the field experience applies not only to academic and professional scientists, but to other groups such as children and decision makers from government and industry. Accessible nature-based experiences will do much to create members of the global community who can respond effectively and creatively to current environmental challenges world-wide.

132: Threats and shortfalls in mammalian conservation on a changing planet

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Mammals are key components of terrestrial and marine ecosystems, and they serve critical roles in all aspects of ecosystem function. Mammals face multiple severe threats to their existence from habitat loss and fragmentation, overexploitation, disease, and climate change. These factors interact, resulting in declining populations, changing species composition, loss of large mammals, and local to global extinction. National and international programs, like the US Endangered Species Act, gather data on the threats and status of species to feed into legislation, and conventions and agencies that focus on conservation policy. There remain severe shortfalls in the availability of data, something that mammalogists must address. The IUCN Red List influences the decisions of major international conventions, including the Convention on Biological Diversity, yet struggles to maintain assessments current. Given the pace of environmental change, recent knowledge is essential to the complex world of national and international policy and funding mechanisms, complicating the bridge from science to policy. The planet is in ecological, technological, socioeconomic, and political transformation. Our baseline for restoration and recovery is a quickly moving target and the composition of both ecosystems and mammalian communities are in constant flux. New technologies offer novel but highly controversial solutions, and the demographic and social changes afoot will influence policies into the future. I see a growing need for scientifically informed activism if we are to save mammals.

133: Understanding variation in topical bat communities: gradient, landscape, and metacommunity perspectives

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A fundamental goal of ecology is to characterize the assembly of species into communities, and to understand the environmental characteristics that lead to the emergent structure of metacommunities. Because of their high local biodiversity based on abundance, phylogeny, and function, tropical bats represent an ideal group for exploring such ecological phenomena. I provide a broad overview of metacommunity structure and the processes that mold it. Then, I review the effects of various environmental characteristics on bat species distributions along gradients in the New World. Differences in the elevational distribution of bats in the Andes, unlike that of rodents and birds, lead to a nested metacommunity structure, likely resulting from species-specific tolerances to cold temperatures and resource availability. In the highly fragmented landscape of the Caribbean Lowlands of Costa Rica, metacommunity structure is guild- and season-specific: Gleasonian in the dry season and Clementsian in the wet season for frugivores, and random in the dry season and in the wet season for gleaning animalivores. Metacommunity structure on Caribbean islands depends on guild and island group. For herbivores, structure is random in the Bahamas and Clementsian in the Lesser and Greater Antilles; for carnivores, structure is nested in the Greater Antilles and Clementsian in the Bahamas and Lesser Antilles. Generally, endemic species do not greatly affect those structures regardless of guild and island group.

134: Unusually large upward shifts in cold-adapted, montane mammals as temperature warms

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The Rocky Mountains have warmed considerably due to anthropogenic climate change. Herein we examine how 47 mammal elevational ranges (27 rodents, 4 shrews) have changed their historical distributions (1886–1979) to their contemporary distributions (post–2005) along 2400 m elevational gradients on two Colorado mountains. Historical elevational ranges were based on geo-referenced museum and publication records. Contemporary elevational ranges were based on systematic field sampling and museum specimens. We constructed Bayesian models to estimate the probability a species was present, but undetected, due to undersampling at each 50 m elevational bin for each time period and mountain range. These models leveraged individual-level detection probabilities, the number and patchiness of detections across 50 m bands of elevation, and a decaying likelihood of presence from last known detections. We compared 95% likelihood elevational ranges between historical and contemporary time periods to detect directional change. Responses were variable as 26 mammal ranges changed upward, 6 did not change, 11 changed downward, and 4 were extirpated locally. The average range shift was 131 m upward, while exclusively montane species shifted upward more often (75%) and displayed larger average range shifts (346 m). The best predictors of upper limit and total directional change were species with higher maximum latitude in their geographic range, montane affiliation, and the study mountain was at the southern edge of their geographic range.

135: Reflections of Grinnellian and Eltonian niches on distribution of phyllostomid bats in Atlantic Forest

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Ecological niches are complex and result from interactions with both biotic and abiotic components of the environment. One recent distinction is between Grinnellian niche characteristics that reflect influences at large spatial scales such as climate and Eltonian niche characteristics that reflect influences at the local level such as distribution of resources and their allocation among species. I estimated Grinnellian and Eltonian niche characteristics of phyllostomid bats distributed throughout the Atlantic Forest, examined degree of phylogenetic non-independence of distribution and niche characteristics, and estimated relative contributions of niche characteristics to distribution across this large Neotropical region. Phylogenetic signal was weak for Grinnellian and strong for Eltonian niche characteristics. Both suites accounted for significant unique variation in distribution of phyllostomid bats in Atlantic Forest. Grinnellian niche characteristics accounted for more than five times the variation in distribution than Eltonian characteristics. Distinct Grinnellian and Eltonian perspectives on the niche provide valuable insights into the distribution of species. Indeed, diets and environmental tolerances are important constituents of ecological niches and have significant effects on distribution of species. For bats in Atlantic Forest, how species respond to the relatively long environmental gradients experienced there may be more important to distribution than does their responses to spatial variation in dietary resources.

136: Elevational patterns of the seven forms of rarity in small mammals

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The seven forms of rarity have framed much of the work on rare species. Rabinowitz (1981) developed a framework that dichotomizes three components of rarity: geographic range size, local abundance, and habitat specificity. In this framework a species is classified as rare or common in each of these three components, resulting in eight forms: seven forms of rarity and one form of commonness. Distinguishing between the different forms of rarity has most commonly been motivated by a desire to assess species vulnerability, but the local composition of species in these forms may have meaningful implications for coexistence and biodiversity. Here, we explored regional and local patterns of the seven forms of rarity in small mammals (rodents, shrews) at 32 sites on four elevational gradients in two mountain ranges in Colorado. First, we examined the regional (mountain range) composition of species in these eight forms by calculating the elevational range size, maximum local abundance, and habitat specificity for each species. Then, to assess differences in rarity composition among sites based on species richness, we examined the local composition of species in regional rarity forms. In both mountain ranges, the regional composition of species rarity forms did not differ substantially from null expectation, but local compositions of these eight forms varied greatly among sites. Scale differences in rarity have important implications for assembly of biodiversity across space.

137: Diversity, biogeography, and evolution of Sulawesi?s remarkable shrew fauna

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After nearly a decade of small mammal inventories on Sulawesi, a large island in the Wallacean biogeographic zone of central Indonesia, we described 14 new species of shrews. In total Sulawesi is home to 21 species of *Crocidura* (Soricidae), all but one of which are members of an endemic radiation. Although this shrew fauna has evolved in just a few million years, it is far richer than any other insular shrew fauna. Using their phylogenetic relationships and geographic distributions, we will discuss the completeness of our taxonomic assessment, local-scale patterns of morphological diversity and species richness, and plausible mechanisms of diversification.

138: Unpacking patterns in mammal functional and phylogenetic diversity in the Anthropocene

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Patterns in functional and phylogenetic diversity reflect ecological and evolutionary relationships among taxa, and thus can offer insights into mechanisms behind species distribution and community structure.

Anthropogenic impacts have strongly altered modern species distributions, yet these effects are largely ignored when characterizing large scale patterns in biodiversity, potentially skewing our understanding of their underlying mechanisms. Here, we investigated global patterns in mammalian functional and phylogenetic diversity using current ranges as well as estimated present natural ranges in the absence of anthropogenic influence. We used the PHYLACINE 1.2 dataset to generate species lists for 91x91 km grid cells under both scenarios. We then measured mean pairwise distances and mean nearest neighbor distances in phylogenetic and functional space for each regional community, as well as the ratio of functional to phylogenetic distance between species pairs. Results were compared to a null model to tease out significant drivers of community assembly across latitude. We find that harsher environments such as deserts and tundra exhibit lower mean functional distance, potentially indicating environmental filtering. However, nearest functional neighbor distances are often greater than expected, which implies farther spacing between species within functional space, despite lower community-wide functional breadth. Patterns in functional and phylogenetic diversity are largely similar under present natural ranges except in the New World, suggesting the impact of historic and pre-historic biodiversity decline is greatest in these regions.

139: High elevation-specialist mammal species weigh more than their relatives down the mountain in Eastern Africa

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We collected non-volant small mammals from four sites (2900, 3250, 3600, and 4000 m a.s.l.) along the western slope of the Simien Mountains in Ethiopia. Over a four-week period we recorded 13 species, 10 of which shared a genus with another species (five species "pairs"). Although not initially included as one of the objectives of our study, we found a correlation between elevation and body weight among congeners. For each of the five genera represented by two species (*Crocidura*, *Dendromus*, *Mus*, *Otomys*, and *Stenocephalemys*), the highest average weight consistently belonged to that of the higher elevation sister. Rupp and Yalden & Largen had also noticed this elevational arrangement of Ethiopian endemic mammals, a pattern which may be explained by Bergmann's *initial* rule (i.e. *interspecific* variation in body size), but as a function of elevation instead of latitude as it is classically defined. While numerous studies have investigated the merits of Bergmann's Rule intraspecifically within mammals by latitude, few have by elevation, but none so far have tested the prediction between closely related taxa as it relates to elevation. Our preliminary findings suggest that this pattern may not be restricted to Ethiopian endemics, as consistency has been found among congeners on other prominent mountains in the region as well.

140: Tricolored bat microsite use changes in response to white-nose syndrome

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Although tricolored bats (*Perimyotis subflavus*) have experienced significant declines due to white-nose syndrome (WNS), little research has been conducted on their responses to the disease. Our objective was to document tricolored bat roost site use pre- and post-WNS and relate it to microsite temperatures, ambient conditions, and population trends. We censused a tricolored bat hibernaculum in northwestern South Carolina each year in late February 2014-2020 and monthly during 2020-21 and 2021-22, and recorded species, section of the tunnel, distance from the entrance, and wall temperature next to each bat. The number of tricolored bats in the hibernaculum dropped by 90.3% during the first three years after the arrival of WNS, then stabilized and increased from 2018 to 2022. Prior to the arrival of WNS, 95.6% of tricolored bats roosted in the back, warmest portion of the tunnel. Post-WNS we observed a significant increase in the number and proportion of bats using the front, colder portions of the tunnel, particularly during the period of population stabilization and increase. Monthly censuses demonstrated bats used the front portion of the tunnel throughout the hibernation season. Our results suggest that greater use of the colder sections of the tunnel by tricolored bats may have led to increased survival. Thus, management actions that provide cold hibernacula may be an option for long term management of bats, particularly in southern regions.

141: Two shakes of a mouse's tail: swimming kinematics of salt marsh harvest mice (*Reithrodontomys raviventris*)

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The endangered salt marsh harvest mouse occupies the brackish marshes of the San Francisco Bay estuary, where it is subjected to natural tidal and managed flooding regimes. Previous radiotelemetry work has indicated that mice tend to remain in their habitats despite flooding. Of particular interest is whether salt marsh harvest mice possess specialized swimming capabilities that allow them to tolerate such periods of tidal inundation. We conducted controlled swimming trials to compare the swimming performance of salt marsh harvest mice to other co-occurring rodents in the Suisun Marsh. We digitized high-speed videos of voluntary swimming behavior to obtain estimates of a range of kinematic variables typically used to evaluate swimming performance in aquatic and marine mammals, focusing on the use of the tail, to uncover the functional significance of their relatively long tails compared to coexisting congeneric western harvest mice. Our preliminary results reveal kinematic differences among species, primarily in body pitch angle, tail tip cycle frequency, tail wave amplitude, trailing edge lateral velocity, and wave speed, reflecting differences in their efficiencies for moving through the water. Furthermore, tail trailing edge velocity increases with increasing tail length across species, suggesting a functional link between tail length and speed. These data may help explain differences in microhabitat use among species, based on differences in their locomotor capabilities.

142: Comparative hearing of vocal rodents

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Comparative studies are critical for understanding ecological and evolutionary principles that give rise to the diversity of mammalian communication systems. The matched-filter hypothesis predicts a correspondence between tuning of the auditory system and properties of species-specific vocalizations. Cricetid rodents are emerging as important models for studying the interaction of hearing and vocal production. We evaluated predictions of the matched-filter hypothesis in six cricetid rodents (*Baiomys*, *Neotoma*, *Onychomys*, *Peromyscus*, *Reithrodontomys*, *Scotinomys*) by comparing properties of social vocalizations with hearing abilities derived from auditory brainstem responses. In general, cricetid rodents produced a diverse repertoire of low- and high-frequency vocalizations. Low frequency (< 20 kHz) vocalizations primarily served as long-distance advertisement signals, whereas high frequency (> 20 kHz) vocalizations were used in close-distance social interactions. All species were able to hear tones between 8-42 kHz, with a broad range of hearing sensitivity that overlapped frequencies of long-distance vocalizations. However, we found a positive association between center hearing frequency and peak frequencies of long-distance vocalizations. Our findings suggest that the peripheral auditory system of cricetid rodents is tuned to their long-distance communication signals, highlighting the importance of communication signals in shaping trait diversity.

143: Characterization and discrimination of the ultrasonic calls of northern and southern flying squirrels

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Passive acoustic monitoring has been used for field identification of numerous species, but efforts to identify flying squirrels have had mixed success. Because *Glaucomys volans* and *G. sabrinus* are sympatric in some areas, and because traditional sampling methods are labor intensive and increase the risk of mortality, we evaluate several statistical models for identification of the ultrasonic calls of Glaucomys in general, and discrimination between *G. volans* and *G. sabrinus*. We use field and lab recordings of ultrasonic calls for both species. Field recordings for *G. sabrinus* are derived from work in the northwest, while those for *G. volans* were obtained in Missouri. Laboratory calls were obtained from colonies housed in an animal care facility. We obtained 4,193 *G. volans* calls and 14,577 *G. sabrinus* calls. Stepwise discriminate functions within SAS provided significant discrimination between species. We discuss extension of the models to scenarios where the two species are sympatric.

144: Sociospatial organization of nilgai antelope in south Texas

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Nilgai antelope (*Boselaphus tragocamelus*) are an exotic ungulate species with over 30,000 free-ranging individuals in South Texas. Although nilgai have been present in Texas for almost a century, there is little information on the movements, behaviors, and social interactions of nilgai. Recently, there has been increased interest in nilgai ecology due to their role as a competent host for cattle fever ticks (*Rhipicephalus (Boophilus) microplus* and *R. (B.) annulatus*), which can negatively affect the livestock industry. The goals of this study were to: 1) investigate the spatiotemporal overlap among nilgai dyads and 2) explore genetic structuring within the population. We used hourly locations of 40 GPS-collared nilgai to help understand the interaction of individuals with overlapping ranges. We analyzed dynamic interactions of 64 nilgai dyads that had ? 10% overlap. We observed dyads interacting closely for several days to weeks, followed by a multi-day or week separation, then interactions resumed. Our results indicated that nilgai have a loose social structure that changes throughout the year. Our genetic analysis revealed that female-female dyads with higher overlap were less likely to be related, while male-male dyads were generally more related regardless of overlap. The social interactions of nilgai can aid in the understanding of population dynamics, space use, and provide insight for disease management strategies.

145: Dispersal and exploratory movements infer early life-history processes in mule deer

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Mammalian space use is characterized by home ranges, where resource acquisition occurs, and sometimes territoriality. Occasionally, individuals depart home ranges exploring adjacent areas or dispersing from natal ranges to avoid inbreeding depression and competition. Juvenile fine-scale movement data is often lacking, and spatial drivers of mammals navigating unfamiliar landscapes are poorly understood. To further understand this mechanism, we GPS-collared 30 juvenile mule deer along the Canadian River in the Texas Panhandle and tested the hypothesis that dispersal is male-biased and seasonal, while exploratory movements are not. We identified excursion via net squared displacement to assign resident or non-resident status. We used velocity, duration, distance, and fidelity to categorize excursion movements as either exploratory or dispersal. Currently, 27% have exhibited excursion including 4 dispersals and 4 exploratory movements. Dispersals were male-biased at 75% and occurred mainly during the parturition season while exploratory movements were not seasonal or sex-biased. Mean dispersal and exploratory movement lengths were 33.64 ± 26.25 km (x ± SE) and 83.88 ± 40.80 km, respectively. Resident velocity averaged 116.50 ± 0.56 m/hr (x ± SE) compared to non-resident individuals at 130.68 m/hr ± 1.20 m/hr overall but 252.71 ± 28.04 m/hr during excursion movements. With 27% of our sample exhibiting movement away from natal ranges, our results support juvenile dispersal and exploratory excursions are important

146: The impact of oral rabies vaccination targeting raccoons across an urban gradient in Burlington, Vermont

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The raccoon variant of the rabies virus (RABV) is intensely managed in the eastern United States and Canada via distribution of oral rabies vaccine (ORV) baits. Understanding how ORV distribution impacts seroprevalence rates of rabies neutralizing antibodies (an index of population immunity) and case reduction in urban areas is critical for RABV elimination. In Burlington, Vermont, previous estimates of seroprevalence rates in raccoons (*Procyon lotor*) are below thresholds necessary for elimination. However, rabies cases are infrequent, suggesting that actual seroprevalence rates may be higher. Using raccoon capture data from twelve sites in the greater Burlington area in 2015–2017, we used a Bayesian multinomial N-mixture model to 1) estimate abundance, seroprevalence, and capture rates across the urban gradient, 2) understand what factors may explain low observed seroprevalence, and 3) make recommendations for improving ORV baiting strategies. Urban development classes varied significantly in abundance: high development sites had more raccoons than low development sites. However, there were no clear patterns in seroprevalence across development classes. Estimated seroprevalence increased with spatial coverage of ORV baits, but not bait density. Seroprevalence estimates were also lower in sites with a higher juvenile-to-adult ratio. These results suggest 1) rabies management plans must consider the spatial pattern of bait distribution, not just bait numbers, and 2) raccoon populations with proportionally more juveniles may require additional approaches to reach target seroprevalence rates.

147: Effectiveness of artificial ecological trap for mitigating chronic wasting disease in white-tailed deer (*Odocoileus virginianus*)

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Infectious disease is an increasing concern for mammal conservation. Addressing this concern requires novel strategies for reducing the likelihood of disease outbreak. One strategy which may reduce the likelihood of a Chronic Wasting Disease (CWD) outbreak in white-tailed deer (*Odocoileus virginianus*) populations is utilizing an artificial ecological trap (AET). An AET is an area which a species perceives as favorable but will actually decrease survival through greater harvest mortality. Our objective is to model the potential effectiveness of an AET in a habitat corridor connecting CWD positive populations in northeast Illinois and CWD negative populations in northwest Indiana. To test the effectiveness of an AET, we used an agent-based modeling framework, *Ov*CWD, to simulate a realistic white-tailed deer population. We then simulated the spread of CWD in the model deer population with and without the AET. Effectiveness of the AET was measured using demographic competence, CWD prevalence, and population size. Each scenario was simulated 100 times and all models were implemented using NetLogo version 6.2.2. Model explorations indicate that AET strategies can be assessed for their impact on the probability of CWD establishment in the regional deer population. Model-based assessments can provide valuable information on the potential effectiveness of an AET and other strategies for mitigating CWD in white-tailed deer prior to field implementation.

148: Modeling rodent-virus interactions in North America from different biodiversity dimensions using machine learning

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Understanding the eco-geographic ’rules’ of host-pathogen interactions is needed for developing fine-grained tools for predicting the risk of different wildlife pathogens being transmitted to humans (i.e., spillover risk). However, the expected host-host, host-environment, and host-pathogen interactions under different amounts of human disturbance remain poorly understood for reasons ranging from poor data quality to inappropriate models. Here we used machine learning to analyze how environmental, geographic, and phylogenetic variables influence the incidence of viral sharing in the Rodentia-to-Hantaviridae system. We show that this methodology is capable of providing reliable geospatial susceptibility predictions for this host-virus system, even when using a small amount of incidence data (e.g., 20% of information in a public database). This new analytical approach makes it possible to: (1) evaluate the probability of new potential hosts to different pathogens given the phylogenetic, geographic, and environmental distances of known host-pathogen interactions; and (2) generate risk assessment maps given the model outputs. We find that

hantavirus sharing among rodents is mostly affected by phylogenetic factors and by an interaction between phylogeny and geography, with environmental variables being of lesser importance. This work indicates that coevolutionary processes have largely driven the current pattern of hantavirus sharing, but also highlights large data gaps in the surveillance of hantaviruses in North America.

149: Suburban striped skunk behavior, contact networks and implications for rabies transmission

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Transmission and maintenance of zoonotic disease depends on how wildlife that harbor the disease interact. The striped skunk (*Mephitis mephitis*) is an important reservoir of the rabies virus, and we studied striped skunk behavior in suburban Flagstaff Arizona USA in the context of understanding dynamics of rabies in an area where there has been a recent host-shift of rabies from bats to skunks. Our studies demonstrated 1) the ecological potential for an alternate mode of rabies transmission via scavenging of dead bats by skunks, 2) the potential for inter- and intraspecies contacts and transmission near dens and roosts in human made structures and at sites where humans supplement food by providing bird feeders and pet food, and 3) potential maintenance of the disease through contacts between individual skunks via dynamic social networks that changed during winter due to den shifts by females and short-term visitation to female dens by males. Overall, our studies suggest several avenues for managing rabies in striped skunks, including focusing trap-vaccinate-release efforts at sites where humans provision food, and targeting vaccination during autumn to reduce the probability of disease maintenance through social contacts during winter.

150: Moving from hantavirus to tick-borne disease testing of NEON rodent blood samples

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The National Ecological Observatory Network (NEON) is an NSF-funded continental-scale observatory that collects long-term, open access ecological data. Since 2014 NEON has used enzyme-linked immunosorbent assay (ELISA) to test more than 10,000 rodent blood samples for hantavirus. This has yielded a robust dataset with more than 200 positive samples spread across 29 sites in the continental US. Starting in 2020, NEON began testing small mammal ear and blood samples for tick-borne pathogens using PCR methods. This presents several advantages including: (i) improved linkages between tick and small mammal datasets, (ii) greater public health relevance (iii) opportunities for novel research questions on pathogen emergence, co-infection, and prevalence changes and (iv) archival DNA extracts. Here, I present graphics summarizing the spatiotemporal extent of the hantavirus dataset and key findings so far. I also provide details surrounding implementation of the new tick-borne disease testing paradigm for small mammal blood samples. NEON now has at least one year of tick-borne pathogen data available, and the results of the tick-borne pathogen analyses from 2021 will be summarized.

151: How to prevent disease transmission in wildlife? Experiments in social conditioning of nilgai antelope

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Cattle fever is among the most important vector-borne diseases of livestock and is caused by a protozoan parasite that is spread by cattle fever ticks (CFT). Alternative wildlife hosts, including white-tailed deer (*Odocoileus virginianus*) and exotic nilgai antelope (*Boselaphus tragocamelus*) have facilitated recent outbreaks of CFT in South Texas. White-tailed deer are known to readily use feeders to consume bait, providing regular opportunities to deliver oral and topical treatments. While captive-raised nilgai are commonly conditioned to feeders, reports of free-ranging nilgai using feeders are rare. Our objectives were to determine if free-ranging nilgai would learn to use a feeder if exposed to feeder-conditioned nilgai. We conducted the study in 2 phases where we introduced captive-raised nilgai that had been pre-conditioned to feeders into large enclosures that included free-ranging nilgai and white-tailed deer. We monitored feeder sites with cameras for approximately 3 months in each phase and calculated indices of use for each species in each phase. We collected over 15,000 photos of nilgai at feeders over both phases, yet only captured a single event where a young naïve bull may have consumed feed. While our results may have varied with a longer duration or different range conditions, our results do not suggest that release of feeder-conditioned nilgai would be useful for developing an effective treatment delivery method for eradicating cattle fever ticks from nilgai.

152: Predicting ecology using multivariate data yields novel insights into diets of cryptic and extinct taxa

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An organism's phenotype often relates to its ecology in a well-characterized manner, enabling us to predict ecology from phenotypic measurements for taxa without direct ecological information such as extinct or cryptic species. Diet is a critical component of a species' ecology, and broadly corresponds to a species' dental morphology. However, in order to predict diet, diet first needs to be codified. Establishing metrics for diet that effectively summarize dietary variability without unreasonable information loss has remained challenging. Here we treat diet as a multivariate metric, using information on the composition of species diets derived from the literature to assign relative importance to individual dietary items. We then use this relative importance data to predict carnivoran diet from various dental and phenotypic metrics using Bayesian multi-level modeling. We find that there is no "one size fits all" model for predicting diet, rather different phenotypic traits perform better at predicting individual food items. Using these models derived from living species with well-characterized ecologies we were able to predict the diet of extinct and cryptic carnivoran species. Our approach need not be limited to diet as an ecological trait of interest, the phenotypic traits used here, or carnivorans as a clade of interest, rather this framework serves as a general approach to predicting ecology from phenotypic traits.

153: Allen's rule in *Peromyscus sonoriensis* (Rodentia)

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Peromyscus sonoriensis, (phylogroup L in Bradley, et al., 2019), is a widespread clade in North America and should demonstrate Allen's rule (shorter extremities in colder environments). Two databases were used to study the morphological variation of their appendages. Both databases showed a strong, positive, significant correlation between tail length and the average January temperature. In addition, there is an equally strong, but negative, correlation between tail length and average July temperature. Similar results are seen for feet and skulls. On the other hand, ear length does not seem to follow Allen's rule. When broken into ecoregions, prairie deer mice are least likely to demonstrate morphological responses to climate.

154: Elbow and knee joint measurements yield the most accurate predictions of body mass in Ruminantia

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Predicting body mass is critical for inferring aspects of extinct mammal ecology. For example, the unique digestive physiology of extant ruminant artiodactyls is suggested to place constraints on their body mass depending on the type of food resources available. Thus, reliable body mass estimates could provide insight into extinct ruminant habitat preferences. However, most regression equations proposed thus far have used craniodental predictors or have relied on measurement that require complete limb elements, which are infrequently preserved in the fossil record. I used multivariate phylogenetic regressions and 65 postcranial measurements to establish predictive equations for body mass in 85 species of extant ruminant artiodactyls, focusing on measurements at the proximal and distal ends of long bones and articular surfaces. I find that subsets of proximal and distal measurements perform as well as equations including measurements from entire elements. The individual measurements that best predict body mass are found at the elbow (distal humerus and proximal radius) and knee (distal femur and proximal tibia) joints, which likely has biomechanical implications for limb loading related to an upright limb posture. Measurements found in commonly fragmented pieces of long bones can be just as powerful for predicting body mass as measurements using an entire bone.

155: Do ankle extensor muscles match locomotor behavior in rodents?

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The hindlimb hypertrophy and augmented power in the limb extensor musculature of bipedal rodents, like kangaroo rats and jerboas, hypothetically better equip them to escape depredation than their quadrupedal counterparts. Visualizing and measuring hindlimb musculature allows us to better understand the differences that elicit rapid responses in bipedal rodents needed to escape from incoming predators. We used DiceCT and digital segmentation to visualize and measure the volume of the ankle extensor muscles of 14 rodent species, representing two bipedal lineages alongside quadrupedal outgroups. Generally, bipedal rodents had larger ankle extensors relative to their body size. For example, *Dipodomys ordii*, a North American Heteromyid, has the most massive lateral gastrocnemius relative to body size. However, *Napaeozapus insignis* also has large ankle extensors relative to body size. They represent an “intermediate" between quadrupeds and bipeds and are known for explosive jumps. We report a reduced or absent soleus muscle in bipedal Dipodidae. Our data supports the hypothesis that bipedal rodents have larger and more powerful ankle extensor muscles that facilitate powerful leaps in order to escape from potential threats such as those from an owl or rattlesnake attack. We propose that bipedal hopping coevolved with larger ankle extensors to perform these explosive, high-powered jumps. We contrast the putatively convergent morphological adaptations of kangaroo rat and jerboa lineages and discuss their evolutionary trajectories relative to quadrupedal counterparts.

156: Locomotion, body mass, and phylogeny are reflected in trabecular bone of Philippine ?earthworm mice? (Chrotomyini)

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Trabecular bone (spongy internal bone tissue) presents an interesting case of limited phenotypic plasticity in the skeleton: it is remodeled throughout an animal’s life in response to its mechanical environment, but like other morphology, it is also subject to genetic influences. However, the relative influences of factors controlling trabecular bone architecture (TBA) are poorly understood. The Philippine endemic murid rodents known as earthworm mice exhibit a range of locomotor modes and body mass within a single radiation, making them an ideal group for a tractable study of these influences. We used Bayesian multilevel models to investigate the relationship among mass, TBA, locomotion, and phylogeny across 11 species of earthworm mice. We considered four aspects of TBA: bone volume fraction (BV.TV), trabecular thickness (Tb.Th); degree of anisotropy (DA); and connectivity density (Conn.D). Phylogenetic signal (λ) is low across the four metrics (all < 0.5); body mass is a strong predictor for all metrics except DA. Semifossorial animals have relatively high Tb.Th, and ricochetal animals have relatively low Tb.Th and BV.TV; terrestrial species have relatively low DA. Differences among locomotor groups are slight, and their posterior probability distributions exhibit high uncertainty due to the inclusion of phylogenetic correlation structure. However, even a weak locomotor mode signal in the TBA of these animals makes sense because of the different characteristic bone loading schemes for different types of locomotion.

157: Challenges and opportunities in the study of sexual dimorphism in fossil carnivorans

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Sexual body size dimorphism is common in small carnivorans, yet putative carnivoran species pairs in the fossil record are frequently distinguished largely or entirely based on size. Conflating species and sexes has the potential to impact taxonomy and affect paleobiological analyses by artificially inflating diversity. It may also mask patterns and trends in the evolution of sexual dimorphism. But how widespread is such conflation? Using published measurements of fossil specimens and body mass data from extant species in

museum databases, we compared body size differences between three putative pairs of extinct species (within the basal feliform *Palaeogale* from two Miocene sites in Germany and the mustelid *Trigonictis* from the Pliocene of Oregon) to those between males and females in extant musteloids. In all cases, size differences were consistent with those seen between males and females in extant sexually dimorphic species. Our results do not, however, conclusively demonstrate that these fossils represent single, sexually dimorphic species, due to small sample sizes that make it difficult to discern population-level patterns. A thorough survey of putative species pairs in the pre-Pleistocene record of small carnivorans coupled with development of body size proxies that allow the inclusion of a larger fossil sample will be invaluable for not only carnivoran taxonomy, but for the study of the evolution of sexual dimorphism and of body size trends through time.

158: Coevolutionary interactions between Tasmanian devils (*Sarcophilus harrisii*) and a species-specific transmissible cancer

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Emerging infectious diseases (EIDs) are a leading threat to biodiversity, often necessitating rapid evolutionary responses to the novel and intense selection pressures they impose. The global spread of EIDs that can occur in days often select for both the pathogen and the host to evolve quickly, therefore providing opportunities to study coevolution in action. The Tasmanian devil (*Sarcophilus harrisii*) and its transmissible cancer, devil facial tumor disease (DFTD), affords such an opportunity to assess incipient host-pathogen coevolutionary dynamics *in situ*. DFTD arose from a Schwann cell in a female Tasmanian devil and is an EID that is nearly 100% fatal. Since its discovery in 1996 in northeast Tasmania, DFTD has spread westward across nearly of the entirety of the devil's geographic range and reduced the total population by ~80%. Multiple lines of evidence suggest (1) devils are evolving in response to DFTD, and (2) DFTD is also evolving, yet evidence of coevolution is lacking. Here, we sequenced the genomes of ~500 devils and ~500 tumors and used a two-way genome-wide association mapping approach to detect genotype-by-genotype interactions underlying variation in force of infection (i.e., the rate at which susceptible devils became infected). Genotype-by-genotype (GxG) interactions explained >40% of the variation in force of infection, highlighting the importance of the extended phenotype in coevolving systems.

159: The genomic basis of venom resistance in hispid cotton rats

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According to the Life-Dinner Principle, greater selection pressure is expected on prey than predators in arms-races; failed hunters go hungry, while those failing to evade hunters die. Therefore, we should expect a tendency for prey to adapt to local predators and win the arms-race. However, rodents have repeatedly been found to be locally maladapted to venomous snakes, raising the question: why are rodents losing these races? Prey local maladaptation could be explained by low standing genetic variation, swamping of adaptive alleles by migration or drift, and/or diffuse selection due to interactions with other predators. Understanding coevolution between venom and venom resistance requires understanding the genetics of both traits because the fitness of one depends on the other. Although the genetics of snake venoms have received significant attention, few venom resistance mechanisms have been documented. Resistance, like venom, is likely a polygenic trait best understood using integrated genomic and ecological approaches. An island and mainland pair of hispid cotton rat (*Sigmodon hispidus*) populations in Florida provides an opportunity to investigate the genetics of prey resistance, as members of these populations have been shown to possess lower venom resistance against sympatric than allopatric eastern diamondback rattlesnakes (*Crotalus adamanteus*). Here, we first present a mainland cotton rat genome assembly. Second, we present candidate venom resistance loci discovered using pooled whole-genome sequencing of 50 individuals each from both populations.

160: Mito-nuclear discordance explains the ambiguous phylogenetic relationship of the Red Fox and Rüppell's Fox

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Interspecific hybridization can lead to introgression, but its genomic impact depends on the interplay of selection, drift and gene-flow. The arid-adapted Rüppell's Fox (*Vulpes rueppellii*) has previously been suggested to be the sister species of the Red Fox (*Vulpes vulpes*), albeit presumably nested within its mtDNA diversity. This paraphyly could indicate recent divergence of *V. rueppellii*, questioning its classification as a distinct species. We generated high-resolution mitochondrial and genome-wide ddRAD data from both species from across North Africa and the Near East. We identified five mitochondrial clades, confirming with high support the paraphyly of *V. vulpes*. All *V. rueppellii* individuals fell within two subclades in a Palearctic clade, intermingled with - but not shared with - *V. vulpes*. In contrast, autosomal loci showed the two species as strongly differentiated, but with evidence for some rare, recent hybridization. Genetic diversity was higher within *V. vulpes* populations than in those of *V. rueppellii*. Our findings are consistent with the well-known successful adaptability of *V. vulpes*, allowing this generalist to cope with environmental and food availability changes. In contrast, the desert inhabitant *V. rueppellii* appears more vulnerable to habitat and environmental changes, with scarcity of resources promoting population fragmentation and increased inbreeding. Furthermore, the mito-nuclear discordance suggests an early divergence and extended time for adaptation in *V. rueppellii*, followed by introgression – supporting classification as a distinct species.

161: A target capture kit for efficient, hierarchical genomic sequencing across the weasel family (Mustelidae)

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Whole genome sequencing is increasingly tractable for non-model mammal systems, but is not necessary for every question. Popular reduced-representation methods (e.g. RADseq, UCEs) are more time and cost effective, and still provide sufficient resolution to address many phylogenetic, evolutionary, and demographic questions, but not without caveats. For instance, RADseq randomly samples sites from across the genome, but has limited repeatability due to batch effects, and UCEs can be difficult to fit into evolutionary models due to their conserved nature. In contrast, target capture makes use of existing genomic resources to sequence pre-selected regions of the genome, and is thereby scalable, customizable, and replicable across sequencing runs. To exemplify its utility for non-model mammals, we developed a target capture kit for the weasel family (Mustelidae). Using 18 whole genomes from across the family, we built a bioinformatic pipeline to identify 15,000 high-quality, orthologous, unlinked, and variable targets across the genome. While anchored in exons, each target includes a portion of surrounding introns. In total, we target ~11,000,000 bp (~0.3% of the genome). Our probe design is intentionally hierarchical: the entire probe set is informative for family-wide genomic analyses, but can be subsampled to address questions on shallower timescales, such as within genera or subfamilies. Our targeted, modular approach provides a set of neutral and functional markers to investigate ecological and evolutionary processes across the Mustelidae.

162: Shrew hybridization across an Arctic ecotone signals progressive loss of a tundra specialist

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The Arctic is experiencing increasing disturbance associated with climate change that includes exacerbation of species interactions as boreal forest communities shift northward and encroach on Arctic tundra. These interactions include increased sympatry among related species, potentially resulting in competition and hybridization, with unknown consequences for evolutionary trajectories. To investigate the

evolutionary consequences of environmental perturbation in northern Alaska, we sampled masked shrews (*Sorex cinereus*; forest; n=250) and barren-ground shrews (*S. ugyunak*; tundra; n=75) to determine the dynamics and spatio-temporal extent of hybridization. We used double-digest restriction-site associated DNA sequencing to recover >10,000 single nucleotide polymorphisms for genomic analysis of species-specific diversity and demographic trends, and for identifying and characterizing hybrids. Our results show low diversity across both species, with a signal of expansion for *S. cinereus* and contraction for *S. ugyunak*, consistent with modeled trends. Although less that 5% of samples are of hybrid origin, all hybrids are well within the current distribution of *S. cinereus*. Hybrids are evidently viable with multi-generational back-crossing in both directions between species, but with the majority of back-cross breeding of hybrids occurring with *S. cinereus*. First generation hybrids are also present. Our results strongly suggest that as *S. cinereus* expands northward, the tundra-associated *S. ugyunak* is experiencing both competitive exclusion and genomic swamping and may be at imminent future risk of continued decline.

163: A time-calibrated supertree for geomorph rodents that includes fossil taxa informs their diversification

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The roles of climate, habitat, and tectonics remain important questions in understanding the rise to dominance of rodents during the Cenozoic. Such analyses are best conducted in clades that include diverse ecologies, high taxonomic diversity, and a rich fossil record. One such study system is found with the Geomorpha, a clade that includes two of the most species-rich rodent families in North America today, the Geomyidae (pocket gophers) and Heteromyidae (kangaroo rats, pocket mice, and their relatives), as well as several extinct families (e.g., Florentiamyidae, Heliscomyidae) distributed over the past 50 million years. We combine existing molecular data with new expanded phylogenetic analyses of morphological data to reveal new relationships within the clade and build a time-calibrated supertree of geomorphs including 181 species (comprising 81 fossils). We use this tree to reconstruct geomorph diversification, including speciation and extinction patterns, while accounting for ghost lineages. Our results show that lineage diversity within Geomorpha remained low until 30 million years ago (Ma) when the very rapid radiation of the extinct entoptychine Geomyidae led to a peak in diversity. Despite a decrease in diversity around 28 Ma, geomorphs remained a species-rich group throughout the Oligocene and Miocene with the evolution of numerous groups now extinct. The modern diversity of the clade is rooted in the Miocene with the contemporaneous radiation of geomyines and crown-group heteromyids circa 13 Ma.

164: Litter size variation among North American small mammals

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Digitizing global biodiversity data provides new resources for scaling up study of organismal phenotypic and life history diversity and their differential response to environmental change. This is especially true for reproductive traits including the timing and intensity of breeding which, in many taxa, are among the most sensitive to climate shifts. Unfortunately, for most species, the available data remain too sparse to simultaneously model both intraspecific and interspecific drivers of life history trait variation. Using a new data set curated from digitized museum specimens and historic census efforts, we explore here how climate context shapes a key life history trait – litter size – within and among 39 common North American small mammal species that vary in habitat preference, diet, and life history strategy. We find that two metrics related to ecosystem productivity, Hargreaves evapotranspiration index and mean annual precipitation, best explain litter size at the interspecific level. In particular, litter size is maximized in the coolest and driest habitats where the timing of resource pulses are temporally most constrained. Our results highlight the importance of digitized biodiversity records and their utility for large-scale ecological and life history research capable of extending past traditionally used mean values for species traits. Developing these data sets is key to understanding how organisms will continue to manage the tradeoffs between energetic supply and demand in a changing world.

165: Mammals of the Tapichalaca Reserve, Zamora-Chinchipe Province, Ecuador

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We surveyed the mammalian diversity of the Tapichalaca Reserve in Zamora-Chinchipe Province, Ecuador. The habitat at Tapichalaca can be described as mountain cloud forest of the eastern Andes. The location is 4° 29' 31.90" S 79° 07' 38.99" W, and the elevation is 2522 m. The steep mountain slopes and high rainfall in this habitat cause frequent landslides that result in dense secondary growth forests. The reserve was established for the protection of the Jocotoco Antpitta (*Grallaria ridgelyi*) that is only known form Tapichalaca and a few other nearby mountain forests. The species we documented include *Marmosops caucae*, *Didelphis pernigra*, *Caenolestes convelatus*, *Caenolestes condorensis*, *Anoura peruana*, *Sturnira bidens*, *Sturnia erythromos*, *Myotis oxyotus*, *Sciurus granatensis*, *Oreoryzomys balneator, Akodon aerosus*, *Thomasomys aureus*, *Thomasomys caudivarius*, *Thomasomys taczanowskii*, *Thomasomys vulcani*, *Nephleomys albigularis*, *Cuniculus tazanowskii*, *Coendou rufescens*, *Leopardus tigrinus*, and *Nasuella olivacea.*

166: Patterns of urban tree squirrel occupancy show strong city-level effects across their geographic range

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Tree squirrels play critical roles in urban ecosystems as important seed predators and dispersers and prey for urban predators. Currently, our knowledge of urban squirrel distributions is based largely on studies from single cities that may not be translatable across their range. Multi-city analyses indicate eastern gray squirrels (*Sciurus carolinensis*) and fox squirrels (*S. niger*) respond differently broad landscape variables such as urban intensity, land cover, and housing density, yet we still lack knowledge regarding how squirrels respond to more specific attributes (e.g., tree canopy, impervious surface cover) that may influence their patch use choices. We leveraged camera trap data from 10 North American cities to build single-species, multi-season occupancy models to identify relationships between squirrel site occupancy and land use, tree canopy, and impervious surface cover. Across their geographic range, both species were more likely to occupy sites with above average canopy and grass cover, however, the strength of these relationships exhibited high among-city variation. We also found high within-city variation in responses to these variables (e.g., gray squirrel occupancy probability ranged from 0.5 to 1.0 on sites with 0% grassy cover in Madison, WI), potentially influenced by the relative abundance or scarcity of particular cover types in each city. Understanding tree squirrel site occupancy patterns in response.

167: Integrated evidence-based extent of occurrence for North American bison since 1500 CE and before

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Following the near extinction of bison (*Bison bison*) from its historic range across North America in the late 19th century, novel bison conservation efforts in the early 20th century catalyzed a popular, widespread conservation movement to protect and restore bison among other bison species and places. However, since Allen's initial delineation (1876) of the historical distribution of bison, subsequent restoration attempts have been hampered by knowledge gaps about distribution before and following colonial settlement. For the first time, we apply a multi-disciplinary approach to assemble a comprehensive, integrated geographic database and meta-analysis of bison occurrences over the last 200,000 years BCE, emphasizing the last 450 years Before Present (circa 1500 CE). We combined 4,376 observations from existing online databases, museum collections, published literature, and first-hand exploration journal entries covering the disciplines of paleontology, archaeology, and historical ecology. We illustrate the historical maximum extent of occurrence (EOO) of bison — project commissioned, and methodology guided by the International Union for Conservation of Nature (IUCN) Bison Specialist Group — using a concave hull polygon based upon observations since 1500 CE (n=2,946). While historical distributional margins represent an EOO, it does not replace a density-based approach reconstructing potential historical range distributions which identify core and marginal ranges. However, we envision this database will contribute to future research in the increasingly evidence-based disciplines of ecology, evolution, rewilding, management, and conservation.

168: Den site selection of bobcats (*Lynx rufus*) in the Black Hills, South Dakota

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The bobcat (*Lynx rufus*) is an important furbearer across the United States. However, management of bobcats can be difficult because of their elusive nature. Little is known about bobcat den site selection and this project aims to provide resource selection of bobcat den sites in the Black Hills, South Dakota. Our objectives for this study are to compare habitat characteristics of den sites to random sites within a bobcat's home range at two spatial scales: (1) the den site (10 m radius around the den) and (2) the den area (100 m radius). Adult female bobcats were captured and radio collared (n = 35) and we located the dens (n = 27) of these collared adult female bobcats using ground triangulation. We collected information on variables including slope, aspect, horizontal cover, canopy cover, and distance to roads at den and random sites. We evaluated bobcat den site selection using discrete choice analysis. Bobcats selected dens that had significantly higher horizontal cover compared to random sites at the den site scale. Bobcats selected dens that had significantly higher horizontal cover and terrain ruggedness compared to random sites at the den area scale. These results suggest that den site selection is perhaps strongly driven by the need for concealment from predators and other disturbances.

169: A review of three neglected species of tuco-tuco: *Ctenomys johannis*, *C. famosus* and *C. coludo*

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The genus *Ctenomys* is one of the most speciose among South American rodents, whose systematics have not yet been fully elucidated. One of the difficulties clarifying the identity of its species is the scarce information available on some of them, erected more than a century ago and of which only the original descriptions, generally very poorly detailed, are known. Our study provides original information about *Ctenomys coludo* Thomas 1920, based on the collection of topotypes that allowed us to perform morphological and molecular analyses. We then compare them with information referred to the holotype, with other specimens deposited in museum collections, and with other species of the genus to which it is considered to be related. Our results also enable us to place *C. coludo* as a member of the "*Ctenomys mendocinus* group", and to propose *C. famosus* Thomas, 1920 as a junior synonym of *C. coludo*. We also recognize *Ctenomys johannis* as a valid and separate species, and provide unpublished information obtained from specimens collected at the type locality. We also extend the distribution of these species and subspecies and present their phylogenetic relationships.

170: Prairie small mammal surveys and behavioral observations using bait stations with trail cams

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The gold-standard of small mammal surveys are the ubiquitous Sherman live traps. However, some work suggests that several small mammal species avoid such traps and it is impossible to observe behavior in the traps. In small mammals, different behaviors and interactions can be triggered by various factors including food availability, competition, predation, and social encounters. We built bait stations consisting of a trail cam facing downward over a tray of oats inside of a large enclosure to survey small mammals in Kansas and observe and score their behaviors. More species were observed in the bait stations compared to Sherman trapping surveys in the same area. Among the most common behavior of rodents in the bait stations was feeding and moving. While intraspecific and interspecific chasing was recorded, few interactions appeared to be aggressive, suggesting that rodents may avoid fights with both conspecifics and heterospecifics despite resource availability. The behaviors recorded in the bait stations would be difficult to observe using other methods since the bait stations allowed small mammals to come and go freely. This suggests that bait station observations, when used in conjunction with other survey methods, are an effective tool to understand the ecology of small mammal populations.

171: Microsite characteristics selected by bats roosting in bridges in the Texas Trans-Pecos

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Resource selection is a foundational concept in ecology. Knowing what resources an organism selects for at multiple scales is crucial when developing and executing management and conservation decisions. Bats present an interesting model group, as they are volant and therefore might have access to more resources than other mammals of similar body size. One of the most crucial components of bat habitat is where they roost. Finding an appropriate roost can present a challenge and roost selection can be critical. Roosting sites serve many functions by providing a place for daily torpor, hibernation, resting, feeding, and rearing of young. Consequently, a roost can influence survival rate and fitness. For example, at a fine-scale, roost microclimate can affect spermatogenesis, pup growth rates, stress levels, and energy expenditures necessary for thermoregulation. Here, we predict that bats are selecting roosts based on microclimate when roosting in bridges. We set iButtons under 13 bridges to record data for used roosts, available roosts, and ambient conditions. These iButtons recorded temperature and relative humidity at specified intervals. Roost dimensions of depth and width were also recorded. Using t-tests and linear mixed-effects models, we test whether bats were selecting for particular roost conditions within a bridge or if use was random at a fine-scale. Identifying the structural and environmental conditions bats seek within a microsite can aid in their management and conservation.

172: Integrating Organismal Biology into NEON

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The National Ecological Observatory Network (NEON) is a National Science Foundation-supported observatory documenting environmental change through 30 years of consistent data collection at research sites across the United States. NEON presents a unique opportunity to produce novel insights into fundamental biological questions, but the potential of NEON and its associated infrastructure have not yet been fully realized by organismal biologists. However, NEON is well-suited for answering some major questions in organismal biology, which uses diverse and integrative approaches to understand variation in the behavior, physiology, and life histories of organisms and how these multiple traits interact across environmental gradients and produce population differentiation. Through NEON, there is great potential for organismal biologists to help reveal how genotypes become phenotypes and discover new patterns at spatiotemporal scales that have not previously been possible. We are organizing a Research Collaboration Network (RCN) that will develop a professional network of organismal biologists who are diverse in

background, expertise, and career stage, host workshops and symposia that focus on the potential of NEON to answer key questions in organismal biology and provide training experiences for the next generation of researchers through research exchanges. This RCN will diversify and strengthen NEON usage by incorporating organismal biologists into the community of NEON users and by promoting interactions between ecologists and organismal biologists.

173: What?s going on upstairs? - testing Dehnel?s phenomenon in small mammals of the Appalachians

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Energetic trade-offs in mammals present in a wide variety of forms, and function in many different ways to achieve one ultimate goal: maximizing survival and fitness despite periods of extreme stress. This is particularly pertinent to mammals facing the ravages of winter, when individuals must balance thermoregulation against lowered resource availability. Dehnel’s phenomenon is an adaptation which involves reversible reductions in brain mass, bone density and total weight so far observed in a handful of small mammals - shrews, stoats and weasels - during winter months. However, this phenomenon has not been widely examined since its first observation in 1949, and rarely outside of Eurasia. This project aims to fill the gaps in Dehnel’s documentation in North American small mammals, with a focus on deer mice (*Peromyscus maniculatus*), masked shrews (*Sorex cinereus*) and smoky shrews (*Sorex fumeus*) from the Appalachian Mountains of the eastern U.S. Using high-resolution CT scans from specimens collected during each season from 2021-22, we compare cranial morphological differences across seasons, taking account of age class. This work is providing a test of Dehnel’s phenomenon in new species and regions of the world, improving our understanding of energetic trade-offs of wild mammals.

174: Examining methodologies and dietary diversity across the ringtail (*Bassariscus astutus*) distribution

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Like many generalist species, the diverse foraging strategies of ringtails (*Bassariscus astutus*) allow them to inhabit a wide range of ecoregions across North America. As omnivores, ringtails are known to eat a wide range of plants, insects, small mammals, and other food items. In this study, we conduct a literature review of ringtail diet studies (n = 40) to compare analysis methodologies, describe ringtail dietary diversity across ecoregions, and highlight gaps in the current understanding of ringtail diet. We identified studies through a systematic literature review and supplemented them with our own field-collected data from Zion National Park, Utah. Within each study, we documented identified diet items, their taxonomic rank, methods, sample size, and location. We then constructed rarefaction curves of identified diet items for all studies, as well as compared between ecoregions and methodologies. We hypothesize that fresh scat analysis will show the highest taxonomic richness, as it provides a wider dietary snapshot and experiences less environmental degradation than other physical methods. Observational studies were examined for unique diet items to describe their usefulness in dietary analysis. Finally, we analyzed ringtail diet composition across three ecoregions by comparing the relative abundance of the most common identified diet items at the order level. This study sheds light on the various methods utilized for mammalian dietary analysis and informs the dietary diversity of a flexible mesocarnivore.

175: Relationships between sex ratios and habitat fragmentation in urban white-footed mice (*Peromyscus leucopus*)

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Urbanization fragments habitats, potentially reducing ecological functionality by isolating populations of organisms. This isolation increases risk of local extinction in habitat patches that can escalate to regional extinction. The effects of fragmentation vary with organism size such that smaller species with lower dispersal abilities, may be more vulnerable than larger ones. Female mammals are also less likely to

disperse far distances than males, especially if the areas are more fragmented or isolated. Fragmentation may therefore alter sex ratios of small mammals by limiting female dispersal. Subsequently reducing reproductive success in local populations could threaten overall evolutionary stability. We used linear regression to identify the relationships between a habitat fragmentation metric, contagion, and the sex ratios of white-footed mice (*Peromyscus leucopus*) populations surveyed using live trapping on 45 sites in the Iowa City, Iowa area. Vegetation connectivity was positively related to the proportions of female mice trapped, indicating few females are present at isolated sites. Because male-skewed populations of polygamous animals are more vulnerable to local extinction, this finding suggests a potential extinction vulnerability for isolated, urban populations of white-footed mice. Given the key role mice play in food webs, disruption to these populations may have broader implications for urban plants, predators, and local human residents.

176: Sepia short-tailed opossum of the western Andes: first record of Monodelphis in the Chocó-Andino, Ecuador

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The genus *Monodelphis* (Didelphidae: Didelphiomorphia) comprises 25 species broadly distributed in South America. The sepia short-tailed opossum, *Monodelphis adusta*, the only species in the genus reported for Ecuador, is known by a few voucher specimens collected from the Eastern side of the Andes, although researchers have hypothesized it should also be present in the western Andes. Records of *M. adusta*, indicate that this species is distributed from the eastern Darien in Panama, through the eastern side of the Andes in Colombia, Ecuador, and Peru to northern Bolivia. Herein, we report the first known records of *M. adusta* from the Western side of the Ecuadorian Andes, based on two specimens collected in the Chocó Andino Biosphere Reserve in the Pichincha Province. Sampling was carried out in three elevational and disturbance gradients (from 500 to 2000 m), including pastures, secondary, and primary forests in the basin of the río Pachijal. Additional sampling was carried out at primary forests of Mashpi Protected Forest (818 m). This report constitutes a first step in the study of the poorly known marsupial faunas from Northwestern Ecuador. Future endeavors will include deep morphological, geographic, and genetic analyses. This discovery enhances the importance of continuing scientific research and conservation efforts on the western side of the Ecuadorian Andes, one of the most biodiverse and threatened ecosystems in the country.

177: Use of whole-genome sequencing to investigate the evolutionary history of island spotted skunks

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Island species have long been considered an important tool for understanding speciation and to investigate the evolutionary forces driving DNA sequence evolution. The Island spotted skunk (*Spilogale gracilis amphiala*) is an endemic insular carnivore found on two of the Channel Islands off the coast of southern California: Santa Rosa Island and Santa Cruz Island. Island spotted skunks are morphologically nearly indistinguishable from one another and from their mainland counterpart, the western spotted skunk (*S. gracilis microrhina, S. gracilis phenax*), fueling the original idea that spotted skunks arrived on the Channel Islands in recent history. However, genetic studies using microsatellites and mitochondrial DNA found significant differences between the two island populations and between the islands and mainland populations, suggesting a longer evolutionary history of spotted skunks on the islands. Still, the degree to which island spotted skunks are diverged from one another and from their mainland relative remain unclear. To further investigate the evolutionary history of island spotted skunks and the forces driving their divergence, we used whole genome sequencing to estimate genomic differentiation, diversity, and inbreeding. Our preliminary results show evidence of high genomic differentiation between all three populations, lower diversity in island populations, and increased inbreeding in island populations, suggesting that island spotted skunk populations are more diverged from one another and from the mainland western spotted skunk than originally thought.

178: Impacts of late Quaternary biodiversity loss on mammal species cooccurrence at a regional scale

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The structure of mammal communities is determined by complex associations between species, their habitats, and their responses to shifting biotic and abiotic factors that differ across spatial and temporal scales. While the effect of biodiversity loss on mammal co-occurrence has been examined at large scales, it is important to examine patterns at other scales. Here we examine changes to a regional ecosystem, the Edwards Plateau in Texas, following the megafaunal extinction in North America during the late Pleistocene. We focus on 15 localities and quantify the proportion of mammal species aggregations and segregations across pre-extinction and post-extinction time intervals. Pre-extinction, only 17% of significant spatial associations involved extinct species. Proportionally, significant pairs decreased by ~60% from the pre- to post-extinction intervals, but the mean strength of associations remained similar. Aggregations make up most significant co-occurrences of species between sites in both the pre- (99.5%) and post-extinction (96.4%) intervals. While co-occurrences of species across trophic guilds shifted significantly through time, only frugivore/granivores and insectivores in the pre-extinction formed pairs more than would be expected given their representation in the community. These regional scale changes in community structure differ from those observed at continental or local scales. Shared climatic and habitat preferences, along with localities experiencing similar environmental changes through time, may lead to more uniform impacts in communities at this scale, obscuring restructuring across biotic interactions.

179: Using museum collections to assess cause-specific mortality of Florida panthers (*Puma concolor coryi*)

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Florida panthers (*Puma concolor coryi*) are a federally endangered species that faced serious threat of extinction until federal protections and management helped restore and protect the population. But they still face high mortality rates due to factors like vehicular collisions, intraspecific interactions, and disease. We examined the cause-specific mortality of the Florida panthers at the Florida Museum of Natural History using a combination of specimen examination, database records, and necropsy reports. Age, sex, date collected, and cause of death were recorded and significant damage on the skulls was also noted. Of the 306 panthers examined, male and adult panthers exhibited the highest mortality rates, at 56% and 74% respectively. Vehicular trauma was the most common cause of death for both sexes, followed by intraspecific aggression. April, June, and November had the highest numbers of vehicular trauma incidents. The most notable types of skull damage included crushed skulls, broken mandibles, missing teeth, and skull fractures. These findings add additional information on panther mortality to pre-existing literature and emphasize the need for wildlife corridors to help further protect the panthers.

180: Variability of home ranges of adult female American black bears (*Ursus americanus*) in northcentral Pennsylvania

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From 2019–2021, the hunting seasons of American black bears (*Ursus americanus*) in Pennsylvania increased in length and changed in structure compared to prior years. Little information exists on factors that influence bear harvest vulnerability during earlier or expanded hunting seasons. Additionally, identifying

variability in movement patterns of bears and their fates throughout hunting seasons can inform management. In a previous study from Pennsylvania, the average home range size of adult females was 41 km^2 (range = 14–84 km^2). However, there is seasonal variation in home ranges and movement patterns of bears. Fall movement patterns of bears have been shown to vary by year and depend, at least in part, on hard mast abundance and distribution. To address these gaps in knowledge, we GPS-collared adult female bears in the Sproul State Forest of northcentral Pennsylvania from 2019–2021 to determine home range sizes and patterns of fall movement. We assessed fall hard mast relative abundance to characterize variability in food resources. Additionally, we evaluated temporal and spatial variation in hunter activity with road-side surveys and camera trapping, respectively. We estimated home ranges with utilization distributions through kernel density estimation. We estimated home ranges for fall beginning in September through den entry or a mortality event. Estimated home ranges will be utilized in future analyses to evaluate third-order resource selection and survival throughout hunting seasons.

181: Skunkoscapes: Range-wide dietary patterns of spotted skunks reveal regional changes in resources use

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Understanding patterns of resource use across a heterogenous landscape can inform on key variation in species ecologies including interaction networks, ecosystem roles, and population trajectories. Here we quantify and compare the broad-scale dietary landscapes of eastern spotted skunks (*Spilogale putorious, S. interruptus*, and *S. ambarvalis*) and striped skunks (*Mephitis mephitis*) across the great plains and southeastern United States to evaluate major environmental factors which drive regional dietary variation both within and across species. Dietary behavior was quantified using carbon ($\delta^{13}C$) and nitrogen ($\delta^{14}N$) stable isotopes sampled from hair, which represents a signal of dietary resource use via known fractionation rates into biological tissues. Categorization and regression tree analyses were used to assess the relative importance of environmental variables impact on diet for each skunk taxa, with outcomes used to model range-wide dietary niche landscapes (i.e. isoscapes). Isoscapes for each taxa were compared as predictions of resource use with known plant and rodent baselines to infer regional shifts from expected dietary niche. Results suggest clear differences in several factors driving dietary variation between species, with spotted skunk range-wide dietary variability impacted less so by human abundance than stripped skunks. Regions where predicted isoscapes greatly differ from observed suggest potential populations under increased threat of extirpation amid ongoing landscape and climatic change.

182: Evolutionary history and phylogeographic relationships of Eurasian shrews in the *Sorex caecutiens* complex

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Shrews of the *Sorex* genus are an evolutionarily successful group that diversified during the Pleistocene. *Sorex* includes over ninety recognized species that are widely distributed across Eurasia and North America. However, diversification and phylogeographic relationships for most taxa and some major clades remain incompletely explored. In this study, we will obtain mitochondrial cytochrome *b* sequences (cyt*b*) for nearly 300 samples across the *S. caecutiens* complex, which includes six extant species. We will then develop phylogeographic perspectives that include reconstructing and testing alternative biogeographic scenarios and demographic histories. We also evaluate diversification rates, which we expect to conform to major Pleistocene events. Thus, we predict that climate oscillations during the last 3 million years have contributed to the diversification of this clade. In contrast to northern North America, the lack of massive glaciers across eastern Eurasia enabled multiple forest-associated taxa to evolve, potentially in distinct refugia. Expanding on these ideas, we will develop spatio-temporal hypotheses for the evolution and geographic dispersion of individual lineages associated with differing ecoregions across central Eurasia.

183: Are bats commensal with bovids?

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Bison (*Bison bison*) and Brahman cattle (*Bos taurus indicus*) are frequently harassed by flies (Diptera), a vector for endoparasites. Bovids cannot completely avoid flies or endoparasites, especially when foraging in the summer when flies are abundant. However, bats are a predator of flies and have been reported capturing flying insects around ungulates. If bats are commensal with bovids, bat counts should be greater on sites with bovids. We used acoustic monitoring and insect traps to count bats and insects from March to May 2021 in Central Texas at 7 sites: 2 sites with bison, 1 site with cattle, and 4 control sites without bovids. We used the Shannon diversity index and mixed model regressions to examine the effects of bovids on bats and insects over time. We identified 19 species of bats and 13 families of flies. Bat counts and the diversity of bats increased through spring but were not affected by bovid presence, which suggests that bats are not commensal to bovids in this region. Bat counts were not affected by insect counts, but the diversity of bats decreased as insect counts increased, which suggests a complex interaction between bats and their prey. Control sites had more insects than the sites with bovids, likely due to the use of insect control measures for bovids. Consequently, bovids may not improve foraging opportunities for bats.

184: A comparison of genetic structure between the tundra vole, *Alexandromys oeconomus,* and their cestode *Paranoplocephala jarrelli*

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Though hosts play a dominant role in influencing the geographic distributions of parasites, shared host-parasite population histories can yield different evolutionary outcomes for hosts and their associated parasites. Here we contrast the genetic structure of *Alexandromys* (formerly *Microtus*) *oeconomus* to that of its cestode parasite, *Paranoplocephala jarrelli* (Anoplocephalidae), to investigate the degree to which the phylogenetic trajectories of the host and parasite are concordant. Phylogeographic analyses of the *A. oeconomus* show a history of allopatric divergence, with four parapatric clades distributed across the Holarctic. *Paranoplocephala jarrelli*, which relies predominantly on *A. oeconomus*, shares the widespread distribution of its host, yet consists of only three major clades, none of which closely align to the host's genetic structure. The discrepancy between host and parasite clade distributions suggests that dispersal by the parasite was not impeded across apparent barriers that maintained host lineage boundaries. In addition to reconstructing the genetic structure of *P. jarrelli*, we test for concordance between host and parasite in terms of the depth of divergence between clades and the demographic signal of population expansion. This study provides insight into factors that allow parasites to follow evolutionary trajectories that are distinct from those of hosts, even when apparent host-specificity is strong.

185: Like father, like son? Estimating breeding values for antler size in male white-tailed deer

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Luxury phenotypic traits, such as horns or antlers are used as both a tool and target for management in populations of ungulates. Because luxury traits are heritable, there is potential to change genetic traits associated with horn or antler size. However, there have been few studies of trait heritability in wild populations. Our goal was to investigate how closely phenotypes are correlated with genotypes in a managed population. We analyzed a long-term data set consisting of several generations of wild white-tailed deer (*Odocoileus virginianus*). Twenty adult males sired 322 buck fawns during temporary confinement in experimental pens from 2007 to 2021. Fawns were captured, ear-tagged, and then released into a 400-ha game-fenced pasture. Each autumn, we captured marked bucks and recorded antler size. Twelve males fathered 101 sons that survived to maturity (≥5.5 years old). We estimated the heritability of

antler size and individual breeding values for each sire, which is the difference between his male offspring's mature antler score and the average mature antler score in the experimental population. The heritability of antler scores was 0.34. This is similar to previous estimates for captive and free-ranging cervids. The correlation between individual breeding values and sire antler size was weaker than expected, indicating that antler phenotypes may not be as closely related to genotypes as commonly believed, especially in variable environments.

186: Can livestock leave room for wildlife? Competition and facilitation in a multi-use landscape

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Protected areas often are too small to house populations of wide-ranging species. Viability of wildlife populations therefore can depend on whether interactions with humans and their livestock living outside protected areas are negative, neutral, or even positive. In central Iran, we quantified interactions between globally endangered onagers (*Equus hemionus onager*) and livestock through a combination of remotely-sensed vegetation metrics, manipulation of livestock grazing, GPS telemetry, and assays of diet quality for onagers. Resource selection by onagers depended on both season and the presence of livestock. During the dry season, livestock reduced forage biomass compared to pre-grazing periods, demonstrating potential for competitive suppression of onagers by livestock when resources are scarce. Additionally, and during both seasons, selection for forage biomass by onagers was accentuated at night when livestock were absent, indicating onager avoidance of livestock. During the wet season, onagers exposed to livestock exhibited higher-quality diets than those that did not co-occur with livestock, suggesting that livestock grazing may enhance forage quality for onagers. Ours is the first in-depth investigation of one of the globe's two remaining populations of onager, and highlights restoration potential for a large, endangered mammal alongside livestock production. Similar to other cases in multi-use landscapes, a shifting dynamic of competition (both interference and exploitative) and facilitation—driven by seasonal rainfall—may characterize wildlife-livestock interactions in Iran and elsewhere in Asian rangelands.

187: Bat species composition of bridges spanning the Rio Grande

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Many bat species utilize manmade structures when natural roosts are unavailable. In arid regions, it is unsurprising that bat activity centers around water. Previous studies suggest there is extensive use of bridges spanning the Rio Grande as bat roosts throughout Dona Ana county. However, it is unclear why bats utilize some bridges and not others. Thus, we sought to understand how human activity and seasonality, impact roosting behaviors. Bridges were regularly examined for presence of bats and species, sex and counts noted. We estimated species richness relative to the degree of urbanization (using GIS) at each site and changes in occupancy across time (seasons). We present data for a full year of surveys from 8 bridges, each with diverse degrees of urbanization spanning 100 kilometers of the Rio Grande. We describe roost use relative to presence of people and relative urban density. To date we have documented 5,320 individuals from 8 species of bats that occur differentially across sites and noted that seasonal patterns follow trends observed in the literature. This project will create a record of bats in the region and expand our understanding of how roost use is affected by urban density and seasonality.

188: Salt marsh harvest mouse appendage propulsion and swimming efficiency

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The salt marsh harvest mouse is a federal and California state-listed species endemic to the San Francisco Bay Estuary. As such, it is subjected to periods of natural tidal and managed inundation. The proposed research explicitly focuses on salt marsh harvest mice captured within the Suisun Marsh to analyze their swimming performance in comparison to three other co-occurring rodents: the California vole, the western harvest mouse, and the house mouse. Preliminary data reveal similarities in swimming performance between the salt marsh harvest mouse and surface swimming muskrats, based on the synchronicity of tail and hindfoot strokes. Here we employ an approach for analyzing body drag and thrust power output of propulsive appendages of muskrats after Fish 1984 (J. Exp. Biol. 110: 183-201). We combined *in-vivo* kinematics of voluntary swimming behavior from high-speed videos with a cadaveric study of body drag using a recirculating water channel and a drag balance. We expect results similar to those of muskrats, in which the tail produces minimal thrust output relative to the hindlimbs for propulsion during surface swimming. These results could elucidate how the swimming efficiency of the salt marsh harvest mouse compares to that of other species and help explain how they navigate flooded habitats.

189: Movement and resource selecton of wild pigs in relation to growth stages of corn

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Wild pigs (*Sus scrofa*) are one of the most successful invasive species and frequently implicated in wildlife-agriculture conflicts. Damage to crops is common and expected to increase as pig populations expand, threatening food supply and increasing economic costs of food production. The overall goal of this research was to identify spatial ecology of wild pigs in an agriculture-dominated landscape. Specific objectives were to determine movement responses, space use, and selection within home ranges relative to resource availability and landscape features that drive wild pig behaviors. We monitored hourly movements of adult wild pigs relative to corn crops using GPS collars during 2019 and 2020 in Delta County, Texas, USA. We conducted separate analyses during 5 primary growth stages of corn. We generated movement metrics, home ranges, space use analyses, and step selection functions to quantify selection for corn and landscape context for each growth stage, by sex. Activity and movements of wild pigs were consistent with previous studies, where males had overall larger movements and space use than females. Space-use of pigs was dependent on corn growth stages, with more use of corn as the crop matured. Most wild pigs were categorized as residents, yet some did make seasonal long-distance movements to corn. This information of wild pig spatial ecology can improve management strategies aimed at the alleviation of crop damage.

190: Tourist-provided resources modify rock squirrel (*Otospermophilus variegatus*) behavior, diet, and parasite communities

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Resources and parasites can regulate populations. Eliminating constraints of one, such as saturating an environment with resources or providing anti-helminthics, may lead to dramatic changes in population dynamics and the health of individuals. Natural parks offer an opportunity to study the impact of resource provisioning by visitors to wild animal populations. Here, I explore diet-infection relationships of rock squirrels (*Otospermophilus variegatus*), a human-habituated park mammal. I surveyed 122 squirrels in sites of varying human-use in Zion National Park, Utah in different seasons in 2021. Squirrel fur was combed for flea species, measuring species richness and infestation level, and collected for isotope analysis. Observations of animals enabled the calculation of population-level activity budgets, including time spent foraging, moving, and grooming. I found that squirrels in habitats and seasons of high tourism were more abundant, consumed more diverse foods, and hosted greater ectoparasite diversity and burdens than low tourism sites. Notably, squirrels in campgrounds were infested by an invasive flea species (*Echidnophaga gallinacea*), perhaps due to contact with domestic animals. Activity budgets showed that squirrel behavior was dependent on tourist habitat type: campground squirrels increased grooming and conspecific interactions compared to trail squirrels that spent more time begging for food and interacting with people.

This work demonstrates how individual behaviors scale up to population-level health outcomes, as well as fine-scale wildlife responses to anthropogenic changes in resources.

191: How far is too far? Genetic diversity and connectivity of collared pika (*Ochotona collaris*) populations

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Predicting how species will respond to climate change represents a key conservation challenge of our time. With rapidly changing environmental conditions, gene flow and standing genetic variation are two important factors that can influence the probability of persistence or extinction of a population and can often be important aspects of conservation planning. Understanding these factors may be particularly important for climate-sensitive species, such as pikas. Here, we used a reduced-representation genomics approach (3RAD) to generate data for 5 collared pika (*Ochotona collaris*) populations in Alaska to better understand connectivity, isolation, and genetic diversity. Populations show considerable gene flow at 5-10 km, but connectivity diminishes significantly around 20-30 km. Estimates of genetic diversity are correlated with habitable area, with those regions that have greater talus (broken rock) exposure maintaining greater standing diversity. Genetic diversity (measured by pi and Watterson's theta) was generally lower than that in American pikas. These results may suggest that some populations of collared pikas might be at higher risk of extinction in comparison to America pika populations because of their lower genetic diversity. Additionally, the results provide a baseline for understanding the potential for extirpated localities or for habitat that becomes suitable due to climate change at range margins to be colonized by natural dispersal processes.

192: Ultraviolet fluorescence in living specimens of rodents and marsupials from eastern Brazilian Amazon

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The occurrence of ultraviolet (UV) fluorescence in vertebrates is an area of active study, but the biological relevance behind this phenomenon remains to be investigated. In mammals, potential explanations for positive responses to UV light include intraspecific communication, predator avoidance, and adaptation to nocturnal-crepuscular light environment. Although fluorescence has been observed in museum skins for various marsupials, placentals, and one monotreme, rare reports include observations on live specimens. Therefore, fluorescence in living mammals has yet to be broadly documented, and this data are essential to further investigate the ecological function of fluorescence in mammals. Here we report the results of an attempt to provide data in living mammals UV fluorescence. During a field-survey conducted at Floresta Nacional de Caxiuanã, eastern Brazilian Amazon, we explored the prevalence of naturally occurring fluorescence across species using ultraviolet-induced visible fluorescence photography (UVP) and video (UVV) (wavelengths at 365 nm). We were able to UVP- and UVV- process five different species, including one marsupial (*Marmosops woodalli*) and four rodents (*Oecomys bicolor, Mesomys stimulax, Proechimys roberti, Makalata* sp.). All species showed some degree of fluorescence, with different species showing differences in intensity, colors, and predominant UV fluorescence in different body parts. These are the first records of fluorescence for families Echimyidae and Cricetidae.

193: Decadal change in the distribution and genomic composition of a woodrat hybrid zone

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Mammalian response to climate change often results in the expansion or contraction of species ranges. As such, quantifying ecological and genetic dynamics at range margins is fundamental to understanding how

species respond to environmental change. Periodic sampling at range margins can provide insight into the magnitude and direction of range-edge change as well as ecological and evolutionary dynamics associated with distributional shifts. Here, we present a 10-year comparison (2011 vs. 2021) of range edge movement and changes in genomic composition of a secondary contact zone between two woodrat species (*Neotoma fuscipes* and *N. macrotis*). During 2007 – 2012, the smaller-bodied species, *N. macrotis*, showed a survival advantage over the larger-bodied species, *N. fuscipes*, in years with dry winters. This survival advantage led to an expansion of *N. macrotis* into the range of *N. fuscipes* and augmented hybridization between the species. Here, we use weather conditions from 2013 – 2021 to predict change in the range margins between the two species and test this prediction with new field sampling and genomic data collection. Our results show continued directional movement of the center of the hybrid zone and provide insight into ongoing ecological and genetic interactions between the two species.

194: A diverse flea (Siphonaptera) assemblage from the small mammals of central New Mexico

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The geographical ranges of many mammals and their associated parasites are dynamic. Comprehensive documentation of these communities over time provides a foundation for interpreting how biotic and abiotic drivers may influence host-parasite interactions and community structure. Here, we characterize the flea and small mammal community of El Malpais in Cibola County, New Mexico, by conducting field surveys for three years collecting in all seasons. We aimed to evaluate the following questions. What is the relationship between flea prevalence and flea mean abundance? Is flea abundance dependent on the biotic and abiotic variables of host sex and seasonality? We calculated the infestation parameters of flea prevalence and flea mean abundance. We then used statistical analyses to determine the relationship of host sex and seasonality on flea abundance. Among 898 mammalian specimens, 925 fleas representing 29 species were collected from 18 host species. *Neotoma stephensi* had the highest flea mean abundance, and *Thomomys bottae* had the highest flea prevalence. *Pleochaetis exilis* was the most abundant flea, and *Aetheca wagneri* had the highest prevalence. Our initial findings show that for this flea and mammal assemblage, flea prevalence and flea mean abundance are positively correlated and that flea abundance is dependent on host sex and seasonality. Assessing relationships between infestation parameters and identifying biotic and abiotic variables that drive host-parasite communities provide valuable insight into evaluating community dynamics overtime.

195: Investigating occupancy drivers across the two American pika subspecies in ROMO

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The American Pika (*Ochotona princeps*) is a cold-adapted lagomorph that lives mainly in alpine and subalpine regions in the mountains of North America. American pika populations are disproportionately vulnerable to direct and indirect climate change impacts and are projected to decline throughout North America. However, this projected population decline is not consistent across the five spatially separated subspecies of *O. princeps* in North America. Two pika subspecies are known to occupy Rocky Mountain National Park (ROMO), one in the north (*O. princeps princeps*) and one in the south (*O. princeps saxitilis*), with a hybridization zone near the Colorado River headwaters. Although both ROMO pika subspecies are expected to be negatively impacted by climate change through changes in suitable habitat, modeling predicts that the southern subspecies is disproportionally vulnerable to local extirpations. The goal of this study was to conduct pika habitat occupancy surveys along elevational gradients across the park to identify differences in occupancy patterns between the southern and northern subspecies. We detected an upslope range retraction only in the southern subspecies. These results have significance for pika management in ROMO, potentially indicating that different management plans should be considered for the two subspecies.

196: Characterization of the prion protein gene in eight breeds of Ethiopian camels

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Camel Prion Disease (CPD) is a transmissible spongiform encephalopathy (TSE) originally detected during antemortem slaughterhouse inspections in the Ouargla region of Algeria. TSEs are contracted through a variety of means including consumption of infected flesh or milk, or contact with bodily fluids. The discovery of CPD draws questions surrounding the safety of contact between humans and domestic camels or infected camel tissues. Meat from Camelus is distributed for widespread consumption in Africa and the Middle East, and is emerging as exotic meat in the Western world. Although the interspecies transmissibility of CPD is unknown, TSEs are known to cause severe motor and cognitive degradation over time in both humans and other animals. Changes in certain codon positions in exon 3 of the prion protein gene (PRNP) may indicate susceptibility or resistance to the contraction of CPD. By examining exon 3 in PRNP of Ethiopian dromedary camels and subsequent genotypic characterization of individuals may allow determination of potential susceptibility to CPD (i.e., some individuals may be predisposed to develop CPD based on their genotype). A recent study examined the cytochrome-b gene and microsatellite data representative of Ethiopian camels and did not detect unique genetic lineages; consequently, there has been no prior linkage to resistance or susceptibility to CPD. Considering that PRNP is under strong purifying selection, we hypothesize that all individuals will exhibit the susceptible genotype.

197: Wildlife mammal species inventory with the use of trail cameras in Sonoran sky islands

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The Madrean Archipelago refers to a set of mountain ranges surrounded by grasslands and desert habitats in southeast Arizona, southwest New Mexico, and north-central Sonora. The majority of the land in Sonora's sky islands is privately owned; thus, information about the wildlife species present in the area is scarce. The Commission for Ecology and Sustainable Development of the State of Sonora (CEDES), the Secretary of Agriculture, Livestock, Water Resources, Fisheries, and Aquaculture (SAGARHPA), and the Arizona Game and Fish Department (AGFD), as members of the Arizona-Mexico Commission, expressed interest in increasing the knowledge base with regards to the wildlife species that inhabit the Sonoran sky island ecosystems in order to inform future conservation actions and policies for the proper management and conservation of shared wildlife species. Thus, a binational wildlife inventory project was implemented at two private properties located in the Sierra Chivato and the Sierra Azul/San Antonio in 2019-2020. Since trail cameras were the main tool utilized, the focus was on wild mammal species detection. A combined total of 49 wild mammal, bird, and reptile species were captured by the trail cameras. The findings obtained thus far are a glimpse into the biological richness of Sonora's sky islands.

198: Mt. Graham: the state of the squirrel

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The Mt. Graham red squirrel (MGRS; *Tamiasciurus fremonti grahamensis*) was federally listed as endangered in 1987 and we have conducted population monitoring and research since 1989. Squirrel population estimates have fluctuated (range: 35-549), with current estimates in fall 2021 of approximately 100 animals. During this same period, the Pinaleño mountain range has experienced three major forest fires and three waves of insect infestation exacerbated by drought conditions. In order to understand the potential of disturbances to impact MGRS, for the past 20 years we have focused on radiotelemetric studies of space use, habitat and nest site selection, reproductive success, survival, and competition. MGRS have home ranges nearly 10 times larger than other red squirrel populations in western North America. Avian predation is the cause for the majority of MGRS mortalities, and most animals don't survive past their first reproductive attempt. In addition, litter sizes of MGRS are smaller than other populations, while juvenile dispersal distance is up to 9 times farther. The increasingly severe disturbance events in the Pinaleños have caused drastic habitat loss, with over 50% of known squirrel territories affected by moderate/severe fire damage. Current research includes continued assessment of population trends and habitat use, monitoring of remote areas previously thought uninhabited by MGRS using passive acoustic recorders, and study of vocal communication to inform the conservation and management of this imperiled species.

199: Effects of rabbit hemorrhagic disease virus 2 emergence on population estimates of New Mexican lagomorphs

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The emergence of novel pathogens in wild host populations can have strong influences on host demographics, including a reduction of survival and fitness. This reduction in vital rates can lead to an overall decline in estimates of host abundance and density. With the recent emergence of rabbit hemorrhagic disease virus 2 (RHDV2) in wild populations of black-tailed jackrabbit (*Lepus californicus*) and desert cottontail (*Sylvilagus audubonni*) in New Mexico, there is a need to document and understand the impacts of this novel pathogen on these two ecologically important species. RHDV2 has previously been documented to cause declines in lagomorph populations in Europe, but its impact on North American lagomorphs is uncertain. From September 2020 – November 2021 we conducted repeated spotlight surveys of 17-25 transects to assess populations of lagomorphs across southern New Mexico. A subset of these transects were originally surveyed between 2014–2015 as part of an unrelated study and we replicated the methods for this study. This data provided us with the opportunity to contrast estimates of jackrabbit and cottontail population measures pre- and post emergence of RHDV2. Preliminary findings indicate declines in black-tailed jackrabbit and desert cottontail population estimates following RHDV2 emergence. Further analysis will include the addition of temporal, spatial, and other covariates into models to improve estimates and better understand lagomorph population dynamics following the emergence of RHDV2 in New Mexico.

200: Assessing long-nosed bat food availability by using remote sensing imagery to build an *Agave* classifier

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Populations of long-nosed bats (*Leptonycteris yerbabuenae* and *L. nivalis*) migrate from south-central Mexico to the southwestern United States, following a hypothesized "nectar corridor" of flowering cacti and *Agave spp.* Following the removal of the lesser long-nosed bat from the U.S. endangered species list in 2018, the U.S. Fish and Wildlife Service has required post-delisting monitoring of bat populations at key roosts and estimates of local forage availability. However, the mosaic of landownership types surrounding roosts can render large portions of foraging areas inaccessible to researchers which impedes measurements of food availability. We used remote sensing products paired with ground truthing in southwestern New Mexico to map *Agave* distribution and phenology—the primary food source of long-nosed bats in this area. We tested the predictive power of two models, a random forest model and a generalized linear model (GLM), to create a classifier for flowering *Agave* through satellite imagery. Models were built using a previously constructed *Agave* species distribution model, normalized difference vegetation index (NDVI) values at 10-meters resolution, and preliminary flowering *Agave* data. The random forest model outperformed the GLM and was able to predict *Agave* occurrence for all know individuals and accurately identify flowering *Agave* patches across the landscape. Future work will focus on distinguishing flowering *Agave* from non-flowering *Agave*. Our findings will be useful for studying vegetation characteristics relevant to other bat conservation applications.

201: Describing mammalian predator impacts on interior least tern nests

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Causes of colony failure in interior least terns (*Sternula antillarum antillarum*) have been a prevalent topic for researchers investigating this previously endangered species. In Arkansas, these colonies are primarily located on sandbars formed along the McClellan-Kerr Arkansas River Navigation System, whose high regulation and channelization restricts natural sandbar formation and quality. Reduction in nesting site quality may put this sensitive species at a greater risk for predator encounters. I identified which sandbar characteristics result in higher frequencies of predator encounters at least tern colonies and which predator species were involved. I used colony, site characteristic, and camera surveys from summer 2020 and 2021 nesting seasons for my investigations. Generalized additive models were used to identify the relationships of major mammalian predator groups with thirteen site characteristics and interior least tern reproductive success. Best models of mammalian predator encounters contained variables like sandbar shape, upriver sinuosity, and the count of logs on a sandbar. Commonly identified predators included coyotes (*Canis latrans*), domestic dogs (*C. familiaris*), and northern raccoons (*Procyon lotor*). This study suggests that, while interior least tern conservation management usually focuses on local habitat features, landscape-scale features may be driving mammalian predator encounters on Arkansas River sandbars. Better understanding these relationships will help inform managers on conservation actions that need to be taken to best support the ongoing recovery of this species across its range.

202: How do microclimate and microhabitat influence seasonal territory occupancy of collared pikas?

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Alpine ecosystems are highly sensitive to climate change. Collared pikas (*Ochotona collaris*) are cold adapted alpine lagomorphs of western Canada and Alaska appear to be vulnerable to many direct and indirect effects of climate change, especially related to temperature fluctuations within their dens during winter, and changes in forage during the spring and summer. However, we do not yet know to what extent they can adapt to these changes. The goal of this research is to identify which microclimate and microhabitat characteristics influence individual collared pika territory occupancy across years. We trapped and fit colored ear tags on 175 pikas, took measurements of territory characteristics, and set temperature loggers within dens across 3 study areas of contrasting climate gradients in southcentral and interior Alaska from 2018-2021. We are examining changes in pika den occupancy by estimating annual colonization and extinction rates through a dynamic occupancy model with forage availability, den size, winter den temperatures, and snowpack as the explanatory variables. Our results will shed light on the importance of microhabitat and winter microclimate of pika dens as a proxy for seasonal territory occupancy, which have been relatively understudied and may be important to consider when making management decisions.

203: Mammal collections in Brazil: overview and database

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Advances in our knowledge on the planet biodiversity have been largely dependent upon biological collections. Recently, the Brazilian Society of Mammalogists established the Mammal Collections

Committee (CCM-SBMz) aiming to collect, organize and share information on the mammalian collections in Brazil, as well as support their management. As a first step, our goal is to provide a diagnosis of mammal collections in Brazil, and the CCM-SBMz contacted 100 collections and successfully registered 71, distributed in all five Brazilian regions. These collections house ca. 372,200 specimens, with 60% of these concentrated in three institutions: MNRJ, MZUSP, and MPEG. The database is completely digitized or in process of digitization in most collections, however, this information is not widely available online. The geographic coverage of the collections is mainly regional or national. In number of specimens, Rodentia is the most frequent order in the collections, followed by Carnivora. At the family level, Didelphidae, Cricetidae, and Felidae are the more frequent taxa. This study shows that Brazil houses an important volume of mammalian specimens. However, considering the country's continental size and high mammal diversity, these numbers are still far from a sufficient representation of the Brazilian mammalian diversity. The results summarize the first efforts of the CCM-SBMz and the committee will continue monitoring the mammal collections in Brazil, as well as working to help the management and growth of collections.

204: A graduate research methods class assists students in defining their main and interrelated research areas

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The most critical task for a graduate student is to learn to structure their research program. Designing a research program is not intuitive, but few graduate programs in organismal or evolutionary biology offer instruction in achieving this goal. We address this issue by offering a graduate Research Methods class. The initial assignment: define the main and related areas of research interest of each student. The purpose is to encourage students to think about how to define their research community. They then illustrate interrelatedness among those fields using a Venn diagram or bubbles connected by arrows that link their main field of interest to contributing fields. Students are told to expect that some diagrams will be more complex than others, depending on whether they are interested in one or more research area, depth, or breadth, and the level of detail they depict. Second, students create a set of diagrams detailing the most appropriate high-quality professional conferences and journals to which they can submit research. Papers presented or published in these areas can assist students in identifying research role models. Next, students give short in-class presentations interpreting their diagrams. Finally, we conduct a group discussion to provide peer feedback, and to let students know about others' research interests. This group work promotes a sense of community to help students generate a research-oriented system of mutual support.

205: A once in a lifetime opportunity: COVID-19 lockdown highlights the effect of humans on wildlife

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As the spread of COVID-19 pandemic increased rapidly, the whole world adopted extensive lockdowns to reduce the transmission of virus. This lockdown phase had a complex effect on wildlife as reduced human disturbances allowed wildlife to venture outside the forest area to explore novel habitats. While at the same time, decrease in forest-related law enforcement in large parts of countryside led to a substantial increase in poaching activities. We conducted a study in forested and nearby areas of a fragmented landscape using camera traps to understand the effect of lockdown on the behaviour and distribution of wildlife. To investigate the change in habitat use and temporal use of wildlife, we considered four widely distributed and highly poached mammalian species, namely leopard *Panthera pardus,* four-horned antelope *Tetracerus quadricornis*, wild pig *Sus scrofa*, and black-napped hare *Lepus nigricollis.* We used single-season occupancy models for habitat use analysis and kernel density estimates of activity patterns for temporal use analysis of study species. Species-specific change in the activity patterns of study species was observed with increased diurnal activity. All four species expanded their habitat use during lockdown period, but it was non-uniform across species. Studies of the impact of COVID-19 lockdown on the behaviour and distribution of wildlife contribute knowledge regarding the impact of human disturbances on wildlife and may aid in planning conservation actions for biodiversity maintenance.

206: Behaviorally Mediated Coexistence of Ocelots, Bobcats, and Coyotes

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The competitive exclusion principle suggests ecologically similar species will have difficulty coexisting due to overlapping resources. Yet, similar species coexist across the globe. Some mechanisms of coexistence have been proposed including fine-scale habitat partitioning, temporal separation, or shifts in dietary preference. Behaviorally mediated differences in habitat use are less studied and may contribute to coexistence. We monitored 12 ocelots (Leopardus pardalis), 19 bobcats (Lynx rufus), and 5 coyotes (Canis latrans) on the East Foundation's El Sauz Ranch and the Yturria Ranch in South Texas, USA, that were fitted with a GPS collar that collected locations every 30 minutes. We characterized behavioral states using hidden Markov models. We assumed low turning angles and longer step lengths to represent patrolling territory, larger turning angles with shorter distances between successive points would represent hunting behavior, and low angles and minimal movement would indicate periods of rest. We predicted 1) ocelots moved further (i.e. territory patrolling) in open areas and rested in dense cover 2) temporal variation in behavior within and across species. We found ocelots and bobcats remained closer to heavy cover when resting and foraging and used open areas more when patrolling territory while coyotes showed the opposite pattern. We also observed differences in the timing of behaviors within and across species suggesting fine-scale, behaviorally mediated spatial and temporal partitioning may explain coexistence of these three carnivores.

207: Unraveling carnivore conflict in an ecological framework: caracals on Namibian farmlands

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In regions where carnivores and livestock coexist, conflicts are virtually inevitable. Throughout southern Africa, caracals *(Caracal caracal)* are regarded as vermin due to livestock predation. Goals of our research were to examine specific life history traits that render caracals susceptible to conflict with humans, to understand the impacts of human persecution on caracal ecology, and to offer alternative strategies for coexistence that work within the context of caracal natural history. We collected data from 34 radio-collared and 208 necropsied caracals on working farms throughout Namibia. We also calculated relative frequencies of prey items in caracal diet from analysis of 202 caracal stomachs, 688 kill sites and 250 caracal scats (N=1140 samples). We recorded a total of 106 species consumed by Namibian caracals. Mammalian prey made up 83.2% of diet, yet livestock comprised only 2.1% of caracal diet despite their abundance throughout the study areas. In addition, we assessed demographic parameters including survival and reproduction and generated life history schedules and Kaplan-Meier survival curves to determine whether caracal populations on Namibian farmlands can withstand current high anthropogenic mortality. Our data indicate that caracal populations are projected to decline in one of the last strongholds of the species, if extensive persecution pressure continues. Understanding the drivers of this conflict is fundamental for developing mitigation strategies that promote coexistence and curtail further ecological trophic cascades.

208: Mechanisms and scope for adaptive rescue in polymorphic populations facing impacts of climate change

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One of today's great challenges centers on how to maintain biodiversity as climate change takes course. Our ongoing research project examines the propensity for standing variation inherent in polymorphic systems to act as a buffer against effects of climate change by providing an opportunity for

species to adapt in place (adaptive rescue). We investigate a known polymorphism in seasonal molting (color change triggered by daylight length) for snowshoe hares residing in the Oregon Cascades, which has resulted in populations comprised of both winter white and winter brown individuals, where proportions roughly follow a gradient in seasonal snow cover. I present plans for collection of population vital rates and behavioral data from GPS-tracked winter white and winter brown morph snowshoe hares along this gradient. Examination of results will allow us to a) directly link the strength of predation-induced natural selection to phenotypic variation in winter coat color on camouflage mismatch, b) measure phenotypic plasticity in behavior to reduce camouflage mismatch or mortality consequences, and c) estimate movement and dispersal attributes of the different morphs. The fitness-based consequences, potentially mediated by plasticity, will be incorporated into integrated population fitness models to quantify both mean fitness of different color morphs and overall expected resilience (population growth) of the populations along the gradient as weeks of snow cover decrease.

209: Elucidating pathways of rodenticide exposure of an urban carnivore

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Widespread use of anticoagulant rodenticides to control rodent pests continues to prompt concerns about exposure of non-target species. Scavengers and carnivores can be exposed secondarily to rodenticides by consuming dead or dying prey, yet the routes through which secondary exposure occurs are complex and under-studied. Our lab group has investigated possible pathways of rodenticide exposure of coyotes (*Canis latrans*) in urban southern California. We have used multiple approaches (stomach contents, molecular genetics, stable isotopes) to describe the diet of coyotes across gradients of urbanization to identify food items that might be associated with rodenticide exposure. We have used remote cameras to examine visitation by wildlife, including coyotes and native prey, of rodenticide bait stations and rat carcasses. We have also tested livers of coyotes for rodenticide residues and conducted necropsies to look for evidence of rodenticide-related mortality, as well as possible sub-lethal effects. Our results show that nearly all coyotes in southern California are exposed to anticoagulant rodenticides at some level, and that exposure is related to diet and land-use. We will discuss this evidence, what appear to be the most likely routes of exposure, and what additional information is needed to evaluate the impacts of rodenticides on coyote populations in the region.

210: Patch size and connectivity predict patch occupancy of an endangered habitat specialist rodent

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Patch occupancy theory predicts that patch size and connectivity are positively associated with occupancy probability. We tested assumptions of patch occupancy theory in the endangered salt marsh harvest mouse (*Reithrodontomys raviventris*), a salt marsh habitat specialist occurring in highly fragmented habitat. We surveyed for salt marsh harvest mice at 47 marshes throughout their range using a novel non-invasive genetic survey technique. We used occupancy modeling to estimate the effects of patch size, patch connectivity, matrix urbanization, and several habitat characteristics on occupancy probability. We found that patch size, connectivity, and matrix urbanization all had significant effects on patch occupancy, with connectivity potentially having the strongest influence. Within patches, fine-scale occupancy was positively related to the presence of high tide escape vegetation. Our data also revealed the potential extirpation of salt marsh harvest mice at numerous sites in the mid-bay region, a poorly understood part of their range. Additionally, occupancy modeling suggested our non-invasive survey approach had a very high detection probability. Our study showed that patch occupancy theory accurately predicted relationships between landscape characteristics and occupancy of a habitat specialist small mammal. In addition, our models provide important guidelines of patch size and connectivity that can inform habitat conservation and restoration for this endangered species.

211: Ancient gene introgression but no recent gene flow among Myotis crypticus and M. nattereri (Chiroptera)

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There is growing evidence that cryptic lineages exist in many morphologically conservative species of bats. It is, however, challenging to assign a meaningful taxonomic rank to these lineages, as species delineation is often complicated by conflicting data sets. Conflicting data sets may result from different types of characters (e.g. phenotypic versus genotypic) or even from different compartments of the genotype (e.g. mitochondrial versus nuclear markers). Historical, demographic or selective factors may be invoked to explain discrepancies, but final decisions regarding the species status of each lineage are often dependent on appropriate geographic and genetic sampling. The cryptic Myotis (Myotis crypticus) is a typical example where morphological characters can hardly differentiate it from its sister species the Natterer's bat (M. nattereri), whilst mitochondrial and nuclear markers show little evidence of introgression between them. We used an array of 11 highly variable microsatellite markers genotyped in 320 individuals from 21 populations sampled across Western Europe to investigate more precisely the porosity of interspecific barriers between those two species. Results based on Bayesian assignment of individual nuclear genotypes and hybrid simulations suggest that the two species are not connected by recent gene flow, confirming their status as fully isolated, biological species. However, local mitonuclear discordance indicates that ancient introgression occurred when these formerly allopatric species entered into secondary contact during postglacial range expansions.

212: Complex diversification with gene flow challenges species delimitation in tree squirrels (*Guerlinguetus*)

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Accurate estimates of species diversity lay the foundation and provide cascading effects in biodiversity research. However, delimitation of cryptic lineages can be challenging and heavily influenced by data source and methodological approach. Analyses of morphological data have suggested only two species within the widespread genus of South American squirrels, *Guerlinguetus*; conversely, molecular delimitation using mitogenomes supported the recognition of at least four distinct species. Here, we integrated phylogenomic inferences based on Ultraconserved Elements (UCEs) with fine-scale population genetic analyses using a dataset of Single Nucleotide Polymorphisms (SNPs) phased from UCEs to estimate species limits within *Guerlinguetus* and to examine evolutionary processes underlying the differentiation among putative species. Population structure analyses estimated from six to nine distinct groups representing our 64 samples. Higher genetic segregation was detected among groups from the southern portion of the Amazon basin (coinciding with major river drainages), whereas groups from the northern region exhibited lower pairwise fixation values consistent with more accentuated gene flow. Isolation by distance was only detected within the Atlantic Forest group. The most conservative scenario (six independent lineages) corresponded to highly supported clades in all UCE inferences and were confirmed as putative distinct species in a coalescent delimitation approach. Our results revealed a complex diversification pattern within *Guerlinguetus*, especially in the northern Amazon lowlands, and underlined the great potential of UCE-based SNPs to unlock cryptic species diversity.

213: Phylogenomics and morphometrics of *Sorex trowbridgii* supports latitudinal differentiation through western North America

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Forest mammals of Pacific states and provinces are associated with mesic coniferous forests of the Sierra Nevada, Cascade, and Coastal Ranges. These habitats span a latitudinal precipitation gradient and multiple potentially influential biogeographic features that have shaped mammalian diversification. Trowbridge's shrew (Sorex trowbridgii) is endemic to these western forests and ranges from southernmost British Columbia south through California, where the distribution splits to west and east of the Central Valley. Based on this distribution and knowledge from other co-distributed species, we hypothesize that intra-specific phylogeographic structure may reflect 1) rangewide connectivity with isolation by distance across latitude, 2) ring-species dynamics around the central valley, or 3) discrete regional phylogeographic structure. We collected data from the mitochondrial cytochrome b gene, morphology, reduced representation genomes, and niche modeling to test these hypotheses. The Cytb data show a clear latitudinal phylogeographic break within California, rendering the southern lineage disjunct across the Central Valley region. Morphometric data are moderately concordant with genetic data obtained so far, but with gradation of measurements across the transition zone that may indicate gene flow where lineages are parapatric. Pending genomic and niche modeling data should provide complimentary insight. The observed evolutionary history of this shrew further supports California as a hotspot for generation of regional biodiversity. We also provide insight towards the systematic placement of S. trowbridgii with respect to Mesoamerican shrew species.

214: Systematics of the Eastern cottontail rabbit (*Sylvilagus floridanus*) from Southwestern North America to South America

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The Eastern cottontail, *Sylvilagus floridanus*, with putative subspecies distributed from Canada to Venezuela, has one of the broadest distributions among extant mammal species, including populations resilient to anthropogenic activities, and occurring at high densities. As such, the conservation status of the species is listed as "Least Concern" in the most recent version of the IUCN Red List. Our current operative taxonomic paradigm, based on recent research into forest rabbits of the *S. brasiliensis* species group, suggests that there is a tighter correspondence between ecology and taxonomy of *Sylvilagus* species than may heretofore have been appreciated. In light of the potential for speciation to have occurred over this broad range, we examined the holotypes of all the subspecies of *Sylvilagus floridanus* from Mexico to Venezuela. We examined discrete character variation as well as mitogenomes from modern and historical specimens, including some of the holotypes and paratypes, and compared holotypes, paratypes, and contemporary and historical topotypical material of *S. floridanus*. Our findings demonstrate that, far from constituting a single species, the *floridanus* group of *Sylvilagus* in fact is constituted by a number of species–level taxa generally congruent with biogeographic regions. Here, we describe the morphological attributes and molecular data, and their joint bearing on speciation and biogeography of *Sylvilagus* in general, and taxa associated with the *S. floridanus* species group in particular.

215: Analysis of biodiversity data suggests that mammal species are hidden in predictable places

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Research in the biological sciences is hampered by the Linnean shortfall, which describes the number of hidden species that are suspected of existing without formal species description. Using machine learning and species delimitation methods, we built a predictive model that incorporates some 5.0×10^5 data points for 117 species traits, 3.3×10^6 occurrence records, and 9.1×10^5 gene sequences from 4,310 recognized species of mammals. Delimitation results suggest that there are hundreds of undescribed species in class Mammalia. Predictive modeling indicates that most of these hidden species will be found in small-bodied taxa with large ranges characterized by high variability in temperature and precipitation. As demonstrated by a quantitative analysis of the literature, such taxa have long been the focus of taxonomic research. This analysis supports taxonomic hypotheses regarding where undescribed diversity is likely to be found and highlights the need for investment in taxonomic research to overcome the Linnean shortfall.

216: Mammal Species of the World Next: platform for curating taxonomic intelligence to extend biodiversity data

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Wild mammals are a bellwether taxon for biodiversity conservation and zoonotic disease monitoring. Mammal taxonomy is subsequently at the center of modern biodiversity science, since no species can be conserved until it is taxonomically recognized, and no pathogen can be understood until the host's evolutionary history is resolved. However, mammal taxonomy is in constant flux: several hundred one-to-many splits since 2004 have resulted in >25% more recognized species and rendered ambiguous prior observational data for ~6,500 extant species. Here we outline progress on new infrastructure, a community platform for taxonomic intelligence called Mammal Species of the World Next (MSWx), that aims to maximize the accurate species-level linking of observational data (e.g., specimens, tissues, images, parasites, pathogens, measurements). MSWx is extending the traditional capacity of taxonomic authorities beyond species checklists to the digital extraction of published taxonomic evidence: (i) species' range maps depicting their extent of occurrence; (ii) verified DNA sequences of barcode genes like cytochrome-b; (iii) type specimens pertaining to species names; and (iv) taxonomic treatment articles depicting diagnostic traits of name usages. As a proof of concept, we geospatially disambiguate the concept labels of GBIF points for North American rodent species. Scaling of this project's tools and workflows beyond mammals and across the Tree of Life has promise for enabling biodiversity databases to stay taxonomically updated in lockstep with future progress.

217: Mosaic variation of genetics, morphology, and vocalizations among African yellow house bats, Genus *Scotophilus*

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The yellow house bat genus *Scotophilus* includes ~20 recognized species of vesper bats, which are the only extant members of the tribe Scotophilini (Vespertilioninae). Four species occur in southern and southeast Asia, 3 on Madagascar, and the remainder in Africa; most recognized species occur in Equatorial forests and/or in eastern Africa. Our recent genetic surveys in East Africa showed evidence of several additional cryptic lineages, whose integrity as distinct evolutionary lineages was supported by species delimitation analyses on 6 introns. Here we evaluate those clades with analyses of additional nuclear introns as well as with external and craniodental morphometrics, pelage variation, and quantitative analyses of vocalizations. We clarify problems with the group's nomenclature, which arose as four new species were proposed for Kenya in 2014 without reference to *Scotophilus nigrita colias* Thomas, 1904; all five species are currently recognized as valid. We also offer additional characters for species diagnosis in the field. Our integrative analyses demonstrate that species of *Scotophilus* are remarkable for their mosaic pattern of character variation; mosaic variation challenges both definition of species limits and the group's nomenclature.

218: Ultraconserved elements resolve phylogenetic relationships and biogeographic history among African bent-winged bats (Miniopteridae)

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The genus *Miniopterus* is morphologically conservative. With the help of genetic analyses, 40 species are now recognized, doubling the number recognized only 15 years ago. However, knowledge of phylogenetic relationships and species limits in *Miniopterus* has not kept pace with species discovery, and there is poor support for relationships among species. The diversification of *Miniopterus* on Madagascar has been assessed as a cryptic adaptive radiation, but continental African species remain greatly understudied, which

has resulted in vague species limits, imprecise distributions, and taxonomic uncertainty. To infer the diversification history of *Miniopterus* we sequenced thousands of ultraconserved elements from *Miniopterus* sampled from both named and undescribed species across Africa and Madagascar. We used maximum likelihood and species tree approaches to resolve evolutionary relationships within *Miniopterus* and coalescent-based species delimitation to infer evolutionary independence. Finally, biogeographic hypotheses of dispersal and vicariance events among *Miniopterus* species were inferred using time-calibrated species trees and ancestral area reconstruction. These findings indicate historical patterns of diversification for African tropical bats across the continent.

219: Species limits and population genomics within the *Phyllotis xanthopygus* species complex in Chile

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Establishing species and population boundaries is a necessary first step in any study aimed at associating genetic variation and phenotypic traits among wild organisms. Improper taxonomic or population designation can lead to spurious correlations when assigning underlying genetic variation to traits of interest. The *Phyllotis xanthopygus* species complex, composed of roughly 8 species, is widely distributed across South America ranging in elevations from sea level to > 6,000 meters, and as such, represents an ideal system for investigation of adaptation to high elevation. However, this group is known to contain substantial cryptic diversity complicating genotype-phenotype analyses. We sequenced whole genomes for more than 70 *Phyllotis* specimens sampled across an elevational gradient in northern Chile, including the highest elevational occurrence of any mammal ever recorded at 6,739 meters above sea level, to determine species diversity along this gradient and establish boundaries for subsequent analyses. Preliminary data suggest at least four distinct *Phyllotis* species are represented in this dataset and are roughly partitioned by elevation. These data add a nuclear genetic perspective to previous mitochondrial DNA-based species delimitation, allow insight in to intraspecies population differentiation, and provide the necessary foundation to further investigate mammalian adaptations to living at high elevations.

220: A constraint-based model of dynamic island biogeography in the face of global change

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We present a conceptual model showing how hysteresis can emerge in dynamic sky island systems given simple constraints on trait-mediated processes. Many sky island systems cycle between phases of increasing and decreasing size and connectivity to a source pool. As these phases alternate the dominant process driving species composition switches between colonization and extinction. Both processes are mediated by interactions between organismal traits and environmental constraints: colonization is affected by a species' ability to cross the intervening matrix between a population source and the island; extinction is driven by the minimum spatial requirements for sustaining an isolated population. Because different suites of traits can mediate these two processes, similar environmental conditions can lead to differences in species compositions at different points of time. Thus, the Constraint-based model of Dynamic Island Biogeography (C-DIB) illustrates the possible role of hysteresis—the dependency of outcomes not only on the current system state but the system's history of environmental change—in affecting populations and communities in insular systems. Importantly, it provides a testable framework to study the physical and biological constraints on populations and communities across diverse taxa, scales, and systems. We will discuss the utility of the C-DIB for projecting past, present and future biota of sky island systems in the USA and Mexico.

221: Historical and contemporary genetic connectivity patterns on tropical sky islands.

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Mountains harbor a significant number of the World's biodiversity, both on tropical and temperate regions, and are sources of high species richness and endemicity. Biogeographic features that have acted as historical barriers, jointly with landscape characteristics, shape mountain species distributions at historical and contemporary scales. In the southeast México and Central America mountains, the *Peromyscus mexicanus* species group shows patterns of allopatric distribution along with parapatric and altitudinal segregation and diversification of lineages. High altitude lineages exhibit signs of population decline since the Last Glacial Maximum, while low elevation ones had population increments during the same period, or earlier. In a different sky islands system, along temperate forest highlands on two slopes of the La Malinche volcano, the black-eared mouse *Peromyscus melanotis* shows reduced genetic variation, limited connectivity, fewest immigrants and significant isolation in higher elevation populations compared with lower ones, in agreement with the Valley-mountain model. Landscape genetics results indicate that local environmental variables differed per slope, where normalized vegetation index (NDVI) and tree height were the main factors promoting connectivity, whilst tree height, NDVI and litter cover were key in different slopes. Based on the three-dimensional data, we identified additional factors limiting connectivity, including dirt roads, grasslands, and disturbed areas. We demonstrate that significant variables associated with higher connectivity are found at highest elevations of both slopes where the forest is less disturbed.

222: Biodiversity in the borderlands: post-fire surveys and non-invasive eDNA metabarcoding to assay trans-boundary mammalian biodiversity

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The international border between Arizona and Mexico is a biodiversity hotspot increasingly threatened by the anthropogenic impacts, including fire. Chiricahua National Monument (CHIR) and adjacent borderlands are threatened by increased anthropogenic fire. In 2011, the human-caused Horseshoe 2 fire, the 5th largest in the state at the time, impacted all of CHIR; 55% of the Monument experienced moderate to severe burn severity. The Chiricahua fox squirrel (*Sciurus nayaritensis chiricahuae*) (CFS) is endemic to the Chiricahua Mountains and is one of 69 species of mammal that comprise the remarkable biodiversity there. We aimed to assess how unique mammalian assemblages, particularly species of conservation concern, within CHIR and beyond have responded to recent fire and subsequent changes to forest composition. We visited 293 of 303 historic CFS nest, searched for CFS sign, and recorded burn severity and forest structure. Further, we placed camera traps and sampled water and soil for eDNA metabarcoding at CHIR and Cuenca Los Ojos across the border in Sonora, MX. We did not detect any Chiricahua fox squirrels or their sign within Chiricahua National Monument (CHIR), and 73% of historic sites experienced moderate to severe burn, and 61.2 % of sites had no Chiricahua fox squirrel habitat remaining. Vegetation structure and composition following moderate – severe fire is altered, compromising connectivity for CFS between CHIR and the greater Chiricahua mountains.

223: Recent changes in precipitation, not temperature, drive trends in suitability in a Neotropical montane shrew

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Many range shifts, both pole-ward and upslope, are being detected for species around the globe in response to climate change. Ecological niche models (ENMs) are commonly used to estimate potential geographical shifts in response to these changes. Typically, ENMs are built using a single set of climate information, making it impossible to identify changes in the environmental margins and geographic limits of the species' distribution. Here, I used climatic time series to detect trends in habitat suitability for a montane cloud-forest species. Using a single twenty-year CHELSA climatic period, I built an ENM with Maxent for the Mexican small-eared shrew (*Cryptotis mexicanus*), a species whose distribution is constrained by humidity and temperature. Then, I transferred the tuned model to twenty-year periods based on monthly data between February 1979 and January 2016 (n = 205 periods: 240 consecutive months each). A Mann-Kendall test detected trends in habitat suitability and climatic variables in individual cells. The detected extent and direction of suitability trends are not as simple as the pole-ward or upslope shifts expected under warming conditions. Comparison between suitability and variable trends suggests that precipitation, not temperature, plays a more critical role in explaining changes in climatic suitability. Detecting suitability trends using a time series of bioclimatic variables could anticipate where and how range limits may have changed according to recent climatic changes.

224: Small mammal and viral biogeography of the Santa Catalina Mountains: a pilot study

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The Santa Catalina Mountains comprise one of the five major ranges that surround the Tucson metropolitan area and one of the constituents of the Madrean Sky Islands of southwestern US and northern Mexico. Characteristic of other sky islands, the Santa Catalinas exhibit stark changes in biotic communities along an elevational gradient due to changes in temperature and aridity, with corresponding changes in small mammal species diversity. In 2021, we began a research program to examine how contemporary and historic changes in biotic communities has influenced the evolution of small mammal populations and their associated viral pathogens in the Santa Catalinas, as a pilot study to the same patterns in small mammals of the Madrean Sky Islands more broadly. Our surveys have have so far yielded 11 species totaling 67 vouchered specimens and 42 nonlethally sampled individuals. We observed maximum per-site species richness of 8 rodent species, with an average richness of 5.2, and 2.1 average species turnover among sites; species turnover among slopes (South, North, and Peak) was similar at 1.94. Using these specimens, we aim to determine whether small mammal hosts exhibit similar biogeographic patterns as their pathogens. We present preliminary results from 8 species of Santa Catalina rodents for which we sampled host mitochondrial and viral genomes from the feces and liver of 24 individuals.

225: Habitat selection informs biogeography and conservation of mammals in the Southwest Sky Islands

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An important component of the mammalian diversity of the Madrean Sky Island Archipelago is an assemblage of species that have Rocky Mountain affinities. These species, adapted to relatively cool, mesic environments, are generally restricted to more northern and higher elevation mountaintop islands within the archipelago. Most biogeographic analyses and conservation decisions are based on species habitat requirements. However, knowledge of habitat for small mammals is generally anecdotal or focused on use, neither of which can be interpreted as habitat requirements. To better inform conservation, we investigated multiple scales of habitat selection for three endemic subspecies of chipmunks (*Neotamias*) occurring on Sky Island mountaintops. Habitat selection is a behavioral process whereby an organism selects from available resources, which allows for identification of habitat requirements. We found that these chipmunks were more restricted in their habitat selection than suggested by existing natural history information. Rather than being a habitat generalist, our results indicate the Peñasco least chipmunk (*N. minimus atristriatus*) selects a specific vegetation structure--meadows with high visual obstruction provided by shrubs and scattered trees. Rather than occurring in montane coniferous forests, the Oscura Mountains chipmunk (*N. quadrivittatus oscuraensis*) selects old-growth pinyon woodlands, while the Organ Mountains chipmunk (*N. q. australis*) selects arroyos as climate refugia. These habitat requirements have direct implications for biogeographic studies and conservation plans.

226: Inter-Class competition: A new direction in foraging ecology in the Shenandoah Valley, VA

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Life in the epigeal layer often goes unexplored, although shrews (Soricidae, 1910) have been foraging in this microhabitat for millions of years. Two shrew species that inhabit the Shenandoah Valley of Virginia, the least shrew (*Cryptotis parva*) and northern short-tailed shrew (*Blarina brevicauda*), were the focus of this study. Foraging trails and caches for these species were found at 6 study sites in a campus arboretum. A computer-controlled monitoring station, patented at the start of this study, was used to attract shrews and non-invasively obtain weight and morphological data. Also of interest was fate of invertebrate caches that shrews leave along foraging trails. Some birds and small mammals are known cachers and will in turn pilfer others' caches. However, inter-Class pilfering behavior between birds and mammals remains unstudied. Study sites included provisional food for birds, and controls had no provisioning. Cameras were used to observe visiting bird species and whether they foraged in shrew trails or at caches. Ground-feeding and caching birds were the most prolific visitors ($p = <0.01$), and are the species most often seen near foraging trails ($p = 0.01$) and caches ($p = 0.04$). Treatment sites had significantly more visits ($p = <0.01$) and treatment shrews displayed a non-significant pattern of weighing less. The information presented here provides a much-needed foundation for future studies focused on foraging interactions across taxa.

227: The SNAPSHOT USA model for large-scale mammal distribution surveys

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Managing wildlife populations in the face of global change requires regular data on the abundance and distribution of wild animals but acquiring these over appropriate spatial scales in a sustainable way has proven challenging. To address this challenge, we launched the SNAPSHOT USA project, a collaborative survey of terrestrial mammal populations using camera traps across the United States. Since the inaugural surveys in 2019, we have sampled ~1500 camera trap locations across 100+ arrays from nearly all 50 states. We continue to expand our cooperator network for surveys each fall, and our model is inclusive for diverse groups from academic institutions, museums, government agencies, Native American nations, and other NGOs. Here we present an overview of the SNAPSHOT USA model and how to join the upcoming Fall 2022 surveys. Finally, we present preliminary findings from the first three years of data showcasing patterns of mammal diversity along urban-wild gradients, and the influence of apex predators on community assembly. All data in the first two years were managed in the eMammal platform but all 2021 and future data iterations are managed in Wildlife Insights—the data are made public each year in the form of a published data paper that includes all cooperating teams. We hope this presentation encourages expansion of our network and showcases the utility of the data for ecological and conservation inferences.

228: The effects of reintroducing an apex carnivore on an insular community of carnivores

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Apex carnivores are one of the most extensively reintroduced taxonomic groups worldwide; however, little experimental evidence exists quantifying the consequences for co-occurring subordinate carnivores. Isle Royale National Park is home to the longest running predator (wolves *Canis lupus*) -prey (moose *Alces alces*) study on record. After their natural functional extirpation in the 2010s, the 2018-19 reintroduction of wolves offered a unique opportunity to study how apex carnivores shape a simple, insular community of carnivores. In a before-after framework, we quantified the demographic, spatial-behavioral, and dietary effects that the reintroduction of wolves had on a carnivore community of red foxes (*Vulpes vulpes*) and American martens (*Martes americana*). Wolves initially decreased the abundance of foxes, and the individuals that survived were associated with occupied human campgrounds, consuming higher proportions of human foods. During this period, martens increased in abundance and expanded their space use, but only to patches with high forest heterogeneity. Following wolf-pack coalescence, foxes increased in abundance and expanded their space-use. Meanwhile, marten numbers declined slightly, being most likely to persist in heterogeneous forests. Our results suggest that the cascading effects of apex carnivore reintroductions are at first strong, then appears to relax. Importantly, although apex carnivores have strong effects on carnivore communities, humans can provide a buffer for tolerated meso-carnivores, which can have negative consequences on the persistence of small carnivores.

229: Testing relationships among isotopic niche breadth, habitat structural complexity and functional divergence in sympatric rodents

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Ecological niche breadth is hypothesized to correlate with environmental heterogeneity and competition. Generalist species are presumed to thrive in heterogeneous environments with diverse resources and low competition, while specialists are presumed to thrive in homogeneous environments with evenly distributed resources and/or higher competition. We tested these hypotheses via analysis of isotopic niche breadth (δ13C and δ15N) in two sympatric rodents, *Peromyscus maniculatus* (dietary generalist) and *Perognathus mollipilosus* (dietary specialist), along the Steens Mountain elevation gradient in SE Oregon. We predicted increased population isotopic niche breadth in structurally complex and diverse mid-elevation habitats, and that *P. maniculatus* populations would be more sensitive to spatial differences in habitat and competition (estimated using functional divergence, FDiv). Surprisingly, population isotopic niche breadth was broader for both species on the basin floor (1220-1300m) than at higher elevations (1300-2968m). Habitat structural complexity and FDiv were inversely related to population niche breadth in *P. maniculatus*. *P. maniculatus* populations in habitats that were less structurally complex but had greater plant resource diversity showed broader isotopic niches, as did populations from communities with lower FDiv and thus increased competition. As predicted, population niches of the specialist, *P. mollipilosus,* did not respond to habitat or community predictors. Our findings highlight the relative importance of competition over habitat complexity in driving resource specialization for generalist species even in homogenous habitats.

230: Home range of sympatric striped skunks (*Mephitis*) and plains spotted skunks (*Spilogale*) in southeastern Texas

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In eastern Texas, striped skunks (*Mephitis mephitis*) occur sympatrically with plains spotted skunks (*Spilogale interrupta*), a smaller-bodied mesocarnivore facing population decline due to habitat loss and urbanization. We examined home range size of co-occurring striped and plains spotted skunks on Katy Prairie, a portion of the West Gulf Coast ecoregion in southeastern Texas. Our study site, Warren Ranch, is managed for cattle production, prairie conservation and is a mosaic of native prairie, minimally managed pastures, and heavily grazed pastures. From February 2019 to June 2021, we fitted striped and spotted skunks with GPS-transmitters programmed to record spatial locations 4 times per 24-hour period. We recorded spatial fixes sufficient for seasonal home range analysis (n ≥ 30 locations per season) on 20 striped skunks (10M: 10F) and 16 spotted skunks (9M: 7F). Cumulatively, data collected represent 36 striped skunk seasonal home ranges (21M: 15F) and 48 spotted skunk seasonal home ranges (31M: 19F). Using kernel UD and minimum convex polygons, we determined mean seasonal 95% isopleth home ranges of striped skunks (297 ± 66 ha) and spotted skunks (196 ± 65 ha). Previous reports suggest that home range size of both species is significantly influenced by both seasonality and sex. Ongoing analysis is examining influences of season and sex on home range size between the two species.

231: Niche tracking of dry conditions in the Spotted Bat (*Euderma maculatum*)

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Euderma maculatum ranges from British Columbia in Canada to central Mexico, crossing the United States over the Rocky Mountains. Despite being easily detected given its audible echolocation calls, little is known about the biology of this species, or the types of habitats it occupies across its distribution. We explored the present-day potential distribution of *E. maculatum* using ecological niche modeling (ENM), to evaluate the available suitable habitat for this species and document the ecoregions where it is likely to be found. Furthermore, we used model projections to the past and the future to quantify if there have been significant changes in available suitable habitat for *E. maculatum* across time. Our predictive ENMs revealed a broad area of suitable habitat for *E. maculatum* extending its potential distribution from 27 ecoregions suggested by its observation records to 87 ecoregions spanning dry areas and deserts. From the Last Glacial Maximum to the present, the projected distribution showed a northeastward shift with higher suitability in Mexico in the past than in the present. Future climate change scenarios show that its potential distribution will shift further northward into British Columbia, but with a small magnitude of change between the best- and worst-case greenhouse gas emission scenarios. Our modeling framework provides novel information to help conservation biologists refine biological inventories of one of the least known North American bat species.

232: Dietary analyses: insights from old vs. new approaches in a Chilean small mammal assemblage

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Dietary studies have classically utilized microhistological features of food items in stomachs and feces to characterize composition. Almost 50 years ago, an analysis of a small mammal assemblage in semiarid north-central Chile revealed three trophic guilds, each with two species; *Octodon degus* and *Abrocoma bennettii* were folivorous, *Phyllotis darwini* and *Oligoryzomys longicaudatus* were granivorous, and *Abrothrix longipilis* and *Thylamys elegans* were insectivorous. In addition, *Abrothrix olivacea* was omnivorous. In each guild, the first species listed was notably more abundant than the other suggesting consequences of interspecific competition. Recently, stable isotope analysis (SIA) of blood plasma of several assemblage members was conducted to examine population-level dietary variation and overlap among species. Preliminary results show strong evidence for interspecific niche partitioning, which was unexpected in this C_3-dominated ecosystem. The two broadly herbivorous species *P. darwini* and *O. degus* had distinct isotopic niches, which suggests partitioning of resources that may be the result of more granivory in the former. *A. olivacea* and *T. elegans* had distinct carbon and/or nitrogen isotope values relative to the herbivores. SIA results also suggest that an invasive omnivorous mammal (*Rattus rattus*) is a significant predator on native small mammals in remnant fog forests. The combination of such methods offers unique opportunities for studying energetic and nutritional aspects of community trophic structure against a background of changing environmental conditions.

233: Ecological impacts of a tornado blowdown on shrews in eastern deciduous forest in western Pennsylvania

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Tornadoes and other extreme climatic events (ECEs) are recognized as drivers of contemporary and future ecological dynamics. An EF2 tornado associated with a derecho touched down at Powdermill Biological Reserve in western PA in the summer of 2012. The tornado blowdown was experimentally divided up into salvage-logged and non-salvage-logged sections, with control forest on each side. As part of our long-term study at this site in eastern deciduous forest, we assessed population dynamics of small mammals inhabiting the blowdown and control areas. This present work focuses on shrews found at the site. The predominant shrew trapped at our site was the N short-tailed shrew, *Blarina brevicauda*, with much smaller numbers of masked (*Sorex cinereus*) and pygmy (*S. hoyi*) shrews. To date, we have trapped 67 *B. brevicauda* (17 blowdown, 50 controls), 3 *S. cinereus* (2 blowdown, 1 control), and 3 *S. hoyi* (2 blowdown, 1 control). The blowdown was used by all species of shrews and differences between use of salvage and non-salvage areas was not significant. *B. brevicauda* use between the blowdown and control strongly was in favor of control areas. Trap mortality of shrews was higher in control as compared to the blowdown. Body mass in *B. brevicauda* was greater in control (x=15.44 g) than in non-salvage (x=14.91 g) and salvage (x=14.83 g) areas, which is consistent with results from the rodent assemblage.

234: Habitat selection and water dependency of feral burros in the Mojave Desert

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Expansion of feral burro (*Equus asinus*) populations across the Southwest are causing rangeland degradation, competition with native species, and human-wildlife conflicts. On Fort Irwin National Training Center (NTC), California, feral burros interfere with military training and are involved in vehicle collisions and other conflicts. Limited data on burros poses a challenge for the development of management plans. We estimated home range area, water use frequency, and 2nd and 3rd order seasonal habitat selection by adult female feral burros from 2015 to 2017. Mean home range sizes (151.8 km^2) did not differ among seasons or between burros that resided close to or far from urban areas. Burros visited water sources more often during the hot-dry season (every 22 hours) compared to the cool-wet seasons (every 39.7 - 45.9 hours). Water use was consistent with habitat selection; burros selected areas near water in all seasons and at both spatial scales, but selection was stronger in the dry season and at the landscape scale. When available, burros strongly selected for areas near urban areas. Burros consistently selected for areas with green forage and at lower elevations, but selection for other topographical features was variable. Our results suggest that urban areas, and resources therein, and water sources have the strongest influence on burro resource selection, and management plans could focus mitigation efforts on these areas.

235: Influence of predation risk from the recovering Mexican wolf population on elk behavior

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Predators change prey behavior, demographics, and movements. These changes have the potential to decrease the fitness of prey through a reduction in foraging time, increased stress levels, and use of lower quality habitat. Although the magnitude of these indirect effects are debated, if strong enough, these indirect effects can reduce birth rates and decrease neonate survival. Prey have the ability to reduce the indirect effects of predators through behavioral changes, such as increased vigilance and multitasking. This study aims to quantify the effects of the Mexican gray wolf (*Canis lupus baileyi*) reintroduction to Arizona and New Mexico on elk (*Cervus canadensis*) behavior. We captured, GPS collared, and conducted behavioral observations of adult female elk across an area of varying wolf density. We developed multiple spatiotemporal predation risk indices using GPS locations of collared wolves and elk killed by wolves. We compared predation risk indices while incorporating pertinent environmental and demographic variables via a priori models to determine the best predictors of elk behavior and multitasking. Elk behavior was best predicted by predation risk and herd size. As predation risk increased so did the probability of vigilance and foraging of adult female elk while the probability of resting decreased. Increasing herd size was inversely related to the probability of vigilance by adult females. Multitasking was predominately explained by predation risk which increased the probability of multitasking.

236: Litter size in mule deer (*Odocoileus hemionus*): Do deer experience reproductive senescence?

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Evolution favors individuals with life-history traits that maximize fitness. Life-history traits that likely have the greatest influence on fitness include age at first reproduction, number of reproductive events per lifetime, and litter size. While litter size is highly variable across mammalian species, mule deer (*Odocoileus hemionous*) are known to have litter sizes of one, two, or rarely, three. Many mammal species increase their allocation of energy to current reproductive potential as residual reproductive potential decreases consistent with the terminal investment hypothesis. Conversely, other species follow the reproductive restraint hypothesis, or allocate less energy to reproduction with an increase in age. Our objective was to identify factors that influenced litter size in mule deer. Further, we determined relative support for the terminal investment and reproductive restraint hypotheses. We sampled 124 litters from mule deer with known measurements of body condition and age (collected at time of capture). We analyzed how maternal body mass, body length, condition (indicated by ingesta-free body fat) and age influenced number of fawns born per litter. We found a strong positive relationship between maternal body mass and litter size. Additionally, age strongly influenced litter size; likelihood of producing twins was greater for prime-aged females than for yearlings and older females. Our results provide evidence for reproductive senescence in mule deer and support for the reproductive restraint hypothesis.

237: Inbreeding avoidance or social learning? Examining the dispersal behavior of a migratory ungulate

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Dispersal is common in mammals and can be driven by inbreeding avoidance, competition for mates, and competition for resources. The three drivers of dispersal are evident in various species of polygynous ungulates, such as red deer and white-tailed deer. However, it is unclear if these factors impact the dispersal of a highly migratory ungulate such as mule deer, whose knowledge of migratory corridors may be more important than dispersal to adult ranges. Our objective was to determine if inbreeding avoidance, competition for mates, competition for resources, or migratory learning influence the dispersal rates and distances of male and female mule deer. We captured six-month old mule deer fawns throughout Utah, USA and fitted each individual with a GPS tracking collar. Using location data obtained from these collars, we classified each individual as "dispersed" or "not dispersed" and tested the influence of male to female ratio, density, and sex on the propensity to disperse and the distance of dispersal. We found that males dispersed more frequently than females, while females dispersed farther. Density and male to female ratio had no impact on either dispersal rate or dispersal distance, and dispersal was uncommon relative to other ungulates. We concluded that there was little support that competition for mates or resources drives dispersal, however inbreeding avoidance and migratory learning appear to influence the dispersal behavior of mule deer.

238: New analytical tools for studying habitat selection in terrestrial mammals

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The study of habitat selection is a foundational component of basic and applied animal ecology. Today, habitat selection in mammals is primarily studied using resource selection functions, a class of models that uses logistic regression to compare "used" to "available" habitat. However, these models have several statistical problems, including rampant pseudoreplication from failing to account for autocorrelation in modern animal movement data, no clear guidelines for sampling available habitat, and large amounts of numerical error from sampling too few available points. These problems are widely acknowledged but have no generally accepted solutions, so we propose three new methods for addressing them: likelihood weighting, Gaussian availability sampling, and numerical convergence checks. We demonstrate the practical advantages of these methods over conventional approaches using simulations and empirical data on a water mongoose (*Atilax paludinosus*), a caracal (*Caracal caracal*), and a serval (*Leptailurus serval*), and briefly demonstrate how to apply our methods to animal tracking data using the 'ctmm' R package. Broad uptake of these methods could substantially improve our estimates of habitat selection in mammals.

239: Climbing kinematics of co-occurring rodent species in the Suisun Marsh, California

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We investigated climbing performance of three co-occurring rodent species in the Suisun Marsh, California. Gait metrics and tail use were compared among *Reithrodontomys raviventris* (n=12)*, Reithrodontomys megalotis* (n=1)*,* and *Mus musculus* (n=1) to determine possible differences in their locomotor capabilities. Individuals were filmed traversing dowels of different orientations (horizontal, 45° descent, vertical descent) and diameters (5, 10, and 20 mm) at 250 fps from which the duty factor (durations of limb support), tail contacts, and tail coiling were quantified frame by frame. Preliminary data suggests greater use of asymmetrical gaits than symmetrical gaits across all dowel orientations and diameters. Both *R. raviventris* and *Mus musculus* showed equal use of forelimb and hindlimb support with overall higher duty factor on narrow horizontal substrates. During descents, *R. raviventris* exhibited higher duty factors overall on both substrate diameters than *R. megalotis,* and relatively higher forelimb duty factors, suggesting they use their forelimbs more for breaking. The higher duty factors employed by *R. raviventris* suggest slower, more cautious movement on narrow and inclined dowels. *Reithrodontomys raviventris* used their tails more on narrow and inclined descents compared to *M. musculus* on the same substrates. These patterns partly reflect expectations for scansorial species, suggesting that salt marsh harvest mice are well adapted for climbing, which may be critical for their survival during tidal inundation in their brackish marsh environment.

240: Seasonal foraging trends in two sympatric ungulates

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Many factors influence foraging decisions of animals. While most large herbivores forage to maximize nutrient gain and minimize energetic cost, interspecific competition and seasonality may play a role in foraging choices of sympatric ungulates. Here, we investigate diet patterns of two sympatric ungulates in the Chihuahuan Desert, the introduced aoudad (*Ammotragus lervia*) and the native desert bighorn sheep (*Ovis canadensis*). We seek to assess the extent of foraging niche overlap between these species, and if seasonality influences potential interspecific competition. We obtained fecal samples from aoudad and bighorn sheep in the Sierra Vieja Mountains, Texas. We used DNA metabarcoding of fecal samples collected over multiple seasons to determine diet composition of both aoudad and bighorn sheep. In addition, we use nonmetric multidimensional scaling ordination (NMS) to assess potential niche overlap by these two species. We also use mixed-effects models to assess relationships between diet composition and seasonality. Preliminary findings suggest that both species consume high proportions of sumac (*Rhus spp.*) and have similar diet breadth. Understanding the extent of niche overlap of these species provides insights into potential interspecific competition between these sympatric ungulates.

241: Sound pressure levels of southwestern red squirrel rattles

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Sound pressure levels of animal vocalizations play a key role in determining signal active space and provide important insight into the mechanisms and function of communication. Red squirrels (*Tamiasciurus*) produce rattle vocalizations to defend territories centered around a larderhoard. In this study, we report amplitude-calibrated measures of rattles produced by southwestern red squirrels (*T. fremonti*) in Arizona. We used a calibrated sound level meter to record rattles and a rangefinder to estimate the distance and elevation angle to focal animals. We corrected for background noise and applied an equation that accounts for spherical spreading to infer amplitude values at 1 m from the source. We discuss our findings in relation to mechanisms of vocal production, territorial behavior, and practical considerations for passive acoustic monitoring.

242: A preliminary investigation of the landscape ecology of restored tallgrass prairie small mammals

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Tallgrass prairies are among the most globally threatened ecosystems, with only one percent of the historical extent remaining. Prairie restoration is an essential strategy to preserve biodiversity and reestablish threatened species. Practitioners use management tools to shift the landscape context of prairie restoration sites, such as prescribed fire and land cover change, as well as through indirect impacts. Small mammal live trapping was conducted over six years at Nachusa Grasslands, a tallgrass prairie restoration site in North-central Illinois. During those six years, different portions of the preserve were burned annually, the preserve area increased, and the land cover changed. We used various metrics of management practices and land cover to spatially analyze species-specific patterns of small mammal populations, including both categorical and quantitative analysis of prescribed fire. Our objective is to gain a better understanding of the landscape ecology of small mammals in restored tallgrass systems and to examine the landscape impacts of tallgrass prairie restoration on a ubiquitous prairie clade. Preliminary results support previous conclusions about species-specific impacts of local- and landscape-scale factors on small mammals. Visual inspection of the number of captures at individual traps within trapping grids revealed species-specific patterns associated with habitat types. Understanding the impacts of landscape context change on small mammals will support land managers in making more informed decisions to best conserve this rare ecosystem.

243: Mustelids on my Mind: Camera trapping reveals species-specific responses to forest disturbance in Maine, USA

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There are four species of mustelid predators native to Maine, in the Northeastern United States: fisher (*Pekania pennanti*), American marten (*Martes americana*), long-tailed weasel (*Neogale frenata*) and American ermine (*Mustela richardsonii*). All four species are trapped within regulated harvest seasons, but the records from recent years have been unreliable for tracking changes in their occurrence patterns. Efficient and consistent monitoring is essential to manage these species as local and global perturbations continue to impact them. To this end, we conducted a large-scale, four-year camera trapping experiment across a gradient of forest-disturbance intensities in the central and northern Maine. We collected over 800,00 images, and recorded fisher at 85% of our 197 stations, marten at 63%, American ermine at 54% and long-tailed weasel at 16%. We examined intraguild dynamics for marten and fisher, as well as the influence of forest disturbance and composition. We found that both species preferred older stands, and although we found no evidence that the larger-bodied fisher is a limiting factor on marten, the smaller marten appears more constrained by intensive logging activity. For the two weasel species, which are very similar in appearance, we incorporated uncertain detections in our analyses. Although data on long-tailed weasel were limited, both these species appear positively associated with recent timber harvest activity, but they may have opposing preferences for forest stand composition.

244: Scaling issues in the study of livestock depredation by carnivores

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Studies of livestock depredation by carnivores are becoming increasingly common as the need for interdisciplinary strategies to promote coexistence grows. Much research has focused on the magnitude of conflict as well as suggested techniques by which to mitigate it; however, it remains unclear how insights into the severity of local conflict, or its associated drivers, may vary with the spatio-temporal scale of observation. Scale, comprised of resolution and extent, is often under-reported in conflict studies, potentially muddying inferences across studies. We evaluated peer-reviewed literature on livestock depredation by carnivores to extract information on the spatio-temporal scale of observation and magnitude of observed conflict (N=214 papers published from 1985-2022). As possible, reported conflict data were converted into a common currency of either 1) total number of animals killed, 2) total number of incidents (i.e., attacks in which multiple animals may have been killed), or 3) percent loss of stock. Metrics were determined for all livestock combined as well as for cattle and sheep/goats separately. Plotting these responses against observation extent (on a log-transformed scale) revealed a decay in number of animals and incidents with increasing spatial extent, a trend that did not vary with carnivore body mass. Understanding scaling relationships in conflict metrics should help provide more robust insights into and management interventions for human-carnivore conflict.

245: Yearly variation in gray bat activity in the Clinch River Watershed, Virginia

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The gray bat (*Myotis grisescens*) is a cave-obligate species strongly associated with riparian habitats. The species has been listed as federally endangered since 1976 after a sharp decline in population size due to human disturbance at hibernation and maternity caves. In recent years, the gray bat population has been growing thanks to protection efforts and potentially due to competition release resulting from the decline of other bat populations decimated by white-nose syndrome. As part of a project with the Virginia Department of Transportation, we continuously monitored 12 riparian sites along the Clinch River Watershed using acoustic detectors from April through November for three years (2018-2020). Monthly activity was similar

between years, but the overall number of nightly gray bat calls increased with each passing year, perhaps echoing the growing population trend. We used 15 different landscape and weather-related variables to create and compare several generalized linear mixed candidate models to determine what might impact gray bat activity. Our top-ranking model included seven variables. Year, nightly temperature, and nightly wind speed were positively correlated with gray bat activity. Total nightly precipitation, distance to the nearest hibernaculum, and amount of urban development within two kilometers of a detector were negatively correlated with gray bat activity. Our exploratory modelling of gray bat acoustic activity reexamines habitat selection and will inform management decisions and regulations as this population recovers.

246: Taxonomic revision of the genus *Megistopoda* parasites of New World leaf-nosed bats (Chiroptera: Phyllostomidae)

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Bat flies (Diptera: Streblidae and Nycteribiidae) are obligate, blood-feeding ectoparasites of bats, parasitizing only bats. Bat fly species belonging to the genus *Megistopoda* are characterized by presenting the femur III longer, thorax shieldlike, and stenopterous wings. *Megistopoda* species are therefore unable to fly and their ability to move among host individuals is restricted and this lack of flight can lead to strong host associations. The genus *Megistopoda* is composed of three described species *M. aranea*, *M. proxima* and *M. theodori*, each of which has been found to be associated with host species belonging to the New World leaf-nosed bats (Chiroptera: Phyllostomidae) genera *Artibeus* or *Sturnira*. With only three widely distributed species, *Megistopoda* is an understudied genus and species delimitation has not been rigorously assessed. Most of the used characters to identify *Megistopoda* species are ambiguous and intraspecific variation is usually not considered. In this talk, I will present the results obtained during my master's studies, where we analyzed morphological characters and a total of 12 body measures of 852 *Megistopoda* individuals (obtained from museum collections and recent fieldwork) from across their geographic range. We identified nine putative species, six new to science, but describing diagnostic characters. Future research will include phylogenetic analyses using morphological and molecular data to determine relationships, host associations, and geographic distributions among *Megistopoda* species.

247: The scale of effect for bobcat habitat selection in a brush managed landscape

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Understanding the spatial scales at which ecological processes occur can elucidate important effects of landscape conditions on wildlife and reveal scales at which species perceive and respond to their environment. In southern Texas, range management typically includes the removal of woody plant species in a systematic pattern resulting in unique landscape configurations with alternating strips of brush and open areas at a precise interval. This management strategy optimizes habitat structure for game species and livestock production; however, it is unknown on how this management impacts other species including bobcats (*Lynx rufus*). Starting in May 2021, we affixed GPS collars on 9 bobcats in La Salle County, Texas on a private ranch to evaluate how landscape composition and configuration influences resource selection and the scale at which bobcats respond strongest to fragmentation. We calculated landscape metrics using a moving window analysis at 10 spatial scales from 30 meter to 800 meters. We then investigated bobcat habitat selection using 3rd order resource selection functions. We found that bobcats selected for woody cover and avoided herbaceous cover. Negative effect of edge density and positive effect of contagion both emerged at the same characteristic scale suggesting that bobcats respond differently to various aspects of fragmentation, but at the same scale of 300 meters. Our results reveal the scale at which bobcats perceive the landscape and respond to landscape configuration.

248: Mule deer response to a pinyon-juniper removal treatment: effects on winter range resource selection

Jason J. Gundlach, University of Nevada, Reno, Reno, NV

Populations of mule deer (*Odocoileus hemionus*) are in decline throughout the Intermountain West for a multitude of reasons, including competition from wild and domestic herbivores, wildfire suppression, energy and urban development, and expansion of woody plants. A primary conservation concern for mule deer in the Great Basin ecosystem is expansion and infilling of Single-leaf pinyon pine (*Pinus monophylla*) and Utah juniper (*Juniperus occidentalis*), which provide minimal nutritional value to mule deer while outcompeting herbaceous vegetation in the understory. We investigated how removal of these trees affects resource selection of mule deer, specifically on winter range. We captured 36 adult female mule deer in the Toiyabe Range of central Nevada from April 2018 through March 2019, with all individuals being fitted with GPS collars. Pinyon-juniper trees on mule deer winter range were removed by the U.S. Forest Service with an impact area of roughly 2,600 acres. Data obtained from GPS collars was modeled within a resource selection function framework utilizing mixed-effects logistic regression. We found that mule deer exhibit strongest selection towards annual and perennial vegetation, signaling an herbaceous vegetation response to the pinyon-juniper removal treatment. Understanding which habitat covariates have the most predictive influence on movement for this population following a pinyon-juniper removal treatment will allow wildlife managers the ability to better assess areas of ecological importance for mule deer populations throughout the Intermountain West.

249: Resource selection of introduced California bighorn sheep

Emily Hagler, Pyramid Lake Paiute Tribe, Reno, NV

California bighorn sheep (Ovis canadensis) are native species of the Great Basin, occupying high elevation, precipitous terrain. Bighorn sheep selection of resources and movement are likely driven by the distribution of escape terrain, water sources, and the quality and availability of seasonal forage. Individuals translocated into a new range must find adequate resources in order to survive. As bighorn sheep become familiar with their new range, their selection of resources reflects their ability to acclimate to their new environmental conditions. The Lake Range in the northwest region of Nevada is an isolated landscape primarily within the Pyramid Lake Paiute Reservation. Our objective was to evaluate how female bighorn sheep seasonally select habitat as they become familiar with introduced habitat. We captured and translocated 21 bighorn sheep into the Lake Range in January of 2020, including 9 adult females. Each individual was fitted with a Vectronic GPS collar that collected twelve locations points per day. Seasonal selection of resources was evaluated to determine how translocated bighorn alter their habitat selection in their first year as compared to the second year. Our results show that female bighorn sheep narrow in their selection of resources the second year post translocation as compared to the first year.

250: Landscape history and mammal diversity

Catherine Badgley, University of Michigan, Ann Arbor, MI

One of the striking gradients in mammal diversity today is the concentration of species in topographically complex regions, such as mountain ranges and rift valleys. These areas contain hotspots for diversity worldwide and many small-range endemic species of high conservation concern. Since climate change is occurring fastest at high elevations and latitudes, species in montane regions are experiencing rapid changes to their ecosystems. Thus, understanding processes that generate and maintain diversity in topographically complex landscapes is highly relevant, requiring integration of information from mammalogy, the fossil record, and earth sciences. We present perspectives on the biogeographic processes that underlie the topographic richness gradient with studies based on the geohistorical record and on current biogeographic gradients. For example, western North America provides a 30 million-year record of landscape history and mammal diversity, during which a massive highland was pulled apart to form the Basin and Range. The mammalian fossil record shows the highest species richness when global warming coincided with rapid changes in topographic complexity. Phylogenetic and paleontological data indicate that speciation and range shifts both contributed to the peak in species richness. Functional diversity changed gradually as long-term cooling and drying altered the distribution of habitats across spatial and elevational gradients. Landscape history influenced regional diversity and spatial turnover more than local diversity, a pattern that persists to the present day.

251: Mountains as biodiversity hotspots through time: integrating fossils with tectonics and climate

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Mountains across the globe are biodiversity hotspots for several groups of plants and animals; however, the deep-time relationship between mountain building and biodiversity remains elusive. To investigate the formation of these patterns over geologic time, we integrated the fossil record of several mammalian families in western North America with regional models of tectonic activity, paleotopography, and paleoclimate over the past 30 million years. We found a significant positive relationship between the rate of tectonic extension and species richness, with mammal diversity peaking during elevated tectonic extension (17 to 14 Ma). During this period, faunal similarity across the region was best explained by models including paleodistance, paleotopography, and paleoclimate variables. Focusing on the species-rich and numerically abundant fossil record of rodents, we found high rates of species origination from 20 to 15 Ma and low, variable extinction rates over the Neogene. Origination rates were positively correlated with rates of tectonic extension and negatively correlated with diversity, implying a role for diversity dependent dynamics. In contrast, extinction rates were negatively correlated with the global temperature record. Taken together, our results reveal marked shifts in the dominant drivers of macroevolutionary dynamics through time, with interactions between tectonics and climate generating an origination pulse in the middle Miocene. Furthermore, mountain passes were more effective barriers during this period, shaping the regional species pool and faunal turnover.

252: Surface process contributions to elevational diversity gradients

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How and why biodiversity varies across space remains a central question in ecology and biogeography. Elevational gradients have become a popular means by which to investigate generality in the pattern of biodiversity and its underlying causes. Among causal drivers, area has been suggested to influence patterns of species richness through a variety of mechanisms including resource and/or habitat heterogeneity, colonization and extinction processes, and sampling effects. Geomorphological features of the landscape, however, have rarely been included in area hypotheses despite clear links between topographic complexity and diversity. Here we investigate the role of geomorphology in shaping diversity of small mammals along an elevation gradient within Lamoille Canyon in the Ruby Mountains of northeastern Nevada. We directly incorporate measurements of topographic relief, hypsometry, and terrain roughness into a multi-model analysis that includes environmental factors (habitat heterogeneity, productivity, temperature, precipitation), using AICc for model selection. We find evidence that topographic relief and hypsometry of the canyon are important predictors of richness along this local gradient. Our findings suggest integration between ecology and geology can advance our understanding of the role of topography in the generation and maintenance of biodiversity. Future work will include extension of this analysis to elevational gradients along river profiles with different incision patterns in other mountain ranges of the Great Basin.

253: Patterns of rodent richness and morphological disparity in South America

Renan Maestri, Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil

Mammalian biodiversity tends to increase in topographic complex regions of South America. Using rodents as a study case, we show patterns of richness and beta-diversity across South America and what is their relationship to topographically complex regions. After depicting the richness patterns, we explore how morphological disparity is distributed across geography for the most species-rich clade of South American rodents, the sigmodontines. This allow us to answer questions related to the origin of species diversity and phenotypic diversification across South America. For that, we calculated morphological disparity of skull size and shape after measuring 2877 specimens from 239 species of sigmodontines using geometric morphometrics. Biogeographic occurrence data was used to map the average species richness and disparity across assemblages. The relationship between morphological disparity and species richness was found to be saturated in around 20 species, with the peak of both richness and disparity concentrated in the Andes Cordillera. Nevertheless, morphological disparity standardized to control for richness indicated that the Andes and the Amazonia have lower disparity (despite high richness) compared to mountainous regions in Atlantic regions of South America. In general, eastern South America, in special mountainous regions of the Atlantic forest, seem to be the hotspots of morphological disparity while still maintaining one of the highest richness hotspots for these rodents.

254: Disentangling explanations for diversity in topographically complex regions

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Two environmental factors are widely thought to explain high diversity of topographically complex regions: topographic discontinuity and environmental heterogeneity. Distinguishing their separate and joint contributions to diversity is difficult because they commonly co-occur geographically. They may, however, be distinguishable in their effects on the relationship between diversification and ecological divergence. Traditionally, adaptive radiations are attributed to “ecological opportunity”, which is the opportunity to evolve along diverse ecological axes afforded by unoccupied ecological space, such as the ecological space opened by extensional tectonic processes. A distinctive feature of adaptive radiations is that speciation is driven by ecological divergence. Non-adaptive radiations, in contrast, are characterized by speciation without ecological divergence. The traditional model of an adaptive radiation needs to be modified for cases in which ecological opportunity is temporally staggered, such as when open ecological space is arrayed along an environmental gradient, making dispersal a key part. Nevertheless, a causal relationship between speciation and adaptation is still expected. In contrast, topographic discontinuity, by itself, can promote allopatric speciation, and in disconnected landscapes, speciation can proceed without adaptive divergence. An alternative to both models, which similarly highlight accelerated speciation rates, are two that emphasize processes maintaining high diversity regardless of speciation rates, by promoting coexistence within diverse communities at different elevations or across heterogeneous microenvironments. We exemplify analyses that distinguish among these processes.

255: Aridity effects on rodent elevational diversity patterns: Implications for global change

Brooks Kohli, Morehead State University, Morehead, KY

Mountains harbor extraordinarily high biodiversity and play a critical role in conservation efforts. While much has been learned about the factors that affect mammal species richness patterns on mountains, we still lack a clear understanding of the community assembly processes that drive elevational diversity gradients. Here I will describe the results of the first large-scale comparative analysis of mammalian functional and phylogenetic diversity patterns on elevation gradients. Comparing diversity patterns across 49 mountains containing 374 rodent species revealed a stark contrast between wet mountains and dry mountains, despite a common hump-shaped species richness pattern. Specifically, functional and phylogenetic richness and dispersion decline with elevation in wet mountain systems but increase with elevation in dry mountains. Wet-mountain lowlands and dry-mountain highlands harbor the most functionally and phylogenetically diverse rodent communities, indicating that water availability is a critical environmental filter for montane small mammal assemblages. This general dichotomy between wet and dry mountains suggests that a mountain’s climate context should inform its global change predictions. To investigate some potential implications, I present a case study from small mammal surveys spanning nearly 90 years in a dry mountain range and protected area in the western US. Shifts in functional diversity indicate complex community responses to climate and habitat change across elevation.

256: An isotopic approach to ecological patterns among wolf-like canids of the Southern Great Plains

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Human persecution of North American wolf-like canids (subfamily Caninae, genus *Canis*) has severely reduced their range and diversity. This is notably evident in the Southern Great Plains of the U.S., spanning Oklahoma, Texas, and New Mexico. Prior to roughly 1950, this region supported the now extinct Great Plains wolf, and locally extinct gray and red wolves. Mexican wolves are restricted to sparse releases and recovery program area in New Mexico, and current diversity is largely comprised of the coyote and domestic dog. As interspecific antagonism and competitive exclusion is known to affect canid behavior and resource access, reduced diversity poses important ecological questions. Were niche partitioning or dietary shifts employed to reduce competition during historical overlap? Following wolf eradication, have coyotes overtaken the "wolf niche?" To address these questions, we isotopically analyzed adult skeletal specimens from institutional collections grouped by taxon, subregion, and collection date. Analyses included radiocarbon dating for chronological age, and stable carbon (^{13}C) and nitrogen (^{15}N) isotopes for dietary composition and relative trophic position, respectively. Radiocarbon dating revealed ages 385 to 125 +/- 15 years before present. Preliminary stable isotope data demonstrated no significant changes in values of pre-1950 and post-1950 coyotes. Unchanged coyote trophic position and dietary composition could be due to insufficient time for change to occur or human influences. Additional specimens will provide more robust taxonomic, geographic, and temporal coverage.

257: Population viability analysis of Ohio?s recovering bobcats

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Understanding how wildlife populations fluctuate in response to anthropogenic change is important for management and conservation. Bobcats were extirpated from many midwestern states in the mid-1800's due to habitat loss and overharvesting and recently recolonized Ohio spiking interest in a trapping season. However, demographic factors and viability of this population are unknown. We conducted a spatial population viability analysis incorporating age and sex-specific road mortality utilizing data from roadkill bobcats, habitat suitability using data from verified sightings, and included fecundity, age and sex specific survival rates drawing on data of other unharvested populations. We simulated trapping considering two scenarios based on the population structure of the harvested animals; "all-animals", in which all ages have an equal probability of harvest and "adults-only" where ages 2+ are harvested. We modeled current and proposed trapping scenarios of varying harvest intensity for 40 years with 300 trajectories. Under current conditions, the median population reaches carrying capacity in approximately 10 years with an interquartile range = ~7000 – 8000 individuals. With low harvest intensity, the final population size for the "adults-only" scenario is lower (median = ~7400) than the "all animals" (median = ~7800). Under high harvest intensity, the population reaches a median of ~6300 and ~7000 individuals for "adults-only" and "all-animals" scenarios, respectively, and many trajectories showed declining populations. Findings will be used to inform decisions on population-level management.

258: Mixed-severity wildfire shapes habitat use of ungulates and large carnivores

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Wildfire is a widespread form of ecological disturbance and can have both positive and negative effects on animals. Further work is necessary to understand how large mammalian herbivore and carnivore populations respond to the gradient of fire severity. The overall objective of this research was to understand the relative roles of bottom-up and top-down factors across the gradient of fire severity on populations of ungulates (i.e., elk and mule deer) and large carnivores (i.e., black bear, mountain lion, and gray wolf) seven years post fire. Remote wildlife (RW) cameras sampled the gradient of fire severity seven years post a large mixed-severity wildfire (Wallow Fire, year 2011, 2,177 km^2) in the White Mountains of Arizona, USA. We evaluated RW camera data using single-species occupancy and Royle-Nichols (relative habitat use) models. As predicted, large mammals (black bear, elk, mountain lion, mule deer, and wolves) exhibited high occupancy and/or habitat use in relation to higher levels of fire severity and/or fire heterogeneity, which was likely related to bottom-up factors related to increased food resources. Some species (black bear and elk) also exhibited relatively high use of unburned forest. If high occupancy and/or habitat use by wildlife in

areas experiencing higher fire severity and heterogeneity translates into increased populations of animals, wildfire might be beneficial to humans, focal wildlife populations, and fire-adapted ecosystems.

259: Spatial capture-recapture and LiDAR-derived metrics reveal high ocelot densities on private ranchlands in Texas

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Reliable estimates of population density and size of a species are crucial population parameters in wildlife conservation and management, especially in the context of the Endangered Species Act. In the United States, ocelots were listed as federally endangered in 1982, but no formal population estimates have ever been quantified. Although vegetation structure has been linked to ocelot habitat use, its effects on encounter probabilities are poorly known. We integrated LiDAR-derived canopy metrics and spatial capture-recapture models to estimate ocelot density, encounter probabilities, and population size on private ranchlands in southern Texas. From September 2020 to May 2021, we conducted camera surveys (42 camera stations) on the East Foundation El Sauz Ranch. We observed a high density of ocelots (17.6 ocelots/100 km^2) with a local population size of 36.33 ocelots (26.10–58.60). Encounter probability of ocelots increased with increasing canopy cover at 2 m and decreasing proximity to woody cover, and movement parameters decreased as canopy height decreased. Use of LiDAR-metrics allows us to understand where ocelots are likely to be detected, which serves as an important aspect of population monitoring for this regionally endangered species. The estimates of population size and density in this analysis reflect the most current estimates and are the first empirical population estimates of ocelots in a portion of their range in southern Texas.

260: An adaptation of dual-frame sampling for estimating bat population trends in multi-hibernacula systems

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Abundance estimates are the most informative metric of population status but are difficult and costly to achieve for rare or elusive species. For bats, which are highly mobile and nocturnal, abundance estimates are usually only possible at their roosts. Although they are relatively easy to census in individual roosts it is often unclear whether observed trends are representative of broader populations trends. Dual-frame sampling is useful for monitoring wildlife populations which exhibit site fidelity and are highly visible but where the proportion of the population comprised by known sites is unknown. We adapted a dual-frame sampling approach to estimating abundance of Townsend's big-eared bats (*Corynorhinus townsendii*) hibernating in system of nearly 800 caves at Lava Beds National Monument in northern California. Following 4 years of surveys we began substituting survey-informed estimates for some site-types to improve efficiency of the monitoring effort. After 8 years of survey, we estimated that approximately 2285 bats hibernated at the study site and observed fluctuations of up to 15% around the mean population estimate and as much as 30% from the previous year. Because our analytical approach generates unbiased population estimates while accommodating annual variability in survey effort among years, it should be attractive to wildlife managers faced with shifting priorities and resources.

261: Gliding towards extinction: drivers of decline in an urban population of the Australian squirrel glider

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Determining causes of population declines is often challenging. In Australia, many species of arboreal mammal are in decline across the continent. The squirrel glider (*Petaurus norfolcensis*), a small gliding possum, has historically occupied native eucalypt forest and woodland in a wide arc along the east coast of Australia. Changed land use from urban development and agriculture has permanently altered and fragmented its habitat. In sub-tropical Brisbane, Queensland, remnant forest patches provide valuable habitat to many native mammals, including the squirrel glider. The focus of this study is a population that occupies a small urban forest remnant (~90 ha). The glider population has shown a steady decline over 20 years of regular monitoring, whereas a population occupying a much larger remnant has not. This study considered the potential causes of this decline, investigating three hypotheses; (i) genetic condition and breeding success, (ii) anthropogenic disturbance and land use changes, and (iii) environmental conditions and predation. This study provides insight into the complexities of identifying the causes of declines, despite our established knowledge of this species' population ecology. Although a useful case study on small and urban populations, this study may also contribute to a broader understanding of declines in similarly threatened species, and how best to conserve and manage such species in the future.

262: Morphometrics of white-tailed deer are correlated with fine-scale patterns of soil composition

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Body size of large mammals varies across the landscape because of differences in environmental conditions. This pattern is recognizable at large spatial scales because of the wide gradient in environmental conditions. We investigated whether environmental conditions at relatively fine spatial scales influenced morphometrics of white-tailed deer (*Odocoileus virginianus*). During 2011–2018, we captured 4,561 deer on 7 sites in South Texas and recorded morphometric data. The 7 sites were located on a ~145 km gradient from coastal to inland; soil characteristics ranged from sandy (>70% sand) to loamy. We used the von Bertalanffy growth function to generate asymptote values of total body length, body mass, and antler size for each sex captured on each site. Asymptote values were negatively correlated with % sand for male antler size (r = -0.62), total body length (female r = -0.76, male r = -0.81), and body mass (female r = -0.76, male r = -0.75). Relative to the sandiest site, mean asymptote value from the 6 sites was higher for antler size (2%), female total body length (3%), male total body length (4%), female body mass (8%), and male body mass (18%). Our data indicate that soil composition is correlated with biologically meaningful variation in morphometrics of white-tailed deer at fine spatial scales. We hypothesize that nutrition is the ultimate driver, influenced by quality or quantity of vegetation.

263: Effect of anthropogenic development on the Sonoran pronghorn population in the Pinacate Reserve, Sonora, Mexico.

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The Sonoran pronghorn (*Antilocapra americana sonoriensis*) is one of the recognized subspecies of pronghorn, endemic to the Sonoran Desert and considered threatened in Mexico and the United States. The main threats for this subspecies are the altered and fragmented habitat structure due to human disturbance, reduction of forage availability, predation, loss of genetic diversity, and high mortality rate due to drought and poaching. Sonoran pronghorn population in El Pinacate Biosphere Reserve in Sonora, Mexico has been isolated for decades because highways, roads, fences, and walls create effective barriers on the northern and eastern boundary of the Reserve. We deployed camera traps to analyze occupancy to better understand the effect of human development on the pronghorn population and habitat use. Sampling sites were set at different distances from the roads, highways, and physical barriers to evaluate their effect on the pronghorn. The results obtained during three years of sampling are analyzed and discussed. We recorded very few individuals along the highways, different to sites located at 750 and 1,500m. Preliminary findings suggest that highways are the covariate with the most significant adverse effect on pronghorn occupancy. This information is relevant for the management of the Sonoran pronghorn in the area, since their subpopulation will remain isolated from the rest of the distribution range, which implies the urgency of decisions to solve this connectivity problem.

264: Risk from a top predator and habitat complexity influence scavenging by smaller carnivores

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Large carcasses serve as hotspots of encounters among carnivores, so subordinate species must weigh the risks and rewards associated with scavenging, which can be influenced by a variety of intrinsic and extrinsic factors. In the southeastern United States, white-tailed deer hunting provisions a massive amount of carrion, which appears to be an important food source for coyotes (a novel top predator), but we know little about how coyotes influence the scavenging behavior of smaller carnivores. In this study, we evaluated the relative importance of risk from coyotes, vulture activity, habitat, and remaining food on carnivore scavenging by deploying 71 deer carcasses within a managed forest in South Carolina in January 2020 and 2021. Long-term risk from coyotes was positively related to bobcat discovery of and time spent at carcasses, and short-term risk reduced feeding by bobcats and opossums. Habitat effects were also scale-dependent, where tree attributes were related to carcass discovery for bobcats and raccoons, and minimal understory cover facilitated gray fox and bobcat scavenging, despite short-term risk from coyotes. Vulture activity appeared to serve as a cue for gray foxes. Collectively, we highlight how coyotes had species-specific, scale-dependent effects on smaller carnivores, which were mediated by vegetation structure. Future research should investigate these interactions during other seasons and try to quantify the ecological effects from human-provisioned carcasses on populations and communities.

265: Predators of Africa's largest mammal migration

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Large seasonal animal aggregations can dramatically alter food webs, as seen with the bears at salmon runs and predators at wildebeest migrations. The straw-colored fruit bat (Eidolon helvum) migration stopover in Kasanka, Zambia established it as the numerically largest concentration of mammals in Africa. Every year in October and November 1.4 million bats come to roost in the 25ha bat forest, resulting in an incredible density of animal biomass at 14,400kg/ha. These bats spend the day in the swamp forest, leaving each night to feed on fruit in the surrounding community. One family of eagles is known to hunt the bats from above, but nothing is known about the terrestrial predators. We used camera traps to census predators in the forest before, during, and after the bat migration to test three hypotheses. First, we predict that predators will increase their use of the swamp forest when the bats are in residence, especially mammalian carnivores (e.g. leopards, mongooses) and snakes. Second, we predict that predators will time their reproductive cycle to take advantage of this abundance with more young offspring when the bats are present. Finally, we expect the normally nocturnal mammalian predators will become more diurnal to hunt the resting bats. We completed field surveys in February 2022 and I will present our findings showing the ecological impact of the Africa's largest bat congregation.

266: Human impacts disrupt the functional relationship between traits and environment in large mammal communities

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Large mammals, important contributors to ecosystem function, have been affected by the modern biodiversity crisis, either directly by purposeful extermination or indirectly by land-use changes. As such, they may be useful indicators of human impact on ecosystem function. We use ecometrics, functional-trait modeling, to examine the relationship between vegetation cover and locomotor traits of carnivorans and artiodactyls and the extent to which human influence has disrupted that relationship. We show that predictive power is better when locomotor traits of both primary consumers (artiodactyls) and secondary consumers (carnivorans) are combined ($\kappa = 0.73$, $p < 0.001$). We then demonstrate that geographic regions where the model's predictive power breaks down are those that have experienced the greatest human influence, particularly in Europe ($\kappa = 0.38$, $p < 0.001$), though it is prevalent across highly impacted areas of other continents. Our findings confirm that anthropogenic impacts disrupt the expected relationship between functional traits and environment in large mammal communities ($y = -0.006x + 0.79$, $R^2 = 0.21$, $p < 0.001$), suggesting that the functional relationships within those communities may have become compromised. Further, our models of communities capture the cascading interactions between taxa, traits, and anthropogenic modifications of environments. Conservation and restoration practices should carefully consider how the suites of functional traits of communities interact with the broader environment when working to maintain or reestablish ecosystem functions.

267: Influence of Mexican wolves on elk habitat selection

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Predation is a primary limiting factor for prey and in addition to direct impacts (killing of prey), it establishes risk, which indirectly influences prey behavior and ecology. We evaluated the influence of Mexican gray wolves (*Canis lupus baileyi*) on habitat selection and spatio-temporal predator avoidance strategies of elk (*Cervus canadensis*). We fit 866 adult female elk with GPS collars across areas of varying wolf densities within the Mexican wolf experimental population area (MWEPA) of eastern Arizona and western New Mexico. Using step-selection analyses we examined relative intensity of elk use in relation to habitat attributes, predator/prey diel activity, and multiple measures of risk, including predicted wolf presence—a function of wolf habitat selection, utilization distributions, and pack size—as well as openness, and predicted risky places, modeled from attributes of sites where wolves killed elk. Preliminary analyses reveal the effect of risk on elk habitat selection was variable, but across all seasons, relative use by elk was best explained by incorporating an interaction between day period and predicted risky places. This behavior supports evidence that in ecosystems where predators and prey are highly mobile and largely overlap in space, responding to predictable and relatively static environmental cues which influence encounter and kill rates may better balance energetic trade-offs than spatially avoiding predator presence or resources in proportion to predator activity.

268: Is niche overlap greater among closely related species in a Mojave Desert rodent community?

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The determination of niches is important for interpreting how communities can respond to environmental change and, in settings where management is needed, can support decisions of conservation scientists. Niche overlap in communities is advantageous to maintain ecosystem function through redundancy. However, a high degree of overlap, which might be expected among closely related species, may also lead to competition and, potentially, competitive exclusion when resources are limited. We employed stable isotope analysis to examine the trophic niches of 14 rodent species in the Mojave Desert, including 4 *Peromyscus spp*., 4 *Dipodomys spp*. and 6 species without congeners included. Samples were taken primarily from specimens collected in spring (February - June) 2015-2019 as part of the Grinnell Resurvey Project conducted by the Museum of Vertebrate Zoology. We compared δ15N and δ13C signatures from 649 fur samples analyzed using a CHNOS Elemental Analyzer. We predicted that species would display trophic and spatial variation in nitrogen signatures; samples collected from locations with greater nitrogen deposition in recent decades as well as folivorous and herbivorous species should display enriched isotopic values compared to others. Preliminary analyses support this prediction, but species also segregated along the C axis, which may suggest differential use of C3 and C4 plant parts. Continuing analyses will illustrate if niche segregation is particularly pronounced among congeners.

269: Drivers of beta diversity among cricetid and heteromyid rodents in rangeland habitats

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Understanding the ecological causes and processes that shape distribution and abundance and ultimately patterns of biodiversity remains a fundamental task in ecology and biogeography. In particular, understanding the influence of generalists and specialists on patterns of community composition may provide insights on the role of environmental and spatial patterns in structuring these systems. Beta diversity is a useful measure of biodiversity that accounts for differences among local communities in a region. We surveyed rodent communities at 35 rangeland sites across north-central Texas and partitioned beta diversity into balanced variation in abundance (i.e., turnover) and abundance gradients (i.e.,

nestedness) to make inferences about processes underlying spatial patterns of rodent community composition. We captured 14 species of cricetid and heteromyid rodents; results suggest high beta diversity among rodent communities, primarily due to high turnover, although there was no overall relationship between beta diversity and environmental variation or distance between sites. However, heteromyid beta diversity was more strongly related to turnover and we identified a significant correlation between heteromyid beta diversity and precipitation in the previous year and distance between sites. These patterns may be due to greater ecological specialization and dispersal limitation in heteromyids relative to cricetid generalists. Results from our work improve understanding of rodent community structure and the degree to which important life-history differences among taxa influence spatial variation in biodiversity in rangeland systems.

270: Exploring the National Ecological Observatory Network (NEON) small mammal collections, samples and data

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The National Ecological Observatory Network (NEON) is a continental-scale project designed to facilitate monitoring and forecasting of ecological and evolutionary change. Expected to continue for 30 years, the observatory produces and openly publishes 181 ecological, climatological, and genomic data products collected from 47 terrestrial and 34 freshwater aquatic field sites. In addition to providing these rich datasets, NEON simultaneously collects over 100,000 physical samples and specimens each year. The NEON Biorepository at Arizona State University curates these samples into more than 60 unique collections and enables their use in research. Mammals are a strong Biorepository focus, as these collections include blood, hair/whisker, tissue, DNA, and fecal samples from small mammals, as well as voucher specimens and their endo- and ectoparasites. The samples and specimens result from NEON's standardized capture-recapture sampling conducted at 45 terrestrial field sites. Specimen and sample data (including images) are made available to the research community through the NEON Biorepository data portal (biorepo.neonscience.org) and are also accessible via the Global Biodiversity Information Facility (GBIF) data portal. At this time, more than 55,000 mammal-derived samples are available for a wide variety of research purposes. We invite you to come learn more about this fast-growing and diverse collection and how the NEON Biorepository may support your research.

271: Ecomorphological shifts across a rodent community since the Ice Age extinctions

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Small mammals can tell big stories of ecological and environmental change—such as toward the end of the last Ice Age ca. 11,700 years ago, a period marked by megafaunal extinction, climatic transition, and human arrival that set the stage for modern ecosystems. This period is recorded at the Rancho La Brea asphalt seeps in Los Angeles, California, USA, which preserves a rich Pleistocene to Holocene assemblage, including small mammals. Here, we quantify potential resource-use shifts in the local rodent community over the last 55,000 years using two-dimensional geometric morphometric analyses of the dentary, or lower jaw, of eight fossil genera, comparing these to the dentaries of 10 modern local rodent species. We predicted shifts in dentary morphology reflecting changes in diet likely stemming from shifts in plant diversity and environment. All eight fossil genera still inhabit the area today, showing relative stability in taxonomic composition: *Dipodomys*, *Microtus*, *Neotoma*, *Perognathus*, *Peromyscus*, *Reithrodontomys*, *Spermophilus*, and *Thomomys*. However, we recovered shape differences in four genera and size increases from fossil to modern-day representatives of three genera. Detailed analyses may reveal species turnover, although this is not currently possible given coarse taxonomic resolution. Despite time-averaging, these preliminary differences suggest a gradual but perceptible response by the small-mammal community to large-scale abiotic and biotic change, highlighting how paleoecological records can illuminate baseline resilience and ecosystem function preceding anthropogenic effects.

272: Sky islands and desert seas: the importance of the conservation of biodiversity in the borderlands

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The Madrean Archipelago in the borderlands of SW US and NW Mexico are recognized as an area of megabiodiversity harbored in a landscape of mountain islands and desert seas. For mammalogists, the region has incredible diversity at the intersection between the flora and faunas of the Rocky Mountains to the north, the Sierra Madre to the south, the Sonoran Desert to the west, the Great Plains to the northeast and the Chihuahuan Desert to the east. The sky-islands region also has been important in the history of ecology from early surveys along the US-Mexico border that cataloged the initial diversity to the formation of foundational ideas on life zones across altitudinal gradients, island biogeography theory and climate change. More recently, the sky islands have been a focus of high profile conservation and management efforts for mammals with leadership in wildlife crossings, reintroduction of Mexican wolves, desert bighorn and black-footed ferrets, collaborative efforts to manage black-tailed prairie dogs in a multi-state conservation agreement, challenges to border crossing populations of endangered jaguars and Sonoran pronghorn and the declines of high elevation montane endemics like the endangered Mt. Graham red squirrel. I will weave our 30 years of work on mammals of the region in a celebration of this biodiversity with an appreciation of the historical significance of the borderlands tempered by an examination of future challenges.

V-1: Female choice for exploratory male personalities through signal location by meadow voles

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Some animals demonstrate mate choice based on personality. However, it is not well known how animals assess the personality traits of others. Individuals may assess conspecifics through variation in signal composition and use. We determined the personalities of male meadow voles (*Microtus pennsylvanicus*) and then tested how these males placed odor marks across their environment as they explored a clean open field arena. We found that exploratory voles placed more marks in the center of the field than non-exploratory voles. As well, voles that were bold and less anxious marked less than bold and anxious voles. Conversely, cautious and less anxious voles marked more than cautious and anxious voles. However, despite these numerical differences, only exploratory male voles made proportionally more center marks. We also exposed female voles to sets of odor marks of males. Marks of the two males were placed either in the center or on the edge of an arena; later, females preferred odor marks associated with the center of the field. Together, these results imply that a male meadow vole's personality can be expressed, assessed, and preferred by a potential mate through differences in their odor mark location. Differences in signal use, rather than composition, may allow active mate choice of personality traits.

V-2: Identifying potential reservoirs of *Borrelia burgdorferi* sensu lato among central Florida rodent species

Sean Beckmann, Stetson University, DeLand, FL

Lyme borreliosis, caused by *Borrelia burgdorferi* sensu lato, is the most common tick-borne disease in the United States. While there are several foci of Lyme borreliosis, the disease has been reported throughout the contiguous US. Additionally, while ticks must first acquire the pathogen from a reservoir host before being able to transmit it, cases are routinely reported in several areas outside of the range of the primary reservoir, *Peromyscus leucopus*. The focus of this study was to identify candidate reservoir species in central Florida. Tissue samples were collected from 302 rodents from 2019-2021 in multiple habitat types and tissues were screened for *B. burgdorferi* sensu lato via genus specific PCR amplification of Flagellin B and Outer Surface Protein B, followed by sequencing of PCR products. Four rodent species were sampled: *Neotoma floridana, Peromyscus gossypinus*, *Podomys floridanus*, and *Sigmodon hispidus*. *Borrelia burgdorferi* was identified in all four species with high prevalence (>30%). *Podomys floridanus* exhibited the highest prevalence (>60%) and harbored three pathogenic *Borrelia: B. burgdorferi* sensu stricto, *B. bissettiae*, and *B. garinii*. *Sigmodon hispidus* harbored both *B. burgdorferi* sensu stricto and *B. bissettiae*, while *P. gossypinus* and *N. floridana* only harbored *B. burgdorferi* sensu stricto. These data suggest that several species of rodents in central Florida may represent reservoirs of pathogenic *Borrelia*. However, additional research is needed to verify these findings and assess transmissibility.

V-3: Ecology and conservation of Asia?s smallest antelope in the land of the lions

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The four-horned antelope (*Tetracerus quadricornis*) is Asia's smallest antelope species and is endemic to the Indian subcontinent. Though widely distributed, it is nowhere found in high abundance and has always been known as a shy and elusive creature. From its reported distribution at the turn of the 20th century, the species has experienced dramatic range reductions with present populations surviving in isolated forested patches. The IUCN Red List has designated the species as Vulnerable and recommends the need for detailed scientific investigation to fill knowledge gaps. Gir forests, globally known for the last free ranging population of Asiatic lions form the western most distribution limit of the four-horned antelope with its population disjunct from peninsular India. The current study was carried out in the Gir protected area to assess the abundance and understand the factors governing the distribution of the species. The abundance estimation was carried out using distance sampling through data collected on vehicle transects. Presence only models were developed using Maxent to understand the factors that governed the distribution of the species in the study area. The density estimate of the species in the Gir protected area was found to be 0.17±0.06 (SE). Vegetation, elevation and proximity to water chiefly contributed to the species' distribution in the landscape. Conservation awareness and sensitization about the species among different stakeholders was generated through various media.

V-4: What is missing in the phylogenetic tree of Vampyressine bats (Phyllostomidae: Stenodermatinae)?

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Vampyressine bats are a highly diverse subtribe within phyllostomids. Numerous phylogenies have been reconstructed with different methods and characters, but so far it is not clear how the early diversification of the subtribe could have occurred, due to low support and incongruencies in basal nodes. Here, we explored the phylogenetic information that skull shapes may have as characters in a phylogenetic reconstruction, using 2D geometric morphometrics to describe the shape of two modules (neurocranium and rostrum) from the dorsal, ventral and lateral view of the skull of 14 species representing each genus of the subtribe Vampyressina. In combination with morphological and molecular characters, we performed a phylogenetic analysis using Parsimony criteria to obtain a reference tree and the phylogenetic indexes to each shape character. Additionally, we performed a phylogenetic signal test to each module using a molecular-based tree. We obtained low support in the same early diversification node of the subtribe, but the topology matched with recent proposals. We found that the shape of the rostrum and palatine have phylogenetic information, contrary to the shape of the neurocranium. We identified shape synapomorphies that could be related to olfactory systems, echolocation and feeding. We aimed for further research in the anatomy of the sensorial systems of vampyressines, that may add valuable phylogenetic information that will help to elucidate their evolutionary history.

V-5: Cranial morphology supports two well-differentiated groups within Central American brocket deer *Mazama temama*

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The Central American brocket deer (*Mazama temama*) is widespread across the Mesoamerican forests, yet it remains largely unknown. Three subspecies are recognized currently based on pelage coloration. However, it remains unclear if there is any pattern of morphological variation throughout its distribution.

Here, we compared two models of morphological subdivision, namely the traditional subspecies and another based on biogeographic provinces via 2D geometric morphometrics and ecological niche modeling. The second model presented a better fit to the observed variation in cranial shape and size. We found divergence in size between individuals from Mexico and Guatemala (northern group) relative to specimens from Honduras, Nicaragua, Costa Rica, and Panama (southern group), the latter being 8% larger than the northern group. Centroid size showed a significant correlation with geographic distance suggesting an isolation-by-distance pattern. We also found evidence of niche conservatism with low geographic overlap between the two groups. Hence, late Pleistocene dispersal from South to Central America and differences in available resources with subsequent isolation due to climatic barriers may have promoted differentiation in size but not yet extensive changes in shape. The Motagua-Polochic-Jolotán fault system probably plays a key role in promoting morphological differentiation by climatic isolation. Finally, we suggest that subspecies *M. t. temama* (Kerr, 1792) and *M. t. reperticia* Goldman, 1913 should remain as valid names for the two differentiated groups detected here.

V-6: Stem density of invasive shrubs facilitate increased winter seed removal by small mammals

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Small mammals can have profound effects on plant communities by consuming plant seeds. Small mammal granivory may be particularly important to understand in the context of invasive shrubs because invasive shrubs may alter habitat structure and thus increase foraging of prevalent small mammal granivores, such as *Peromyscus leucopus*. Despite evidence that invasive shrubs can amplify small mammal granivory, it remains unclear whether the effects of invasive shrubs on small mammal granivory are highly seasonal, producing pulses of strong mortality during times of the year when seeds are most vulnerable. We manipulated the presence of a widespread invasive species, *Rhamnus cathartica*, in a deciduous oak-maple forest to track rodent granivory of three native tree species and *R. cathartica* across summer, autumn, and winter. We measured rodent activity using camera trap photo data to predict correlations between activity and invasive shrubs. Our results reveal a significant interaction of season and invasive shrubs: in summer and autumn, there was no effect of invasive shrubs on overall seed removal, but winter removal was 21% greater in invaded habitats. Habitat characteristics, like stem density, could be an important driver in seasonal seed removal within invaded habitats when vegetative cover is no longer present. Therefore, understanding when and where small mammals are most active may have important implications for overwinter seed survival within invaded habitats.

V-7: Effects of anthropogenic noise and light pollution on nest-site selection of Formosan giant flying squirrels

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With increasing global human population and expanding urbanization, anthropogenic noise and light are now recognized as a pollutant of international concern. In this study, we aim to understand the effects of anthropogenic noise and artificial light at night on nest-site selection of Formosan giant flying squirrel (*Petaurista philippensis grandis*) in urban forest. We installed 175 nest boxes at 6 study sites in Taichung, Taiwan. We measured noise and light level at each nest box every 3 months. We checked nest boxes every 1-2 weeks and recorded if the nest box was occupied by flying squirrels. We used generalized linear models to examine effects of noise and light level and other environmental characteristics on probability of use of nest boxes. From November 2019 to November 2021, forty (22.85%) nest boxes were used at least once by flying squirrels. Average noise level and maximum noise level during the day were significantly lower at nest boxes used by flying squirrels. The results of the generalized linear model showed that the probability of use of nest boxes was negatively affected by average noise level in the day time, but was not affected by light level at night, after account for effects of canopy cover. In the future, we will estimate noise and light level within home ranges of flying squirrels to investigate the effects of noise and light pollution on animals.

V-8: Towards filling the gap: Lagomorpha evolutionary puzzle

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The globally distributed mammalian order Lagomorpha comprises two living families: Leporidae (hares and rabbits) and Ochotonidae (pikas), with 12 genera and 106 species. Reconstructing comprehensive genus- and family-level phylogenies has remained challenging due to a high degree of homoplasy in morphological characters. The phylogenomics research so far, has been focused on the most speciose genera *Lepus* and *Ochotona*. Recent genomic studies on these genera also revealed ancient hybridization and recurrent introgression, making species-delimitation difficult. Hence, thorough taxon sampling is critical to resolve the Lagomorph enigma. Here, we tried to fill some of the remaining gaps. The leporid *Sylvilagus* (second most speciose leporid) and monotypic genera (e.g. *Brachylagus*) lacked more complete genomic data till now. We sampled 10–100 year old muscle and skin tissues of museum collections (University of Washington Burke Museum and Field Museum of Natural History, Chicago, USA) to generate complete mitochondrial genomes with custom-designed mRNA probes. Extraction protocols for both modern and ancient DNA were used, prior to enrichment and Illumina sequencing. We assembled de novo six mitogenomes of *Lepus alleni* (Mexico), *Lepus nigricollis* and *Ochotona rufescens* (Afghanistan), *Sylvilagus floridanus, S. aquaticus*, and *Brachylagus idahoensis* (USA). Furthermore, our study concerning some unidentified *Lepus* specimens from Iran indicates the existence of *Lepus tibetanus* in this area. Preliminary phylogenomic analysis supports the hybridization among *Lepus* and returns *Brachylagus* as a sister lineage to *Sylvilagus*.

V-9: Wet and warm season: when the pacas come out to play

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Cuniculus paca is a medium-sized frugivorous rodent of Neotropical forests, a preferred bush meat, and prey for pumas and jaguars. We studied the activity pattern of *C. paca* in Campos do Jordão State Park (PECJ, 8341 ha), a rare remnant of seasonal upland Atlantic Mixed Forest in southeast Brazil. We sampled 24 sites (May 2021- March 2022) using camera traps (1-1.5 km apart) and obtained 155 independent records of *C. paca* in 14 wooded sites (119 records in preserved forested areas; 19 in forest with *Pinus* plantation; and 17 in shrubland-forest transition). Pacas were absent in 10 sites, 3 of which were grasslands and 7 forest. In the cold dry season (n = 689 trap-days), 27 records were collected, whereas 128 in the warm wet season (n = 1576 trap-days; X2 = 12.37, df = 1; p = 0.001). As a frugivore rodent, fruit abundance was probably driving paca increase in the wet (and reproductive) season, when paca cubs were also photographed. Site elevation ranged from 1210 to 1869 m asl, with paca records at all elevations. Pacas were nocturnal, with most records between 8 pm and 4 am. Our results show that poaching is likely unimportant inside this protected area. PECJ conservation policies are seemingly effective in guaranteeing the persistence of this, and other game species.

V-10: Storage effect to the evolutionary rescue: Persistence in temporally varying environments

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Global climate change is leading to increased environmental variability, particularly temperatures and precipitation, which is forcing many populations to rapidly adapt or go extinct. Populations are more likely to rapidly adapt to environmental change if selection acts on balanced genetic variation in populations. One evolutionary mechanism that could allow populations to maintain genetic variation is the storage effect. The storage effect occurs when a subset of individuals is under reduced selective pressure compared to the rest of the population, effectively storing genetic variation. Previous studies have shown that storage effect is possible under a variety of population dynamics but did not explore storage effect in populations whose sizes are allowed to vary or to decrease to extinction. Hence, we do not know if the storage effect can evolutionarily rescue populations from extinction. Here we expand on a previous model of the spatial-storage effect to model varying population sizes, including logistic population growth, and evolve populations forward-in-time in silico. We examine the model under a range of varying selection strengths and periodicities, migration rates, and mutation rates. Preliminary results indicate that populations with storage effect have an increased rate of persistence than those where it is absent, which may lead to evolutionary rescue in natural populations. This is particularly relevant for structured populations that experience multiple litters per year, as seen in many rodent populations.

V-11: Female reproductive state changes vocal characteristics in North American red squirrels

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Fluctuations in reproductive hormones such as estradiol and progesterone can be communicated through the acoustic characteristics of mammalian vocalizations. This variation in vocal characteristics may act as an important mechanism for coordinating reproductive behaviour. In North American red squirrels (*Tamiasciurus hudsonicus*), both males and females defend spatially distinct territories year-round using territorial 'rattle' vocalizations. Females enter estrus only once or twice a year, allowing males onto their territory to mate. Given the long distances travelled and synchronous timing of male arrival, we hypothesized that variation in female vocalizations associated with estrus may provide a cue which males use to find receptive females. To test this hypothesis, we analysed the acoustic parameters of 897 rattle vocalizations collected from 108 female red squirrels between 2018 and 2020 and compared them across reproductive states using generalized additive models. While we found that fundamental frequency significantly decreased throughout pregnancy and weaning of pups, this did not correspond with female estrus, suggesting that it is unlikely that males use vocal cues in orienting towards receptive females. These change in frequency directly following pregnancy may provide important cues which other females can use to time their own reproductive events. These findings are novel in demonstrating distinct changes in female vocalizations of a territorial mammal associated with reproductive condition.

V-12: Do scavenging rates of small-mammal carrion differ in primary and secondary forests?

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Small-mammal carrion is a unique resource with spatially and temporally patchy distributions that has important effects in trophic webs and nutrient cycling. The availability of small-mammal carrion in ecosystems is difficult to determine, but estimates suggest that a significant proportion of small-mammal mortality results in carrion sequestered by scavengers and/or decomposers. Here, we investigate the fate of small-mammal carrion and test if the rates of scavenging differ between primary and secondary forests and/or across forest strata in a lowland, Neotropical rainforest. We conducted our study in La Selva Biological Station, Costa Rica, where we deployed 202 mouse carcasses on the ground and ~1 m above ground level on trees and lianas in primary and secondary forests. We deployed trail cameras on each carcass, and surveyed carcasses daily to calculate scavenging rates for carcasses placed on different forest strata, across the two forest types. We found scavenging rates to be extremely fast, and no significant difference in scavenging rates between primary and secondary forests, regardless of forest strata placement. Scavenging of small-mammal carrion was dominated by invertebrates, particularly bullet ants and burying beetles. These results highlight that secondary forests, in comparison to primary forests, can maintain similar levels of ecosystem function particularly in regards to scavenging. Additionally, small-mammal carrion is a highly sought-after resource that is quickly sequestered in Neotropical rainforests.

V-13: Size- and state-dependent effects of invasive plants on antipredator behavior of white-footed mice (*Peromyscus leucopus*

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Invasive plants can provide refuge from predators that significantly reduce perceptions of risk for small mammals, leading to important changes in antipredator behavior (e.g., increased activity and spatiotemporal avoidance). Mammalian behavior can depend critically on individual condition (e.g., body size) and individual state (i.e., reproductive status). Individuals may increase or decrease risk-taking behaviors to satisfy the demands of changes to body condition or reproductive state. However, we have little understanding of how individual condition and state affects the nature and magnitude of the effect of invasive shrubs. Therefore, we experimentally manipulated the presence of invasive shrubs (*Rhamnus cathartica*) to determine if plant invasions generate changes in the prevalence of antipredator behavior in white-footed mice, *Peromyscus leucopus*, of varying condition and state. We used live-trapping to measure individual body size and reproductive state, and conducted three standardized behavioral assays: an emergence test, a handing bag test, and an open field test. Preliminary findings suggest the presence of invasive shrubs reduced the prevalence of antipredator behavioral traits regardless of individual condition and state. When invasive shrubs were removed, the expression of antipredator behavior was dependent on the body size and reproductive status of an individual. Our findings suggest that plant invasions may reduce the variation in the antipredator behavior of rodents because the need to engage in conditional risk-taking behavior declines within homogenous environments perceived as safe.

V-14: The influence of drought on fecal corticosterone and dispersal-related behaviors in wild *Peromyscus boylii*

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Associations between behavioral attributes or hormonal profiles and dispersal phenotypes are common across vertebrate taxa. More bold, exploratory, or active individuals tend to disperse farther or at a higher frequency compared to more shy and less active individuals. Corticosterone may influence dispersal decisions by enhancing dispersal-related behaviors, and these relationships can be mediated by ecological pressures. Here, we tested the hypothesis that precipitation, sex, and age affect fecal corticosterone levels and that fecal corticosterone levels correlate with activity and boldness in brush mice (*Peromyscus boylii*). We also tested for direct influences of precipitation, sex, and age on activity and boldness. We measured boldness and activity using video-recorded open field tests and quantified fecal corticosterone metabolites. Fecal corticosterone levels were higher in years with below average precipitation, and in females. We did not find an effect of fecal corticosterone levels on activity or boldness. Finally, activity and boldness were not directly affected by sex, age, or precipitation. Further analysis of the relationships between drought, fecal testosterone, and dispersal-related behaviors is in progress and will also be discussed.

V-15: Functional Impacts of High-Effect Mutations Associated with dog Hyper-Sociability

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A significant amount of variation in human-directed dog social behaviors can be traced to a polymorphic transposable elemental (TE) insertion that lies within the *General Transcription Factor* 2-I (*GTF2I*) gene. However, not much is known about the molecular impacts of this polymorphism. TEs can cause changes in chromatin looping that lead to altered *cis*- regulatory contacts. We found that dogs containing the TE formed a loop with the gene *Elastin (ELN)*, which incidentally plays a key role in the penetrance of phenotypes in humans with Williams Syndrome. This loop was absent for dogs lacking the TE. Subsequently, we found a significant difference in expression of *LAT2*. This gene is located between *GTF2I* and *ELN,* which make the two ends of the chromatin loop, and is involved in the glutamate-glutamine cycle of the brain. We also found a modest change in expression of *ELN* (p=0.19), yet we need more power to detect these differences. Co-expression analyses reveal that genes functionally related to *ELN* and *LAT2* differ in expression between samples containing and lacking the TE. Hence, the high effect TE locus can regulate several genes that affect the complex phenotype of behavior.

V-16: Prevalence and persistence of *Anaplasma phagocytophilum* in a northern Illinois prairie ecosystem

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Anaplasma phagocytophilum is a tick-borne pathogen that is the causative agent of human granulocytic anaplasmosis. Human anaplasmosis is one of the most common vector-borne zoonotic diseases in the United States. While many tick-borne pathogens are well understood, there is still much to learn about *A. phagocytophilum* with regard to prevalence and persistence within prairie-dwelling hosts over time. To assess this, prairie dwelling rodents were sampled from 2014-2018 in northern Illinois. Tissue samples were then screened for *A. phagocytophilum* using nested PCR. Evidence of *A. phagocytophilum* was present in *Ictidomys tridecemlineatus* in as early as 2014. Prevalence rose by 2016 and was consistent throughout the rest of the study. Additionally, *I. tridecemlineatus* had a significantly higher prevalence of *A. phagocytophilum* than any other rodent species in any year. These data suggest that *I. tridecemlineatus* is a potential reservoir of *A. phagocytophilum* in prairie ecosystems.

V-17: Taxonomic boundaries in Lesser Treeshrews (Scandentia, Tupaiidae: *Tupaia minor* Günther, 1876)

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The Lesser Treeshrew, *Tupaia minor* Günther, 1876, is a small mammal from Southeast Asia with four currently recognized subspecies: *T. m. minor* from Borneo, *T. m. malaccana* from the Malay Peninsula, *T. m. humeralis* from Sumatra, and *T. m. sincepis* from Singkep Island and Lingga Island. A fifth subspecies, *T. m. caedis*, was previously synonymized with *T. m. minor*; it was thought to occur in northern Borneo and on the nearby islands of Banggi and Balambangan. These subspecies were originally differentiated based on pelage color, a plastic feature that has proven to be an unreliable indicator of taxonomic boundaries in treeshrews and other mammals. To explore infraspecific variation among *T. minor* populations across the Malay Peninsula, Borneo, Sumatra, and smaller islands, we conducted multivariate analyses of morphometric data collected from the hands and skulls of museum specimens. Principal component and discriminant function analyses reveal limited differentiation in manus and skull proportions among populations of *T. minor* from different islands. We find no morphometric support for the recognition of the four allopatric subspecies and no support for the recognition of *T. m. caedis* as a separate subspecies on Borneo. Our study highlights the importance of reevaluating infraspecific taxonomic boundaries with nonarbitrary data to better understand and protect mammalian diversity in threatened regions.

V-18: Ancient mitogenomes reveal population dynamics of Holocene bison in the northern Great Plains

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Millions of bison occupied the Great Plains prior to their almost complete extermination in the 19th century. Their population dynamics and genetic diversity in the Great Plains between the terminal Late Pleistocene and the recent anthropogenic bottleneck remains unknown. To infer the Holocene demography, bison bones and teeth were collected from archaeological sites across the northern Great Plains. The radiocarbon age of the bison samples varied from 12,226 to 167 calibrated years before present. Dual-indexed DNA libraries were generated from single-stranded DNA isolated from bones and teeth. The DNA libraries were enriched for bison mtDNA sequences using RNA baits and sequenced on MiSeq platform. Mitogenomes with a high coverage were assembled from 40 bison specimens. An extensive mitogenome variation in the Holocene bison from the northern Plains encompassed the mtDNA lineages from modern bison and the latest *Bison priscus* from western Canada. The Bayesian skyline analysis demonstrated the bison population growth in the northern Plains starting ~14,000 years ago with melting the ice sheet and the replacement of spruce forests with the grassland. The population reached its maximum ~5,000 years ago followed by small population reduction in late Holocene starting ~3,000 years ago. The historic fluctuations of effective size of the local bison population caused by environmental and anthropogenic factors are relevant to effective management of conservation herds and protection of ancient mtDNA lineages.

V-19: Co-occurrence of free-ranging dogs and northern tiger cats in the Brazilian semi-arid Caatinga shrub-woodlands.

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Free-ranging domestic dogs (*Canis familiaris*) impact carnivore populations through competition, disease transmission, and direct predation. In protected areas (PAs) across Latin America, free-ranging domestic dogs tend to be ubiquitous, especially in small PAs within fragmented landscapes. Among the many species impacted by domestic dogs, the northern tiger cat (*Leopardus tigrinus*) stands out due to its threatened status, and the fact that large swaths of its remaining range are known to have free-ranging dogs. Thus, discerning spatial interactions between free-ranging dogs and tiger cats is important for the latter's conservation. With this in mind, we surveyed a small private reserve in the Brazilian dry forests with camera traps. We assessed landscape use of both species and whether they avoid each other through multi-species occupancy models. We also analyzed their respective activity patterns to test for temporal segregation. Finally, we estimated the density of each species through spatially explicit capture-recapture models. Preliminary results suggest a positive co-occurrence between tiger cats and domestic dogs in the study site, sharing the landscape without spatial segregation. Both species exhibited a high degree of temporal overlap as well. This implies a high risk of disease transmission and direct killing by domestic dogs for tiger cats and that mitigating action should be taken.

V-20: Systematics of the New World *Eptesicus* and *Histiotus* bats indicate a South American origin

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Biodiversity is the key to evolution and conservation yet is underestimated in many taxa and the mechanisms generating biodiversity are often unclear. Bats (order Chiroptera) are the second largest mammalian order with >1,400 species and global distribution, making them an ideal model to study biodiversity. Here we focus on the cosmopolitan genus *Eptesicus* (family Vespertilionidae) where the New World species have been found more closely related to *Histiotus*, a South American morphological genus with enlarged ears, than to the Old World *Eptesicus* species. However, phylogenetic relationships among the New World species remain unclear. In this study, we estimated the New World phylogeny using the ultra-conserved elements (UCEs) and extensive geographic and taxonomic sampling, including 8 of 10 nominated New World *Eptesicus* species and 6 of 8 nominated *Histiotus* species. We found four monophyletic New World clades, namely the *E. fuscus* clade, *Histiotus* clade, and two Neotropical *Eptesicus* clades that indicated cryptic diversity. Both concatenation and multi-species coalescent analyses showed a novel topology where *Histiotus* is more closely related to *E. fuscus* than their sympatric Neotropical *Eptesicus*. The ancestral state reconstruction identified a Neotropical origin of the New World clades and a Saharo-Arabian origin of the most recent common ancestor of the New World and Old World clades, indicating a cross-Atlantic colonization route from northern Africa to South America.

V-21: Genetic diversity and abundance in two Neotropical cervids of Quintana Roo Mexico

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Knowing the genetic diversity and abundance of a species is of the utmost importance for its management and conservation, however, the capture of some species of cervids is difficult due to the dense vegetation in its tropical distribution areas. Therefore, we use a non-invasive genetic capture-mark-recapture analysis using feces, which has proven to be a useful tool for obtaining the abundance and genetic diversity of a species. The objective of this work was to determine this genetic diversity and abundance of *Odocoileus virginianus* and *Mazama pandora* in a human dominated landscape in northwestern Quintana Roo. We

extracted and amplified DNA from 360 cervid scats during 2018-2021. We used the cytochrome b mitochondrial region for species identification and the characterization of haplotypes. We used six microsatellites to identify individuals. In addition, we estimated the population size of both species using a capture-recapture model. We found five unique haplotypes for both species, 19 and 21 individuals identified for *M. pandora* and for *O. virginianus* respectively. The genetic diversity for both species was high in all the analyzed loci compared to what was previously reported; these results suggest both populations still have genetic flow with other populations.

V-22: Biodiversity Literacy in Undergraduate Education (BLUE): an example from natural history collections and pathogen data

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Biodiversity Literacy in Undergraduate Education (BLUE) is a diverse and inclusive network of biodiversity researchers, data scientists, museum professionals, and biology educators focused on undergraduate biodiversity education and data literacy. The BLUE network addresses the need to incorporate biodiversity information and data skills into undergraduate education and endeavors to develop competencies, materials, and strategies that infuse biodiversity data into the curriculum, facilitate broad-scale adoption of data literacy competencies, and improve undergraduate biology training to meet increasing workforce demands in data, collections-based, and biodiversity sciences. BLUE is partnering with members of project AIM-UP! (Advancing Integration of Museums into Undergraduate Programs) and the Museums and Emerging Pathogens in the America's (MEPA) virtual community of practice to extend the network. Through this collaboration, we will engage international partners and identify strategies that will support the training and development of diverse, competent, and engaged 21st century workforce who are well-prepared for a broad set of career paths generating and utilizing biodiversity data to address scientific issues of critical national and global importance. We also will develop place-based educational modules that incorporate specimen-based data from museum collections and important concepts in emerging pathogens, develop inclusive materials and translate modules into Spanish and Portuguese, and create culturally relevant and accessible educational materials that meet the needs of a diverse and international community.

V-23: Temporal niche of the Andean tiger cat in cloud forests of the Western Andes, Colombia.

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Closely related predators can coexist if there is divergence in at least one dimension of their niches, this coexistence also has marked effects on prey behavior. Here, we describe the effects of moonlight and the temporal co-occurrence of sympatric ocelots and prey on the activity of the Andean tiger cat (Leopardus tigrinus pardinoides). From 2018 through 2021, we collected data on the diel activity of Andean tiger cats, ocelots, and potential prey through camera trapping. We checked a total of 21 cameras spaced 1 km apart in cloud forests of a private protected area in the western Andes of Colombia. Circular metrics were used to describe the activity patterns of Andean tiger cats, and their temporal overlap with sympatric ocelots and prey were estimated using paired conditional kernel density curves. Andean tiger cats are mainly nocturnal, and, as expected, their activity correlated consistently with that of small rodents though not with terrestrial birds, especially during periods of new moon. Ground-dwelling birds were mainly diurnal and exhibited higher overlap with ocelots than with Andean tiger cats. Ocelot and Andean tiger cat activity overlapped marginally in 2018 and, this time, partitioning increased during the following year. Andean tiger cats increase their chances of encountering prey during darker nights, and the activity shift of ocelots in the area may be helpful in explaining such a pattern.

V-24: Morphological evolution of scapula and pelvis of hystricomorph rodents

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Hystricomorpha is one of the three major lineages in Rodentia and represents ~13% of living rodent species. They have a long evolutionary history and present a great distributional range around the globe. They have evolved distinct morphologies to exploit almost every locomotory niche available to rodents, from subterranean to arboreal, rock-dwelling, terrestrial, scansorial, and even semi-aquatic modes. Because of their great species diversity and morphological disparity, hystricomorphs provide a great opportunity to understand the extent of both ecological convergences and phylogenetic constraints in shaping morphology. Here we investigate morphological diversity of scapular and pelvic girdle of hystricomorph rodents, and assess the effects of phylogeny and locomotor modes in shaping that diversity. We used geometric morphometrics to assess shape and size variation of both structures, and phylogenetic comparative methods to relate them to their evolutionary history and ecological features (e.g., locomotion mode). To accomplish that we analyzed morphological data of ~560 specimens of 106 species of hystricomorph rodents obtained from museum collections, mainly from the Field Museum of Natural History. Preliminary findings suggest that the greatest morphological variation lies between arboreal and fossorial species, for both scapular and pelvic girdle, and size seems to be more constrained in the phylogeny than shape, for both scapular and pelvic girdle. Understanding the evolutionary and ecological features that determine species morphology provides critical information for investigations into adaptation.

V-25: Mexican wolf (*Canis lupus baileyi*) restoration in Mexico: summary of a 10-year effort

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After Mexican wolves were extirpated from the Mexican landscape during the early 1980s, a captive binational program started with the aims of releasing individuals into the wild. Our aim is to describe the restoration process of Mexican wolves from 2012 to 2021 in Northern Mexico. We have released 17 Mexican wolf' pairs and family groups into the wild. Establishment of breeding pairs range from 1 to 4 per year. We have documented 14 litters since 2014, with a minimum of 49 pups sired. Litter size at two-months of age range from two to six. Survivorship is higher for individuals born in the wild than those under human care. Mortality causes include poison, firearms, run over, trapping and unknown. Livestock carcasses are an abundant and widespread source of food for wolves in the landscape, thus making them a scapegoat for poor livestock husbandry in the region. The livestock community and land tenure in terms of size and ownership affect recruitment within the population. Unfortunately, Mexico has not fully eradicated the causes that accounted for Mexican wolf loss at the end of the 20th century. A thorough and more aggressive institutional effort that includes conditional approval of subsidies for agricultural practices, law enforcement and effective compensation programs must be instated to see a successful increase in the population of Mexican wolves in the wild.

V-26: Small mammal community variation corroborates a recent and idiosyncratic biogeographical history of *Restingas* in Brazil

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Restinga is a phytophysiognomy of the Brazilian Atlantic Forest (BAF) Domain, characterized by mosaics of shrublands and forests that evolved on coastal sandy plains formed during the Quaternary. It has been

hypothesized that the colonization of different *Restingas* by animals and plants was recent, idiosyncratic, and involved only a subset of species from the adjacent forest. This hypothesis predicts that *Restinga* communities would share higher similarities with nearby biotas (non-*Restinga* communities) than among each other. Here, we evaluated whether the spatial structure of small mammal communities (Rodentia and Didelphimorphia) from *Restingas* in southern and southeastern Brazil is compatible with the recent colonization hypothesis, using an Elements of Metacommunity Structure approach. A matrix of 34 species presence and absence were generated considering 20 published inventories in *Restingas* areas of the south and southeast region, in addition to museum records from NUPEM-UFRJ collection and Species Link database. The analysis was performed in the R package Metacom. The resulting metacommunity structure was Clementsian, with two compartments, the first formed by *Restingas* from Espírito Santo, Rio de Janeiro, and São Paulo, and the second by *Restingas* from Santa Catarina and Rio Grande do Sul. This spatial structure reflects the BAF's "Paulista" and "Southeast" biogeographic units, therefore, supporting the hypothesis of recent colonization. When evaluated independently, the compartments generated random structures, providing further support to the recent colonization hypothesis.

V-27: Anatomy and postnatal ontogeny of the masticatory muscles of *Didelphis albiventris* (Didelphimorphia, Didelphidae)

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Ontogenetic changes in masticatory muscles are expected as mammals shift from lactation to independent feeding. Here we describe changes in the organization in masticatory muscles along four age classes (from suckling young with no erupted molars to adults with full permanent dentition, named C1 to C4) obtained by dissecting 15 specimens of the Brazilian White-eared Opossum, *Didelphis albiventris*. The most striking changes were seen in the temporalis and masseter muscles. The temporalis originated posterior to the orbit since C1, but only occupies the whole lateral of the skull (enlarged by the sagittal and nuchal ridges) in C3. Its superficial and deep portions insert laterally and medially, respectively, into the coronoid process. It is covered laterally by the deep masseter that, along with the temporal insertion, extends ventrally to the masseteric fossa since C1. The superficial masseter inserted into the inflected angular process and originated posteriorly in the maxilla, continuously with the masseteric fascia in C1, but tendinously above the molar series in C3. In C4, the superficial masseter presents three components and an inferior tendon. The deep temporalis also changed along the ontogeny: in C1 it does not fully occupy the coronoid process, due to the absence of the post-orbital constriction. These changes likely result in increased bite force through ontogeny as joeys are weaned and shift to an independent diet.

V-28: Forelimb specialization as an adaptation for burrowing in kangaroo rats (Genus *Dipodomys*)

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Given their need to burrow, soil substrates can be very important in defining the habitat of kangaroo rat species (*Dipodomys*). Factors such as compaction, density, and particle size, lead to differences in soil friability when burrowing, therefore burrowing may require species-specific specializations related to these edaphic factors. Using morphometric techniques, we tested the hypothesis that forelimb morphology is linked to substrate affinities in *Dipodomys* species. We expected to find specialized morphology among species that inhabit dense substrates consistent with enhanced musculature and a powerful forelimb outforce, manifested anatomically as comparatively short, robust forelimbs. We discovered a significant morphological difference among species, where those inhabiting dense substrates displayed the most robust forelimb morphology. Our results indicate that *Dipodomys* species found in dense substrates may require morphological specializations, whereas those found in less dense substrates may display more generalized morphological traits. *Dipodomys* species also use their forelimbs to load their cheek-pouches as they forage for seeds. This behavior might present a tradeoff with the morphology needed for efficient burrowing such that most *Dipodomys* species (particularly habitat generalists) have morphology adapted primarily for efficient foraging rather than burrowing. Our results will allow us to further characterize the habitat requirements that may limit the geographic ranges of these species, which can help us to better predict species occurrences, build and refine niche models, and protect appropriate habitat.

V-29: Population assessment of the three small cat specialists of the vanishing Brazilian drylands

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The Brazilian savannas (Cerrado) and the semi-arid thorn shrub-woodland of the Caatinga are losing considerable tracts of land due to a series of developments and for being the country's new agricultural frontier. While these biomes have already lost > 50% of their original cover, they comprise the main habitat and range for three small Neotropical cats, the lowland northern tiger cat (*Leopardus tigrinus tigrinus*), the Brazilian Pampas cat (*Leopardus colocola braccatus*) and the jaguarundi (*Herpailurus yagouariundi*). The first is globally Vulnerable, and all of them are listed as Vulnerable in Brazil. In this work, we wanted to understand their population patterns and trends in some of their prime and vanishing habitat types. Population assessment was made by means of camera trapping, with 11 density estimations and seven population trends (of more than 5 years) assessed for the three focal species. Density estimation ranged from 0.001 ind/km^2 to 0.25 ind/km^2, with median values at 0.04 ind/km^2. Values are highly suggestive that they all possess low densities throughout, only rarely reaching higher values (> 0.08/km^2). We noted considerable population drops for a three generations time-period (15 years) of 39.5-77.7%. With increasingly higher rates of habitat loss in the core of their range, low/very-low densities and population drops of significant magnitude, the future of all three species, especially tiger cat and Brazilian Pampas cat is quite worrisome.

V-30: Dental ecomorphology, stable isotopes, and body size reveal ecological shifts in the grasshopper mouse *Onychomys*

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How sensitive is micromammal ecology to climate fluxes and extinction of large mammals? We investigated this question for invertivorous grasshopper mice (Onychomys) at Hall's Cave in Texas, which records the extinction of Pleistocene megafauna and warming from the last glacial maximum to the present. We quantified morphological and dietary changes using (1) microCT-derived 3D dental ecomorphological variables, (2) stable isotope analyses of bone collagen, and (3) dental proxies for body size. Our models show strong support for both climate and extinction driving shifts in body size, isotopic niche (δ13C and δ15N), and dental ecomorphology over time. Overall, temperature best explained body size variation, consistent with Bergmann's rule. The terminal Pleistocene megafaunal extinction also strongly influenced Onychomys, leading to a doubling of body size in the early Holocene despite the warming climate. These individuals represent the largest modern or fossil specimens of this genus known. Interestingly, those Onychomys immediately post-extinction had higher δ15N values relative to earlier or later animals, suggesting the largest mice ate at higher trophic levels. This hypothesis is supported by concomitant increases in occlusal convexity, a measure of tooth pointiness associated with faunivory. We suspect these ecomorphological and isotopic shifts reflect a temporary response to the changing resource availability immediately post-extinction. Our results emphasize the transformative effects of megafaunal extinction in light of modern anthropogenic perturbations to ecosystems in a warming

V-31: Impact of dietary protein on postnatal growth, body composition, and performance in *Peromyscus californicus*

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Dietary protein is a primary component of diet quality and is critical to successful growth and reproduction. This study examines the relationship of dietary protein level in the lab on juvenile growth rate, body composition and performance. *P. californicus* were placed in one of five isocaloric protein diet treatments and were followed from birth through age at first reproduction. The impact of dietary protein on postnatal growth had a threshold effect with growth rate lowest on the lowest protein diet but similar on all other diets containing 10% or more crude protein. Pup swim endurance however increased at a linear rate as dietary

protein levels increased; endurance was not significantly related to pup age or pup mass. Body composition was impacted by dietary protein. Lean mass was greater in pups on higher protein diets and related to faster growth; however lean mass as a proportion of fat-free mass was not significantly different across diet treatments. Total fat as a percent of total mass increased with increasing dietary protein but only in mice that were older than 40 days. The difference in the impact of dietary protein on growth and swim performance may be due to the complex age-related effects of dietary protein on body fat and lean mass.

V-32: Activity patterns of bat species at interstate highway sites with and without wildlife underpasses

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Roads force wildlife to navigate degraded and fragmented habitats across the globe, creating barriers to movement and increasing the risk of mortality. This includes bats, whose movements between foraging and roosting habitats may be impeded by roads. Wildlife crossings structures (WCS) are a common mitigation strategy to increase connectivity, but investigation into bat activity in or around these structures is limited. Our goal was to test whether highway locations with WCS had more bat species and higher activity levels than locations without underpasses. Echolocation calls were recorded at locations along Interstate-90 with and without underpasses, and in the adjacent forest. Calls were analyzed across all species, and separated into 4 guilds based on species-specific frequency ranges. The same 8 species were detected at all locations. Total bat activity was higher along the highway than the adjacent forest but did not differ between locations with vs. without underpasses. Guild activity followed similar trends, with some exceptions. The 40 kHz guild showed significantly higher activity at underpasses than at locations without them. Confounding variables make interpretation challenging, but this study provides important information on bat activity along an interstate highway in Washington State. We highlight the need for more intensive monitoring efforts to better understand the effectiveness of WCS in reducing the impacts roads have on bats in North America.

V-33: Understanding ranging behaviour of elephants in the forest-crop field interface of Rajaji landscape, northwestern India

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Understanding ranging and space use is fundamental in establishing and maintaining protected areas, developing management strategies for the conservation of wildlife, and alleviating human-wildlife conflict. Home range size and space-use pattern can be influenced by interactions between various biotic and abiotic factors, such as distribution of resources, presence of other conspecifics, as well as competitors and predators. Here we studied the ranging behaviour of 4 radio-collared and 15 non-collared bull elephants *(Elephas maximus)*, and identified mixed-sex/female-led family groups in the forest–crop field interface of Rajaji landscape, northwestern India. The study individuals were identified based on various morphological features and intensively followed from March 2020 to March 2022 to understand their behavioural and physiological states and association pattern. Only one bull elephant provided telemetry data for 14 months (24th December 2020 to 25th February 2022). Preliminary findings suggest that bull elephants show crepuscular behaviour, especially during crop-raiding seasons. For the collared elephant, a geographically distinct space-use pattern was observed between Rabi and Kharif cropping seasons. Spatio-temporal ranging behaviour was observed to be similar during musth and non-musth crop-raiding reasons. Elephants involved in crop-raiding were exclusively bull elephants and mostly formed all-male groups. The ranging pattern of elephants in the forest–crop field interface suggests that long-term conservation success in these areas necessitates management interventions beyond the administrative boundary of the protected areas.

V-34: Not alone: burrow sharing by the endangered Elias Atlantic spiny rat (*Trinomys eliasi*, Echimyidae)

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Trinomys eliasi is a rare echymid rat endemic to Atlantic Forest and classified as near-threatened and decreasing in population by the IUCN. Its distribution is restricted to a few lowland forests and “restingas", vegetational associations that suffer the greatest human impacts in the Brazilian state of Rio de Janeiro (RJ). The few studies of the species indicate that its populations are isolated from each other. This spiny rat is described as solitary and nocturnal, but there are no empirical studies supporting these characterizations. The objective of this study was to evaluate the activity pattern of *T. eliasi* and obtain information about its natural history and level of sociality. We installed 12 camera traps (Bushnell Trophy Cam HD) in the legally-protected ReBio União, RJ, Brazil, between July 2019 and April 2020. We obtained 2,233 video records. These include 444 videos of *T. eliasi*, all of which were at night time. Four videos recorded two or more adults sharing the same burrow, and 65 recorded an adult and one or more juveniles, which raise questions about the level of sociality of this rodent. There is another species of *Trinomys* (*T. yonenagae*) that shares burrows and is recognized as social. Considering this and the little knowledge about rodent social systems, we plan to continue observing and describing *T. eliasi* behavior.

V-35: A mammal collection of the Galápagos islands

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The Galápagos islands are famous for their striking biota, magnificent scenery, and association with naturalists and collectors as Charles Darwin and Rollo Beck. The Galápagos are regarded as a living laboratory for studying evolution; however, it is surprising how little known are basic aspects of the natural history and taxonomy of their mammalian fauna. Here, we present an overview of the collection of mammals of the Charles Darwin Research Station in the Galápagos with the intention of promoting the use of this remarkable resource by researchers. The collection contains introduced and native species, being the Galápagos sea lion, *Zalophus wollebaeki,* the most represented taxon. An interesting source of specimens in the collection are owl pellets; native and introduced rodents have been retrieved, including guinea pigs that may represent evidence of a feral population. The collection also contains fossils of the extinct giant rat *Megaoryzomys curioi*. At least 10 species of cetaceans are represented, including some specimens with pathologies, and a complete skeleton of *Kogia sima*. The native bat and rodent specimens may help to resolve some long standing taxomic issues such as the status of *Lasiurus brachyotis* and *Aegialomys bauri*. This collection is an important resource, awaiting to be used, to solve the abundant pending questions regarding Galápagos mammals.

V-36: Gray foxes in the United States midwest: Extirpation in our own backyards

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Gray foxes (*Urocyon cinereoargenteus*) have declined precipitously over the past three decades in the midwestern United States, such as Ohio, Illinois, Iowa, and Missouri. The reason is unknown but is likely a combination of predation, competition, and disease. High harvest rates in the 1970s–1980s may have contributed synergistically. A survival rate and cause-specific mortality study of 14 radiocollared gray foxes was conducted in southeastern Ohio. Within 1 year, 11 (73.3%) foxes died. Two were struck by vehicles, seven died from canine distemper, and two developed systemic infections originating from minor trap-related injuries. Deaths arising from minor lacerations raised the possibility of compromised immunity and an inbreeding depression. Fifty-three gray fox tissue samples were obtained from 22 Ohio counties. DNA from 20 tissue samples was extracted and kindly donated by Luther College, whereas the remaining samples were processed at Capital University. We detected moderate to high levels of genetic variation based on mean observed (H_O = 0.723) and expected heterozygosity (H_E = 0.734), and low levels of inbreeding (F_{IS} = 0.051). We have since constructed a distribution map based on 3 years (2019–2021) of camera trapping data across the Ohio Appalachian Plateau and verified sightings by the public. Gray fox populations occurred in a clumped distribution. The next step is to determine genetic heterozygosity and gene flow within and between clumps.

V-37: Redness signals body size in tree squirrels

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An animal's coloration is associated with a variety of processes and is therefore subjected to multiple selective pressures. Mammals, especially, are typically inconspicuously colored, or cryptic, to avoid detection by predators. Alternatively, an animal may use conspicuous coloration to advertise the presence of an anti-predator defense. The association between signal and defense is called aposematism. Conspicuous black and white coloration has recently been associated with a range of defenses in mammals, including body size (Howell et al 2021). Here we test whether conspicuous red coloration in tree squirrels is associated with environmental variables suggestive of crypsis or with body size. We examined skin specimens of 57 tree squirrel species (n=257) representing 25 genera and continuously measured redness of the dorsum, the ventrum and of red accents. We then associated these phenotypic variables with enviornmental variables using phylogenetic generalized least squares regression. We find that increasing dorsal redness is associated with more humid environments and closed canopies, consistent with prior work that coloration on this part of the body in this group is predominately shaped by a selection for crypsis (Sheets and Chavez 2020). Furthermore, we find that ventral redness and the redness of red accents is associated with large body sizes. Our findings suggest that crypsis and aposematism are not mutually exclusive and that aposematism may be more widespread in mammals than is currently appreciated

V-38: Foraging behavior response of small mammals to different burn severities

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Wildfire causes profound challenges for animals to overcome, especially forest-dwelling mammals, due to reliance on specific vegetation types. This study addresses the impact of 3 types of burn severity forest areas (completely, partially, and non-burn areas) on foraging behavior of a small mammal community in the Pinaleño Mountains (Arizona) using the giving up density experiment approach (GUD). Overall, burned severity affected the perceived predation risk (reflected in the GUD), where in completely burned patches, small mammals spent less time foraging than partially- and non-burned patches. Vegetation characteristics influenced GUD in the 3 burn severity patches. For example, more canopy cover increased GUD (decreased foraging) in both non burned and burned areas, however, number of logs corresponded to lower GUD (increased foraging) in non-burned areas, but opposite trends in partially burn areas. This suggests complicated interactions between levels of vegetation characteristics (ground, medium and upper level) in the perception of predation risk related to burned severity. Fires affected the foraging behavior of the small mammal community but did not impact all species the same. Generalists, such as *Peromyscus* sp., seemed to forage across all burn severities, while specialist species, such as tree squirrels, tended to avoid the completely burned patches. Clarifying the complex impacts of fires on small mammals foraging behaviors contribute to our understanding of the intricate interactions, at micro-habitat levels, between vegetation structure, and behavioral response of

V-39: Fishers in a landscape altered by tree mortality: implications for habitat suitability and connectivity

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Changes in climatic conditions are altering forests in many ways around the globe. In the southern Sierra Nevada, drought conditions starting in late 2012 led to massive outbreaks of beetles and subsequent

extensive conifer mortality from 2015 – 2018. For species such as the fisher (Pekania pennanti), which relies on extensive canopy cover and large decadent trees, the short- and long-term impacts of this landscape level change are uncertain. To better understand fisher habitat use post-tree mortality in this region, we attached Lotek GPS collars to male and female fishers between fall 2017 and late winter 2020 to summarize habitat use relative to selected covariates. Our objectives were to document landscape features which drive fisher use within a landscape altered by tree mortality, characterize how environmental variables contribute to habitat suitability across the landscape, gain insights into fisher movement in post-tree mortality conditions by examining potential landscape connectivity. A resource selection analysis indicated that fishers tended to be in areas with more dense live forest, live forest interspersed with tree mortality, further from roads, closer to streams. and in elevations < 3,000 m. Highest connectivity occurred in areas of dense live forest (with little tree mortality) around 2,000 m; while roads were not necessarily barriers, areas of high road density were avoided. We anticipate these results can help inform management plans.

V-40: Linking macroecological distribution patterns to individual specialization in small mammal communities

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We are at a time when community assembly and biodiversity are recognized vital components of conservation. Thus, it has become more vital than ever to link macroecological distribution patterns to local community niche interactions. We first tested if rodent communities found in the shrubland-grassland ecotone followed the predictions for abundance-occupancy relationship. We then specifically tested: 1.) if widespread species with a high abundance will have wide niche areas according to Resource Breadth Hypothesis. 2.) Whether more abundant species will have less overlap between niche areas than less abundant species according to the Core-Satellite Hypothesis. 3.) If species react to resource limitation by either (a) expanding individual specialization following the Niche Variation Hypothesis or (b) through increased individual generalization following Optimal Foraging Theory. Finally, 4.) whether more widespread and abundant species will show a higher level of individual specialization during resource limiting conditions than a less abundant species. Using stable isotope analysis to quantify dietary niche we found that widespread and abundant species had both wider habitat and diet niche areas as well as higher diet niche overlap than less abundant species. Additionally, not all populations of a widespread and abundant species responded to resource limitation through individual specialization. We found there are not discrete categories species fit into when considering generalist or specialist niche strategy; rather we should consider species falling at different points along the specialization spectrum.

V-41: Habitat use of the Andean tiger cat in a biodiversity hotspot of Colombia.

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The habitat use of small felids is affected in multiple ways by human disturbance, co-occurrence with intraguild prey and predators, and microhabitat and landscape structure. It is important to know how a vulnerable species such as the Andean tiger cat (*Leopardus tigrinus pardinoides)* responds to each of these factors in order to implement viable conservation actions. An 18-month sampling with 53 camera trap stations was carried out to evaluate the main determinants of habitat use of the Andean tiger cat in three protected areas from the middle Cauca basin, Colombia. Habitat use of the Andean tiger cat increased with litter depth and distance from population centers. Andean tiger cats also tended to use more than expected by chance sites with the presence of its prey, and were invariant to the presence of intraguild predators. To implement viable conservation actions on the species, it will be necessary to consider the importance of the structure of the microhabitat, human disturbance, and the co-occurrence of prey as conditioning factors for its use. In protected cloud forests, the Andean ocelot can use its habitat to maximize encounters with prey and decrease the risks associated with proximity to population centers. It will be necessary to expand efforts to determine if the observed trends can be sustained beyond the limits of protected areas.

V-42: The Neotropical cat genus *Leopardus*: a genomic history of rapid speciation and hybridization

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The phylogeny and taxonomy of the Neotropical genus *Leopardus* (Felidae) has always been controversial, owing to the cryptic morphology, rapid diversification and instances of hybridization in this clade. We employ whole-genome sequencing data of 15 samples spanning all 8 recognized *Leopardus* species (IUCN/SSC Cat Specialist Group) to address how speciation, introgression and demographic events shaped their current diversity. We constructed a consensus phylogeny under the assumption of the multispecies coalescent, quantified the phylogenomic discordance found in the genome and conducted introgression tests to distinguish between incomplete lineage sorting and hybridization as sources of conflicting phylogenetic signal. To assess current genetic diversity in *Leopardus*, we estimate genomic divergence, heterozygosity and runs of homozygosity in our samples. We show that the consensus phylogeny supports the recognition of Andean and Central American populations of northern tiger cat (*L. tigrinus*) as a distinct species, not closely related to the NE Brazilian population, and challenge the long-held notion of margay (*L. wiedii*) and ocelot (*L. pardalis*) as sister species. We detect historical hybridization between ocelot and the base of the '*Oncifelis*' clade, and identify introgression between Geoffroy's cat (*L. geoffroyi*) and southern tiger cat (*L. guttulus*). Consistent with a recent radiation, genetic divergence between species is relatively low, yet highly contrasting levels of heterozygosity indicate different demographic histories.

V-43: Species from feces: using eDNA metabarcoding to assess plant diet diversity in feral pigs

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Feral pigs (*Sus scrofa*) are a destructive yet successful invasive species in North America, with some of their success attributed to their dietary plasticity. Feral pigs are opportunistic omnivores, and much of their diet consists of plants. Predation on plants by feral pigs can harm the environment through the disruption of vegetation succession and competition. Environmental DNA (eDNA) is a rapid and low-cost method that allows for fine taxonomic resolution of dietary contents. Here, we apply eDNA metabarcoding to describe the taxonomic and functional diversity of plant diets of feral pigs as well as assess spatio-temporal variation in diets. From October 2018 to March 2021, fecal samples were opportunistically collected from 157 trapped pigs at three locations: private properties in Louisiana (n = 5), Fort Polk, Louisiana (n = 107), and Fort Hood, Texas (n = 46). We are particularly interested in categorizing plant species based on their conservation status and ecosystem role. This study also intends to assess biogeographic variation (e.g., if diets vary across military installations), temporal variation (e.g., if seasonality influences diets), and biological variation (e.g., if age or sex of an individual influences diet). This study aims to further our understanding of feral pig predation and consumption of native and introduced plants in order to better inform feral pig management plans and efforts.

V-44: Shrub encroachment alters trophic interactions in a canid-lagomorph community in the Chihuahuan Desert

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A long-standing question in ecology is how bottom-up (resource-limited) and top-down (predation-limited) processes interact within food webs to structure ecological systems. A key remaining challenge, however, is to anticipate how bottom-up and top-down effects are modified by global change effects. Globally, the conversion of arid and semi-arid grasslands to shrub dominated states is a major form of environmental change with potential consequences for trophic interactions and the dynamics of ecological communities. We examined the effects of shrub encroachment on trophic interactions for lagomorphs (black-tailed jackrabbit and desert cottontail) and canids (coyote and kit fox) at the Jornada Basin Long Term Ecological Research (LTER) site in the Chihuahuan Desert of southern New Mexico. Using 7-years of camera-trap data collected across grassland-to-shrubland gradients, we found that bottom-up processes did not produce simple, direct effects on lagomorphs. Specifically, lagomorphs responded strongly to bottom-up processes during years of high precipitation, but only on sites with high shrub cover. This outcome is inconsistent with the pulse-reserve paradigm and may be explained by changes in perceived predation risk associated with increases in shrub cover. Both canids responded positively to lagomorph abundances, suggesting the presences of bottom-up effects. Predation limited processes on lagomorph abundances were not strongly supported. Finally, we detected intraguild interactions between kit foxes and coyotes. We discuss the implications of our findings in the context of ecological state dynamics.

V-45: Coexistence of three mephitids in tropical dry forest in Tehuacán-Cuicatlán biosphere reserve, México

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The hog-nosed skunk (*Conepatus leuconotus*), hooded skunk (*Mephitis macroura*), and southern spotted skunk (*Spilogale angustifrons*) coexist in Tehuacán-Cuicatlán biosphere reserve (TCBR) sharing a diet based on invertebrates. We aimed to infer the mechanisms that allow their coexistence in a tropical dry forest with ecological integrity, and analyzed the activity overlap and relative abundance among species. We obtained 235 records for hog-nosed, 39 for hooded, and 42 for spotted skunks from 15 camera-trap stations from 1 May 2013 thru 30 April 2020. The hog-nosed skunk showed a unimodal activity pattern ($\mu \pm SE$ = 00:42 ± 00:12 h) with peak around midnight, and the hooded skunk had a bimodal pattern ($\mu \pm SE$ = 01:02 ± 00:33 h) with peaks during crepuscular hours at sunset and sunrise. Mean activity of the spotted skunk was unimodal and differed from the other two species ($\mu \pm SE$ = 01:49 ± 00:23 h, $P = 0.02$). The hog-nosed skunk had the highest relative abundance (2.53 to 7.90) and differed from the hooded (0.44 to 1.21) and spotted (0.83 to 0.96) skunks in both seasons ($P < 0.01$). The smaller species, the spotted skunk, showed the most restricted circadian activity and avoided the activity peaks of the other two species. We inferred that the larger species, the hog-nosed skunk, determined the dynamics of intraguild interactions among mephitids in the tropical dry forest in TCBR, Mexico.

V-46: Foraging Ecology of the Hawaiian Hoary Bat on Maui

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The Hawaiian hoary bat foraging ecology is poorly understood and lack of information is hampering efforts to develop effective recovery plans. We sampled 35 sites in each of 9 habitat types with bat detectors for our 34,226-hectare study area from Sept. 2017 – Sept. 2018. We radio-tracked 16 bats on 109 nights. We calculated the 95% kernel foraging ranges (FRs) and 50% kernel core use areas (CUAs) in R. We used blacklight traps to sample insects in each of the 9 habitat types and determined the diets of bats using a DNA barcode library and analysis of each bat's guano. Bats spent more time foraging in gulch, low-density developed, and grassland habitats, and differences existed between months ($P < 0.01$). The mean CUA was 3,991 hectares and the mean FR was 17,362 hectares. Bats ate primarily moths (68%), as well as flies (12%), termites (9%), orthopterans (5%), beetles (4%), and true bugs (2%). Native and nonnative insects were eaten, and bats were somewhat selective in prey species. Agricultural vegetation, grassland, and low-density developed habitats had the highest dry weight values for insects, while the lowest values were from the forest woodland and high-density developed habitats. Our data suggest foraging flexibility in the species with the use of habitat types changing during different seasons.

V-47: Widespread convergent evolution of venom resistance in African carnivores

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Several African and Asian mammals are known to survive bites from and regularly prey upon venomous snakes. Honey badgers, hedgehogs, pigs, and mongooses have all independently evolved mutations at their nicotinic acetylcholine receptors (nAChr), which prevent binding of snake venom α-neurotoxins. Recently, a published genome of the meerkat (*Suricata suricatta*) shows the same mutations that confer resistance to mongooses present in the meerkat, suggesting that venom resistant nAChR's may be present in (and ancestral to) all Herpestids. Using museum tissues, we sequenced the nAChR for species within Herpestidae as well as the closely related families, Viverridae, and Eupleridae. Results reveal that resistance is present in many species within all three clades and has evolved several times independently. While Herpestids share the same mutations at the same sites, Viverrids and Euplerids have evolved mutations more similar to those found in honey badgers and hedgehogs. Within Viverridae we find an additional novel instance of functional convergence (different mutations at the same sites). This work is the first to show any molecular mechanism of venom resistance in Viverrids and Euplerids. Both pervasiveness and repeated convergence of these mutations suggests this extraordinary adaptation is more common than previously thought, and that the ecological and evolutionary relationships between venomous snakes and mammals have played a key role in the evolution of mammalian physiology.

V-48: The evolutionary history of the urea transporter gene family (SLC14A) in mammals

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Urea transporters (UT) are transmembrane proteins widespread in life, from bacteria to metazoans, transporting urea through cell membranes. Mice and humans have two transporter types encoded by the genes SLC14A1 (UT-1) and SLC14A2 (UT-2), differing in length (UT-2 roughly twice as UT-1) and transcription profiles. The evolutionary history of these mammalian genes and their relationships with the UTs of other vertebrates remain unclear. We annotated UT genes in a representative set of high-quality vertebrate genomes to resolve orthology and construct their evolutionary history. In coelacanths and tetrapods, UT loci are in tandem and flanked by similar orthologs. Coelacanths and amphibians have a single UT gene. All mammals have the two UT loci described in mice and humans; which are separated by about 1 kb. Other amniotes lack UT-1, having instead several UT-2 forms. Phylogenetic analysis allowed us to establish the ancestral state in tetrapods, namely a single UT gene that was preserved in sarcopterygians and amphibians. We inferred two main gene duplication events in amniotes: one originating UT-1, and another, giving rise to a small proto-UT-2. UT-1 is currently restricted to mammals. The second duplication was internal to UT-2, accounting for its internal structure. This internally duplicated gene is found in mammals and sauropsids, whereas a secondary loss of the first half of the UT2 gene is observed in lepidosaurs.

V-49: Sexual dimorphism in the endocast of eastern lowland gorillas in the light of social behavior

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Sexual dimorphism of the nervous system has been reported for a wide range of vertebrates and is commonly associated with behavioral differences. Within gorillas, males and females differ greatly in their social behaviors. However, our understanding of sexual dimorphism in primate cranial structures and brain remains limited. In this study we aimed to investigate the differences between male and female external and internal (i.e. endocast) cranial shape, in the eastern lowland gorilla. To do so, we reconstructed gorilla external crania and endocast from computed tomographic (CT) scanners and used 3D geometric morphometrics techniques to assess the phenotypic differences between the sexes. Our results highlighted a sexual dimorphism for external cranium and endocast as regard for both size and shape. Males display an elongated face associated with a pronounced sagittal crest and an elongated endocast on the rostro-posterior axis compared to females that are characterize by a rounded brain case and endocast. Males also show significantly larger external cranium and endocast size than females. In addition, we described important differences for the posterior cranial fossae (i.e. position of the cerebellum within the braincase), olfactory bulb and endocranial hemispheric asymmetry between the two sexes. In particular, our results highlighted that females have relatively larger posterior cranial fossae and left endocranial hemisphere while males have been characterized by a relatively larger and rostrally oriented olfactory bulb.

V-50: Diet of maternal big brown bats vs. bachelor big brown bats in Kansas

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The public rarely comes into close contact with bats, but if they do encounter one it is generally *Eptesicus fuscus*. These bats historically resided in tree snags and rock crevices but with continued urbanization, *E. fuscus* primarily reside in urban structures. Even though *E. fuscus* are widespread, there is limited knowledge on their dietary preferences. This project will examine seasonal dietary variation and dietary differences between the sexes of *E. fuscus*. In partnership with the Kansas Department of Wildlife, and Parks, guano samples were collected May through August of 2019 and May through August of 2021 from bats captured in mist nets. DNA was extracted from the guano and COI mini-barcodes were amplified. Insect DNA was sequenced using next-generation sequencing protocols and bioinformatics pipelines. Through the sequencing of insect DNA, seasonal variation in *E. fuscus* will be established and we will assess variation between male and female diets. With increased knowledge of *E. fuscus* diet, better management practices that account for variation occurring seasonally and between males and females can be implemented.

V-51: Rodent species as potential reservoirs of pathogenic *Ehrlichia* in a prairie ecosystem.

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Ehrlichiosis is a tick-borne disease caused by multiple species of *Ehrlichia*, which infect humans and companion animals alike. While the ticks responsible for transmission of these pathogens are known, the rodent species that serve as reservoirs are less understood. This study sought to identify possible reservoirs of *Ehrlichia canis* and *Ehrlichia ewingii,* both of which are increasingly common in midwestern states like Illinois. This sudden increase may be tied to preservation and restoration of tallgrass prairie ecosystems in the region. From 2014-2018, 472 tissue samples were collected from three rodent species on a prairie restoration in Boone County, Illinois: *Microtus pennsylvanicus* (n=209), *Ictidomys tridecemlineatus* (n=136)*,* and *Zapus hudsonius* (n=127). Both *Ehrlichia canis* and *Ehrlichia ewingii* were found in all three species as determined via nested PCR amplification using primers specific to each species of *Ehrlichia,* followed by DNA sequencing. Approximately 22% of rodents sampled were positive for *Ehrlichia canis,* and ~14% of rodents sampled were positive for *Ehrlichia ewingii*. There was a significant effect of rodent species on pathogen prevalence, with *Ictidomys tridecemlineatus* and *Microtus pennsylvanicus* more likely to be infected with either pathogen than *Zapus hudsonius*. Additionally, of the infected rodents, ~25% were infected with both species of *Ehrlichia* suggesting a higher than expected degree of coinfection. Data indicate that prairie-dwelling rodent species may serve as reservoirs for these bacteria in the midwestern US.

V-52: Bobcat (*Lynx rufus*) abundance and density in privately owned ranches of northwestern Chihuahua, Mexico

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Population status of wild species is essential when making decisions about their management and conservation. Bobcats (*Lynx rufus*), considered the most abundant wild feline of Mexico; however, there is no solid evidence about its population size in the country. Therefore, our objective was to estimate the population density of bobcats in northwestern Chihuahua, Mexico. In the 2018-2021 period, we collected scats in 21 privately owned properties and using microsatellite markers analysis determined sex and individual identification. We calculated the density of bobcats dividing the number of individuals within a minimum survey area using the mean maximum distance traveled. We identified 181 bobcat scats belonging to 29 unique individuals, including 13 females and 16 males (sex ratio 1:1.23). We recaptured 25 individuals; mean number of recaptures range from 1 – 11. The majority (n =23) of the individuals were present in two years, while the rest (n = 6) appeared in more than three years. On average, we estimated bobcat density at 10.16 ± 5.92 ind./100km^2; (with a range of 1.05 – 45.27 ind/100km^2). Bobcat densities are not uniform in the study area, so the individual identification in different population through genotyped scats is suitable to estimate moderate densities. We recommend more studies on the abundance and population density of bobcats in Mexico, and thus contribute to its conservation status in the country.

V-53: Quantifying bobcat prey abundances between distinct ecoregions of Oklahoma

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Bobcats (*Lynx rufus*) occur throughout most of Oklahoma, yet the state is comprised of a great variety of diverse ecoregions, often representing contrasting environmental conditions. Previous studies of bobcat diet within Oklahoma show variable diet between ecoregions, but apparent preferences for rabbits (particularly *Sylvilagus* spp.) and rodents. Quantifying the relative abundances of potential prey upon the landscape will greatly improve our understanding of bobcat space-use and dietary preferences between these distinct ecoregions. To estimate the abundances of rodent prey at our three bobcat research study sites, we deployed a series of 300m Sherman live-trap transects between March and May of 2020 and 2021. Each study site was partitioned into three or four distinct habitat types and four transects were deployed on each habitat type for three consecutive trap nights. Over the two field seasons, we recorded >1200 captures of 832 rodent individuals, representing >20 species of small mammal. Three genera represented 91% of captures alone, with *Peromyscus* spp. accounting for almost three quarters of all captures, however diversity differed among study sites and habitat types. Initial analyses show that time since prescribed burns had significant effects on the abundance and community assemblages of small mammals within certain habitat types. Predictive modelling will provide estimates of small mammal abundances for our represented habitats, informing bobcat spatial modelling and providing context to much of our collected bobcat data.

V-54: Community structure in a countryside ? testing predictions from island biogeography vs. habitat amount hypotheses

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Elucidating the mechanisms by which landscapes structure wildlife communities in agroecosystems gains in importance at a rate concurrent with habitat loss. Wildlife communities could find sanctuary in an array of professionally managed protected lands dispersed through a matrix of rural privately-owned land. We used camera-traps to survey medium- and large-bodied mammal assemblages for one year in 30 property units of the Lyndon B. Johnson National Grasslands in north Texas to test the ability of island biogeography theory (IBT) and the habitat amount hypothesis (HAH) to explain observed species diversity and intensity of site use via a modeling approach. The IBT 'islands' were defined as the entire protected property unit or only forest patches within and bounded by the property units, whereas forest cover was the focal habitat for HAH. The habitat amount hypothesis was expected to outperform the island biogeography models. Contrary to expectations, neither of the IBT variants nor the HAH were supported. Diversity and intensity of site use had a non-linear negative response with forest amount while the IBT predictors often showed relationships of zero magnitude or opposite than expected. These assemblages appear to be supported by the rural private land and the protected land, and the species likely are utilizing an array of habitat types.

This provides another example of agroecosystems supporting generalist mammal communities, further highlighting their potential for wildlife conservation.

V-55: Are direct observation and playback effective in surveying Japanese pika populations in dense vegetation?

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Wildlife monitoring plays a key role in species conservation with growing importance under the threat of climate change. The Japanese pika (*Ochotona hyperborea yesoensis*) is a presumably vulnerable cold-adapted species, but its high elusiveness hinders fine population surveys. Visual-based survey methods, often used for other pika species, are not applicable in the densely vegetated pika habitats of Hokkaido, Japan. In this study, we alternatively assessed the efficacy of aural detection of the Japanese pika through their vocalizations to survey their occupancy and abundance. We conducted two different point count surveys, namely direct observation and playback, during 2021 in 18 sites in and around Daisetuzan National Park. We then assessed the efficacy of these methods in detecting occupancy and how this is affected by survey duration. For abundance, we investigated whether the indices from both methods were correlated. Japanese pikas were found to be present at 11 of our surveyed sites. We found both direct observation and playback to be effective at detecting presence, but playback was more efficient considering the time-wise performance. We also found abundance indices to be strongly correlated between direct observation and playback. In conclusion, our results demonstrate that both survey methods are applicable for Japanese pika population surveys, even in densely vegetated habitats, and therefore represent valid survey methods that can help understanding the effects of climate change on the species.

V-56: Effect of past and present weather conditions on small mammals in a temperate mountain range

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Small mammals show a strong response to weather, which is one of the main factors shaping their population dynamics. We evaluated abundance and structure of small mammal communities in relation to past and present weather conditions, using trapping data collected during seven years in the Romanian Carpathian Mountains. For each sampling site, we used the interpolated seasonal rainfall and mean temperature in the trapping year and each of the three years before, and some habitat characteristics, among which tree canopy cover had a significant effect. To evaluate the unique and shared effects on the community structure, we used multivariate analyses and variation partitioning among groups of predictors. Present temperatures, but not rainfall, predicted the community structure. Among the past conditions, spring and autumn rainfall two years earlier and autumn temperatures two and three years earlier had significant effects, showing the important delayed effect of climate, mediated by primary production. Most of the variation in community structure was explained by the overlap between temperature, rainfall, and year, while the unique effect of year was not significant. The habitat was a poorer predictor compared to the weather. The abundance of the common shrew (*Sorex araneus*) had a significant negative response to temperature. Therefore, we predict that this species will decline with climate warming. In contrast, the yellow-necked mouse (*Apodemus flavicollis*) was correlated with increased temperatures.

V-57: A battle between crab-eating and hoary foxes in the northern Brazilian savannas? Abundance, spatio-temporal patterns.

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The crab-eating fox (*Cerdocyon thous)* and the hoary fox (*Lycalopex vetulus*) have extensive range overlap and an omnivore diet that could put them as potential competitors. In this work, we compared their activity, habitat use, and abundance in the vanishing northern savannas of Brazil, in Mirador State Park - MSP. Both species exhibited nocturnal habits; while showing differential habitat use preferences. The hoary fox

favors the more open savannas, while crab-eating prefers denser savannas. Meanwhile, crab-eating foxes were way more abundant than hoary foxes, reaching a ratio of 3:1. We managed to estimate the density only for the former, through spatial analyzes in an effectively sampled area of 117.43 km2, with 72 days of sampling effort and 52 detections of 12 individuals in one site (Mel). In the other site (Cágados), the sampled area was 164.81 km2, where we obtained 82 detections of 22 individuals, in 82 days of sampling effort. Thus, crab-eating fox densities at MSP were approximately 0.35 ind./km2 (Mel) and 0.23 ind./km2 (Cágados). These are high values for spatial analysis. Do they battle at MSP? No, they do not seem to do so, and besides, *their known food preferences could ameliorate and be a key factor in segregating them, minimizing direct conflicts.*

V-58: Alteration to daily activity patterns of terrestrial herbivores at a wind energy facility

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Wind energy facilities have become a prominent feature on landscapes across North America. While ecological impacts and behavioral changes to bats and birds near wind turbines have been well studied, it is less clear the degree to which terrestrial species are impacted by these novel structures. Here we investigate if daily activity patterns of two prominent herbivores, mule deer and jackrabbit, differ between mixed agricultural and grassland habitats with and without wind turbines. During 2011-2012, camera traps were deployed at turbine and turbine-free habitats in western Kansas. Daily activity patterns were estimated via kernel density and assessed for differences between treatment groups. Preliminary results indicate that deer shift their daily activity patterns around turbines to become increasingly diurnal, but not lagomorphs. Changes in daily activity pattern of herbivores is not likely in response to changes in human, which also differs between turbine and turbine-free habitats. This suggests that environmental assessments of wind energy facilities should consider potential disruption to herbivore behaviors and consider altering usage during behaviorally sensitive periods.

V-59: Cranial bone calcification process of masked palm civet

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The masked palm civet (*Paguma larvata*) belongs to the family Viverridae, Carnivora, and is a “late-maturing” animal in which pups are born in an immature state during the fetal period. Sufficient knowledge regarding the ossification mode of the masked palm civet skull is lacking. Therefore, we observed the ossification pattern of the skull and appearance time of the fontanelles using ?CT in 40-day fetuses and newborns of masked palm civets. Ossification of the medial plate of the sphenoid pterygoid process, stylohyoid, and tympanic ring was observed in the external skull base of the newborns, but these ossifications were not observed in the 40-day fetuses. In newborns, basioccipital, alisphenoid, basisphenoid, orbitosphenoid, squama, and petromastoid portions of the temporal bone were all ossified. However, in the fetus, squama and petromastoid portions of the temporal bone were hardly ossified. In humans, the posterior fontanelle is said to close first (3 months), following which closure of the anterolateral (6 month), posterolateral (18 month), and anterior (36 month) fontanelles occurs. Therefore, the differences in the ossification process and order of fontanelle closure were thought to be caused by the change in brain development and cranial bone ossification patterns in the course of evolution.

V-60: How does the crab-eating raccoon makes use of habitats in the dry Brazilian Caatinga?

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The crab-eating raccoon (*Procyon cancrivorus*) is a procyonid with a wide distribution in South America. Despite this, its behavior and ecology remain poorly known. Prior studies suggest the species is nocturnal, solitary, and often associated with water. It has been recorded in the semi-arid Caatinga biome, the largest forest ecoregion in the Americas. The biome is experiencing accelerated habitat degradation, and 46% of its original cover has already disappeared. Very little is known about crab-eating raccoons in semi-arid environments. To fill in this gap, we sampled a private reserve in the Brazilian Caatinga with camera traps.

We estimated activity patterns of crab-eating racoons using kernel density estimation. We also assessed the species' habitat preferences using single season occupancy models. We found that the species is nocturnal, with the vast majority of records being at night. Preliminary findings also suggest the species uses all vegetation formations available at our study site and is not negatively affected by human presence. Occupancy rates were high, which suggest the species is adaptable to the semi-arid environment at our study sites. These results enhance our understanding of the crab-eating raccoon ecology in semi-arid landscapes.

V-61: Rodent diversity and distribution in a highly human modified tropical landscape

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Globally, the tropical forests (TF) harbor high diversities of flora and fauna and provide important ecosystem services but they are nonetheless highly disturbed. In Mexico, TF are concentrated in the southeast where they are currently fragmented and reduced in extent due to livestock husbandry, agriculture, and urban and rural human expansion. The purpose of this study was to determine the response of rodent community to fragmentation of the TF in a rural landscape in a buffer zone of a Natural Protected Area in Chiapas. The change in land use over a period of 33 years was determined. The landscape was characterized into different categories using landscape metrics. Rodents were sampled and their diversity evaluated within each landscape category. During the last 33 years, 360 ha of tropical forest have been transformed to pastureland and human settlements. Fragmentation has yielded four categories of landscape: agriculture, pastureland, rural, and tropical forest, generating a mosaic landscape. The most abundant of the ten species of rodents documented were *Peromyscus mexicanus* (n = 65) and *P. beatae* (n = 17). *Scotinomys teguina* was found exclusively in tropical forest. Other species were found in more than one landscape category, for example, *Heteromys desmarestianus* (tropical forest and agriculture coverage). Long-term studies are required to understand the process fragmentation and the evolution of rodent response to rapid and dramatic changes in the landscape.

V-62: Unraveling the role of the Andes in the diversification of the nectar bat *Glossophaga soricina*

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Glossophaga soricina is a generalist species of nectar bat that occupies multiple habitats and ecosystems. It has one of the widest distributions among Neotropical bats, ranging from Mexico to Argentina. According to phylogeographic studies, *Glossophaga soricina* comprises two clades: 1) individuals from South America east of the Andes Mountains, and 2) individuals from Central America, Jamaica, and the western slope of the Andes (Hoffmann and Baker 2001, Rocha-Dias et al. 2017, Hoffmann et al. 2019). However, the limited sampling in previous studies and the use of a single mitochondrial marker (Cytb), prevent us from making strong inferences about biogeographical patterns. Thus, the main goals of this work are to analyze phylogeographic patterns of *G. soricina* in South America, and to establish the extent to which the Andes act as a barrier for *G. soricina* populations. To this end, UCEs (Ultra Conserved Elements) and mitochondrial genomes are being utilized as genetic markers. Our results do support two main clades of *G. soricina*, as reported in previous studies, but their geographic distributions are different. The two groups are not delimited by the Andes; instead, each group has cis- and trans-Andean distributions.

V-63: Audio detectors, camera traps, and live trapping: a look into flying squirrel survey methods

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Species occupancy is often understudied in cryptic species, such as northern and southern flying squirrels (*Glaucomys sabrinus* and *G. volans*, respectively), because they are difficult to detect when present. These issues are particularly challenging with species of conservation interest whose rarity may further limit detection and for which traditional methods such as live traps require an abundance of time and labor and may result in the inadvertent deaths of sensitive species. Recently, surveying with non-invasive methods such as acoustic detectors and camera traps has shown promise in remedying these problems, although widespread testing is needed. We deployed live traps (60), baited camera traps (2), and low-cost acoustic detectors (2; Audiomoths, Open Acoustic Devices) across New York State to target flying squirrels and other small mammals as part of the state-wide New York Mammal Survey. Traps were deployed at each site for 6-12 nights from 2020-2021. Trill calls are diagnostic and easily differentiated between species compared to other common call types. We found audio quality of Audiomoth acoustic detectors was adequate to identify northern versus southern flying squirrel trill calls; however, quality was insufficient to accurately identify other flying squirrel vocalizations to species. Flying squirrel detection rates were highest using acoustic detectors followed by camera traps then live trapping; however, combining camera traps and acoustic detectors yielded the highest per-site detection rates.

V-64: Diversified diet: How do uakaris select fruits infected by insects.

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The ingestion by primates of insects embedded within fruits is a little discussed topic. However, such actions can provide frugivorous and granivorous primates with a substantial source of animal protein, vitamins and micronutrients. Previous studies have shown positive selection for infested fruit for some species in the diet of the Golden-backed Uacari (Cacajao ouakary), a South American primate. The objective of this study was to test whether the weight of a fruit would be enough to reliably inform a monkey whether the fruit is infested or not. We studied 11 plant species shown by previous studies to be actively selected by primate, and which, together, contributed more than 25% of the uacari diet. We used the following predictions: (i) Golden-Backed Uacaris would actively select infested fruits using the mass of fruits (ii) Golden-Backed Uacari would select infested fruits by the volume. We tested these predictions using the Mann Whitney test (on the raw data to verify that, in general, uninfested and infested seeds are significantly different in mass). Results indicate the variable mass is an important factor to indicate to uacaris whether the fruit is infested. However, they do not select by fruit volume, showing, for example, no preference for bigger fruits. This, preference lies within size categories and is based on comparitive mass per volume. Further studies are required.

V-65: From sound to silence: a census of the Santa Genebra?s howler monkeys (Alouatta g. clamitans)

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Brown howler monkeys (*Alouatta guariba clamitans*) are important members of tropical forest dynamics, acting as seed dispersers, however, its populations had suffered an outbreak of yellow fever, becoming a threatened species. One of the last populations that inhabit the state of São Paulo, lives in the Santa Genebra Reserve. Where the last census estimated one of the biggest densities for the species in the biome, but the sights (and vocalizations) of the animals became rarer in the last years. Although the park's management didn't register fatalities related to yellow fever in recent years. We estimate the actual population's density, using Distance software, and simulate different scenarios in Vortex software to determine the population viability since the last census and for the future. All scenarios in our simulations lead to a lower density of howler monkeys in the fragment, and the results suggest that the isolation doesn't affect the local population viability, neither in short or long periods, but the yellow fever has a significant impact, especially in a longer time scale. The biggest factor in the population reduction was the decrease in carrying capacity, showing that the population drop is due to the intense degradation process that the reserve has been going through, such as fires and edge effects. Our results demonstrate the need for greater efforts in the management of the reserve.

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SAVE THE DATE!!!

13TH INTERNATIONAL MAMMALOGICAL CONGRESS

Please join us 14 to 20 July 2023 for the 13th International Mammalogical Congress (IMC-13). The IMC-13 meeting will be hosted by the American Society of Mammalogists - who will be celebrating their 102nd annual meeting - and will be held at the Dena'ina Civic and Convention Center in Anchorage, Alaska.

From the serene waters of Cook Inlet to the exceptional natural wonders of the Chugach, Anchorage encompasses incredible adventures and metropolitan appeals that are larger than life. With 1,500 moose, incredible national parks nearby, and 60 glaciers only a short drive away, Anchorage is a dream destination. Come celebrate modern mammalogy, make new friends from throughout our international community, and enjoy the towering mountains, sparkling glaciers, and amazing wildlife that makes Alaska the Last Frontier.

The scientific program for IMC-13 will include symposia, workshops, and plenary speakers, as well as contributed oral and poster presentations. A full social agenda is being planned that will include field trips and events at local points of interest. Hotel blocks and dormitory housing will be available for meeting attendees. Please be sure to share and follow the meeting on social media using #IMC13!!!

Detailed conference and registration information will be forthcoming on the conference website (imc13.com). For more information about IMC-13, contact the ASM program director, Cody Thompson (mammal.meetings@gmail.com); ASM meeting planner, Kerrell Dunsmore (kerrell@thenextgreatevent.com); or IFM president, Eileen Lacey (ealacey@berkeley.edu).

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