

**97TH ANNUAL MEETING
OF THE
AMERICAN SOCIETY OF MAMMALOGISTS
20-24 JUNE 2017
UNIVERSITY OF IDAHO
-MOSCOW, IDAHO-**



ABSTRACT BOOK



The 2017 American Society of Mammalogists Annual Meeting logo was designed by Audrey DiGirolamo (seated left), who is majoring in Studio Art and Design at the University of Idaho. Associate Professor Delphine Keim's (seated right) graphic design class developed logos with Idaho mammal themes as a class project. The best design was selected by the local committee for use at the meeting.

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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 who 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 6 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 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.

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WELCOME

Dear ASM Attendee,

Welcome to the 97th annual meeting of the American Society of Mammalogists!

We are delighted to be meeting in Moscow, Idaho! Judging from the registration and abstract count, ASM members are excited about the venue and the opportunities this meeting brings. Whether you are a long-term member or have just joined, I can say without hesitation that you are part of a special organization. For those of you who are new members or are attending their first meeting, know that this is a wonderful opportunity to meet fellow mammalogists, share in the latest findings, and learn about upcoming opportunities. This is perhaps our very best opportunity to meet and welcome new colleagues, so please introduce yourself!

A quick look at our schedule will show you a program covering all aspects of mammalogy. We have contributed papers arranged in technical session and identified by topic; symposia on genomic approaches, climate change and small mammals, and the ecophysiology of large body size in changing climates; and workshops on programming applications in *R*, broadening impacts on K-12 education, and writing successful NSF dissertation improvement proposals. You will also find no fewer than five thematic sessions, including our first foray in "lightning talks". Of course we have our two plenary sessions in which we highlight work by recipients of our student awards and showcasing accomplishments of senior mammalogists; and we have a wonderful capstone presentation in store by an ASM Honorary Member. For even more opportunities, we offer two poster sessions to facilitate one-on-one interactions. Learning of advances in mammalogy brings us to the meeting, but I would remind all attendees that ours is a working society, and members are called on to make important decision regarding our governance at our two Members Meetings. Your vote matters and I urge you to attend these important decision-making events.

All work and no play is just no fun at all, so we have sprinkled in plenty of opportunities for socializing. These include the various socials and picnic, an auction, the Run for Research, and a student mixer and mammal crawl in downtown Moscow.

For many of us, the camaraderie at these meetings makes it as much a reunion of extended family as an opportunity to stay current on great science. I know I am just one of many who look forward to this week as a time to indulge my affinity for all things mammalogical, reconnect with old friends, and meet new colleagues. I thank you all for attending and making the ASM a priority in your lives. I especially thank our sponsors, exhibitors and advertisers, whose support is critical to so many of our annual functions. Please take some time during the breaks and socials to visit their tables and displays and let them know how much you appreciate their participation.

Enjoy the meetings,



Robert Sikes
President, American Society of Mammalogists

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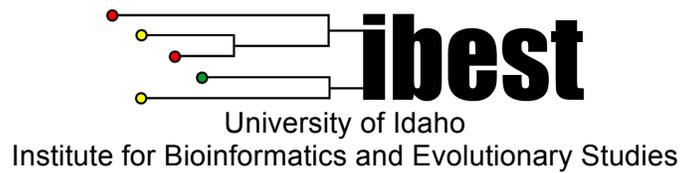
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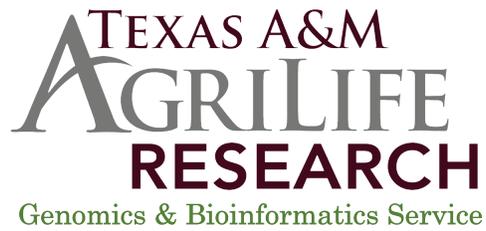
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ABSTRACTS

1^{E,HTA}: Mountain lions support beetle biodiversity through predation

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Carnivore ecology is a broad field, inclusive of novel hypotheses aimed at describing the ecological niche of large carnivores and their keystone roles in natural environments. While numerous gaps have been addressed in this field, many remain open to speculation. Here we present research on an iconic species that, through predation, provides significant amounts of carrion to diverse scavengers in natural systems. We conducted weekly sampling of beetle scavengers at 24 carcasses of ungulate prey killed by mountain lions in the Greater Yellowstone Ecosystem. Approximately 23,000 adult beetles were collected and sent to the Marsh lab at Montana State University for identification to species level. We use Shannon's diversity metrics for each week and over the course of each carcass to calculate beetle biodiversity and evenness over time. We've documented > 300 species of beetles, of which three-fourths were carrion-dependent, emphasizing the keystone function mountain lions have in supporting invertebrate biodiversity. Preliminary data suggests beetle diversity and evenness increase over time at ungulate carcasses. Our results will offer wildlife managers new data demonstrating the keystone function large carnivores have in supporting biodiversity. This new area of research could have important consequences for carnivore conservation, and could be applied broadly to numerous carnivore species across diverse habitats. This research was supported by the 2016 Annie M. Alexander Award awarded to Joshua Barry.

2^{HTA}: Determining carnivore habitat use in a rubber/forest landscape in Brazil using multispecies occupancy models

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Understanding the factors that influence the presence and distribution of carnivores in human-dominated agricultural landscapes is one of the main challenges for biodiversity conservation, especially in landscapes where setting aside large protected areas is not feasible. Habitat use models of carnivore communities in rubber plantations are lacking despite the critical roles carnivores play in structuring ecosystems, and the increasing demand for natural rubber. Our research sought to determine the habitat use of a mammalian carnivore community within a 4,400-ha rubber plantation/forest landscape in Bahia, Brazil. To study the community we set up a 90-site camera trap grid. We used a multispecies occupancy model to determine the probabilities of habitat use by each species. There were significant differences in the probabilities of habitat use of domestic dogs (*Canis familiaris*), crab-eating foxes (*Cerdocyon thous*) and coatis (*Nasua nasua*), with domestic dogs and foxes having higher probabilities of using rubber groves and coatis of using forest. The low detection probabilities (≤ 0.1) of tayras (*Eira barbara*) and wildcats (*Leopardus* spp.) precluded reliable estimation of habitat use probabilities using the occupancy model. The results show the potential of rubber/forest landscapes for the long-term conservation of carnivore communities in the Atlantic forest, especially in mosaics with 30-40% forest cover, and provide insights for making rubber a biodiversity friendly crop. This research was supported by the 2017 Anna M. Jackson Award awarded to Andrea Dechner.

3^{HTA}: Contrasting behavioral and physiological responses to environmental change in two partially sympatric

Talysin T. Hammond*, Rupert Palme, and Eileen A. Lacey
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In the face of environmental change, organisms may increasingly depend upon immediate, phenotypically plastic coping mechanisms to adjust to changing habitats. Behavior and physiology are examples of first-line mechanisms animals can use to respond to environmental change. This research focuses on stress (using fecal glucocorticoid metabolites, FGMs) and activity patterns (using accelerometers) of two California chipmunks that have exhibited divergent responses to the past century of environmental change: the range of the alpine chipmunk (*Tamias alpinus*, TA) has contracted upwards in elevation, while the co-occurring lodgepole chipmunk's (*T. speciosus*, TS) range has not shifted. We collected FGM and environmental (2013-2015) and activity data (2015) to test hypotheses about which factors best predict stress and activity, and to what extent they differ between TA and TS. Our environmental data shows that temperature and vegetation differ in the focal species' habitats. After validating the use of accelerometers, we found that activity patterns, though temporally similar, differ interspecifically in which factors best predict them: TS's activity shows stronger flexibility with environmental parameters and more inter-individual variability. In captivity TA showed a stronger FGM response to a number of stressors, while in the field FGM-environment relationships differed between years, with density and vegetation being strongly predictive. Ultimately, our results reveal a number of interesting disparities between the focal species that help clarify their differential responses to environmental change. This research was supported by the 2017 A. Brazier Howell Award awarded to Talysin Hammond.

4^{E,HTA}: Ungulate migration is a cultural phenomenon

Brett R. Jesmer

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In ungulate populations, migration arises because individuals track seasonal shifts in the spatial distribution of forage. I hypothesized that information regarding spatial and temporal variation in forage quality is socially learned and gives rise to a culture of migrant behavior. I tested this hypothesis using 10 populations of bighorn sheep (*Ovis canadensis*) and moose (*Alces alces*) with varying opportunity for social learning (0 to >70 generations). For each population, I used telemetry data and remote sensing technologies to quantify the amount of information individuals possessed and their migratory propensity. In contrast to the genetic programs that strongly influence most bird and insect migrations, ungulate migration required generations of information acquisition and transfer via cultural transmission. Over the course of a single generation, individuals acquired and transferred small amounts of information, but migrant culture arose only after 25 to >70 generations of information gain and social learning. Because culture ratchets up information gain with each successive generation, the loss of migration will result in generations of information loss and will likely suppress fitness for extended periods. Preservation of migrant culture should be prioritized alongside landscape connectivity in efforts to conserve migratory ungulates. This research was supported by the 2017 Elmer C. Birney Award awarded to Brett Jesmer.

5: Endemic mammals of Colombia: what do we know about them?**

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Colombia occupies the sixth place in global mammal diversity with 526 species, of which 58 are endemic to the country. Endemic Colombian mammals include rodents (31 species), primates (9), bats (8), marsupials (5), and shrews (5). In spite of the growing body of knowledge on South American mammals, there is still an information gap concerning studies of the biology, systematics and diversity of Colombian mammals. This is even more critical for the endemic taxa, which have been historically overlooked. As a consequence, these species are underrepresented in natural history collections and not included in phylogenetic analyses. In order to evaluate the current knowledge on endemic Colombian mammals and

define research priorities, we developed an online platform named “Musaraña” with the aim of compiling all available information of the records and studies on Colombian endemic mammals. Although some primates and marsupials have been studied in relatively more detail, this is not the case for most bats, rodents and shrews. A total of 5 endemic species are known only from their type locality, and it is still unclear whether 3 taxa constitute valid species due to the very small sample size and absence of genetic data. Furthermore, there is a lack of ecological and systematic studies for most small mammals. Research priorities should address threats and population status, species distributions, evolutionary relationships, and the taxonomic validity. This research was supported by the 2016 William T. Hornaday Award awarded to Héctor E. Ramírez–Chaves.

6^{HTA}: Untangling the taxonomy of short-tailed opossums (*Monodelphis*): an integrative approach using molecular and phenotypic data**

Silvia E. Pavan

Coordenação de Zoologia, Museu Paraense Emílio Goeldi, Avenida Perimetral, Belém, Brazil

Short-tailed opossums, genus *Monodelphis*, comprise the most speciose genus of New World marsupials, with 23 currently recognized species ranging from eastern Panama to northern Argentina. Considering its widespread distribution, the genus has potential to be exceptionally informative about biogeographic processes that have shaped the continental fauna. Additionally, the large phenotypic diversity in the group—pelage coloration, behavior, and reproductive strategies—makes it particularly interesting to investigate the evolution and the adaptive significance of phenotypic trait variation. Unfortunately, taxonomic problems and phylogenetic uncertainty have long inhibited evolutionary and biogeographic studies of this group. In my systematic research on *Monodelphis* I used phylogenetic analyses of molecular data and morphological comparisons to test hypotheses about relationships and species limits, with the following principal results: (1) the first phylogenetic hypothesis of the genus based on dense taxonomic sampling and multiple genes; (2) a time-scaled, model-based biogeographic analysis of the genus; (3) a revised subgeneric classification; and (4) descriptions of new species. With these results in hand, ecologists and physiologists have new tools with which to investigate several interesting topics, including the evolution of diurnality and semelparity. This research was supported by the 2015 Alma and Albert Shadle Fellowship awarded to Silvia Pavan.

7^{HTA}: Growth patterns and morphometric consequences of adherence to ecogeographic rules in a widespread rodent**

Angela D. Hornsby*, Miriam L. Zelditch, and Marjorie D. Matocq

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Understanding the generation and maintenance of intraspecific variation is one of the central goals of evolutionary biology. When variation is structured across environments in consistent ways, we may develop ecogeographic rules to describe these presumably adaptive, convergent responses to the same environmental forces. Though the ultimate causes of adherence to these rules are rightfully of wide interest, the mechanisms and secondary consequences are also important for understanding how observed phenotypic patterns arise. To this end, we investigated the mechanisms and consequences of ecogeographic variation in a widespread rodent (bushy-tailed woodrat, *Neotoma cinerea*). We found that body size trends in *N. cinerea* are explained by both temperature (Bergmann’s Rule) and ecosystem productivity (resource availability rule), with smallest body sizes found in warm-unproductive climates. After testing for effects of climate on growth initiation, rate, and termination, we found that differences in body size across climates were established early on, during gestation or nursing. Finally, we used geometric morphometrics to analyze cranial shape and found that, despite their smaller size, adult *N. cinerea* in warm-unproductive climates are not pedomorphic (relatively juvenile-shaped) because they break the size-shape relationship by developing at a faster rate per unit body size. These findings are a beginning step toward understanding the mechanisms through which both primary and secondary ecogeographic variation arises, and could be expanded to investigate body size patterns in other taxa. This research was supported by the 2016 Shadle Fellowship awarded to Angela Hornsby.

8^{E}: Pattern and process in the radiation of ground-dwelling squirrels**

Bryan S. McLean

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Despite many well-known examples of rapid radiation in the mammal Tree of Life, we are only beginning to understand the processes that drive taxonomic, phenotypic, and ecological diversity within these clades. Many mammalian radiations may be responses to ecological opportunity, whereby exploitation of new resources or environments in ecological time drives evolutionary divergence and adaptive radiation. I discuss recent progress in our understanding of lineage and phenotypic evolution within ground-dwelling squirrels (Xerinae: Marmotini), a rapid radiation of sciurids distributed across the Holarctic region. Drawing from a suite of specimen-derived molecular, morphological, and ecological datasets, I compare and contrast evolutionary pattern and process at two different scales (across the tribe and within the genus *Urocitellus*). Commonalities across scales include continuous expansion to new habitats, attendant ecomorphological adaptation, and coordinated evolutionary change among morphological traits. Other patterns are scale-dependent; furthermore, discordant patterns can be found within scales but among morphological traits. This work significantly refines our understanding of phylogeny and diversification dynamics in Marmotini but also reiterates the pressing need for integrative analyses at the shallowest of levels in radiating clades to identify drivers of rapid speciation. This research was supported by the 2016 ASM Fellowship awarded to Bryan McLean.

9: Adaptive use of nonlethal strategies for minimizing wolf–sheep conflict in Idaho

Suzanne A. Stone*, Stewart W. Breck, Jesse Timberlake, Peter M. Haswell, Fernando Najera, Brian S. Bean, and Daniel J. Thornhill

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Worldwide, native predators are killed to protect livestock, an action that can undermine wildlife conservation efforts. An ongoing example is occurring in the western United States, where wolves (*Canis lupus*) were eradicated by the 1930s but are again present in parts of their historic range. Nonlethal deterrents have proven effective in reducing livestock losses to wolves in small-scale farm and ranching operations but are often presumed ineffective or infeasible in large-scale, open-range grazing operations. We report a 7-year case study where we strategically applied nonlethal deterrents and animal husbandry techniques on an adaptive basis to protect more than 10,000 sheep (*Ovis aries*) and several packs of wolves in central Idaho national forest lands. Sheep depredation mortalities in the demonstration study area are compared to an adjacent wolf-occupied area where sheep were grazed without the added nonlethal protection measures. Over the 7-year period, sheep depredation losses to wolves were 3.5 times higher in the adjacent area than in the project area. Furthermore, no wolves were lethally controlled within the project area and sheep depredation losses to wolves were just 0.02% of the total number of sheep present, the lowest loss rate among sheep-grazing areas in wolf range statewide, whereas wolves were recurrently killed in the adjacent area. Our project demonstrates that proactive use of nonlethal techniques applied conditionally effectively minimizes wolf depredation on large open-range operations.

10^F: Forecasting cattle depredation risk by wolves within grazing allotments in Washington: a preliminary analysis

Zoë Hanley* and Robert Wielgus

Large Carnivore Conservation Lab, Washington State University, Pullman, WA 99163 USA

Preventing carnivore-livestock conflicts requires identifying conditions placing livestock at risk and focusing outreach and adaptive management at a local scale. Through reintroductions the mid-1990s, gray wolves (*Canis lupus*) have successfully recolonized portions of their former range in the northern Rocky Mountains and surrounding states. Livestock (primarily beef cattle (*Bos taurus*) and sheep (*Ovis*

aries)) are grazed on public and private allotments across an estimated 31% of wolf-occupied areas in Idaho, Montana, and Washington. I investigated characteristics of cattle depredations by gray wolves within grazing allotments in Idaho, Montana, and Washington (n = 69) to predict depredation risk for all cattle grazing allotments in Washington. Risk models were developed to test hypotheses that cattle depredations by wolves were associated with wolf demographics, cattle abundance, allotment characteristics, and land cover types. Cattle depredation risk increased for larger livestock grazing allotments with more cattle and wolves. Wolf pack reproduction, livestock turnout date, and percent grassland cover indicated high variability in the direction of their relationship with cattle depredation probability. Cattle grazing allotments in Okanogan, Yakima, Ferry, Garfield, and Asotin counties were identified at intermediate (61 – 80%) to high (81 – 100%) depredation risk. These risk models and maps provide locations to focus depredation prevention measures and a template for future analyses as wolves continue to recolonize Washington.

11^{E,HTA}: Determinants of activity patterns in urban striped skunks (*Mephitis mephitis*)

Victor Y Zhang*, Tad C. Theimer, Cory T. Williams, and C. Loren Buck

Center for Bioengineering Innovation (VYZ, CTW, CLB) & Department of Biological Sciences (TCT), Northern Arizona University, Flagstaff, AZ 86011 USA

With the expansion of urban development, the occurrences of human-wildlife conflicts will increase in frequency. The ecology of a species, including their daily and seasonal patterns of activity, likely influence the temporal patterns of these conflicts with humans. Striped skunks (*Mephitis mephitis*) are common to urban/suburban landscapes across North America, but the ecology of these populations is not well described. We used accelerometers to measure the overall dynamic body acceleration (ODBA), an index of activity-specific energy expenditure, in a suburban population of striped skunks across a one-year period. Skunks presented both nocturnal and crepuscular activity patterns, depending on sex and season. Weather influenced nightly ODBA in both males and females, with the effects of various weather parameters dependent on breeding stage. Snow cover significantly decreased activity levels in both males and females, possibly due to low food availability. Seasonal differences in nighttime ODBA were consistent with metabolic and reproductive demands. Activity increased in both sexes during spring/summer when compared to fall/winter, and females were more active than males during late gestation through lactation. Greater moonlight intensity decreased activity of males during the early spring mating interval and decreased activity of females during late gestation through lactation, possibly because of changes in vulnerability to nocturnal predators. Our data suggest that managers of urban wildlife should consider the importance of species activity patterns when developing management strategies.

12^F: Resource-Based Conflicts Between Onagers and Livestock in Central Iran

Saeideh Esmaeili*, Mahmoud-Reza Hemami, Petra Kaczensky, Chris Walzer, and Jacob R. Goheen

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The onager (*Equus hemionus onager*) is an endangered subspecies of the Asiatic wild ass, restricted to two protected areas in central Iran. Agricultural expansion and associated conflicts with locals and their livestock are thought to have contributed to its range collapse over the past four decades. To ground future reintroductions in the best science possible, and in December 2016, we fitted 10 mares with high-resolution GPS collars (the first such effort on any ungulate within Iran) and administered a questionnaire within and 50 km outside the Bahram-e-Goor Protected Area. We interviewed 520 individuals (330 villagers and 190 urban residents) regarding their attitudes toward onagers and their conservation. Fifty-seven percent of villagers were unaware of the endangered status of onagers, and 60% of urban residents were unaware that onagers existed in Iran. The degree of conflict with onagers was negatively related to villagers' tolerance of this species, and future conservation efforts. The most widely supported strategies were to accept compensation for crop depredation (74% support) and government-supported shifts from traditional pastoralism to industrial production of livestock (66%). Our results provide the first step in country-wide restoration of onagers by (1) quantifying local support for a range of potential

solutions for conservation; and (2) mapping the rate and timing of nomadic movements by onagers within and around Bahram-e-Goor.

13: Revisiting dental disease as a trigger for lions to become man-eaters

Bruce D. Patterson* and Larisa R. G. DeSantis

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During construction of the Kenya-Uganda Railway in East Africa, workers camped near the Tsavo River were attacked and eaten by two male lions. Inducing terror, mutiny, and work stoppages, the lions became legendary for literally stopping the British Empire in its tracks. They were eventually killed in Dec 1898 after allegedly claiming 135 victims. Many hypotheses purport to explain their depredations, including prey shortages brought on by (H1) a two-year drought or (H2) a rinderpest epidemic, (H3) the railroad's following a traditional caravan trail often strewn with dead or dying slaves, (H4) incomplete cremation of Hindu workers that potentially invited the attention of scavenging carnivores, and/or (H5) dental disease that precluded normal predatory behavior. H1-H4 all invoke resource scarcity and/or greater reliance on scavenging, which would serve to broaden the man-eaters' diets; in contrast, H5 would likely restrict lion diets. Dental microwear textures of the man-eaters (i.e., low to medium complexity values) fail to support scenarios of them as desperate or habitual scavengers. Instead, their teeth resemble those of zoo lions provisioned with meat; reduced durophagy was likely a consequence of their limited access to human carcasses and/or their inability to scavenge carcasses due to dental disease. Although many lions have missing, broken or abraded teeth and behave normally, those that develop significant pathologies become candidates for dietary shifts like those observed in Tsavo.

14: Changes in ecological interactions within mammal communities after the terminal Pleistocene megafauna extinction

Felisa A. Smith*, Rosemary E. Elliott Smith, S. Kathleen Lyons, Emma A. Elliott Smith, Seth D. Newsome, and Catalina P. Tomé

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Globally, the majority of large-bodied mammals are at risk. The biodiversity crisis is a major conservation concern because the loss of these animals also means the loss of their ecological roles within communities. Growing evidence suggests mega-mammals have a disproportionate influence on the function of ecosystems. Here, we use the late Pleistocene megafauna extinction as a proxy to examine changes in the structure and function of a local mammal community after the catastrophic loss of 80% of large-bodied mammals. Hall's Cave, in the great plains of Texas, has unparalleled temporal resolution over the past 20ka, allowing characterization of the community before and after the extinction event. We employ the null model program PAIRS to evaluate the strength and type of mammal associations over time. The number and strength of interactions yields insights about the cohesion and resilience of ancient and modern ecosystems. We find ancient ecosystems were more tightly structured than modern ones. Not only did extinct species form significantly more species associations, but the average interaction strength was also significantly stronger. Moreover, unlike modern communities, both positive (e.g., predatory-prey) and negative (e.g., competition) interactions were important before the extinction. In particular, extinct carnivores were much more tightly associated with their prey base than modern species. Our results suggest many fundamental aspects of mammalian communities changed with the loss of megafauna at the terminal Pleistocene.

15^E: Spatiotemporal determinants of home range size of imperiled New England and invasive eastern cottontails

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Imperiled New England cottontail (NEC, *Sylvilagus transitionalis*) are a native obligate user of shrubland in the Northeast. Recovery efforts for NEC are hindered by a limited understanding of seasonal behavior and biology and complicated by the invasion of novel plant species in Northeastern shrublands. Further, competition with an introduced competitor, the eastern cottontail (EC, *S. floridanus*), may impede resource use and colonization success. Our objectives were to 1) establish seasonal 95% home range and 50% core area baselines for NEC and EC that can be used to inform management, and 2) assess the impact of habitat variables, including common invasive plant species thought to define habitat quality and impact cottontail survival, on home range and core area size. We modeled home range and core area calculated using adaptive local convex hull (a-LoCoH) kernel methods as a function of a suite of habitat variables and species, sex, and season. We employed Akaike information criterion (AIC_c) corrected for small sample size to assess model fit. Home range differed between sexes, species, and by season. Core area differed between sexes and season. Invasive Japanese barberry (*Berberis thunbergii*) was inversely correlated with home range of NEC and core area of both species in during the summer. Our findings suggest Japanese barberry may be beneficial to the recovery of NEC and highlight the importance of incorporating seasonal dynamics to management planning.

16^E: Are tree bats foraging at wind turbines in the southern Great Plains?

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Although the ultimate causes of high tree bat fatalities at wind farms are not well understood, several lines of evidence suggest that bats are attracted to wind turbines. One such hypothesis is that bats could be attracted to turbines as a foraging resource if insects that bats prey upon are commonly present on and around turbines. To investigate the foraging attraction hypothesis, we conducted a series of surveys at a wind farm in north-central Texas from 2011-2015 to determine if eastern red (*Lasiurus borealis*) and hoary (*Lasiurus cinereus*) bats forage on insects near wind turbines. First, we conducted light trapping surveys to characterize the insect community. Second, we assessed diet composition using DNA barcoding of the stomach contents of 45 eastern red and 23 hoary bat carcasses collected in fatality searches. We then compared the turbine insect assemblage to the diet analysis results. Together, the light trapping and diet analyses revealed that the insects most commonly found in the diets of eastern red and hoary bats were consistently present on and around wind turbines, including several important crop pests. Collectively, these findings provide strong support for the foraging attraction hypothesis. As wind turbines appear to provide a valuable and consistent foraging resource, strategies to keep bats away from wind turbines will need to be developed to reduce collision risk with rotating blades.

17^{E,HTA}: Seasonal temperature acclimatization in pygmy rabbits and the role of burrows as thermal refugia

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Small mammals in habitats with strong seasonal variation in the thermal environment often exhibit physiological and behavioral adaptations for coping with thermal extremes and reducing thermoregulatory costs. Burrows are especially important for providing thermal refugia when above-ground temperatures require high regulatory costs (e.g., water or energy). Our objective was to explore the role of burrows as thermal refugia for pygmy rabbits (*Brachylagus idahoensis*) during the summer and winter by quantifying energetic costs associated with resting above and below ground. We used indirect calorimetry to elucidate the relationship between energy expenditure and ambient temperature over a range of temperatures the animals experience in their natural habitat. We also measured the temperature of

above- and below-ground rest sites used by pygmy rabbits in the summer and winter and estimated the seasonal thermoregulatory costs of resting in the two microsites. Although pygmy rabbits demonstrate seasonal physiological acclimatization, the burrow is an important thermal refuge, especially in winter. Thermoregulatory costs were lower inside the burrow than in above-ground rest sites for >50% of the winter season. In contrast, the thermal heterogeneity available in above-ground rest sites in summer reduced the burrows' role as a thermal refuge during all but the hottest periods of the afternoon. Our findings advance our understanding of the behavioral ecology of pygmy rabbits and indicate the possible importance of burrows as refuges for other sagebrush-dwelling species.

18: A warming umbrella to gauge change and emergent predator-prey systems in the Beringia Arctic

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Declining sea ice and associated changes on land are fueling novelty in species x environment interactions. The vulnerability of the Arctic's largest land mammal, muskoxen (*Ovibos moschatus*), to such events remains unclear. Using field data generated by non-invasive photogrammetry across 8 years at 3 sites in Arctic Russia and Arctic Alaska, we asked how repeated minor rain-on-snow events (ROS) affect skeletal growth in juvenile muskoxen (N=781). When ROS occurred during gestation, body size was compromised for up to three years, a handicap which reveals one mechanism by which changing climates retard growth. Further, concomitant with ice recession polar bear densities increase on land. To understand how muskoxen respond to potential predatory behavior by both polar bears (in Russia) and brown bears (in Alaska), we performed 221 simulated interactions using bear and caribou replicas. Model selection indicated that habitat variables, herd sex ratio, and treatment affect muskoxen defense. Herds were 3x more likely to flee from the simulated approach of bear models than caribou ones, and female-dominated herds were more likely to flee than those male-dominated. Our findings reveal an unanticipated level of phenotypic plasticity in muskoxen secondary responses to climate forcing. Despite difficult rhetoric between Russia and the USA, trans-continental collaboration improves knowledge about the interaction between abiotic factors and ecological systems while enabling geo-political opportunity at the top of the world.

19: Bat behavior in response to ultrasonic signals: implications for reducing mortality at wind turbines

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Broadcasting ultrasonic signals has been proposed as a mitigation strategy to prevent bats from coming into close proximity to the rotating blades of wind turbines. Preliminary studies indicate that high frequency noises may deter echolocating bats from entering any area where such sounds are played. Thus, if ultrasonic deterrents are deployed effectively, bats should avoid entering the rotor swept zone of wind turbines, thereby eliminating the risk of collision. Nevertheless, before such deterrents can be applied as mitigation, we need to understand how ultrasonic signals influence bat behavior and determine the conditions under which they will be most effective. We therefore conducted both lab-based and field experiments in which we tested a set of artificially developed ultrasonic signals that varied in frequency, pulse rate, pulse interval, and amplitude. We then evaluated the responses of bats to each of these signals to identify which signal characteristics hindered bat activity, and in turn led to avoidance. Using video analysis software, we found that responses to ultrasonic signals were species-specific and depended on the type of activity bats were conducting as well as the distance at which the activities were conducted from the source signal. Our results revealed that the frequencies of the ultrasonic signals were important and emphasized that deterrent placement requires careful consideration to effectively and practically reduce bat fatalities at wind turbines.

20: Aposematic variation and the evolution of warning coloration in mammals

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Aposematic prey animals use conspicuous, high contrast color patterns to warn potential predators that they possess a defense mechanism. Avian predators show an innate phobia of bold, contrasting color patterns, and can readily learn to avoid a prey item displaying bold warning coloration. Signal uniformity is important to promote predator learning and memory retention; however, there is documented variation in the aposematic pattern of many species, including the striped skunk (*Mephitis mephitis*). Most aposematism research uses avian predators and insect prey – we know relatively little about how mammalian predators learn about and interact with aposematic prey. This study examined the behavior of captive coyotes (*Canis latrans*) during interactions with baited black-and-white models that were able to spray a dilute skunk oil solution. After learning trials, we also tested their ability to generalize to a variant pattern design modeled after naturally documented variation in striped skunk pelage. The results demonstrate that coyotes show innate wariness of a black-and-white striped model and most can quickly and effectively learn to avoid the model after being sprayed. Variants with proportionately more white incited more avoidance behaviors than darker patterns and similar to the diagnostic black-and-white striped pattern.

21^{E,HTA}: A matched filter between call frequency and auditory sensitivity in northern grasshopper mice (*Onychomys leucogaster*)

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Vocal communication is a critical component of mate attraction and territorial advertisement in a variety of taxa. Optimality theory predicts a strong match between signal properties of senders and hearing sensitivity of receivers, but morphological or physiological constraints may reduce tight correspondence. We recorded vocalizations and measured auditory brainstem responses (ABR) – a *physiological measure of hearing sensitivity* – in northern grasshopper mice (*Onychomys leucogaster*), a species that produces long-distance calls to advertise their presence to rivals and potential mates throughout arid regions of the western United States. Preliminary ABR data indicate heightened sensitivity (32.5 ± 2.0 dB SPL re: 20 uPa) to tones between 10 kHz and 12 kHz ($n=10$), which correspond to the fundamental frequencies ($11.6 \pm .63$ kHz, $n=36$) of long-distance calls produced by senders. Our preliminary findings provide support for the matched filter hypothesis.

22^{E,HTA}: Neighbor familiarity affects intrusion risk and behavioral plasticity in a territorial squirrel (*Tamiasciurus hudsonicus*)**

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It is increasingly acknowledged that the composition of an individual's social environment can vary, and that this variation may have profound effects on behavior and fitness. Using a wild population of North American red squirrels, we investigated the importance of the composition of the social environment in a territorial species by assessing whether the risk of intrusion faced by territory owners varies with the degree of relatedness and familiarity in their social neighborhood. To test this, we conducted temporary removals of territory owners and observed the time until intrusion and the identity of intruding individuals. We found that neighborhoods with low average familiarity had a higher risk of intrusion and that unfamiliar neighbors were more likely to intrude. Using a combination of behavioral observations and audio recordings we then demonstrated that red squirrels respond to this risk in a behaviorally plastic manner by increasing the time devoted to territorial behavior and decreasing nest use in unfamiliar

neighborhoods. The results from our research demonstrate that familiarity with neighbors affects intrusion risk and behavioral time budgets in red squirrels, suggesting that the composition of the social environment may be a previously underappreciated selective pressure in species considered to be 'asocial'. This research was supported by a 2014 and 2016 ASM Grant-in-Aid of Research awarded to Erin Siracusa.

23^E: Invasive shrub alters patterns of seed predation by modifying small mammal use of woody debris

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Habitat features are often useful predictors of small-mammal activity. However, invasive plants can alter animal behavior. We examined whether invasive shrubs alter small-mammal use of woody debris, a microhabitat feature commonly associated with small-mammal activity. We removed an invasive shrub (buckthorn) from 7 of 15 plots in southern Wisconsin. In each plot, we deployed 200 tagged red oak seeds in November 2014. After five months, tags were recovered to track spatial patterns of small-mammal seed predation. Most recovered tags were associated with consumed seeds (95%), providing an indication of small-mammal refuge use. Live-trapping and camera-trapping suggested that white-footed mice (*Peromyscus leucopus*) were responsible for most seed predation. In habitats without buckthorn, most seed predation occurred near woody debris. In habitats with buckthorn, small mammals rarely consumed seeds near woody debris, and seed predation occurred farther from the plot center and was less spatially clustered. Our results underscore the important influence of predation refuge and microhabitat on small-mammal activity, and suggest that changes in habitat-use mediated by invasive shrubs might complicate efforts to predict the fine-scaled distribution of small mammal species. Moreover, post-harvest woody debris manipulations used to promote rare small mammal species may need to account for the presence of invasive shrubs. We conclude that forecasts of small mammal community composition under future management scenarios should account for the novel habitat provided by invasive shrubs.

24^E: Bats are not rats: new method for testing olfactory discrimination in bats

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Olfactory cues mediate a range of mammalian behaviors including foraging, territorial signaling, individual recognition, and mate choice. Rats, mice, and other rodents have functioned as model organisms to investigate the use of odors in mammals. Methods developed in rodents, such as Y-tube choice assays, have since been used in a variety of other terrestrial mammalian systems to demonstrate olfactory preference, discrimination, learning and thresholds. Evaluating olfactory sensitivity is an important first step in understanding the relative importance of different odors in animal lives. Behavioral studies have demonstrated the importance of odors in social interactions and foraging in bats, but few studies have addressed the specific mechanisms by which bats use odors. Additionally, these studies rely on methods designed for terrestrial animals and thus in their application to bat behavior in the field due to the need for pre-test training. Here we present a new method for testing olfaction with minimal training in bats by taking advantage of their natural tendency to seek out small crevices or spaces. Using Mexican free-tailed bats (*Tadarida brasiliensis mexicana*) as a model, we present preliminary data using a behavioral assay to test olfactory thresholds and discrimination in bats. This paradigm can be further modified to investigate olfactory preferences, use of different types of olfactory cues and mechanisms of scent localization across a diversity of bat species.

25^{HTA}: A temperate armadillo: a genomic portrait of the nine-banded armadillo's northward migration

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Both natural selection and genetic drift contribute to variation in genes and morphology across a geographic range expansion. Novel ecological conditions can promote selection during the dispersal and establishment of organisms, while the contribution of genetic drift is important when founder effects are present. Evidence of the myriad neutral and selective forces acting on geographic range expansions may be recorded in the genome. Here, we look at genomic variation in the range-expanding, nine-banded armadillo to uncover links between niche differences and genetic changes. In the last 3 mya the species has dispersed northward from its tropical origins in South America to first reach Texas in 1849 and then to the South and Southeast U.S. states. We use high-throughput genomic data to estimate phylogenetic relationships of populations across the species' expansion gradient and to infer its demographic history. We sampled historical museum specimens as well as individuals at the expansion edge, which allows for an analysis of genomic divergence across the species' broad range over a 127-year period. Preliminary findings suggest that patterns of genomic variation differ between core and edge populations, but further analyses will reveal whether genomic divergence tracks differences in niche. Studying the relationship between genomic and niche divergence will provide clues for understanding whether and how the species has evolved as it expanded its range northward into uncharted territory.

26^{E,HTA}: Phylogeny, not ecology, shapes the mammalian vomeronasal system: evidence from V1Rs and morphology**

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Mammalian social chemical cues are primarily detected in the vomeronasal system. While vomerolfaction is well conserved due to its role in fitness-related behaviors, several mammalian groups have lost function, including Old World primates, some aquatic mammals, and most bats. These losses and gains might relate to ecological variation, such as circadian rhythm, social system, or habitat specialization, but it is unclear if these patterns are related to ecology, phylogeny, or both. We used vomeronasal genetic machinery and morphology to model the evolutionary dynamics of loss and gain vomerolfaction. Vomerolfactory cues are detected by *V1R* receptors in the vomeronasal organ (VNO). Both *V1Rs* and VNO size and shape are highly variable among mammals. We obtained the *V1R* profiles from nearly every mammalian order, and estimated the birth and death rates of gene duplication and loss. We also quantified VNO morphology from iodine-stained soft tissue μ CT-scans. We found no clear connection to ecological explanations of loss or gain. Many mammalian orders have experienced decreased birth rates of *V1R* genes, relative to other mammals. However, many lineages with low *V1R* birth rates still possess a well-developed VNO and retain intact orthologous receptors with distantly related species, suggesting strong purifying selection in light of low diversification. Our study highlights the importance of incorporating phylogenetic comparative methods to understand the evolutionary history of complex traits, such as a sensory system.

27^{E,HTA}: Finding hidden diversity: genomic resolution of a cryptic chipmunk species

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Biodiversity may often be under-estimated due to speciation between cryptic genetic lineages that are morphologically or ecologically very similar. With the myriad of emerging threats to biodiversity, it becomes increasingly important to characterize cryptic species diversity. Here we report genomic evidence for cryptic speciation among sympatric lineages of chipmunks (*Tamias*) within the central Rocky Mountains of North America. We used targeted capture to generate ~ 8 MB of high-coverage Illumina sequence data from over 10,500 genic regions in western chipmunks, with a focus on the yellow-pine chipmunk (*T. amoenus*) and least chipmunk (*T. minimus*) in central Idaho. We then estimated

phylogenetic relationships among several western chipmunk lineages and investigated the extent to which hybridization has contributed to genomic variation within and between these species. Our results reveal genetic and morphological evidence for at least one cryptic lineage of chipmunk, historically described as a geographically restricted subspecies of the yellow-pine chipmunk from Craters of the Moon National Monument (the Craters chipmunk). Surprisingly, we find that the Craters chipmunk appears to be locally abundant and fairly widespread throughout the coniferous forests in south central Idaho. Our surprising results suggest that the ecology, evolution, and systematics of this conspicuous group of diurnal mammals remains unresolved despite over a century of intensive study.

28^{E,HTA}: Adiposity signals and body size predict song effort in Central American singing mice**

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Many signaling theory and sexual selection models assume that elaborate traits are “condition-dependent,” but condition is challenging to define and measure, especially in the wild. Traditional field metrics for condition have included measures of body size as a proxy for energetic reserves, but these estimates are coarse and are a snapshot of the dynamic processes of homeostasis. In this study, we complemented traditional body size measures with information about metabolites that help regulate energy balance to explore the condition dependence of an elaborate trait—the vocalizations of Alston’s singing mouse, *Scotinomys teguina*. These physiological measures included hormones and nutrients that regulate homeostasis in both the short- and long-term. We found that songs of singing mice differ in frequency signatures and in “song effort,” amplitude, trill rate, and song duration characteristics. While song effort in singing mice was predicted by traditional body size measures, it was predicted more robustly by measures of long-term regulatory hormones secreted by adipose tissue. This indicates that adiposity signals may provide additional information able to unmask relationships between costly traits and condition. Finally, frequency signatures were not correlated with any measure of condition and are not under apparent selection, suggesting that these acoustic characteristics may play a role in individual identification.

29^{E,HTA}: The evolution of seasonal camouflage**

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Resolving the mechanisms by which animals adapt to novel environments is central to understanding the origin and conservation of biodiversity. Mismatches between the timing of key life history events and optimal environmental conditions have emerged as an important threat to biodiversity, yet the evolutionary mechanisms underlying seasonal adaptations remain largely unknown. Several species of mammals undergo seasonal molts between brown and white pelage as part of a coordinated suite of phenotypic responses to seasonally varying environments that are cued by photoperiod. In snowshoe hares (*Lepus americanus*), autumn molts to white winter coats closely track the local onset of snow cover. However, some hare populations that inhabit environments with more ephemeral snow cover molt instead to brown winter coats. We have combined population genomics, association mapping, and functional genomic studies to resolve the molecular and evolutionary basis of alternative winter white and brown pelage morphs. Field estimates of coat color-related survival combined with genomic signatures of positive selection at causative coat color alleles reveal strong natural selection on the maintenance of locally adaptive seasonal crypsis. Our results thus provide one of the first examples of a clear genotype-to-phenotype-to-fitness link for a seasonally changing trait. These findings provide important insights into how this crucial component of seasonal flexibility may respond to rapid environmental changes in snowshoe hares and other species. This research was supported by a 2015 Grant-in-Aid of Research awarded to Matthew Jones.

30^{HTA}: Why is the giant panda *Ailuropoda melanoleuca* black and white?

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Most mammals have brown or grey pelage suggesting background matching, but a few have striking black-and-white pelage for which functions remain enigmatic. Most notably, the giant panda *Ailuropoda melanoleuca* has black eye patches and ears set on a white face, with black shoulders, forelimbs, and hindlimbs set on a white torso. To understand the functions of such coloration, we used a comparative approach across mammalian carnivore species and bear subspecies, breaking up the body into separate sections. Based on body section specific associations between fur color and ecological factors, we discovered that the giant panda's white face, dorsum, flank, belly, and rump are adapted for crypsis against snowy backgrounds, whereas its black shoulders and legs are adapted for crypsis in shady subtropical forests. Analyses of fur color and social factors suggest that dark ears may signal ferocity while dark eye patches may be used in individual identification or in dominance interactions between giant pandas. Thus, the external appearance of this species has been molded for several functions. There is no compelling support for giant panda fur color being involved in disruptive coloration, temperature regulation, or reducing eye glare.

31: An ice-age legacy in modern DNA: climate drives cyclic hybridization in high-latitude ermine (*Mustela erminea*)

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Contemporary mammalian biodiversity in North America has been shaped by cycles of population isolation and divergence driven by Quaternary glacial advances, and subsequent expansion and contact during glacial retreats. As a consequence of post-glacial expansion, divergent lineages from independent refugia came into secondary contact, but the extent to which historic admixture intermittently contributed to contemporary diversity in mammals is only now being uncovered using genome level analyses. We investigated the role of introgression in genomic evolution of the Holarctic ermine (*Mustela erminea*) using Illumina whole-genome sequence data. We demonstrate divergence among lineages coincident with 4 distinct refugial centers: Beringia, West, East, and North Pacific Coast (NPC). We also identified multiple bouts of hybridization, including contemporary hybridization at along the Alaska-Yukon Territory border between East and Beringian lineages and an earlier, independent episode of admixture suggests these lineages previously hybridized to form the NPC Island lineage, whose location is consistent with the Coastal Refugia Hypothesis. Isolated in a coastal refuge during the Last Glacial Maximum, the NPC Island lineage subsequently diverged, suggesting allopatric divergence occurred after ephemeral gene flow, a process that may be more common in high latitude and insular species. While hybrid-based divergence in this coastal environment has immediate evolutionary consequences and conservation implications for ermine, it also offers an alternative lens for viewing the role of islands as engines of biological diversification.

32: Adventures in Texas mammalogy: updates from the Light Lab at Texas A&M University

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Research in the Light Lab at Texas A&M University has been exploring several projects related to the ecology and evolutionary biology of Texas mammals. One project investigates geographic range extensions of the North American Porcupine, *Erethizon dorsatum*, with newly documented eastward movement in Texas supported by a specimen collected in Harris County. Another project is exploring possible past hybridization between the White-footed Deer mouse (*Peromyscus leucopus*) and the Cotton Deer mouse (*P. gossypinus*) in Brazos County, Texas. As part of a long-term field project, collected *Peromyscus* presumed to be *P. leucopus* were genetically identified as *P. gossypinus* using the

mitochondrial cytb gene. Brazos County is the western limit of the distribution of *P. gossypinus*, with the most recent specimen on VertNet collected in 1973. Thus, it was unexpected to find multiple individuals of *P. gossypinus* in Brazos County. However, nuclear data (morphology and the genetic markers) support that these individuals are *P. leucopus*. My lab is currently exploring a small data set to determine if past hybridization may have occurred between these two *Peromyscus* species. Lastly, I am involved in a collaboration examining phylogeography of the Baird's Pocket Gopher, *Geomys breviceps*. As part of this research, I have some interesting results to share regarding mito-nuclear discordance and pseudogenes in pocket gophers.

33^{E,HTA}: Morphological comparisons of the Meadow jumping mice (*Zapus hudsonius*) subspecies show few statistical differences

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The meadow jumping mouse (*Zapus hudsonius*) occupies a wide range across North America with 12 subspecies described in the last taxonomic revision before advanced tests were readily available. In general, original descriptions were based on qualitative differences and visual comparisons of characters, plus some subspecies were defined using a limited number of specimens. Recent delimitation tests indicate at least ten evolutionary lineages and four candidate species occur within nominal *Z. hudsonius*, but that await formal revision. Here, we focus on one of those candidate species, which has experienced recent northern expansion resulting in few genetic and ecological differences across 30° latitude. We test whether geographic variation in cranial morphology is consistent with expectations of original subspecies descriptions against those from more recent findings. We photographed, landmarked, and calculated measurements for the original nine characters using original skulls plus newer samples (N = 223). Both univariate and multivariate analyses show few statistical differences among six subspecies with one exception being between two northern subspecies (*alascensis* vs. *tenellus*), but this difference may be an artifact of few available samples. Additionally, we detected greater variation for each character within subspecies than initially reported, suggesting subspecies descriptions may be flawed perhaps resulting in conservation implications. Next steps of this project are to quantify ecophenotypic variation using geometric morphometrics to compare shape change across subspecies, environmental variables, and genetic differences.

34^E: Character displacement using geometric morphometrics for two sympatric Atlantic Forest rodent species

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Character displacement, defined as trait evolution responding to selection pressures, is a proxy for measuring interspecific competition. The Interior Atlantic Forest of eastern Paraguay houses two abundant sympatric species, the terrestrial *Akodon montensis* and semi-terrestrial *Oligoryzomys nigripes*, with high potential for competition and niche partitioning. Using geometric morphometrics we test for character displacement in skull and mandible morphology. We digitized museum samples and compared skull and mandibles of *O. nigripes* (n = 130, 121) and *A. montensis* (n = 144, 124) using 16 and 13 homologous landmarks respectively. We implemented Procrustes analysis, which transforms, scales, and rotates homologous landmarks. We implemented principal component analysis (PCA) to identify the variables that best describe variation between species. We used discriminant function analysis (DFA) to compare differences in shape and permutation tests to test significance between age classes, sexual dimorphism, and interspecific differences (character displacement) between species. PCA identified maximum variation in the rostrum between species. We found evidence for sexual dimorphism in skull morphology of *O. nigripes* and *A. montensis* ($\alpha = 0.0009$ and $\alpha = 0.0360$ respectively), not in mandibles. DFA showed evidence of character displacement between species in skull and mandible ($\alpha = 0.0001$). Most of the variation occurs in the posterior portion of the face and apparatuses associated with eating. This leads us to hypothesize that diet is a major driver for niche partitioning species.

35: Morphological variation in *Peromyscus maniculatus*

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Approximately 5000 museum specimens of *Peromyscus maniculatus* were studied in an attempt to understand intraspecific variation in morphology. As expected, island mice are larger. However, latitude (Bergmann's Rule), altitude, and year trapped (~"climate change") were poorer than expected predictors. Allen's rule does appear to apply to tail length with shorter tails in *Peromyscus maniculatus borealis* in colder areas of their range.

36: Fossil *Bison* and past climates: a long-term trend of body size into the future

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The relationship between body size and temperature of mammals is poorly resolved especially for large keystone species such as bison (*Bison bison*). Bison are well-represented in the fossil record across North America, which provides an opportunity to relate body size to climate within a species. We measured the length of a leg bone (calcaneum) in 1189 specimens from 60 localities that were dated based on stratigraphy and ¹⁴C decay. Average annual temperature was estimated from ¹⁸O values in the ice cores from Greenland. Calcaneal length of *Bison* declined over 40,000 years, that is body mass was 62% larger (935.5±13kg) than today (583.5±7kg). Average annual temperature has warmed by 6°C since the Last Glacial Maximum (~24-18kya) and is predicted to further increase by 4°C in the 21st century (IPCC-AR5, 2013). If body size continues to respond to temperature, bison body mass will likely decline by 48% (301.8±18kg). Changes in body size of bison may be a result of migration or disease but those effects are likely to be local and not likely to persist over the long-time-scale of the fossil record. The strong correspondence between body size of bison and air temperature is more likely the result of persistent effects on the ability to grow and the consequences of sustaining a large body mass in a warming environment.

37^E: Muscle dynamics during vertical jumping by kangaroo rats (*D. deserti*)

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Predation is an important factor that shapes prey's fitness. Kangaroo rats (*D. deserti*) are bipedal hoppers that use vertical jumps to evade their attacker (i.e., snakes and owls). Reported jumps of this animal can reach more than 1 meter, which is over 20 times hip height. The ankle extensors are the primary muscles involved in plantar flexion, and likely plays a key role in propelling the animal upwards during vertical jumping. We examined relative mechanical work contribution by the ankle extensors to the vertical jumps of kangaroo rats and the effects of biarticularity of this muscle tendon unit (MTU). We hypothesize that the amount of work done by the ankle extensors is a fixed percentage of the energy required for a jump. These muscles are biarticular and we predict that the MTU also transfers energy from the larger proximal muscles. We examined the performance of the ankle extensors during vertical jumping by combining high speed video and ground reaction forces for inverse dynamics. Data suggest that our hypothesis is supported. There appears to be a linear relationship between jump height and work done by the ankle extensors. This suggests that the ankle extensors are required to perform more work as the height of the jump-task increases. Furthermore, data shows that the MTU produces and transfers work.

38^E: Anatomical and functional diversification of the bat calcar

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Morphological novelty is ubiquitous throughout Chiroptera and is likely a key to bat diversity. Bats

comprise approximately one-fifth of all mammals and have evolved a wide diversity of morphological adaptations during their ecological radiation. While the anatomy and function of bat forelimbs (wings) have been studied extensively, their highly-modified hindlimbs have received much less attention. In this presentation, we explore anatomical variation in bat hindlimbs with a particular focus on the calcar, a neomorphic skeletal structure in bat feet that is not found in other mammals. Calcar morphology varies extensively across bat species, which may have functional and ecological implications. By integrating data from histology, microCT scanning, and examination of museum specimens, we demonstrate that the calcar varies in shape, size, and tissue composition across the chiropteran phylogeny. Using contrast-enhanced microCT scanning, we also demonstrate variation in the muscles that actively control the calcar. When we examine these results in the context of a biomechanical model for beam bending, we find that this anatomical variation can affect calcar mechanical performance. Together, these results suggest that the calcar has evolved to meet different functional requirements across bat species.

39: Morphological specialization of proximal vs distal muscles of kangaroo rats

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Within large bipedal hopping mammals, adaptations of the ankle extensor muscle-tendon units that facilitate economical elastic energy storage are limit their ability to generate mechanical work when moving up slopes. Therefore, a division of labor exists such that the large proximal muscles behave as motors while the distal muscle tendon units behave like springs. However, unlike larger hoppers, kangaroo rats have relatively thick ankle extensor tendons which are unlikely to stretch during normal hopping loads. In this study we used *in vivo* recordings of muscle length change and activity to directly measure how two major extensor muscles are modulated in response to a range of inclines. Sonomicrometry and EMG data were collected from the distal lateral gastrocnemius (LG) and proximal vastus lateralis (VL) while animals hopped on a motorized treadmill at 0, 10, and 20, degrees incline. Preliminary results show that the VL actively stretches, likely absorbing energy, under all conditions; however, the amount of stretch decreases with increasing incline. The LG undergoes increased active shortening with increasing incline, suggesting that this muscle contributes increased positive mechanical work when hopping up a hill. Therefore, while the knee extensors appear to behave in a similar manner to those of wallabies, the ankle extensors do not, suggesting there is no division of labor.

40: Morphological variation in *Cryptonanus chacoensis* (Tate 1931) (Didelphidae) along a precipitation and temperature cline

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There are many ecogeographical rules that attempt to understand and describe patterns of morphological variation in species along different gradients, including among these are included Allen's, Bergmann's, Gloger's, Jordan's, Rapoport's rules. *Cryptonanus chacoensis* is a species with a broad ecological distribution that is mirrored by a general cline in precipitation with approximately 500mm of rainfall in northwestern Paraguay to more than 1700mm in the southwestern border of the country ranging from Dry Chaco to the humid Atlantic Forest. Recent phylogenetic analyses of this species have verified that these belong to one species. Recent analyses of Atlantic Forest (AF) specimens have shown dramatically larger specimen, showing variation in coloration and saber dentation. Using linear morphometric, I implemented principal components analysis of specimens along the entire distribution. The first PCs were then implemented in generalized linear models, as dependent variables with 19 bioclimatic variables as independent variables thus testing what combination of climate variable best describe skull morphology in *Cryptonanus*. PC1 was best described by max temperature of warmest month and precipitation of coldest quarter, and PC2 was best described by temperature seasonality. We found a clear difference in PC1 scores between forest and Chaco specimens, but not for PC2 and PC3. The Interior AF in Paraguay is unique from the rest of the coastal AF, which has resources unique to the that result in giant specimens.

41: The future of natural history collections: Investing in infrastructure for future mammalian education and research

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Natural history collections are tremendous assets for teaching and research on mammals. Originally developed for studies focused on natural history and biodiversity discovery, advancements in technology (e.g., genomics, high-resolution imaging, stable isotopes) now take advantage of the taxonomic, temporal and spatial coverage represented by museum infrastructure. These new approaches are assessing critical societal questions, especially those related to biodiversity responses to changing environmental conditions. Emerging trends in both specimen-based biology and environmental informatics are also identified. Specimen digitization has rapidly mobilized this biodiversity resource for bioinformatic studies ranging from the genome to large-scale GIS based assessments aimed at understanding how changing environmental conditions are reshaping species. Nevertheless, significant opportunities (e.g., NEON, IsoBank) and challenges (e.g., training, permitting and sustainability) remain to fully integrate and exploit this resource; now is an opportune time to evaluate whether the existing collections and methods we use to build that infrastructure are sufficient to meet the demands of mammalogy in a time of rapid loss of diversity. Using digitized records from VertNet, opportunities and limitations for investigating spatiotemporal changes in mammalian species and communities are identified. A critical need exists to develop a comprehensive plan to more rigorously sample mammalian diversity to stimulate mammalogy in the future.

42: Evolutionary sustainable ungulate management

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Trophy hunting of ungulates involves selective harvest of males based on horn, antler or tusk size. Selection can be driven by hunter preference, regulations, or both. Selection on heritable traits can lead to an evolutionary response. Sport hunting, including trophy hunting, can be a major driver of conservation of ungulates and their habitat. Much research has focused on the ecological sustainability of sport hunting, but possible evolutionary effects of sport hunting are less known and often controversial. Trophy hunting often selects against traits favored by sexual selection. Therefore, an evolutionary response should only be expected if selective hunting pressure is strong, consistent over time and space, and targets the genetic component of antler, horn or tusk size. Mountain sheep (*Ovis* spp.) in most of Canada are under a 'perfect storm' of regulations and ecology that make them more likely than other ungulates to show an evolutionary undesirable response to intense selective hunting. Males reach 'trophy' status 1-3 years before peak breeding success, there are no quotas for residents and hunting continues until potential genetic rescuers exit protected area and are shot. Data clearly show an evolutionary shrinkage in horn length. Because of differences in ecology and in hunting pressure, other ungulates may not respond to selective hunting as drastically as mountain sheep. Trophy hunting is evolutionary sustainable only when regulations account for scientific knowledge.

43: The GUD, the bad and the ugly: revealing the inner selves of animals

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For me it has been a lifelong passion. A quest to create a lockstep between patch use theory and practice. For most it should simply be a useful tool. A tool for getting inside an animal's "head" and revealing its perceptions of risk, state, habitat quality, diet, balancing acts of food safety and/or toxins, climate and even its cognition. Theory tells us that a forager should try to leave a depleting food patch at a quitting harvest rate whose benefits just balance the metabolic, predation and missed opportunity costs of foraging. The dregs from the patch (the giving-up density, GUD) provides a measurable surrogate for the quitting harvest rate. Honed by natural selection, the animal's GUD reveals its cost-benefit analyses. Since 1988, three hundred or so GUD papers reveal that mammalogists have a commanding lead. Measuring variation in perceived predation risk (more accurately, the foraging cost of predation) has been

the largest application. I began in the desert with a little millet buried into a lot of dirt. Now, in the hands of others, food patches take on ever cleverer manifestations complete with remote sensing and cameras. Others too have advanced the theory and broadened its application. Whether it be mechanisms of coexistence, landscapes of fear or behavioral indicators for conservation, much can still be learned by going through the leftovers of an animal's feast.

44^{HTA}: Repeated radiations: caviomorph rodents and other Neotropical lineages as evolutionary replicates to study species diversification

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The Neotropical realm encompasses a vast amount of mammalian biodiversity, for richness comparable only to Indomalaya but with much higher rates of recent species diversification. Understanding the ecological drivers of rate variation among major clades has motivated mammalogists since G. G. Simpson's seminal work on evolutionary tempo and mode. The rise of mammal phylogenomics now enables us to address these questions quantitatively, comparing rates and timing of evolution across thousands of species. Here we present the merits of this approach as applied to replicate Neotropical radiations that differ in their timing of arrival to South America and extant diversities: rodents (Caviomorpha: 40 Ma/264 sp.; Sigmodontinae: 13 Ma/413 sp.), primates (Platyrrhini: 32 Ma/161 sp.), bats (Phyllostomidae: 35 Ma/205 sp.), marsupials (Didelphidae: 44 Ma/106 sp.), and sloths and armadillos (Xenarthra: 67 Ma/33 sp.). Estimated ages and branch lengths are standardized in the same macroevolutionary rate framework across a new supermatrix-based molecular timetree of Mammalia that includes 5911 species in the global radiation (4098 from DNA, else via taxonomy). Within caviomorph rodents we find the highest diversification rate shift of all mammals—a 4.0x up-shift leading to the burrowing tuco-tucos (*Ctenomys*). Phyllostomid bats additionally show a 1.5x upshift at the base of their radiation. We further examine the impact of Miocene aridification in driving biome-related shifts in the diversification of these co-occurring lineages.

45^{E,HTA}: All together now: a phylogeny of all extant rodent families inferred from ultraconserved elements

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Molecular data have revolutionized our understanding of relationships among rodent species and led to the recognition of three clades: the Ctenohystrica, mouse-related clade, and squirrel-related clade. Previous research using mitochondrial, nuclear, and SINE data are conflicted over the relationships among these three clades as well as the relationships among Anomaluroomorpha, Castorimorpha, and Myodonta. These conflicts are probably due to rapid, ancient divergences that generated extensive variation in gene tree topologies. We extracted ultraconserved elements from published genomes and generated new UCE sequences from additional taxa. Our resulting dataset includes all 36 families within Rodentia and notably the first sequences of the genus *Platacanthomys*. We used these data to estimate phylogenetic relationships with both concatenation and species tree approaches. Both methods support sister relationships between Ctenohystrica and the squirrel-related clade and between Castorimorpha and Myodonta. Support for alternative topologies calculated with BUCKy and PhyloBayes will be discussed. Our well-supported and taxon-rich phylogeny is a crucial first step in understanding the biogeographic and temporal patterns of rodent diversification.

46^{E,HTA}: Evolutionary history of the *Hybomys* division (Muridae, Rodentia) and systematic revision of the genus *Hybomys*

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The *Hybomys* Division of arvicanthine rodents consists of three genera (*Stochomys*, *Dephomys* and *Hybomys*) that are endemic to the Guineo-Congolian rainforests. *Hybomys* contains six species separated in two subgenera (*Hybomys* and *Typomys*). In the absence of genetic data for *Typomys*, the inclusion of all six species into a single genus has been controversial, especially given the morphological and karyotypic differences between the subgenera. We present a molecular phylogeny and a fossil calibrated tree of the *Hybomys* Division based on two mitochondrial (Cyt *b* and 12S rRNA) and two nuclear (IRBP and GHR) genes from all genera and subgenera. Maximum likelihood and Bayesian analyses failed to recover a monophyletic clade for the genus *Hybomys*, as *Typomys* was sister to a *Stochomys*, *Dephomys*, and subgenus *Hybomys* clade. The cyt *b* genetic distance between the subgenera *Hybomys* and *Typomys* (K2P = 17.6) was comparable to or greater than distances between genera of African arvicanthines (mean K2P = 18.5) and the subgenus *Hybomys* and *Dephomys/Stochomys* (K2P = 16.0). Divergence of *Hybomys* and *Typomys* was older than most other recognized genera of African Arvicanthini. Repeated aridification events between the Miocene and Pleistocene restricted African rainforests to isolated river basins and upland refugia contributing to the diversification within the *Hybomys* Division. Considering the phylogenetic analyses, large genetic distance and early divergence date, *Hybomys* and *Typomys* should be recognized as separate genera.

47^{HTA}: Conflicting evolutionary histories of the mitochondrial and nuclear genomes in New World *Myotis*

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The diversification of *Myotis* into more than 100 species in just a few million years is one of the most extensive mammalian radiations available for study. Our current understanding of relationships within *Myotis* is therefore biased towards a set of phylogenetic markers that may not reflect the phylogenetic history of the nuclear genome. To resolve this, we sequenced the full mitochondrial genomes of 37 representative *Myotis*, primarily from the New World, in conjunction with targeted sequencing of 3,648 ultraconserved elements (UCEs). We inferred the phylogeny of *Myotis* and explored the effects of concatenation and summary phylogenetic methods, as well as combinations of markers based on informativeness or levels of missing data, on our phylogenetic results. Of the 295 phylogenies generated from the nuclear UCE data, all are significantly different from phylogenies inferred using mitochondrial genomes. Even within the nuclear genome quartet frequencies indicate that around half of all UCE loci conflict with the estimated species tree. Despite the degree of discordance between nuclear UCE loci and the mitochondrial genome and among UCE loci themselves, the most common nuclear topology is recovered in one quarter of all analyses with strong nodal support. Based on these results, we re-examine the evolutionary history of *Myotis* to better understand the phenomena driving their unique nuclear, mitochondrial, and biogeographic histories.

48^E: Mammals escaped the nocturnal bottleneck concurrently with the extinction of non-avian dinosaurs

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Activity patterns are a major element of animal ecology as they determine the type and intensity of biotic and abiotic conditions individuals face. Most modern mammals, including strictly diurnal species, exhibit sensory adaptations to nocturnal activity, thought to be due to a prolonged nocturnal phase, or

'bottleneck', during early mammalian evolution. This temporal partitioning may have allowed mammals to avoid antagonistic interactions with dinosaurs during the Mesozoic. However, understanding the evolution of mammalian activity patterns is hindered by unclear fossil evidence. While reconstructions of ancestral behaviour from extant species could potentially elucidate these patterns, existing studies have been limited in taxonomic scope. We used an extensive behavioural dataset for 2415 species from all extant orders to reconstruct ancestral activity patterns across Mammalia, and to test the predictions of the nocturnal bottleneck hypothesis. We find strong support for the nocturnal origin of mammals and for the Cenozoic appearance of diurnality, although cathemerality may have appeared in the late Cretaceous or immediately after the K-Pg. Simian primates are among the earliest mammals to show strictly diurnal activity 52.4Ma. Our study is consistent with the prediction that mammal-dinosaur temporal partitioning during the Mesozoic led to the mammalian nocturnal bottleneck. However, the expansion of the mammalian temporal niche may have begun in the late Cretaceous, consistent with the line of evidence that dinosaurs were declining before the K-Pg event.

49: Interrogating difficult nodes in the phylogeny of placental mammals

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The advent of molecular systematics revolutionized our understanding of mammalian relationships, but many recalcitrant nodes still defy consistent support. Among these, the (1) the earliest divergence within Eutheria, (2) the position of Scandentia, and (3) the relationships of Perissodactyla have been especially problematic. While many studies have addressed these issues, most have done so with either enormous genomic datasets, but limited taxon sampling, or the inverse, with extensive taxon sampling, but few loci. Here, we target a balanced approach in which we use sequences from thousands of ultra-conserved elements while sampling taxonomic diversity at the family level. We identify consistent species-tree support for Atlantogenata (Xenarthra + Afrotheria) despite only a quarter of individual gene trees containing this relationship. We consistently place Perissodactyla in a polytomy with Cetartiodactyla and Ferae and Scandentia as either the sister to Primatomorpha or in a polytomy with Primatomorpha and Glires. The remaining problematic nodes in the deep-time mammalian phylogeny are sufficiently difficult to resolve that systematists should only view inferred relationships as established when consistent support emerges from distinct datasets. Put simply, there are no silver bullets.

50^{E,HTA}: Does a native mammal facilitate the success of invasive prickly pear cactus (*Opuntia stricta*)?**

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The establishment and spread of introduced prickly pear cactus (*Opuntia stricta*) has had profound ecological impacts across the globe. Prickly pear reproduces either sexually or asexually, with each mode of reproduction conferring different benefits to individuals. The rate of sexual reproduction—the proportion of individuals originating from seeds rather than clones—can affect the outcome of eradication efforts. The olive baboon (*Papio anubis*) is a frequent disperser of *O. stricta* seeds in Laikipia, Kenya. We conducted germination trials to determine whether digestion by baboons, seed dormancy, or both influenced *O. stricta* germination rate, an important component of sexual reproduction. We then tested differences between *O. stricta* density and rate of sexual reproduction between baboon roost sites and control sites in Laikipia. Rates of seed germination increased with dormancy and did not change after digestion by baboons. Both the rate of sexual reproduction and the density of *O. stricta* were significantly higher at baboon roosts than control sites. These results suggest that baboon roosts should be of particular interest for future monitoring efforts, as they may produce many *O. stricta* seedlings after eradication efforts are thought to be complete. This work highlights the role that native mammals play in dispersing an introduced plant. By identifying drivers of mode of reproduction, future control efforts can implement alternative methods to “high risk” areas with substantial deposits of seeds.

51: Body size affects microhabitat and diet use in a marsupial herbivore community

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Body size affects many life-history parameters including diet and predation risk. We examined the influence of body size on diet and microhabitat use in a community of herbivorous marsupials in the Grampians National Park, Victoria, Australia. We quantified microhabitat use by recording the cover of plant functional groups and species at radio-tracking fixes. We quantified diet composition through microhistological faecal analysis, and measured the quality of the plant genera contributing most to the diet of each species. We tested three predictions: as metabolic demand scales with body size, (1) while foraging, smaller animals use habitats with higher-quality forage than larger animals; (2) smaller animals consume the highest quality diets; (3) being more vulnerable to predation, smaller animals will rest in habitats offering greater concealment cover than larger animals. Foraging western grey kangaroos and swamp wallabies used microhabitats as predicted; red-necked wallabies used more open, poorer-quality habitats than expected. For all species resting microhabitats offered greater concealment cover than foraging microhabitats, but body size did not influence the density of vegetation used. The percentage of cellulose explained differences in diets; nitrogen concentration did not. The two (larger) kangaroo species consumed poorer quality diets (higher in fibre) than the smaller wallaby species. In this system, body size influenced foraging microhabitat and diet use as predicted, but only in some species.

52: Isotopic niche partitioning from the Holocene to today: a case study of desert mice

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Desert rodent communities are strongly structured by competitive interactions, with body size dependent uses of microhabitat and seeds believed to promote species coexistence. How stable intra- and interspecific resource use and partitioning are over time, however, is unknown, yet is key to applying a species interactions framework to understand community responses to environmental change. Using ^{13}C and ^{15}N obtained from Modern and fossil specimens spanning the last ~8,000 years, I examine isotopic niche dynamics in four sympatric desert mice species (*Chaetodipus formosus*, *Perognathus longimembris*, *Peromyscus maniculatus*, and *Reithrodontomys megalotis*) in the Smoke Creek Desert of northwestern Nevada. Using Bayesian ellipses and Euclidean distances, I find significant variation in the niche position, niche breadth, and interspecific niche overlap of these species through time. While the niche breadth dynamics of the Murids were positively correlated with one another, the niche breadth of *C. formosus* was negatively correlated to that of all other species. Body size provided no explanatory power. I also found that patterns of resource use and partitioning among the species today differs from that seen in the Holocene past, both in the absolute and the relative position of each species' niche in at least one isotopic axis. This suggests that environmental change is pushing these species past their range of previously-experienced resource variation, with species' responses unfolding individually.

53: A comparison of nutrition and foraging behavior between sympatric mule and white-tailed deer in Washington

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The only 2 extant species of the genus *Odocoileus*, mule deer (*O. hemionus*) and white-tailed deer (*O. virginianus*), are endemic to the Americas. Over the last few decades, white-tailed deer populations have expanded their distribution in many areas along a north-south zone along the Rocky Mountains where the deer species co-occur. To better understand potential for competition, we compared foraging behavior and nutrition of tractable mule and white-tailed deer raised and foraging together in 21 ponderosa pine/Douglas fir stands in northeastern Washington that varied 10-fold in forage biomass. In each stand, we measured forage composition and biomass, recorded deer behavior, and determined harvesting rate

and diet composition, selection, and nutritional quality. The deer species had similar overall activity budgets, a diet similarity index of 58%, and the same preference ranking for 86% of available plants. Mule deer took larger bites and harvested food faster, whereas white-tailed deer moved more while foraging and consumed more diverse diets that were slightly, but significantly, more nutritious. These differences suggest a moderate degree of diet partitioning between the deer species. Therefore, habitat management that affects the amount and species composition of forage might influence the performance of the deer species.

54: The long-haired rat (*Rattus villosissimus*): an ecosystem disrupter in arid Australia

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The northern arid zone of Australia is notable because of the unpredictable rainfall patterns that it experiences. Rainfall, when it does occur in sufficient quantity, results in pulses in primary productivity that can lead to population outbreaks of native rodents (Muridae). Not all species of rodent respond to each resource pulse. Perhaps the best example of this irregularity is the long-haired rat (*Rattus villosissimus*), the largest extant rodent in arid Australia (body mass: 150 g). The species is not resident in our study area in the western Simpson Desert, rather population outbreaks occur every 25-30 years. Such outbreaks have significant impacts on the biotic and abiotic environment. Here, we report on an outbreak that occurred from June 2010 to December 2012 and the subsequent response to the disappearance of the rats. The outbreak resulted in a series of novel ecological interactions in addition to significant levels of soil redistribution and a large spike in rodent biomass. Novel interactions included rat predation on small mammals, invasion by the rats in to refuges of the threatened plains mouse (*Pseudomys australis*), and feeding and associated damage to the threatened keystone tree species (*Acacia peuce*). The sporadic occurrence of the long-haired rat and the intensity and spatial scale of the novel interactions lead us to consider it a disruptive factor in the functioning of the Simpson Desert ecosystem.

55^E: Pulsed resource availability changes dietary niche breadth and partitioning between generalist rodent consumers

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Pulses in food availability can influence the dietary niche of consumers and modify their interspecific interactions. To better understand the mechanisms which structure dietary niche breadth and overlap, we quantified the diets of two generalist rodents (*Peromyscus maniculatus* and *P. leucopus*) during a three-year period in which two food pulses were produced by masting of American beech. We used carbon and nitrogen stable isotope ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$) analysis of hair to reconstruct diets in the summer and fall of each year and to measure each species' dietary niche breadth and interspecific niche overlap. We tested whether dynamics in niche breadth and overlap were consistent with predictions of optimal foraging theory or competition theory. Patterns of niche breadth were consistent with predictions of optimal foraging theory, with both species having narrower niche breadths during masting periods than during non-masting periods. Comparatively, niche overlap was consistent with competition theory with higher niche overlap, or less resource partitioning, during masting periods than during non-masting periods. Overall, dynamics in niche breadth and overlap were closely associated with masting events despite changes in *Peromyscus* abundance over this same time. Our results indicate that competition is modulated by food availability. Because food availability is rarely considered when investigating competition between *P. maniculatus* and *P. leucopus*, our results may explain why evidence for niche partitioning between these species has been equivocal.

56: Identity of mammalian hosts and performance of flea parasites: evolutionary and conservation implications

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Among host species that a parasite is able to exploit, a principal host and auxiliary hosts are distinguished. We report the results of comparative analyses of abundance and laboratory experiments on performance of fleas exploiting different hosts. We found that taxonomic relatedness between the principal and auxiliary hosts determines what abundance a parasite can achieve on auxiliary hosts. Experimental studies supported these findings for energy expenditure of blood digestion and reproductive output of fleas, but only when the analyses were restricted to auxiliary hosts of the same family as the principal host. However, flea performance appeared to be high when they fed on hosts very distant from but co-occurring with their principal hosts. Then, we measured flea performance on hosts that were both distant from the principal host and inhabit other geographic regions modelling thus host invasions. Flea performance was either high or low on different invasive hosts being thus context-dependent. We conclude that among-host variation in parasite performance may result from interplay of several factors including co-occurrence between hosts, susceptibility of a host to parasite attacks, species-specific level of immunocompetence of a host and the level of host specificity of a parasite. High performance in an unusual but co-occurring host may be one of the reasons for host switching to unrelated lineage such as switch from mammalian to bird hosts that happened during evolutionary history of fleas. From the conservation perspective, we also conclude that the response of a resident parasite to an invasive host is unpredictable.

57: Exploring the role of *Blarina* in the Lyme disease cycle in North America

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Human Lyme disease is a bacterial infection caused by members of the *Borrelia burgdorferi* s.l. complex that is transmitted primarily by ticks in the genus *Ixodes*. Since first reported in 1975 in Lyme, Connecticut, Lyme disease has steadily increased both in number of cases and geographic extent. Despite being restricted to eastern and Midwestern states, Lyme disease is the 6th most common reportable disease in the US, with ~300,000 cases annually, of which only 10 percent are diagnosed because the spectrum of pathologies makes early diagnosis difficult. The forest-dwelling white-footed mouse, *Peromyscus leucopus*, is presently considered to be the main competent (amplifying) reservoir host, but our recent studies indicate the potential for a significant role in transmission of *B. burgdorferi* by the short-tailed shrews in the genus *Blarina*. Of 362 ticks removed from *Blarina* caught in live traps in eastern Virginia, 360 were *Ixodes* spp. Tissues from 22 of 33 *Blarina* from eastern Virginia were positive for *B. burgdorferi* s.l., as were 72% of tissues from 25 museum specimens of *Blarina* collected from 1963-1993. *Borrelia*-positive tissues from *Blarina* collected in Minnesota (n = 42, 79%) and Kansas (n = 19, 74%) further indicate the importance of understanding the role of the short-tailed shrew in the transmission of Lyme disease.

58^E: Coyotes (*Canis latrans*) exhibit an immune response to *Rickettsia* spp. in Arizona

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Rocky Mountain spotted fever (RMSF) is a tick-borne rickettsial infection that causes severe disease in humans and animals. In 2003, RMSF was identified in Arizona and local outbreaks affecting humans have occurred since that time. In AZ, the primary vector for RMSF is the brown dog tick (*Rhipicephalus sanguineus*), and domesticated dogs are this tick's primary host. Free-roaming dogs have been implicated in the spread of RMSF on Native American reservations, where most of the RMSF cases occur. Current empirical data are insufficient to explain long-range dispersal between communities, but due to the sudden increase in human RMSF cases, we hypothesize the influence of a wildlife component. Coyotes (*Canis latrans*) are genetically similar to dogs and have larger home ranges, so we hypothesize

that coyotes are contributing to the long-range dispersal of RMSF and infected ticks. To test this, we used an indirect immunofluorescence antibody assay (IFA) to screen for RMSF antibodies in coyote sera. We have demonstrated for the first time that coyotes in Arizona are exposed to *Rickettsia* spp. bacteria and may contribute to the maintenance of RMSF in the wild.

59^{E,HTA}: Lyme disease prevalence as it relates to vector and host distributions on a temporal and spatial scale on Fort Drum Military Installation, New York

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In the Northeast, Lyme disease is the most common vector-borne zoonotic infectious disease spread by black-legged ticks (*Ixodes scapularis*). While host densities influence tick encounters, host specificity influences successful transmission due to varying reservoir competences. Due to the potential for impact, our objective was to estimate abundance and distribution of host populations on Fort Drum to better assess the potential risk of exposure of Lyme disease to active troops and their dependents. Sherman and Tomahawk traps were used to estimate small mammal abundance and diversity through mark-recapture in six habitat cover types. Ticks and ear punches removed from animals were screened at the Army Public Health Command at Fort Meade, MD with a real-time PCR multiplex for *Borrelia burgdorferi*. Species composition among 97 captured individuals was: 36% *Tamias striatus*, 30% *Peromyscus* spp., 21% *Tamiasciurus hudsonicus*. Although approximately 52% of captured mice had an attached tick, compared to 26% of chipmunks, 100% of attached ticks on chipmunks tested positive, compared to approximately 33% of attached ticks on mice. The highest exposure rate of 47% occurred in developed landscape where trapping success and Simpson's diversity index were greatest at 13.54% and 0.57 respectively. We will continue to analyze 2016 field data and develop models for presentation, with our overall goal of developing temporal and spatial management recommendations for troop training, recreation, and habitat management on Fort Drum.

60^{E,HTA}: Effects of mammalian community composition on ectoparasites in the Chihuahuan desert

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Many studies have focused on the relationship between species richness and disease prevalence; few have examined the more nuanced relationship between host community composition and parasite prevalence in multi-host, multi-parasite systems. We examine the effects of mammalian community composition on the prevalence and community composition of ectoparasites (fleas and ticks) in a desert rodent community. We utilize a long-term research site in the Chihuahuan desert in southeastern Arizona, where some experimental plots allow access to all rodents, and others exclude kangaroo rats (*Dipodomys* spp.), the dominant rodent species in this system. We also trapped rodents outside of these plots to assess how the exclusion of jackrabbits and other non-rodent mammals from the study plots might affect the parasite community. We found differences in ectoparasite prevalence among the rodent host species. In November 2015, *Onychomys leucogaster* (northern grasshopper mouse) had the highest prevalence of fleas (56%), whereas *Dipodomys merriami* had a prevalence of 12%, and no fleas were found on several species of *Chaetodipus* (pocket mice). We also found differences in the host specificity of parasites; ticks were found almost exclusively on kangaroo rats. In November 2016, ticks were significantly less prevalent on *Dipodomys* captured within the plots (21% prevalence) compared to outside the experimental plots (80%). Jackrabbits may play a key role in the maintenance of the tick population in this system.

61^E: Effects of sylvatic plague on northern Idaho ground squirrels

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Northern Idaho ground squirrels (*Urocitellus brunneus*) are a threatened species and we have conducted field experiments to test whether sylvatic plague may be responsible for their decline. We evaluated whether experimental removal of fleas (the vector of plague) increases survival of northern Idaho ground squirrels and 3 coexisting species: Columbian ground squirrels (*Urocitellus columbianus*), yellow-pine chipmunks (*Tamias amoenus*), and deer mice (*Peromyscus maniculatus*). Apparent survival was 1.17, 1.03, and 1.01 times higher on flea removal sites compared to control sites for Columbian ground squirrels, northern Idaho ground squirrels, and chipmunks (respectively). In 2016, we also used a plague vaccine on chipmunks and deer mice and compared apparent survival of vaccinated animals to controls. Apparent survival of vaccinated animals was 2.78 times higher than that of control animals. We have collected and identified 1,547 fleas from anesthetized animals on our study sites and have documented 6 species of fleas that are known vectors of plague. Both squirrel species and chipmunks share the same suite of flea species (although proportion of flea species differs among species). Our results suggest that sylvatic plague is contributing to the decline of the northern Idaho ground squirrel (and is reducing survival of sympatric species); more work is needed to understand how this virulent invasive disease is being maintained and how best to manage plague effects on northern Idaho ground squirrels.

62: Home range use of southern flying squirrels in fragmented forest landscapes

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We studied home range use and spatial activity patterns of southern flying squirrels (SFS; *Glaucomys volans*) across fragmented landscapes of west-central Illinois. We calculated seasonal home range sizes and annual survival from 67 animals (36 males, 31 females) captured during 2014–2016. Home-range and core-area sizes were similar ($P \geq 0.14$) among males and females across summer (April–September) and winter (October–March) seasons. Average distance traveled between consecutive locations during a season did not vary ($P = 0.34$) by sex. Similarly, total distance traveled during a season did not vary by sex ($P = 0.91$) or year ($P = 0.46$) and ranged from 1189 to 1661 m between summer and winter seasons. Mean annual composite home range and core area sizes were 10.39 ha (SE = 1.25, $n = 56$) and 1.25 ha (SE = 0.15, $n = 56$), respectively; estimated female home ranges are the largest documented for this species. Our results underscore effects of habitat productivity on seasonal home range dynamics and space use patterns by SFS in fragmented landscapes. Winter communal nesting appears to be influenced by availability of cavity trees, thereby confirming the importance of standing snags in contributing essential habitat to flying squirrel populations in fragmented forests.

63^E: I'd trap that! Trap success and densities of pygmy rabbits across the Great Basin

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Pygmy rabbits (*Brachylagus idahoensis*) are sagebrush (*Artemisia* spp.) and burrowing obligates, only occurring in the intermountain region of the western United States. Because trap success is low for these small lagomorphs, population sizes are relatively understudied and a new method of trapping is needed to increase sample sizes. Most methods of trapping pygmy rabbits rely on chasing the rabbit down a burrow before setting traps, but we set out 100 traps at a time, placing them in burrows and well used runways. Using this new trapping procedure, in summer 2016, we trapped 310 individual pygmy rabbits at several sites across 3 regions in Nevada and southeastern Oregon. Here, we plan to investigate how variables such as mean temperature, precipitation, breeding status, time of day, trap orientation, total time traps were open, age and sex influence trap success. Based on our preliminary mark-recapture data, we estimated population sizes, sex ratios, and age ratios. Although this is an ongoing project, these initial

estimates establish a baseline of how these populations vary in number and density across the landscape.

64: Using the Internet-of-Things to monitor bat roosts

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The Internet-of-Things (IoT) refers to a network of electronic sensors connected together, which exchange data with other connected devices, individuals, or the Internet. IoT makes it possible to remotely monitor animal activity, environmental conditions, and behavior. This technology is used in the “Digital Bat Roost Project”, which uses IoT technology to log roost temperatures, humidity, and light levels on a time schedule set by the user. In addition, bat activity is recorded whenever a bat exits or enters the digital bat house using infrared break beam sensors. Both activity and environmental data are logged to an on-board micro SD card. To retrieve the data from the roost, there are several options. Researchers can simply remove and the SD card, copy the data to a spreadsheet program, and replace the card in the roost. Alternatively, the data on the SD card can be automatically download to a smartphone or tablet using Bluetooth technology. This means that the researcher only needs to be within 30 feet of the roost to sync and download the data. Finally, if the roost is within wifi range, the data can be live-streamed to the internet. Other uses of IoT technology for mammalogy, such as monitoring burrows and the use of GPS tags to log position and send the coordinates via text message, are also discussed.

65^E: Macro- and micro-habitat effects of ocelot occupancy

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The ocelot (*Leopardus pardalis albescens*) is a small endangered subtropical felid found in 2 small populations in the Lower Rio Grande Valley of Texas. Degradation and loss of habitat is one of the principal drivers of a loss of ocelot genetic diversity in the region. Previous research in ocelot habitat use has reported ocelots select for dense closed canopy thornshrub (>75%) and will occasionally use more open land cover types. However, research is needed to examine if these or other habitat variables affect initial occupancy, local colonization and local extinction of ocelots. From 2011-2016, we conducted remote camera surveys on 28 sites on the East Foundation’s El Sauz Ranch, Willacy County, TX. We report initial occupancy was positively influenced by low canopy height and low light intensity, local colonization was positively influenced by thermal cover (e.g., less intense light, low temperatures, low wind speed, and low relative humidity), and localized extinction was positively influenced by increasing patch density of herbaceous vegetation. This research provides information into habitat components most likely to influence where ocelots occur, which is essential for future ocelot recovery and habitat restoration in the Lower Rio Grande Valley.

66^{E}: What does a prudent pika pick? Spatial and temporal dietary trends of an alpine mammal**

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Climate change is driving changes in species and communities worldwide, including range shifts, local extirpation, and population declines. The specific mechanisms remain unclear, but may include physiological limits or the reduction in food sources. Previous research has shown that the American pika (*Ochotona princeps*) is sensitive to increased temperatures, but whether their population declines are directly due to temperature stress or indirectly due to their dietary change is debated. Pikas are central-place foragers that store food for the winter in hay piles, and thus may be particularly sensitive to changes in vegetation. We hypothesize that variation in diet may be an important factor influencing pika populations. We predict that pika populations’ diets will have changed in response to climate change, and that pikas will exhibit seasonal variation in their diet. Using carbon and nitrogen stable isotopes, we characterize the isotopic dietary niche of nine pika populations in the southern Rocky Mountains,

comparing historical and modern populations. We use bone isotope values to compare populations over space and historical time, and fur isotope values to study seasonal variation in diet. We find that there is little change in dietary niche over historical time or latitude, and we find seasonal variation in pika diet. While limited to the southern Rocky Mountains, our findings suggest that pika are constrained in their diet composition across space and historical time. This research was supported by a 2016 Grant in Aid of Research awarded to Marie L. Westover.

67^{E}: Abiotic and biotic habitat characteristics shape the current distribution of a rare kangaroo rat**

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A primary goal of ecology aims to understand which factors influence distribution and abundance of species. Rare species, by definition, have sparse or restricted spatial distributions generally governed by habitat availability. As such, understanding distribution of rare species requires a comprehensive knowledge of their dependence on both local habitat features and interspecific interactions (i.e., positive and negative). We sampled vegetation and soil characteristics and surveyed the rodent community at 35 sites across the historical range of the Texas kangaroo rat (*Dipodomys elator*), a rare and potentially threatened species, to identify biotic and abiotic characteristics potentially limiting its distribution and abundance. Soil type (i.e., clay-loam) and bare ground were important determinants of *D. elator* occurrence across its distribution. Moreover, *D. elator* occurred most frequently with *Chaetodipus hispidus*, another heteromyid species with similar habitat preferences. Results from our work should improve understanding of factors contributing to the rarity of this kangaroo rat species and its vulnerability to habitat change and help inform conservation and management strategies for rare species.

68: Genetic mechanisms of hypoxia adaptation in high-altitude mammals

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High-altitude environments provide ideal testing grounds for investigations of mechanism and process in physiological adaptation. In this talk, I will describe recent efforts to identify and characterize mechanisms of biochemical and physiological adaptation to hypoxia in high-altitude mammals. This work is motivated by questions about the inherent repeatability and predictability of adaptive evolution at the molecular level. Is it possible to predict which molecular mechanisms are most likely to contribute to biochemical adaptation? Can we predict which mutations - or which types of mutation - are most likely to contribute to adaptive changes in protein function? To address these questions we integrate evolutionary analyses of sequence variation with experimental studies of hemoglobin function using site-directed mutagenesis.

69: Evolutionary cascades across multiple mammalian contact zones: methods for genomic investigations within complex host-parasite systems

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Conserving functional mammalian communities will rely on understanding how constituent species have evolved through time and space in response to long-term environmental change. Traditionally, evolutionary biologists focused on individual species through phylogeographic assessments. Decades of mammalian phylogeographic studies have yielded new perspectives utilizing one to a few common loci to perform comparative assessments. However, those comparative approaches analyze co-distributed species generally without considering biological interactions. Further, both long-standing and recent

questions regarding generalizable processes of community assembly, speciation, and co-evolution, to name a few, cannot be answered with traditional sequencing. Genomic approaches allow for increased rigor when investigating the high complexity inherent within interdependent groups of species as they evolve across the landscape. We demonstrate how genomic data are being used to investigate evolutionary cascades among shrews and their related symbiont, mainly parasite, biodiversity. Across North America, shrews of the *cinereus* group form multiple contact zones, and hybridization is evident between several taxon pairs. We ask how gene flow among these mammals influences both speciation of shrews, and contingent evolutionary responses among associated diversity including helminth parasites and microbiomes. Our expectation is that feedback responses through multiple layers of biological organization can in turn impact host fitness and evolutionary trajectories. This type of integrated investigation will rely on refining and standardizing comprehensive field protocols using multiple methods of preservation to maximize next generation approaches.

70: Evolutionary systems biology of high altitude adaptation in deer mice

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Both phenotypic plasticity and genotypic specialization can contribute to performance differences in species that are locally adapted to different environments, but their relative contributions are expected to vary with the spatial and temporal grain of environmental variation. In species that are distributed across steep elevational gradients, environmental conditions change dramatically over small spatial scales, and as a result, adaptive variation may be attributable to transcriptional plasticity in regulatory networks that underlie trait differences between high- and low-elevation populations. Here, a series of common-garden experiments were conducted which were designed to examine the role of regulatory plasticity in evolutionary adaptation to high-elevation conditions in deer mice (*Peromyscus maniculatus*). Using a systems biology framework, I will discuss our efforts to integrate genomic surveys of DNA sequence polymorphism and genome-wide transcriptional profiles with functional assays of metabolic enzyme activities, cellular and tissue-level phenotypes, and measures of whole-animal performance. Highland mice exhibit greater thermogenic capacities than lowland mice under hypoxia, and this trait is associated with increased survival at high elevation. Our recent work has shown that this enhanced performance is associated with up-regulation of transcriptional modules that influence several hierarchical steps in the O₂ transport cascade. Most of these performance-related transcriptomic and physiological changes occur over physiological and developmental timescales, suggesting that regulatory plasticity makes important contributions to fitness-related physiological performance in highland deer mice.

71: Using temporal genomic contrasts to detect rapid evolutionary responses to climate change

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Rapid environmental change threatens global biodiversity and has already led to the decline or extirpation of many taxa. Although phenotypic plasticity may enable populations to rapidly track changing climates, evolutionary adaptation will be essential for the long-term persistence of many species. Disentangling plasticity from evolutionary responses ultimately requires resolving the genetic basis of adaptation. However, it remains challenging to differentiate recent or ongoing positive selection from stochastic genetic changes in populations that are also undergoing extreme demographic changes. Natural history museum collections may hold the key to overcoming many of these difficulties by providing crucial temporal information on species distributions, phenotypes, and population genetic variation spanning periods of recent environmental change. I will discuss our ongoing efforts to recover high quality genomic data from archived museum specimens and to develop sophisticated analytical approaches suitable for such data. Using examples from chipmunks and snowshoe hares, I illustrate how next generation museum population genomics can be used to dissect the genetic basis of ecologically important traits, and to detect rapid evolutionary responses over timescales relevant to anthropogenic climate change.

72^E: Associating host genomic variation with gut microbiota in wild house mice

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Recent advances in microbial ecology have shown that gut microbes can affect digestion, immunity, development, and behavior of their animal hosts. Although this raises the intriguing possibility that gut microbes play an important role in host ecology and evolution, we know little about the forces shaping the composition of the gut microbiota. Here, we combined field and laboratory based approaches to understand the environmental and genetic factors associated with gut microbial variation in natural populations of house mice (*Mus musculus*). Using 16S amplicon sequencing, we characterized gut microbial communities in 10 populations of house mice sampled across North America. Overall microbial variation was correlated with climatic variables, host body size, host diet (determined from carbon and nitrogen stable isotopes), and host genetic distance (determined from exome sequences). Host genetic distance correlated with microbial community distance better than did the geographic distance between hosts. We identified host genomic regions associated with microbial measurements using Latent Factor Mixed Models. A common garden experiment demonstrated that the population differences in microbial composition in wild mice persisted in a laboratory environment after one generation. Together, these results suggest an important role of host genetics affecting variation in the gut microbiota of wild house mice.

73: Lightning talks at the ASM Annual Meeting

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Many researchers, including mammalogists, have research projects that are in the initial stages of implementation or perhaps are even still in development. Such projects may benefit from feedback, but not be advanced enough to fill a standard 15-minute presentation slot. Five-minute lightning talks encourage developing a concise explanation of a project and provide a venue for first-time presenters without the pressure of a full-length presentation. Additionally, lightning talk sessions are a fun way to experience a broad survey of different types of research being conducted. There are other venues that provide opportunities for 5-minute lightning talks, which are well-received. The American Society of Mammalogists is designating a lightning talk session this year to introduce members to this format and highlight the benefits of an abbreviated presentation. This talk will discuss this format of presentation and ways to conduct a successful lightning talk.

74^E: Building a silent desert for behavioral studies of vocal rodents

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A long-standing issue in studies of vertebrate behavior is the disconnect between conditions experienced in nature vs. the laboratory. Field studies often suffer from the inability to control a wide range of factors, such as climate, diet, and interactions between individuals and species. Conversely, laboratory settings permit control over most variables, but generally do not portray realistic spatial or social scenarios. Meanwhile, researchers are increasingly discovering a diversity of sounds used by muroid rodents in a variety of social contexts. In an effort to bridge the gap between field and laboratory settings to better understand acoustic interactions, we are building a 255 m² indoor desert equipped with above- and below-ground cameras and a microphone array sensitive to audible and ultrasonic frequencies. A raised floor with removable plugged holes allows for manipulation of burrow densities, and speaker arrays on soundproof walling enable high fidelity sound playback. Multiple animals can be tracked simultaneously and continuously under fluorescent or infrared light. We discuss several ongoing experiments that utilize this novel arena to better understand acoustic behavior in rodents.

75^{E}: Linking microwear across the dental arcade: do canid m1 and m2s record comparable**

signals?

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Quantification of carnivoran dietary habits via dental microwear texture analysis (DMTA) is instrumental for inferring dietary behavior from modern and paleontological skeletal specimens. Currently, DMTA among canids has targeted the hypoconulid facet of lower second molars (m2), where the widest range of food processing occurs. However, caniform carnivorans have increased occlusal area on the talonid basin of the lower carnassial (m1). If this region is biomechanically analogous to the m2, it could dramatically increase sample sizes of available fossil canid specimens as carnassials are more frequently recovered and more identifiable. We tested if dental microwear textures were similar between analogous facets on the m2 and m1 in two canids, coyotes (*Canis latrans*) and gray wolves (*Canis lupus*). Paired casts sampled from museum collections were analyzed for three microwear indices indicative of diet within carnivorans: anisotropy, complexity, and textural fill volume. Anisotropy (indicative of flesh consumption) and complexity (indicative of durophagy) did not differ between the m1 and m2 of coyotes or wolves (all $p > 0.1$). Textural fill volume, however, differed between the m1 and m2 for coyotes ($p < 0.001$), but not for wolves ($p = 0.11$), which could reflect differences in bite force along the tooth row. Our results suggest that the m1 talonid can be substituted as a comparable facet for the m2 when using dental microwear to reconstruct diets of caniform carnivorans.

76: Diversification rate in mammals and association with genome size and life history

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Mammals are a highly diverse class of vertebrates that occupy a diversity of niches and are globally distributed. However, most of the taxonomic diversity within mammals is represented by a single order (Order Rodentia), and most of the ecological diversity is represented by a single superorder (Superorder Laurasiatheria). Previous work has suggested that the diversification rate of mammals has fluctuated across the 166 million year history of this clade. We hypothesize that fluctuations in diversification rate are correlated to genome size, portion of repetitive elements, and mutation rate. Genome size and portion of repetitive elements are expected to influence neutral variation within species that may also lead to greater speciation potential. Mutation rate is difficult to estimate for most mammals. Instead, we used life history traits that have strong correlation with mutation rate. We examined the relationship between diversification rates in mammalian families and their genome size, proportion of transposable elements, metabolic rate, and longevity. By examining the relationship between genome size, portion of transposable elements, longevity, and metabolic rate with diversification rate, we can examine the relative impact of these genomic and life history traits on speciation and extinction in mammals. As some clades of mammals contain very few extant members and others contain 50% of the diversity of mammals, this type of analysis will improve our understanding of mammalian evolution.

77: Genomics of hybridizing ground squirrels

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The opportunity to understand the process of speciation at the genomic level has increased due to the availability of reduced representation and high-throughput sequencing. Two species of squirrel, Rio Grande ground squirrel (*Ictidomys parvidens*) and thirteen-lined ground squirrel (*I. tridecemlineatus*), hybridize in isolated populations within southeastern New Mexico and west Texas. The hybrid zone is a result of secondary contact due to changes in climate occurring within the past 100 years. We used double digestion restriction-site associated DNA sequencing (ddRADseq) to identify single nucleotide polymorphisms in hundreds of individuals, including known hybrids, to quantify genomic introgression and hybridization in *I. parvidens* and *tridecemlineatus*. Our results demonstrate frequent hybridization between *I. parvidens* and *tridecemlineatus* with substantial genomics introgression between species. In

addition, we identified a number of F2 and backcross hybrids implying that postzygotic reproductive barriers, in the form of selection against hybrid phenotypes, is minimal. Despite high levels of gene flow between species, genomic regions of high F_{ST} were identified in each species. It remains to be seen if there is a breakdown of reproductive barriers in the *I. parvidens/tridecemlineatus* species pair. Regions of high F_{ST} may contain loci responsible for limiting introgression and determining the forces responsible for reproductive isolation.

78: Genetic isolation and a unique disease threatening the island fox

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Island foxes (*Urocyon littoralis*) consist of six subspecies that inhabit six of the eight California Channel Islands. The processes of island colonization and historical bottlenecks, due to limited carrying capacity and anthropogenic threats, have caused a severe loss of genetic diversity within each population of island foxes. Evidence suggests that these genetic changes may contribute to a high incidence of ceruminous gland carcinoma in one subspecies, the Santa Catalina (SCA) island fox (*Urocyon littoralis catalinae*). These cancers form in the ear canals of approximately half of adult SCA foxes, and are associated with chronic inflammation caused by ear mite infection. However, foxes on two neighboring islands suffer high rates of infection with the same mites and some inflammation, yet cancer does not result. We test the hypothesis that the remarkably high incidence of carcinoma in Santa Catalina island foxes is the result of genetic variants for cancer susceptibility, which have increased in frequency due to genetic drift. We apply genomic tools including RAD, whole-genome, and targeted sequencing to identify specific candidate genes that may be involved. Ultimately, we aim to develop a susceptibility panel of genetic loci that would provide an efficient way to genetically assess an individual fox's probability of developing cancer in response to mite infection. This panel could be used for both monitoring and population management in this threatened subspecies.

79: Conservation status of black-and-white snub-nosed monkey, *Rhinopithecus bieti*

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Rhinopithecus bieti, endemic to China, was believed extinct when no observations were reported after the original description in 1897, until 1960 when 8 skins were obtained from hunters in Deqin County, Yunnan. The population since rediscovery was in decline until protections became effective in the 1980s, when some subpopulations began to increase, while others continued to decline or became extirpated. Limited surveys began in 1979, but the first comprehensive survey in 1987-1992 revealed 20 bands or subpopulations. All are found in the Hengduan Mountains between the Mekong and the Yangtze Rivers. Surveys in 2000 found no sign of monkeys in 12 areas where they had previously existed, but 3 new bands were found, leaving 11 extant, of which at least 5 were isolated by barriers such as low-elevation farmland, roads, and higher elevation grazing lands. Subsequently, an extirpated population was rediscovered, or recolonized former habitat. The total population of *R. bieti* recovered from 800-900 in 1986 to about 1,700 individuals in 13 bands by 2002 and 2,500 based on surveys during 2004- 2009. In 2012, the populations in Tibet and Yunnan totaled > 3,000, and about 3,500 in early 2016. This suggests a gradual, sustained rate of increase (λ , lambda) of 1.05 over the last 3 decades. All populations are in national or provincial nature reserves, but logging, hunting and poaching remain threats.

80: Body size determines depth and length of hibernation in free-ranging brown bears

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During hibernation, animals undergo major reductions in body temperature and metabolic rate. The amplitude of metabolic rate reduction in hibernators is dependent on body size; small hibernators have a high metabolic rate when euthermic, making a drastic decrease in core temperature during torpor necessary to reach a very low metabolic rate. The lower magnitude of the decrease in core temperature during hibernation in bears, compared to other hibernators, is thought to be related to body size, although detailed studies on intra-specific variations in body temperature are lacking. Here we document, with data from 34 bears totalling 45 years, relationships between body mass and body temperature, hibernation duration, den exit date, and in a cumulative index of hibernation depth; with the smallest bears having lower body temperatures, hibernating longer, exiting later and saving more energy than large bears. These relationships were consistent across a range of masses from 30 to 233 kg. Our results demonstrate that body size, even in a large mammal determines the cooling process of the bear as they enter the dens and lower the metabolic rate, with smaller bears, which have higher thermal conductance, having lower body temperatures.

81^F: Craniodental integration and facial length in domestic dogs

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In mammals, teeth complete their growth before erupting into the mouth; thus, tooth size is largely decoupled from growth of the craniofacial skeleton. How these separate developmental modules evolve to maintain functional dentition has been a perennial topic in evolutionary biology. While most studies using samples from wild populations have documented patterns of integration in teeth and variability of particular teeth relative to others, relatively little is known about how dentition might respond to changes in tooth row length. We investigated craniodental integration along the axis of variation in relative face length for a diverse sample of crania from adult dogs using 26 repeatable landmarks from 195 dog crania. Integration in the cranium and part of the maxillary arcade was strong and consistent across most of the gradient in face length; however, integration declined rapidly once relative face length became less than relative face width. This inflection point corresponded to shifts in relative sizes of the middle cheek teeth, which remained large as relative face length decreased beyond this threshold. In addition, relative tooth size as a function of face length differed for each tooth considered, contributing to phenotypic (dis)integration in brachycephalic dogs. This pattern in context of the functional tradeoff between skull shape and dentition, suggests that developmental constraints may have arisen to conserve size, and hence occlusion, in functionally important teeth.

82: Testing for adaptive introgression between *Mus musculus domesticus* and *Mus spretus*

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Adaptation requires genetic variation on which natural selection can act. There are three major sources of genetic variation: (1) new mutations, (2) standing genetic variation, and (3) introgressed variants from other species. Introgressed variants are especially intriguing because they may arise faster than new mutations, can include multiple mutations on a single haplotype, and have been tested by selection in the species of origin. *Mus musculus* and *M. spretus* diverged an estimated 1.5-3 Mya, have a genetic divergence of about 1%, and are broadly sympatric. The two species have many morphological and life

history differences. Additionally, there is a significant fitness disadvantage to hybrids; F1 males are completely sterile and genomic incompatibilities exist between the two species. Several previous studies have revealed introgression of alleles from *M. spretus* into *M. musculus*. Here we look for evidence for introgression from *M. musculus* into *M. spretus* populations utilizing previously published and newly generated exome-capture data.

83^E: Management in the anthropocene: conserving the endangered salt marsh harvest mouse in a changing world

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In the San Francisco Estuary (SFE) less than 10% of historical tidal wetlands remain, and those comprise a fragmented mosaic of natural and anthropogenically altered wetlands. Globally, only 5 species of vertebrates, and only one mammal, the endangered salt marsh harvest mouse (SMHM, *Reithrodontomys raviventris*), are restricted to coastal wetlands. SMHM is a unique wetland-adapted rodent endemic to the marshes of the SFE. Conventional conservation practices have favored a push toward tidal restoration as a recovery action for SMHM. However, tidal wetlands are vulnerable to sea level rise and tidal restoration is slow and costly. Understanding the value of alternative habitat types can improve conservation of SMHM. We investigated the relative value of historical tidal and anthropogenic diked wetlands for SMHM. We found that both support similarly sized populations and similar numbers of reproductive females. Habitat use is similar between wetland types, but smaller home ranges in diked wetlands may indicate greater habitat value. Finally, preferred food plants occur at high densities in diked wetlands. This study greatly improves our understanding of the habitat requirements of SMHM. Diked wetlands have high habitat value for SMHM, possibly superior to tidal habitat; this result triples the acreage of “good” SMHM habitat in the SFE. It also illustrates the importance of understanding the value of anthropogenic habitats for conservation of endangered mammals as historical habitat patches dwindle.

84: Filling the void: rapid movement of southern bats into the vacated niche of cave bats killed by WNS in the mid-Atlantic states

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Over the past 10 years, mass mortality of cave bats in the eastern US has occurred due to white-nose syndrome (WNS). Mortality rates from WNS have reached 100% at many sites, and there have been an estimated 6-7 million bats lost in this panzootic. The result is an ecological niche which has been substantially vacated throughout the eastern US. More southern bat species are found to be moving north to occupy this vacated niche, including Mexican free-tailed bat (*Tadarida brasiliensis*), southeastern myotis (*M. austroriparius*), evening bat (*Nycticeius humeralis*), seminole bat (*Lasiurus seminolus*), and northern yellow bat (*L. intermedius*), among others. Northward movements and subsequent range extensions for these bats recently have been detected using bat acoustic signatures. As these bats fill the void left by mass mortality of cave bats, they will continue to press north farther into open niches left by the mass mortality of cave bats. The analysis to explain the northern movement of these bats must also take into account climate change. Ranges of some species have been documented to be shifting north prior to WNS, and these bats moving north likely are responding to climate as well as the open niche. The implications of this great northward movement of bats have both ecological as well as conservation significance, and a change in bat biodiversity already is evident in the mid-Atlantic states.

85: Mandibular shape and diet in foxes

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We used geometric morphometric techniques to explore shape variation in the dentaries of foxes. Dentaries from 17 species of foxes were photographed in lateral view at the Los Angeles County Museum of Natural History, Field Museum, SIU Carbondale Mammal Collection, and University of Kansas Museum of Natural History. We placed 12 homologous landmarks and edgels on each dentary, as well as 50 semi-

landmarks along the margin of the angular process. We performed a Procrustes superimposition to align the specimens, followed by a canonical variates analysis. The analysis revealed significant shape differences between the species, particularly with respect to the shape of the angular process, position of the coronoid process, and position of the masseteric fossa. We estimated the phylogenetic signal associated with dentary shape. Using dietary data derived from the literature, we performed a non-metric multidimensional scaling ordination to reveal the relationship between shape and diet.

86: BAT1K: An initiative to sequence genomes from all extant bat species

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The ability to sequence large numbers of mammalian genomes has only become economical in the last decade. As a result, most major sequencing efforts have targeted single species from distantly related clades to maximize phylogenetic diversity and financial resources. In doing so, few genomic resources have been developed to study lineage-specific evolutionary innovations that arose in closely related taxa. BAT1K is an initiative to sequence the genomes of all ~1,300 extant, bat species in an effort to uncover the genes and genetic mechanisms behind the unusual adaptations of bats including longer life-spans, flight, echolocation and disease resistance. The project is organized into three phases to produce genome drafts for every family, genus, and then species. Members of the consortium will gain early access to the genome assemblies as they are produced. More information is available at www.bat1k.com.

87^{HTA}: Evolution of mammalian parasites: Are there signatures of selection in chipmunk sucking lice?

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Natural selection should lead to adaptations that increase the fitness of parasites. Blood sucking parasites that rely on the same resources from a host may converge on similar adaptations or they may employ different mechanisms to garner those resources. Western North American chipmunks (genus *Tamias*, subgenus *Neotamias*) are parasitized by two species of ectoparasitic sucking louse in two families *Hoplopleura arboricola* (Hoplopleuridae) and *Neohaematopinus pacificus* (Polyplacidae), that are approximately 50 million years divergent. These two louse species have similar life histories and rely on similar resources from their chipmunk hosts. Species trees were estimated for each louse using over 800 nuclear genes assembled from whole-genome sequencing. Phylogenomic reconstructions for the two louse species are distinctive across host-associated lineages, indicating different histories of host-parasite association. Here, we are assessing selection across exons to determine if the two distantly related chipmunk sucking lice exhibit similar signatures of positive selection relative to other mammalian lice. Comparing these louse species provides insight into the prevalence of convergent selection in parasitism of chipmunks.

88: Spatiotemporal heterogeneity in prey abundance and vulnerability shapes the foraging decisions of an omnivore

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To evaluate the interplay between prey abundance, prey vulnerability, and predator space use, we examined black bear (*Ursus americanus*) predation of caribou (*Rangifer tarandus*) neonates in Newfoundland, Canada using data from 329 collared individuals (21 bears, 34 adult female caribou, 274 caribou calves). We found that landscape heterogeneity influenced calf vulnerability, and that bears displayed the strongest selection for areas where they were most likely to kill calves, which suggested they were actively hunting caribou. Initially, the per-capita rate at which bears killed calves followed a type-I functional response, but as the calving season progressed and calf vulnerability declined, kill rates dissociated from abundance. Bears adjusted their foraging strategy when they were less efficient at catching calves, highlighting the influence that predation phenology may have on predator space use. Bears appeared to continue to hunt caribou as calf availability declined, but switched from a strategy of selecting areas of increased calf vulnerability to a strategy that maximized encounter rates with calves. Our results reveal that generalist predators can dynamically adjust their foraging strategies over short time scales in response to changing prey abundance and vulnerability. Further, they demonstrate the utility of integrating temporal dynamics of prey availability into investigations of predator-prey interactions, illustrate shortcomings of common analytical approaches, and move towards a mechanistic understanding of the dynamic foraging decisions of a large, generalist predator.

89: Folivory by desert granivores may regulate post-fire recovery of plant communities

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Small mammals influence and can even regulate the composition of plant communities in desert systems. However, invasion by exotic plants and subsequent increasing frequency of fire in deserts of the western United States is altering the small mammal communities of these systems. Even with fire-induced changes in the small mammal community, these animals continue to exhibit top-down influence on post-fire recovery of the plant community. We used a randomized complete block design to evaluate the interactive effects of fire and small mammals on survival of seeds and seedlings of common plant species in the Mojave and Great Basin Deserts. On average, daily survival of seeds was greater in plots without small mammals (0.96) than plots with small mammals (0.91). Likewise, daily survival of seedlings was greater in plots with small mammals excluded (0.93) than in plots with small mammals present (0.82). Further, in most plots 100% of seedlings were harvested within 8 days of planting. The small mammal influence was not consistent among all species of plants releasing a few species from top-down forces. Our results illustrate that the role of granivorous small mammals extends beyond dispersal and granivory to the seedling stage of plant life cycles. Moreover, small mammal-mediated folivory by granivores may be equally or more important for plant survival than both dispersal and granivory of seeds by these same granivores.

90: Indicators of change in ecological restoration: small-mammals and herbaceous cover

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Assessment of ecological restoration projects is essential for improving their implementation and justifying their costs, but comprehensive monitoring and evaluation are often not incorporated into such projects. We developed a cost-effective monitoring program for lands managed by 5 Native American tribes in northeastern Washington and adjacent Idaho. Key ecological objectives of restoration are that the restored area (1) has an assemblage of species characteristic of a reference ecosystem that provides appropriate community structure, and (2) consists largely of indigenous species. We established 24 reference points representing the best extant representatives of 8 habitat types, and 83 sampling points on 39 management units where restoration was initiated. Composition and structure of vegetation, and composition and relative abundance of small mammals, birds, and larval amphibians were monitored over 3 years for reference points and at 5-year intervals on restoration sites. Similarity matrices incorporating relative abundance (Chao-Jaccard) were calculated to compare managed lands to the reference for each habitat. Non-metric multidimensional scaling was used to visualize the relationships of restoration to

reference sites for each habitat type. Small mammals are appropriate indicators of change for shrub-steppe habitat where clear linkages with herbaceous vegetation were observed. For habitats subject to disturbance (e.g., flooding in wetland meadows), local extinction and colonization events can alter composition and abundance of both plant and small-mammal species, and move habitats away from reference conditions.

91: Evaluating the influence of intraguild predation on the spatial dynamics of kit foxes

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Intraguild predation (IGP) can drive the spatial dynamics of a subordinate predator and may explain space use patterns to deviate from predictions based on resource availability. In deserts, free-standing water was historically scarce, limiting the distribution of large-bodied predators and offering refugia for smaller, arid-adapted species (e.g., kit fox [*Vulpes macrotis*]). In the Great Basin Desert, increased anthropogenic water sources have allowed larger carnivores (e.g., coyotes [*Canis latrans*]) to increase in distribution and abundance. We coupled noninvasive genetic sampling and dynamic occupancy models to investigate the relative influences of habitat characteristics and IGP (coyotes) on the spatial dynamics of kit foxes in western Utah, USA. We employed a multi-stage approach to evaluate the influence of habitat characteristics on coyote occupancy, and then investigated the role of habitat and coyotes on kit fox space use at multiple scales. Coyote occupancy was unrelated to water, but was positively related to shrubland and woodland habitats. Inversely, kit fox occupancy was negatively related to shrubland and woodland habitat. Kit fox probability of local extinction was positively related to site-level coyote activity, and within an occupied site, the probability of kit fox detection was positively related to survey-level coyote activity. Our results support IGP theory predictions. At broad scales kit foxes minimized overlap with coyotes; but at finer scales kit foxes still adhered to expectations of the resource availability hypothesis.

92^E: Responses in the cotton rat (*Sigmodon hispidus*) to the megafauna extinction of the terminal Pleistocene

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About 80% of large bodied herbivores went extinct at the terminal Pleistocene in North America. The extirpation of these large bodied species likely had cascading effects within communities, but to date little work has focused on the consequences on surviving small bodied mammals. Our study examines effects of the extinction on the morphology and diet of *Sigmodon hispidus* (the cotton rat), a generalist herbivore. Our specimens are from the fine-grained temporal record from Hall's Cave in the Edward's Plateau in Texas. Using bone collagen from fossil jaw fragments, we characterized the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ isotope values. From these, we quantified the isotopic dietary niche of *S. hispidus* for the past 15ka using Bayesian-based ellipse areas. Body size was estimated using allometric equations based on first molar length. The diet of *Sigmodon hispidus* varied in breadth, sometimes expanding and contracting by twice the area between time bins, with an expansion directly after the extinction event. The morphology of cotton rats showed an overall increase in body size, despite warming temperatures following an important cold episode after the extinction. These changes suggest either a low level of impact from the loss of taxa or a high level of adaptive behavioral plasticity in response to community-level change.

93: Acoustic partitioning in a desert rodent community

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Acoustic communication mediates resource defense and mate recognition in a wide variety of animals. Divergence in acoustic signals can reduce mismating and/or misdirected aggression among species, but mechanisms causing divergence remain understudied. Grasshopper mice (*Onychomys*) are carnivorous, territorial rodents that inhabit arid environments throughout western North America. Both sexes produce loud, long-distance calls thought to function in territorial advertisement and mate attraction. In this study, we captured and recorded northern (*O. leucogaster*), southern (*O. torridus*), and Chihuahuan (*O. arenicola*) grasshopper mice in the Bootheel of New Mexico where all three species co-occur ($n=15/\text{sex}/\text{species}$). Within species, we found no sex differences in body mass or call characters. However, body mass and fundamental frequency differed significantly among species. In accordance with principles of acoustic allometry, the largest species (*O. leucogaster*) produced the lowest frequencies (34 g; 11.6 kHz), followed by *O. torridus* (29 g; 13.5 kHz) and *O. arenicola* (22 g; 14.9 kHz). Our findings suggest that species differences in size contribute to acoustic partitioning to potentially promote assortative mating.

94: Age and spatial genetic structure affect black bear effective population and neighborhood size

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The idealized concept of a population is integral to mammalian ecology and evolutionary biology. Most models in evolutionary ecology adopt simplifying assumptions to make analyses tractable. Almost inevitably, real species in nature violate these assumptions in various ways, and it is important to evaluate the consequences of these departures. Here we focus on estimation of effective population size (N_e) neighborhood size (N_s) for black bear (*Ursus americanus*) in Michigan. We illustrate the practical application of methods to account for violations of two common, simplifying assumptions about populations: 1) reproduction occurs in discrete generations, and 2) matings occur randomly among all individuals. We estimate male and female vital rates involving 1) age-specific survival 2) age-specific fecundity and 3) age-specific variance in fecundity. We used program AgeNe to calculate the effective number of breeding adults (N_b) for each of nine years and N_e . Estimates of demographic neighborhood size was based on Wright's relationship $NS_{\text{demo}} = 4\pi\sigma^2D$ and genetic neighborhood size (NS_{gen}) was estimated using Rousset's method based on correlations between inter-individual genetic distance and Euclidean distance. By accounting for age- and sex-specific dispersal, fecundity and mortality, we estimate that the ratio N_b/N_e was 0.39 and estimated N_e/N was 0.29. Estimated demographic and genetic neighborhood size were comparable (139 vs 98, respectively). Wahlund variance affected N_e to a greater degree than N_b .

95^{E}: The source and colonization history of Isle Royale's rediscovered martens (*Martes americana*)**

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Home to the longest running predator-prey study on record, Isle Royale National Park holds a unique place in ecological history. Beyond the dynamics of wolves and moose, however, remarkably little is known about the ecology and evolutionary history of the island's other mammalian fauna. For example, anthropogenic disturbances at the turn of the 20th century were presumed to have extirpated many carnivores from the island, including American martens (*Martes americana*); yet, a small and potentially unique marten population was recently rediscovered. To identify the source and colonization history of this population, we genotyped martens from Isle Royale and potential source populations in neighboring Wisconsin, Minnesota, Michigan, and Ontario using a suite of polymorphic microsatellite markers. We then employed Bayesian cluster analyses to characterize the genetic structure of martens in the Lake Superior basin, and quantified genetic distances between putative populations. To estimate phylogenetic relationships, we then sequenced mitochondrial genes from a subset of individuals within each identified

cluster and constructed neighbor-joining trees. Finally, we coupled phylogenetic measures with nuclear divergence estimates to develop the first evolutionarily significant units for martens in the Lake Superior basin, and employed coalescent simulations to estimate the colonization history of Isle Royale martens. Our analyses present the first phylogenetic assessment of Isle Royale martens and provide unique insights on the evolutionary history of native Isle Royale mammals.

96^E: Processes of diversification in sigmodontine rodents: the genus *Akodon* as a first approximation

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Two main hypotheses proposed to explain the differences in richness among clades are the clade-age hypothesis (i.e. species-rich clades are older) and the diversification-rate hypothesis (i.e. species-rich clades diversify more rapidly). The latter is prevalent in lineages encountering novel and/or underutilized resources (ecological opportunity), as has been hypothesized for the diversification of South American sigmodontine rodents. Using alternative methods of analyses (ARC and rase), calibrated molecular phylogenies and geographic ranges of species from the genus *Akodon* - one of the most diverse clades within Sigmodontinae - were used to test previous hypotheses of diversification for the genus. Although there is no clear signal for a unique pattern of speciation in *Akodon*, sympatric speciation can be considered rare. In addition, linear distance and range asymmetry analyses suggest that speciation in parapatry was the most frequent pattern. Estimates of ancestral distribution revealed that the origin of the group ~3.4 Mya can be centered between central Paraguay and northern Argentina, in contrast to long accepted hypotheses. The split between the Andean and the southeastern Brazilian groups happened early in the diversification of the genus, and consequent diversification and dispersal occurred longitudinally with a second Argentinian colonization happening ~1 Mya after the first. As with most groups, the evolutionary history of *Akodon* cannot be attributed to a single process, but instead to the combined effect of ecological and historical processes.

97^E: The utility of zonadhesin in examining a potential reproductive isolation mechanism in rodents

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Species-specificity in mammals is crucial to maintain reproductive isolation boundaries and prevent interbreeding and dilution of the gene pool. It has been hypothesized that gamete recognition is one of the first steps in establishing post-mating isolation mechanisms. Gamete recognition is a known pre-zygotic isolation mechanism in certain invertebrates, but its significance in vertebrates, such as mammals, is not well established. One of the proteins crucial in this process is zonadhesin (ZAN), a rapidly evolving, sperm protein that mediates species-specific adhesion to the egg's zona pellucida. It has been suggested that the evolution of ZAN correlates with reproductive isolation in mammals and is an adaptive gene found only in certain internally fertilizing mammals. Substantial intra-species differences are known to exist in human and pig ZAN and might be under strong selective pressures. Thus, transcript evolution of those transcripts of the gene might contribute to the speciation process. Therefore, by examining alternative transcripts and the protein-coding sequence of ZAN both between and within species, both closely and distantly related, we can determine the level of variability and conservation of the gene and further establish if the subsequent protein might be acting as a reproductive isolation barrier. To address this question, we examined genetic variability in multiple rodent species including *Peromyscus*, *Ictidomys*, *Dipodomys*, and *Sigmodon* in order to assess sequence variation across a hyper-variable region of the gene.

98: Converting fossil information into Bayesian priors for calibrating molecular clock analyses in rodents

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Genetic data are often analyzed with the goal of inferring evolutionary divergence times, but these analyses require calibration, usually based on fossils. Using the oldest known fossil in a clade (the “hard minimum”) underestimates ages, because the divergence occurred before it shows up in the fossil record. When using node-based calibration, a prior shape that allows for an earlier divergence than the hard minimum should be used. Unfortunately appropriate shapes of these priors are difficult to determine and often arbitrary. We compare two approaches to generating these prior shapes. “Phylogenetic bracketing” methods create priors based on the “soft maximum”, focusing on information in the fossil record that is potentially older than the node in question. In contrast, the recently developed penultimate gap (PenG) and ghost lineage length (GLin) methods create a well-defined calibrating prior shape by applying information gleaned from the fossil record that is more recent than the node in question. We evaluate how these different approaches perform in simulations and how they estimate the radiation of caviomorphs and murid rodents. The methods yield similar results overall, but we encourage researchers to look beyond the soft maximum, and pay more attention to the median value on their calibrating priors and how their parameters might be creating a “soft minimum” that is having an outsized influence on their results.

99: Phylogenomics of the *Tamias quadrivittatus* group.

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The degree to which species boundaries are subject to introgression has received increasing attention over the last two decades. Here, we examine introgression among six species in the *Tamias quadrivittatus* group by comparing 51 mitochondrial DNA genomes with exon-capture data from the nuclear genomes of the same individuals. Coalescent simulations have demonstrated that the degree of cytonuclear incongruence in this group exceeds that which can be attributed to incomplete lineage sorting, and one species in particular (*T. dorsalis*) exhibits fixation on introgressed mtDNA wherever it contacts other members of the group. Furthermore, signatures of selection were detected in the introgressed mtDNA genomes. Phylogenetic analyses of the nuclear data provide a well-resolved hypothesis of relationships and each species showed little evidence of introgression in the nuclear genomes.

100^{E,HTA}: Unexpected genetic composition of a reintroduced carnivore population

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In an attempt to maximize genetic diversity, species reintroductions often target numerous source groups and occur over multiple years. However, the serial introduction of individuals from disparate locations can create unique patterns of genetic structure, with potential implications for demography and population connectivity. To investigate the genetic structure and connectedness of contemporary populations of serially reintroduced American marten (*Martes americana*) in Wisconsin, we sampled both the source populations of Colorado, Minnesota, and Ontario, and the two reintroduction sites within the state. In a relatively small area (~7000 km²), we detected four distinct genetic clusters, partitioned according to the original source groups. Source groups exhibited differing degrees of success, with Minnesota and Ontario signatures persisting and Colorado disappearing from the landscape. One of the genetic clusters had an unknown source not attributable to the reintroduced populations, potentially arising from an early reintroduction attempt or the persistence of a cryptic native population of martens. Limited admixture between clusters was detected, yet we found evidence for the occasional dispersal of martens from one site to the other. Our results suggest that reintroductions can create strong and novel patterns of genetic structure – unseen for this species elsewhere or other vertebrates in the region – across small spatial scales.

101^{E,HTA}: Old marker, new tricks: sequencing *cytochrome-b* to investigate metapopulations dynamics of kangaroo rats in Texas

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Due to its sequence variation, lack of recombination, general synteny and remarkable ease of amplification, the mitochondrial *cytochrome-b* gene has been evaluated to tackle an assortment of phylogenetic questions in a variety of organisms. Here, we present another use of this marker: to examine metapopulation subtleties across the current range of the Texas endemic kangaroo rat, *Dipodomys elator* (family Heteromyidae). In 2015 and 2016, we live-trapped *D. elator* along county roads and on private and state lands in north-central Texas. We non-invasively sampled DNA from these rats by pulling whiskers. From these we amplified *cytochrome-b*, sequenced and analyzed the PCR products to determine any genetic differentiation among localities. To add a temporal layer to our analysis, we incorporated 30-year-old *D. elator* toe snips from museum specimens. We hypothesize that, based on geography and initial analysis via MEGA, there could be at least two distinct subpopulations, which form factions in the west (Cottle, Childress, and Hardeman Counties) and in the east (Wilbarger and Wichita Counties). *D. elator* is rare and threatened in Texas, and its candidacy for federal listing under the Endangered Species Act is being evaluated. These preliminary results provide key data for future conservation efforts of *D. elator* and give us a valuable starting point for further population genomic analyses.

102^{HTA}: Is the Brazilian free-tailed bat (*Tadarida brasiliensis*) a ring species?

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The Brazilian free-tailed bat (*Tadarida brasiliensis*) is a widespread and highly mobile bat that is broadly distributed throughout North, Central, and South America and in the Caribbean. A recent genetic study of *T. brasiliensis* in the Bahamas documented a major break in population structure between individuals sampled on the Little Bahama Bank (LBB; Abaco and Grand Bahama) and the Great Bahama Bank (GBB; Long Island and Eleuthera). These two banks are separated by the Northwest and Northeast Providence Channels. This break was surprising given their high dispersal capabilities, as the shortest distance across the channel between Abaco and Eleuthera is only about 60 km. This study expands the geographic sampling of *Tadarida* to investigate the phylogeographic structure of this species and trace the colonization of the LBB and GBB through the sequencing of *Cytochrome b* and *Rag2* loci. *Cytochrome b* revealed two strongly supported groups: one comprising individuals from North and Central America as well as the LBB individuals, and a second group comprising South American and Antillean populations along with the GBB individuals. Only one individual from the LBB was intermixed with the second clade containing GBB. *Rag2* was relatively uninformative for any structure. We present scenarios for the colonization of *T. brasiliensis* throughout the Caribbean and mainland and discuss whether *T. brasiliensis* meets the definition of a ring species based on our findings.

103^{HTA}: Comparing ecology and phylogeographic history in Asian pikas

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The phylogeographic history, species limits, and evolutionary relationships of mammals in Central Asia would provide a foundation for detailed ecological, physiological and evolutionary research, yet these key studies have been stymied for most of this fauna due to inadequate geographic sampling. Taxonomy and

evolutionary history of pikas (genus *Ochotona*) in Central Asia, in particular, have been especially problematic. We focus on 4 species that occur in Mongolia, *O. pallasii*, *O. hyperborea*, *O. alpina*, and *O. dauurica*, and that have distinctive behaviors and habitat preferences. Using a comparative phylogeographic approach, we address the following questions: 1) How does the contemporary distribution of each species reflect geologic and demographic history? 2) Have differences in ecology among species influenced demography or distributions? and 3) Do the demographic histories of Mongolian pikas expand our understanding of the evolution of the genus *Ochotona*? Our study reveals that *O. pallasii* reflects a largely panmictic population across its range resulting from probable long-term persistence across this region of Central Asia. This history does not appear to be shared by the 3 other species of pika in Mongolia, whose geographically structured populations are consistent with isolation and subsequent expansion. Distinctive biogeographic histories highlight differential response of close relatives to changing environmental conditions.

104^{E,HTA}: Investigating population structure and barriers to gene flow in the American badger of British Columbia

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Peripheral populations are often characterized by small population size, habitat fragmentation, and low genetic diversity, with many at risk of extirpation. Such threats can be even more pronounced in human-modified landscapes. The western American badger (*Taxidea taxus jeffersonii*) is an endangered mammal inhabiting the southern interior of British Columbia. Human development and forest encroachment have reduced badger habitat, leading to habitat fragmentation and population isolation. Road mortalities continue to hamper badger recovery by reducing population size and hindering effective gene flow. We used haplotypic data from the mitochondrial DNA control region and genotypic data at 14 nuclear microsatellite loci collected for 287 samples from across BC and neighboring regions in Canada and the United States of America to study phylogeographic structure, population subdivision, and barriers to gene flow in western American badger populations. Phylogeographic analyses suggest historical connectivity between western BC and Washington state, with a large proportion of shared haplotypes in this region. Conversely, genotype analyses suggest isolation within western BC and subdivision into two distinct units, with the transition zone corresponding to a major highway. Using resistance surface modeling, we identified landscape features acting as barriers to gene flow on both local and broad scales. Mitigating the impact of these barriers as well as increasing connectivity between populations in BC and with populations in the USA will be essential for conserving genetic diversity.

105^E: Body condition, behavior, and genetic comparisons among coyotes along an urban-rural gradient

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Urban conditions such as habitat fragmentation, development, and food availability may cause some species to alter their behavior to exploit the landscape. However, although predators may react differently than prey due to life history strategies and interactions with people, research on behavioral and genetic differences of predators in urban ecosystems is lacking. Our objective was to determine relationships between urbanization, behavior, and genetics. First, we hypothesized that coyotes (*Canis latrans*) will exhibit different individual behaviors. Secondly, that there will be different frequencies of behaviors and genetics based on environment type. To test these hypotheses, we quantified coyote behavior in an extreme urban-suburban gradient and determined if there were allelic differences by population in dog behavioral gene regions. Behavioral data, such as the actions of a coyote during capture, processing, and manipulation test, were recorded for over 80 Chicago Metropolitan Area coyotes during 2014-2017. For each coyote, observers independently assigned a 1-7 score for bold and aggression, and eight gene regions were sequenced for a total of 20 single nucleotide polymorphisms and two microsatellites. We

found differences between dog and coyote sequences, as well as behavioral differences between coyotes and habitats. To better manage coyote populations in cities, it is important to understand relationships between urbanization and predator behavior. Understanding the mechanisms, both environmental and genetic, behind boldness and aggression is crucial towards mitigating human-coyote conflicts.

106^{HTA}: Do striped skunks utilize different defense strategies based on type of predatory threat?

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Prey species defend themselves from predators with behavioral and morphological defenses and occasionally utilize varied defenses against different predators. These species must assess risk and weigh the costs and benefits between mutually exclusive behaviors such as defense versus foraging to maximize survival. Striped skunks (*Mephitis mephitis*) possess a slew of antipredator behaviors, and have bright white stripes that warn predators of the danger of their noxious anal gland secretions. Evidence suggests skunk defenses are effective at deterring terrestrial predators, but how skunks assess the risk posed by different predator types has not been examined empirically. Skunks were presented with audio playbacks of coyote and great horned owl predators (the primary terrestrial and aerial predators of skunks, respectively), as well as the diurnal peregrine falcon and white noise as control. Behavioral responses to each were measured to investigate potentially contrasting antipredator defenses. Preliminary results suggest that skunks flee more frequently in response to owl than coyote vocalizations, and spend a longer time foraging when exposed to coyote than owl vocalizations. Few studies have explored aposematic behavior and risk assessment in mammals or antipredator behaviors in striped skunks specifically, and no study has measured striped skunk behaviors in response to aerial predators. This research will help elucidate how organisms adapt to differing predatory threats, especially when one defense is not effective against all major predators encountered.

107: Pen trial of estrogen-induced egg aversion in raccoons (*Procyon lotor*)

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Aversive conditioning is a promising but unproven non-lethal approach to reducing mammalian predation on the eggs of ground-nesting birds, terrapins, and sea turtles. We tested the efficacy of oral estrogen (17 alpha-ethinyl estradiol) deployed in chicken eggs as an aversive agent for raccoons (*Procyon lotor*). Nine treatment raccoons received 6 treated eggs (injected with 10 mg of estrogen) every other day for 14 days, followed by a combination of 2 treated and 4 untreated eggs every other day for 14 days. Nine control animals received 6 untreated eggs on the same schedule. None of the 9 treatment animals showed signs of illness immediately following estrogen ingestion. Nevertheless, all became averse and reduced egg consumption by 50% after 1-8 feedings. The control animals ate 99.7% of all eggs presented and never reduced egg consumption. The aversion was neither absolute (1 treatment animal ate 91.7% of the 84 eggs presented) nor persistent (all of the animals later "sampled"). Raccoons could not distinguish between treated and untreated eggs. We observed no changes in behavior and no detrimental health effects, except for the death of 1 pregnant female, which was almost certainly a consequence of the estrogen. These results suggest that a full-scale field trial of estrogen is likely to be productive under circumstances where all of the target population is subject to treatment.

108: Evaluating nest site selection of southern flying squirrels in west-central Illinois

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Southern flying squirrels (SFS; *Glaucomys volans*) nest in natural cavities in snags and hardwoods trees in mature, undisturbed forests. Forest fragmentation across Midwestern landscapes may limit the availability of nesting trees relative to other regions characterized by contiguous forested habitat, though has not been extensively studied. Our study objective was to evaluate nest tree use of SFS in west-central Illinois. From October 2014 to April 2016, we used radio telemetry to track SFS to 109 nest tree

sites (83 live trees, 26 snags). Our results indicated that diurnal nest trees were characterized by significantly more ($\chi^2_1 = 4.41, P \leq 0.02$) live, larger diameter oak trees than random locations. We documented greater ($\chi^2_1 \geq 3.97, P \leq 0.04$) use of live, intact canopy trees by female squirrels whereas nest tree use by male squirrels was characterized by fewer numbers of tree species and greater use of snags in more advanced stages of decay. Selection for live trees by female SFS may be attributed to increased energetic demands while rearing young. Further, SFS used a variety of forest types for nesting, including riparian and floodplain forests. Flexibility in nest site selection by SFS may be related to variation in forest patch sizes that characterize fragmented Midwestern landscapes. Thus, future research quantifying potential effects of habitat fragmentation on SFS nesting ecology is warranted.

109^{E,HTA}: Island biogeography of small mammals in Ozark glades while accounting for imperfect detection

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Island Biogeography Theory (IBT) explains and quantifies large-scale ecological patterns among islands and isolated habitat patches. IBT predicts the number of species per habitat patch differs as a function of area, isolation, and complexity as a result of local colonization and extinction. Estimates of species richness are central for application of IBT, but differences in detectability of species can lead to bias in empirical data sets. Hierarchical community models correct for imperfect detection by leveraging information from across the community to estimate species-specific occupancy and detection probabilities. Using the fragmented Ozark glades as our model system, we constructed a hierarchical community model to 1) estimate site-level and regional species richness while correcting for detection error, and 2) determine environmental covariates driving species-specific occupancy. Based on IBT, we predict site-level species richness will be a function of area and isolation. Additionally, we predict that the perimeter/area ratio and total vegetation cover will affect species-specific occupancy. We sampled 16 glades in southwest Missouri from May–July 2016 and quantified mammal community structure within the glade network. The detected species pool included 8 species: *Peromyscus attwateri*, *P. leucopus*, *P. maniculatus*, *Reithrodontomys fulvescens*, *Sigmodon hispidus*, *Neotoma floridana*, *Tamias striatus*, and *Sylvilagus floridanus*. Results from the model yielded a regional species estimate of 8.5 species. A multiple regression analysis yielded significant effects of perimeter/area ratio on detection-error corrected richness estimates.

110^{E,HTA}: Restoration of native baboon-plant mutualisms following eradication of the invasive prickly pear cactus (*Opuntia stricta*)

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Frugivorous primates play important roles as seed dispersers around the world, but these interactions can be to the detriment of native plants if they begin to prefer the fruits of non-native species. We assessed whether olive baboons (*Papio anubis*) select for the fruits of an invasive prickly pear cactus (*Opuntia stricta*) on the Laikipia Plateau in Kenya. By eating the fruits of *O. stricta*, baboons facilitate the establishment and spread of the cactus. We collected scats from baboon roosts, then identified, counted, and weighed the seeds in each scat. We conducted vegetation surveys of the baboon roosts and quantified fruit availability. Using a two-sample t-test, we compared the cactus fruit availability, and the proportion of individual scats' masses that were *O. stricta* seeds, between 2014 and 2016. Fruit availability decreased substantially between 2014 and 2016 ($p < 0.014$), however, the proportion of *O. stricta* seeds in the scats did not decrease significantly ($p=0.07$). Following such a marked decline in *O. stricta* fruits in 2016, we expected the proportion of *O. stricta* seeds in the baboons' scats to decrease proportionately. Our data, however, suggest that baboons appear to be consuming a disproportionate amount of *O. stricta* fruits relative to availability. This has important implications for our understanding of mutualisms between native mammals and introduced plants, as well as management of *O. stricta* around the world.

111: Source-sink dynamics and sexual dimorphism in Alaskan and Canadian North American wolverines (*Gulo gulo luscus*)

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The circumboreal wolverine (*Gulo gulo*) is ideal for studying responses to environmental perturbation in the North due to a history of glacial refugia and post-glacial recolonization, as well as more recent impacts of anthropomorphic harvest and climate and habitat change. Because genetic variation provides clues to distributional changes, our research uses microsatellite DNA variation to identify source and sink populations to inform conservation strategies for wolverines as well as explore potential barriers to gene flow in the future under changing conditions. Male and female dispersal patterns are compared using 20 microsatellite loci across 360 sampled individuals from approximately 270,000 square kilometers of Canadian boreal forest and 80,000 square kilometers of Alaskan tundra. With a focus on source-sink dynamics and sexual dimorphism in dispersal, trap susceptibility, and establishment in new areas we examine recent (1995-2015) wolverines of the study areas. Cranial morphology is also examined to determine if morphology reflects genetic differences in the sampling regions above, as well as in larger sampling of North America to explore subpopulation differentiation, ecomorphological adaptation to food resources, sexual dimorphism, and population health through craniodental pathologies.

112: Phylogeographic assessment of the Heermann's kangaroo rat (*Dipodomys heermanni*)

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Heermann's kangaroo rat (*Dipodomys heermanni*; Rodentia: Heteromyidae) is endemic to California and primarily found in the dry, gravelly grassland and open chaparral habitats of the San Joaquin Valley. Current taxonomy (based on morphology and habitat use) recognizes nine subspecies within this kangaroo rat. Current management practices of *D. heermanni* are based on these historical classifications; however, these classifications may not accurately reflect the unique lineages in need of conservation. This study aims to assess the phylogeography of *D. heermanni* across its geographic range. In doing so, we will gain insight into the diversification of *D. heermanni*, determine what, if any, barriers to gene flow exist among unique lineages, revise subspecific taxonomy (if necessary), create predictive models for the geographic ranges of each unique evolutionary unit, and make recommendations for conservation and management. We present a preliminary mitochondrial dataset that indicate recognition of all nine subspecies is likely unwarranted. Further molecular work will add additional markers and samples, including analysis of museum specimens in a dedicated ancient laboratory. Morphological analyses of 12 cranial measurements from museum specimens from across the species range representing all subspecies also will be performed. Lastly, distribution records from GBIF and VertNet will be analyzed using MaxEnt to predictively model the geographic range of *D. heermanni*.

113^{E,HTA}: Crowd sourcing, citizen scientists, and collecting nontraditional data: the search for the eastern spotted skunk

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The eastern spotted skunk (*Spilogale putorius*) is a diminutive mesocarnivore distributed in the southeastern and great plains regions of the United States. While historically common, the species has undergone a drastic, range-wide decline, the reason for which is currently unknown. Efforts to learn more about this skunk have been hampered by incomplete knowledge of the species, including full range and distribution, due to a lack of prior study. A search for historical museum records from Texas yielded 196 records, yet only 11 since 2000. To create species distribution models, unique methods were required to find verifiable presence data. To wit, we initiated non-traditional methods such as requesting observations from academic, biological, and wildlife rehab groups, distributing "wanted posters" to citizen scientist groups, and collecting additional historical observations by searching the "brag a little" section of early trapping periodicals. Finally, follow up trail camera surveys, led by citizen scientists, were initiated at locations of verified or suspected skunk observations. The result of all efforts has been 89 verified observations of spotted skunks in 24 counties since 2003. The effort to locate additional historical

observations resulted in presence-only data in 27 counties from 1906 through 1918. In total, efforts have resulted in an additional 210 observations from 37 counties. Our results confirm that utilizing nontraditional methods can be an important tool when searching for rare species.

114^E: Cryptic variation of two sympatric *Akodon* species in Interior Atlantic Forest remnants of eastern Paraguay

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Akodon montensis and *A. paranaensis* are two abundant sympatric species in forest remnants in the Interior Atlantic Forest of eastern Paraguay. The original description of *A. paranaensis* did not include comparison with *A. montensis*. These two species are very difficult to identify in the field, based on external features. Using the *cyt-b* gene we were able to discriminate between these taxa. We implemented geometric morphometrics on skulls and mandibles in order to compare interspecific morphological differences. We used principal component analysis (PCA) to identify the portion of the skull with the most variation. Discriminant function analysis (DFA), followed by permutation test was implemented to test shape differences between species. Based on preliminary results of multispecies PCA we found most of the variation in the rostrum. DFA showed considerable differences between species and permutation test showed significant differences between species (skull $\alpha \leq 0.0001$ and mandible $\alpha \leq 0.0001$). Our DFA showed most of the variation in the anterior portion of the rostrum, the zygomatic arches, and molars. Proper discrimination between these species is valuable for understanding the ecological role of these species in these forest remnants. Given their abundances, identifying these species will also allow for improved biodiversity metrics for conservation and management efforts. Improved understanding of these species is valuable for long term mark recapture studies, which are currently unreliable in these forests.

115^{E,HTA}: Investigating elevational gradients as a predictor for host-parasite relationships

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Information regarding the factors influencing parasitism of mammals remains limited, especially how environments, land use, disturbance, and presence of hosts jointly regulate parasite loads. Collection of parasites is often an afterthought with little emphasis on testing ecological patterns or assessing factors likely responsible for facilitating parasite success. In this study, we assess how elevation alters parasite assemblages, while controlling for change in structure of the mammal community. We trapped small mammals along an elevational gradient of a sky island in the Great Basin across eight sites ranging from 1,316 to 3,382 meters. We captured and vouchered 618 individuals using holistic approaches. From these, we screened 565 for ectoparasites and 534 for endoparasites. Overall, our analyses showed a weak ($R^2 = 0.396$, $P = 0.09$) negative trend in parasite detection with increasing elevation. However, we detected a more complex pattern for ectoparasites indicating a significant relationship of fleas occurring at higher elevations ($P < 0.005$) with mites showing an inverse pattern ($P < 0.001$) suggesting that fleas and mites may either interact with elevation or perhaps each other. Conversely, endoparasites and elevation appear to be unrelated, suggesting other factors, perhaps riparian habitat availability, could be regulating endoparasites. Next steps include an investigation of how habitat characteristics and particular mammal assemblages are related to parasite assemblages.

116^E: Testing ecogeographic variation in *Microtus* – signals of insular gigantism

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Availability of resources influences the evolution and ecology of organisms leading to predictable ecogeographic patterns. Body size is often strongly influenced leading to reasonable expectations of patterns exhibiting either insular gigantism or dwarfism. In this study, we use morphological analyses to test alternative hypotheses of these patterns of ecogeographic variation in island-associated mammals. More specifically, we test for skull variation among 15 populations of voles including *Microtus breweri* and

three subspecies of *M. pennsylvanicus* that occupy both islands and the mainland of the Northeastern Coastal Zone ecoregion in the northeastern United States. Recent phylogenetic analyses of this clade indicate there is a lack of genetic differences among these species and subspecies and at least one subspecies may now be extinct. However, initial analyses of skull variation indicate that island-associated populations are larger when compared to mainland populations, suggestive of insular gigantism. Next steps of this study are to evaluate how localized environments and isolation interact to contribute to ecophysical allopatry and test how genetic mechanisms influence phenotypic patterns observed in this system.

117^F: Red fox (*Vulpes vulpes*) colonization of Wisconsin

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In the contiguous United States, red foxes (*Vulpes vulpes*) are believed to be native only in mountainous regions (Rocky, Cascade, Sierra Nevada, and Appalachian mountains), the Great Basin, and the South Atlantic states. Fox colonization in the Great Lakes Region is unknown and it is unclear whether wild foxes naturally expanded from Canada following glacial retreats, or if farmed foxes colonized the landscape after the peak of fur-farming in the 1930s. To determine origin of red foxes regionally, we collected tissue samples of foxes from three groups in Wisconsin: 1) contemporary wild foxes from fur trappers; 2) pre-1930 wild foxes from museum collections and; 3) farmed foxes from contemporary fur farms. By assigning each fox to a haplotype of a known origin and reconstructing a network of North American foxes to include Wisconsin samples, we will identify relationships between wild, historical, and farmed foxes, and determine the role of natural versus human-assisted colonization. We hypothesize that pre-1930 wild foxes from Wisconsin will exhibit haplotypes indicative of natural range expansion from Canada, but that contemporary wild fox haplotypes will align with farmed fox origins. Determining the origin of recolonizing carnivores, in general, and foxes, in particular, will not only reveal the pattern of genetic and taxonomic diversity in altered landscapes, but also guide regional management efforts.

118^{HTA}: Spatial patterns of species richness and functional diversity of Appalachian mammals: implications for conservation

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Functional diversity is a measure of the number of functionally disparate species within an area and can yield alternative perspectives when compared to species richness and may improve the understanding of connections between biodiversity and ecosystem function. Conservation planning can benefit from an enhanced understanding of the factors that influence these potentially complex relationships. In this study we apply Species Distribution Modeling (SDM) to evaluate spatial patterns of species richness and functional diversity of mammals occupying the Appalachian Ecoregion. Using predicted distributions for at least 60 species, we apply spatial regression techniques to assess the influence of environmental, biological, and anthropogenic factors on both measures of diversity. As expected, patterns differ for each measure with richness focused in the southern Appalachians that differs from at least two discrete functionally important regions. However, perhaps more surprising is that species richness was most affected at local scales, whereas functional diversity was best explained at the regional scale. Furthermore, we detect a mismatch between actively protected areas and areas important for both biodiversity measures. Consequently, conservation programs may need to revisit priorities to optimally capture both functional diversity and species richness to maximize ecological and evolutionary interactions that are expected to shift in the near future.

119: Food habits of coyotes (*Canis latrans*) in a southern California urban landscape

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Increased availability of human-related food sources is an often cited but poorly understood explanation for attracting and sustaining wildlife populations in urban environments. Southern California is one of the largest metropolitan areas in the United States, yet populations of coyotes (*Canis latrans*) can still persist here. My goal is to describe the diet of coyotes living in the urban areas of Los Angeles and Ventura counties. Coyotes should be successful in urban environments because of their ability to utilize human-related resources. I will use standard fecal analysis techniques that examine samples for teeth and fur belonging to prey. Preliminary analysis of Los Angeles coyote scats show a high proportion of anthropogenic subsidies in the diet (50% of scats), including trash (19%), ornamental plants (17%), and pet food (5%). Preliminary analysis of Thousand Oaks scats also show a high proportion of anthropogenic subsidies (47% of scats), with a large portion of scats containing ornamental plants (36%). Although the sample sizes vary between study sites, it appears anthropogenic subsidies are still an important food source for suburban coyotes. Identifying the diet of urban coyotes will help us understand how these carnivores persist in human-dominated landscapes. Wildlife biologists will use our results to identify areas where coyotes are more likely to consume human-related resources and provide stronger guidance on how to reduce human-coyote conflict.

120^E: Ontogenetic changes in the long bone microstructure in the nine-banded armadillo (*Dasybus novemcinctus*)

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Analysis of ontogenetic changes in long bone microstructure aid in vertebrate life history reconstructions. Specifically, osteohistological examination of common fauna can be used to infer growth strategies of biologically uncommon, threatened, or extinct vertebrates. Although armadillo biology has been studied extensively, work on growth history is limited. Here we describe long bone microstructure in tibiae and femora of an ontogenetic series of nine-banded armadillos (*Dasybus novemcinctus*) to elucidate patterns of bone growth. The primary cortex of the smallest individual is composed of primary woven bone of fibrolamellar organization. The primary tissue is then remodeled extensively and larger specimens lack primary tissue and show signs of extensive cortical drift including the presence of compact coarse cancellous bone in the cortex and erosion on the periosteal and endosteal surfaces. Larger specimens also have an outer circumferential layer (OCL) of avascular lamellar bone. The OCL forms in tibiae before femora, indicating tibial growth rates begin decreasing earlier than femoral in *D. novemcinctus*. Additionally, intratendinous metaplastic tissue is found in the tibiae and femora. Intratendinous metaplastic tissue is typically associated with tendinous attachments, however, in the tibia of *D. novemcinctus* portions metaplastic tissue are found in regions unassociated with tendinous attachments. Growth trends in common fauna like the nine-banded armadillo can be used as a foundation for understanding life histories of related, but uncommon or extinct, species of cingulates.

121^E: Spatial variation in sexual-size dimorphism of the American black bear in eastern North America

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Spatial patterns of sexual-size dimorphism for the American black bear (*Ursus americanus*) from 12 localities in eastern North America were investigated. Forty-four measurements from 371 (187 males and 184 females) adult specimens (≥ 4.5 years old) were recorded using digital calipers. Males were larger than females for all characters except braincase width and length of m3 for specimens from Virginia. Averages of mean values for the degree of sexual-size dimorphism across localities ranged from 4.1-22.5% with most being from 6.6-17.0%. For 39 of the 44 characters (88.8%), there was no statistically-significant difference in degree of sexual-size dimorphism across localities, indicating it was

approximately the same at each locality. This was supported further by results of principal component analysis. Results followed a similar pattern reported for *U. americanus* in western North America that supports a growing generalization for medium-sized and large-sized terrestrial carnivores of a uniform pattern of sexual-size variation across geographic space; this is likely due to bioenergetic factors associated with growth and reproduction with selective pressure responsible for size dimorphism acting uniformly throughout the range of the species.

122: Fleas from *Peromyscus* in the collection of the Denver Museum of Nature & Science

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Parasites of a particular host genus may be overlooked on initial examination of host species although many museum collections routinely include both hosts and their parasites. Focusing on ectoparasites, we examined 188 fleas from 154 *Peromyscus maniculatus*, 20 *P. truei* and 4 *P. boylii* in the collections of the Denver Museum of Nature & Science (DMNS). Hosts were collected from Colorado (14 counties), Wyoming and Idaho (one county each) between 1991 and 2015. Fleas represented 3 families; Ceratophyllidae (155 fleas), Hystrichopsyllidae (24 fleas), and Leptopsyllidae (9 fleas). The ceratophyllid *Aetheca wagneri* (Baker 1904), represented 62.8% (118/188) of the fleas collected from *Peromyscus* spp. Female *P. maniculatus* infested with *A. wagneri* exhibited a flea mean intensity (MI) of 3.63 in contrast to males, which had a flea MI of 2.07. Male *P. maniculatus* exhibited a much greater diversity of fleas (17 species) than females (9 species). These results are most likely the result of the males' wide-ranging while females remain closer to nesting areas. Less common fleas collected included *Malareus telchinus*, *Opisodasys keeni*, *Orchopeas leucopus*, *Catallagia decipiens*, and *Callistopsylla terinus terinus*, associated with small mammals and often shared with *Peromyscus* spp. We did not find any range extensions or new host records. <http://arctos.database.museum>.

123^{E,HTA}: Sublethal effects of predators on prey behavior and stress physiology within individuals and populations

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Predator-prey relationships represent one of the most important interactions occurring within ecosystems, potentially affecting community structure and dynamics. Primarily, in these relationships ecologists focus on the direct impacts predators have on prey density through consumption. However, this only represents a portion of the total effect that predators have on prey. Another is sublethal—a result of a prey's anti-predator responses to risk. These responses to increased predation risk can cause a decline in body condition, reproduction, and foraging behavior, leading to changes in population dynamics and, ultimately, community structure. Here we examine how sublethal mechanisms, both acute and chronic, can alter dusky-footed woodrat (*Neotoma fuscipes*) behavior, stress physiology, and fitness in Southern California. By using giving-up densities and enzyme-linked immunosorbent assay, we concurrently examine the behavioral and physiological impacts of increased perception of predation risk. Risk was manipulated using native predator urine. Current results indicate no significant changes in fitness, foraging, and stress hormones under long-term stress, suggesting that a chronic stress response did not evolve within this species. This likely represents one of the few empirical mammalian studies demonstrating that response to chronic stress may be adaptive under specific life history traits, evolving to maximize fitness under chronic stressors. Lacking this insight into the impacts that sublethal effects have on predator-prey relationships may limit the success of future conservation and management strategies.

124^{E,HTA}: Individual specialization and multiple pathways to dietary generalism in a small mammal community

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In recent years our understanding of niche breadth has shifted from viewing a species niche as uniform across conspecifics to recognizing the variation and plasticity in resource use by individuals. "Population-level" generalist species can be comprised either of individuals whose resource use mirrors that of the population, or individuals who use a narrow subset of those resources. We sought to quantify resource use by individuals of a dietary generalist (fringe-tailed gerbil; *Gerbilliscus robustus*) in a savanna small mammal community. We asked whether individuals consumed a diversity of foods at all times throughout the year or switched their diet to reflect temporal shifts in availability. We compared *G. robustus* to a dietary specialist (Hinde's bush rat; *Aethomys hindei*) to investigate these questions. Through blood plasma carbon and nitrogen isotopes, we quantified individual-level diet breadth from individuals sampled repeatedly March 2015 – September 2016. The *G. robustus* population was comprised of both individual generalists and individual specialists. Surprisingly, the *A. hindei* population also exhibited diet generalism by individuals, although most were specialists. While generalist individuals of *G. robustus* tended to consistently eat a mixed diet, the few individuals of *A. hindei* that displayed dietary generalism demonstrated diet switching. Different dietary strategies between individuals and populations could be a mechanism to reduce competition and cope with environmental stressors in this ecosystem characterized by rainfall-driven resource pulses.

125^E: Using stable isotope analysis to understand competitive interactions between sympatric pocket mice, historically and today

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Co-occurrence models are increasingly being used to highlight interspecific interactions within a community. Sympatric species that co-occur less frequently than expected by chance may be competing, which can lead to niche partitioning. Niche partitioning can be independently assessed through the analysis of carbon and nitrogen isotopes. Carbon and nitrogen values from tissues provide information about an individual's habitat, trophic level, and diet composition. Co-occurrence models of *Perognathus mollipilosus* and *Perognathus longimembris* in the Toiyabe mountain range indicate that historically, these two species were not significantly segregated. Yet today, in the same system, they are significantly segregated. To evaluate a potential change through time in the interspecific interactions between these species, we analyzed $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values from their hair, historically and today. We found that historically, there is minimal overlap in the isotopic niche space for these two species, indicating that resources may have been partitioned. Analysis of modern specimens suggests increased overlap in resource use and an overall contraction in the isotopic niche space of *P. mollipilosus*. These results may reflect a previously demonstrated upslope shift of *P. mollipilosus* out of the range of *P. longimembris*, and thus reduction in aggressive behavior towards *P. longimembris* by the larger *P. mollipilosus*.

126^E: The importance of residential swimming pools as an urban water source for bats

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Habitat loss is the primary cause of declining bat populations globally and urbanization represents a major contributing factor. Yet, studies have indicated that urban parks, green belts and tree-lined suburbia can support a diverse and abundant bat community. These areas must, therefore, be providing suitable and readily available resources, such as water. However, in hotter environments many natural water sources are ephemeral. Thus, we propose that bats may be relying on residential swimming pools as a water source. To explore this hypothesis, we used camcorders with night vision capabilities and bat acoustic detectors to record bat activity at a pond in a local park along with four nearby swimming pools in Fort Worth, Texas. Video and acoustic data was then analyzed to determine if bats were using swimming pools and how frequently. Our study revealed that bats drank at all four swimming pools. One pool was used by bats every survey night with multiple drinking events being recorded, while drinking frequency increased at the other three pools as the local pond began to dry up. These results indicate that swimming pools represent an important water resource for bats. The next stage would be to determine what characteristics of swimming pools are bat friendly and use this information to promote healthy, stable bat populations in urban habitats.

127^{E}: The current number of recognized mammals with a chronology of described species**

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The number of recognized mammal species has rapidly increased in the genetic age, by both original description and validation of prior synonyms. The jump from 4629 recognized species in the 2nd edition of *Mammal Species of the World* to 5416 species in the 3rd edition exemplifies this increase. Here we perform a review of mammalian taxonomic literature, especially publications after 2005, revealing an updated count of 6250 recognized mammal species. At least 84 species are recently extinct leaving 6165 extant, resulting in 832 species recognized since 2005, a value that compares to 787 species from 1993-2005. A chronology of species descriptions finds major increases in the 1840's, late 1800's to early 1900's, and in the early 21st century. The most speciose mammalian orders, Rodentia and Chiroptera, respectively contain 2481 and 1388 species (together 62.8% of mammalian richness). The mouse-related families Muridae (820 species) and Cricetidae (764) are the richest among mammals, followed by Vespertilionidae (497) and Soricidae (440). The mouse-eared bats *Myotis* and musk shrews *Crocidura* are the richest mammalian genera (131 and 197 species, respectively). The ASM's new Mammal Diversity Database will make this listing publicly available and updateable, eventually with full synonym listings and citations, to raise mammalian taxonomy to the standard of amphibians and birds. This research is funded by the ASM Mammal Biodiversity Committee.

128: The Mammal Collection at California State University, Long Beach

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The mammal collection at California State University, Long Beach (CSULB) contains 12,220 specimens, making it the 6th largest mammal collection in the state of California. The holdings represent thorough geographic coverage of the small mammals of southern California and northeastern Mexico, including a 700-specimen survey of Joshua Tree National Park and vouchers for the parasitological and systematic research of CSULB faculty. Rodents form 77% of the collection and bats another 14%. Most specimens were collected between 1940 and 1985 and consist of a paired skin and skull, although a number of bats are preserved in ethanol. The collection has recently been digitized and specimen data are searchable through the CSULB Biological Collections website (<http://web.csulb.edu/colleges/cnsm/collections/mammals/>) by taxon, locality, and date. CSULB's proximity to the Natural History Museum of Los Angeles makes it easy to visit both institutions in a single trip. Please contact Suellen Jacob, suellen.jacob@csulb.edu, for visitation, loan, or data enquiries.

129: A guide to Southern California terrestrial mammals

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The purpose of this guide is to provide biologists and amateur naturalists with a written and spatial guide to the terrestrial mammal fauna of Southern California. There is currently no technical or interactive comprehensive guide to the terrestrial mammals of Southern California, and, as such, many field biologists perform surveys without a complete knowledge of the mammals that may exist within a survey area. Most surveys performed for public or private development projects are focused on endangered, threatened, or sensitive species. This results in a limited list of potentially occurring species and so limits the results to a subset of an area's mammal fauna. Thus, information on other species is not recovered. This project grew out of the primary author's work to provide field staff with more complete information on the mammals of Southern California, so that the mammal fauna can be accounted for accurately in reports and impact analyses. While compiling information for the written guide, the authors also investigated creating a spatial guide using Geographic Information Systems (GIS) technology. The spatial guide would allow biologists direct access to a list of mammals and known occurrences while in the field. We investigated four mapping and delivery methods. To date, accounts and maps for all mammal species

in Southern California have been completed, and the project is currently being expanded to include all of California.

130: Environmental and hormonal influences on dispersal-related behaviors in brush mice (*Peromyscus boylii*)

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Behavioral traits such as exploration, activity, and boldness can influence dispersal movements of young animals, as can hormones such as corticosterone. We investigated variation in dispersal-related behaviors in free-living brush mice (*Peromyscus boylii*) during periods of varying environmental harshness. We conducted open-field and novel object tests to quantify boldness, activity, movement rate, and response to a startle, and quantified fecal glucocorticoid metabolites (FGMs). We found that age, sex, and FGMs interacted to affect dispersal-related behaviors. In particular, juveniles were bolder and less responsive to a startle, and there was a positive correlation between FGM level and activity in adult females and juveniles of both sexes. Juveniles also displayed increased boldness and activity under drier conditions. Our results suggest that behavioral traits and hormones previously implicated as influences on dispersal in other species may be elevated during the juvenile life stage, and are influenced by environmental conditions; future work will incorporate detailed movement data from radio-tracked individuals. This research was supported by a 2014 Grants-in-Aid of Research awarded to Rebecca Kelley.

131^F: A genomic-level perspective on immunogenetic variation and mate choice in a monogamous mammal (*Peromyscus californicus*)

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Variation at Major Histocompatibility Complex (MHC) genes is thought to be an important mechanism underlying mate choice in vertebrates. However, analyses based on individual MHC loci have generated contradictory results regarding the role of these genes in disassortative mating. To provide a comprehensive assessment of relationships between MHC variation and mating behavior, we used an exome capture approach to characterize 13 MHC loci, 312 innate immunogenes, and 1,044 non-immunogenes in 50 free-living, monogamous pairs of California mice (*Peromyscus californicus*) from two distinct populations. Pairwise genotypic comparisons and SNP-based allelic differences revealed monogamous pairs in both populations to be more dissimilar than non-pairs at MHC, innate and non-immunogenes ($p < 0.01$). Consistent with the functional role of immunogenes, the populations were highly differentiated at MHC and innate genes ($F_{st} = 0.56$ and 0.57) but not at non-immunogenes ($F_{st} = 0.007$). Concomitantly, we found animals within each population to be closely related at MHC genes ($r = 0.12$). Together, these results suggest that inbreeding avoidance – not MHC-based disassortative mating – may be driving mate choice decisions in California mice. Further, our data suggest that locus-specific patterns of genetic variability commonly interpreted as evidence for MHC-based disassortative mating may instead reflect genome-wide dissimilarity between reproductive partners. As a result, locus-specific evidence for disassortative mating may have biased previous interpretations of the role of MHC genes in mate choice.

132^F: Best practices in stable isotope ecology: correcting stable isotope signals measured in formalin fixed specimens

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Museum collections contain a wealth of untapped data about an animal's niche which stable isotope analysis can elucidate. Specifically, ^{13}C reflects an animal's diet while ^{15}N captures trophic position. Although study skins have been the most common method of specimen preparation over the last century, fluid preservation has become common in recent decades as it preserves all tissues and morphology.

Fluid storage involves fixation of whole animals with formalin followed by long-term storage in ethanol. Formalin alters carbon isotope signals of tissues by methylating proteins with isotopically light carbon. To quantify this phenomenon, we analyzed $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values from hair from seven rodent species from the Ruby, Toiyabe, and Pine Forest Mountains. Hair was serially sampled from specimens prior to preservation and post-preservation for 1 – 6 years of ethanol storage. As expected, differences in $\delta^{15}\text{N}$ values between years were not significant, but $\delta^{13}\text{C}$ signals were depleted by approximately 0.75‰ after fixation and 1 year of ethanol storage. This offset continued to grow (due to residual formalin in the body) at a decreasing rate for 4 years, then stabilized. We found a final $\Delta^{13}\text{C}$ of -1 ± 0.2 ‰ after 4 years. This is a biologically relevant $\Delta^{13}\text{C}$ and should be accounted for when inferring diet and performing analyses using fluid-stored museum specimens, and when comparing across museum preparation types.

133: Benefits of sociality: a Type IV functional response in a South American fox

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The per capita behavioral responses of predators to variation in prey species abundance is characterized as the functional response (FR). Most vertebrates exhibit either Type II (consumption increases to a plateau with increasing prey abundance) or Type III (sigmoidal, reflecting prey switching as prey increases from low to modest abundance) FR. A Type IV FR is similar to a Type II or Type III except that per capita consumption declines at very high prey abundance. Type IV FR are best known among invertebrates but were originally postulated for vertebrates foraging on group-living prey such as schooling fish. The degu (*Octodon degus*) is a social hystricomorph rodent, and degus foraging in large groups detect predators more rapidly than those in smaller groups, suggesting that predation rates should decline at high degu densities. A key predator of degus is the culpeo fox (*Lycalopex culpaeus*), which is characterized as a generalist rodent predator that exhibit numerical but no FR. We monitored degu and culpeo numbers over two decades, and we characterized culpeo diet with traditional scat analysis. Using 23 years of observations our data show a clear Type II FR for rodents in general, but for the highly social degu, per-capita consumption clearly declines at the highest degu density. To our knowledge this is the first demonstration of a Type IV FR for a mammalian predator.

134^F: Individual-based modeling of interactions between ungulates and wolves

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We are developing individual-based models (IBMs) of how deer (*Odocoileus* spp.) and elk (*Cervus elaphus*) select seasonal home ranges to understand how wolves (*Canis lupus*), in turn, select territories in response to ungulate behavior. IBMs are used to model individual behaviors, which provide predictions of population-level patterns. Our models are based on the expectation that animals are adapted to select home ranges and territories efficiently based on spatially distributed resources. Animals should select habitat that maximizes benefits acquired from resources (e.g., food) against costs of acquiring them (e.g., travel costs, predation risk, etc.). We are using our models to predict how deer and elk select seasonal home ranges. We predict how wolves select territories in response to density and distribution of deer and elk. Preliminary results suggest that ungulate home ranges and wolf territories are smaller and of higher quality where food resources are more clumped. This means that wolf territories should vary in size based on ungulate behavior, which varies by species and season. We are parameterizing the models with data from real landscapes (e.g., terrain, vegetation, etc.), allowing us to estimate size and location of actual wolf territories in relation to ungulate distribution. Biologists will be able to predict wolf pack

locations and abundance in absence of extensive empirical data to help inform management decisions for both ungulates and carnivores.

135: Molecular phylogenetics of tylomyine rodents (Rodentia: Family Cricetidae)

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The purpose of this study is to develop a molecular phylogenetic hypothesis of relationships among all four genera of cricetid rodents within the subfamily Tylomyinae using both a mitochondrial gene (cytochrome *b*) and a nuclear marker (intron 7 of *Beta-Fibrinogen*) and enhanced taxon and geographic sampling. Here we demonstrate that the genera *Tylomys* and *Ototylomys* are monophyletic and are sister taxa. Within *Ototylomys* there is an undescribed species from central Chiapas, Mexico. Within *Nyctomys* there are two well-differentiated clades. One is distributed in low elevation dry forests from the west coast of Mexico south through El Salvador, and a second is found in relatively high elevation cloud forests from southern Mexico south through Guatemala.

136: Abundance and survival of northern flying squirrels in late-successional forests in the Central Oregon Cascades

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Northern flying squirrels (*Glaucomys sabrinus*) have been the focus of many small mammal population dynamic studies in the Pacific Northwest. Much of this research was initiated due to the importance of northern flying squirrels as a prey species for federally threatened northern spotted owls (*Strix occidentalis caurina*), and assessed the demographic consequences of forest management. Few studies have assessed the spatial heterogeneity of northern flying squirrel demographic processes within old forests. Here, we report on analyses of a six-year mark recapture study of northern flying squirrels and other small mammals from late-successional forest in the H.J. Andrews Experimental Forest, near Blue River, OR. We quantified northern flying squirrel abundance and survival on nine trapping grids over six years, and relationships between spatial and temporal demographic patterns and habitat measurements. We estimated abundance and survival using a robust design modelling framework in Program MARK with spatial and temporal covariates. Our results suggest strong multi-year temporal and spatial variability in northern flying squirrel abundance and survival estimates. Initial abundance estimates range from 172 to 420 individuals and initial survival estimates range from 75% survival to 40% survival across all nine grids. Estimates of northern flying squirrel abundance and survival as well as demographic associations with habitat variability will inform old forest ecosystem management across the Pacific Northwest.

137^F: Baseline camera-trap study in the Amazonian Yasuni Biosphere Reserve

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Thirty percent of mammalian diversity is found in the Amazon Rainforest. However, these mammals are hard to study due to elusive behaviors and camouflage. By using camera traps at the Shiripuno Lodge Yasuni Biosphere Reserve, we non-invasively captured natural behaviors of mammals. The purpose of this study was to document mammalian diversity in the Reserve. Motion-activated cameras were placed along trails for 2-6 weeks between 2013 and 2015. In total, we captured 2,593 photos and videos, 299 of which were mammals (29 species). The most common species were peccaries and agoutis. Rarely-seen mammals included Brazilian Tapirs and Jaguars. Bats were also very common throughout the evenings in areas near water. Without camera traps, these elusive creatures would be difficult to observe. The images serve as a baseline of mammal diversity in the area, but more research will be necessary to document changes in populations and behaviors. Because poaching is common, there may be differences in mammalian populations and behaviors in different areas of the Amazon. The Amazon stores over 48 billion tons of carbon dioxide in its trees. Recent studies suggest that if large mammals are

lost from a forest, the large trees will also be lost because their seeds will not be dispersed. Documenting the presence and populations of large mammals in the Amazon is therefore essential for the preservation of the entire ecosystem.

138^E: Changing diets and chiseling away dogmas regarding saltbush specialization in *Dipodomys microps*

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Dipodomys microps, the chisel-toothed kangaroo rat, is a small desert rodent occurring in a region that has undergone substantial ecological changes due to rangeland expansion.

Although generally considered a saltbush specialist, the natural diet of *D. microps* consists of saltbush (*Atriplex confertifolia*) a C4 plant and blackbush (*Coleogyne ramosissima*) a C3 plant.

To determine if human-driven environmental change has impacted the natural diet of *D. microps* we took advantage of natural differences of carbon stable isotopes between C4 and C3 plants.

We predicted that increased abundances of blackbush due to rangeland expansion and corresponding decreases of saltbush will have led to diet shifts in *D. microps*. To test this prediction we sampled fur of kangaroo rats from Inyo County, California housed in the Museum of Vertebrate Zoology from three time periods: before the landscape change (1917, N=10), during the disturbance (1973-1978, N=10), and recent samples (2008-2009, N=8).

We observed minor shifts in percent of saltbush in diets of *D. microps*. In 1917 saltbrush consumption averaged 48%, in the mid 1970s saltbrush ingestion averaged 47%, and by the late 2000s the average consumption dropped to 37%. These observations are consistent with my prediction that environmental factors caused kangaroo rats to favor blackbush. However, the low percentage of C4 reliance suggests this species may not be a true *Atriplex* specialist as previously thought.

139: American pikas (*Ochotona princeps*) as a platform for public engagement in climate change

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Identifying changes in species distributions is key to mammalian conservation. Enlisting the help of public volunteers (termed “citizen scientists”) has recently become a popular way to monitor sensitive species while also engaging the public in science and conservation. American pikas (*Ochotona princeps*) are small, climate-sensitive lagomorphs that are ideal for volunteer monitoring because they are charismatic and generally easy to identify. These traits, paired with concerns about recent climate-mediated pika population declines, have made pikas a popular target for citizen science throughout the western United States: six formal projects across four states are currently training citizen scientists to monitor pikas. Some specifically target K-12, but student engagement is often limited by liability issues. Here, we summarize recent progress and current challenges to public participation in pika research. Volunteer observations have led to important discoveries about pika biology, and surveys suggest that participation enhances volunteer awareness of climate change. However, data synthesis across projects is difficult due to limited funding opportunities. Increased funding would facilitate volunteer training and retention, development and use of compatible survey protocols, data sharing, and expanded data collection in areas of high conservation priority. Overall, pikas can be a powerful platform for public engagement in science. However, future attention is needed to balance educational, scientific and management objectives in project design, and more resources are needed to coordinate these projects.

140: Mammalian reproduction: a female perspective

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Perhaps more than any other class of organisms on Earth, female mammals possess extraordinary control over their reproduction. They regulate major aspects of mating and conception as well as offspring survival, growth, and development. They do this using a combination of internal conception, in-utero development, and lactation, all of which provide mammalian females unprecedented influence on their reproductive success. Yet, historically, the female perspective has been given short shrift. One of the most striking aspects of historical terminology is that features of indeterminate sex may be given male names. For example the enlarged clitoris (aka “pseudopenis”) of female hyenas or the “female” prostate. In an unusual methodological twist, male traits have historically been employed to measure female behavior. Two particularly interesting cases of this include “induced” versus “spontaneous” ovulation and estrus. Our poster reviews specific examples of how the historical perspective in reproductive biology has led us to, in some cases, misunderstand that biology. We offer alternatives to help move the field forward in a gender-neutral way.

141^F: Estimating recruitment of wolves with limited data

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Successfully managing a species can require information on basic demographics such as survival and reproduction. Recruitment is particularly important for harvested species because it determines the level of harvest that can be sustained by the population; thus, this information can be used to improve harvest decisions. When management occurs across large spatial scales, however, these data can be costly or highly difficult to collect and are often unavailable at the scale needed to inform management decisions. Management of gray wolves (*Canis lupus*) in Montana could benefit from information about the spatial and temporal variation in recruitment. Existing data are insufficient for traditional methods to estimate recruitment of wolves, therefore a new approach is needed. Our objectives are to develop a method to estimate and ultimately determine the factors that explain the spatial and temporal variation in wolf recruitment using available data. Integrated population models can be a useful tool for demographic analyses from limited data sets, and can increase precision in estimates. We developed an integrated population model to use collar, hunter survey, and group count data to estimate recruitment of wolves. We will ultimately use this model to evaluate the spatial and temporal variation in this demographic parameter. These data are available from ongoing monitoring and this method does not require collecting any additional data. This method can help reduce costs associated with monitoring wolf populations while providing valuable information needed to help inform management decisions.

142: Effects of species traits and landscape configuration on small mammal occurrence in human-dominated landscapes

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In human-dominated landscapes, agriculture and urbanization eliminate natural habitats for wildlife and fragment remaining habitat patches. Responses of wildlife to anthropogenic disturbance differ across space and among species. Identifying the underlying reasons for these differences in response informs both species ecology and wildlife conservation efforts. We assessed the relative contributions of two factors that potentially influence wildlife distribution in fragmented landscapes: (1) inherent species traits, including niche breadth and proximity to range boundary; and (2) landscape characteristics, including habitat abundance and degree of landscape fragmentation. We tested how these two factors influenced distribution of 12 species of small mammals across 35 different human-dominated landscapes in north-central Indiana, USA that differed in extent of agriculture and composition and configuration of forest, grassland, wetland, and edge habitat. We improved on previous efforts to quantify small mammal distribution in these landscapes by accounting for imperfect detection and phylogenetic non-independence among species using a multi-stage modeling approach. Preliminary results indicate that

species-specific characteristics, particularly niche breadth, played a more important role than landscape composition or configuration in driving patterns of small mammal occurrence across the study landscapes. Comparisons with naïve models indicate that failing to account for imperfect detection and phylogenetic relationships altered inference for several model parameters. Future work will extend our modeling approach to additional taxa in the same landscapes, including bats, turtles, and breeding birds.

143: Development of a long-term bat monitoring program at Fort Indiantown Gap - National Guard Training Center, Pennsylvania

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Federal lands are required to monitor the effects of land use on threatened and endangered (T&E) species according to the Endangered Species Act. Over the last decade, White-nose Syndrome (WNS) has drastically reduced populations of several bat species, leading to calls for these species to be federally listed. Given the likelihood of new T&E bat species in the future, natural resource managers will need to know the level of survey effort required to collect historical data on a wide range of increasingly rare bat species. In 2016, we began developing a long-term bat monitoring program at Fort Indiantown Gap - National Guard Training Center, Pennsylvania. We surveyed the bat community from May-September using a combination of mist-netting and acoustic techniques (stationary monitoring, driving and walking transects). We used SonoBat 4.0.7 to identify recorded calls to species. We then used these data to: (1) determine the differences in bat species detected between survey methods; (2) compare the relative effort required to detect a given species using each method; and (3) determine whether extending the survey season detected additional migratory species. Long-term monitoring programs will become increasingly important at federally-owned properties as WNS continues to push additional species towards extinction. The most effective programs will be based on data that indicate the technique(s) required to efficiently and confidently detect all bat species present.

144: Identifying a neo-sex chromosome via deep resequencing in a hybridizing primate species

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It is well established that sex chromosomes play an important role in speciation, and some have attributed rapid divergence to sex chromosome turnover in clades with multiple sex chromosome systems (MSCS). However, empirical research has been mainly restricted to taxa with non-complex sex chromosomes. Thus, the role of neo-sex chromosomes in driving divergence is unclear. In most primate lineages, the ancestral mammalian sex chromosome system (XX/XY) is retained. However, in New World primates, several species have evolved MSCS via translocation events between autosomes and sex chromosomes. Howler monkeys (Atelidae: *Alouatta*) are unique in that there is evidence for MSCS in almost every recognized taxon and neo-sex chromosomes vary in number and identity across species. The role of MSCS in driving divergence in this system and the evolutionary breakpoints for these neo-sex chromosomes remain to be understood. Here, we use deep resequencing to analyze differences in mapping depth between the sexes to identify sex-linked contigs and map the evolutionary breakpoint for the translocation producing the neo-X chromosome in *Alouatta palliata* (X_1X_2Y), a species that forms a narrow hybrid zone with its sister taxon, *A. pigra* ($X_1X_2Y_1Y_2$). This work is a necessary first step to enable downstream analyses that address sex chromosome evolution and the role of sex chromosome rearrangements in reproductive isolation.

145: An association between differential expression and adaptive divergence in the Patagonian olive mouse (*Abrothrix olivacea*)

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The Patagonian olive mouse occupies a broad range of habitats in southern South America. We used RNA-seq to obtain transcriptomic data of 38 individuals from four localities (two in the Patagonian steppe, two in the Andean forest). We assembled a reference transcriptome of > 17,000 genes, assessed differential gene expression between forest and steppe individuals, and genotyped > 180,000 SNPs to assess genetic divergence and departures from neutrality. Expression profiles clearly distinguish forest and steppe samples, and 2,881 loci are differentially expressed between these biomes. These include, but are not restricted to, multiple solute carriers and other genes involved in urine concentration, detoxification genes, and genes of the immune system. The distributions of Tajima's D within habitats were displaced toward negative values, reflecting a history of demographic expansion of this species, especially in the steppe. D values of differentially expressed and baseline genes overlapped broadly, but the former tended to be right-shifted, indicating a greater presence of intermediate frequency polymorphisms in these genes. F_{ST} also varied broadly in both classes of genes but, again, tended to be larger in differentially expressed genes, indicating that these genes tend to be more differentiated between habitats. Our results indicate that both differential expression and adaptive allelic variation are important in the occupation of contrasting habitats by the Patagonian olive mouse.

146: March Mammal Madness: communicating science and art across social media

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Annually since 2013, in honor of the NCAA College Basketball March Madness Championship Tournament, the blog "Mammals Suck... Milk" features simulated combat competition among ~65 species of animals in a virtual tournament, March Mammal Madness. Scientific literature is cited to substantiate likely outcomes should two animals or two groups of animals encounter one another, and battle outcome is a probabilistic function of the two species' attributes within the battle environment. Thousands of people play March Mammal Madness each year, including students in primary, secondary, and high schools, college biology and anthropology courses, museum collections staff, and families. Animal combat bouts during March Mammal Madness are described in near "real time" using the microblogging site Twitter. Each evening the results are aggregated, along with public commentary, via the social network repository Storify and linked from the hosting blog as well as shared through online social networks. Through the scientific information embedded in the bout descriptions and peer contributions from animal aficionados and experts in a variety of fields, participants learn about inter-species interactions, the importance of ecological context, how natural selection has shaped adaptations, conservation management, and the significance of art and the sciences in education and research. March Mammal Madness is a pedagogical innovation that engages people from around the globe, creatively integrates digital technologies, and inspires awe for the natural world.

147: Estimating quantity and quality of moose forage in northern Idaho

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Several populations of moose (*Alces alces shirasi*) in northern Idaho have declined in recent decades for

unknown reasons. Limitations in quality or quantity of forage have been proposed to drive or contribute to these declines, but relatively few data are available to assess this hypothesis. To fill this information gap, we 1) evaluated diet selection using microhistological analyses of fecal samples collected across northern Idaho, 2) conducted field sampling and modeled forage availability as a function of physiogeographic variables, and 3) analyzed shrub samples for crude protein, tannin protein-precipitating capacity, and digestible energy. Proportion of preferred shrub species (e.g., *Salix* spp., *Ceanothus* spp., *Amelanchier alnifolia*, *Acer glabrum*) in diets differed among sampling locations, and availability on the landscape also varied across our sampling region. We used data on demographic trends from 21 populations and examined associations with forage quantity and quality parameters. Preliminary results suggest substantial variation in diet, availability of shrubs, and forage quality parameters among populations, which could be contributing to population declines.

148: Fate of the immigrant: post-translocation survival of southern Idaho ground squirrels (*Urocitellus endemicus*)

Teresa Tarifa, Eric Yensen, Tyler Fleming, and Cristian Noya-Rada

Managers often consider translocation as a tool for resolving human-wildlife conflicts or mitigation of development projects. However, translocations can have uncertain outcomes. The southern Idaho ground squirrel (*Urocitellus endemicus*) is under pressure from human-wildlife conflicts in its small geographic range (2,400 km²) in southwestern Idaho. Between 2012 and 2014, we translocated 315 squirrels from a ranch with a kill permit and captive-born individuals from Zoo Boise to a site without squirrels using a “soft-release” technique. Previous translocations of this species lacked monitoring. We tracked fates of translocated squirrels and those subsequently born at the site using life trapping. Wild-caught squirrels had higher survival rates than captive-born individuals. First year survival of wild squirrels was 21 to 39% vs. 10 to 16% from the Zoo. By the second year, only 10 to 11% of wild and no captive-bred squirrels survived. By the third year, only 6% of wild squirrels survived. Survival of squirrels born at the release site was 51 to 56% for the first year and 28% for the second year. Females survived better than males in all groups. Many factors contribute to high mortality of translocated animals. *Urocitellus endemicus* was a Candidate Species until 2015, but anthropogenic threats continue. Maintenance of viable populations is a challenge, but use of translocation must be considered a last alternative. There is no place like home.

149: Tolerance of foraging constraints in female barren-ground caribou (*Rangifer tarandus granti*)

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Wild ungulates experience large seasonal variations in food supply but their ability to tolerate foraging constraints are poorly understood. We measured daily intake of 20 female caribou from mid-pregnancy (January) through parturition (May) to breeding (September). Restriction of available food for 14 days in winter reduced intake to $55 \pm 2 \text{ g} \cdot \text{kg}^{-0.75} \cdot \text{d}^{-1}$ from ad libitum intake of $91 \pm 5 \text{ g} \cdot \text{kg}^{-0.75} \cdot \text{d}^{-1}$, but animals maintained body mass and returned to a similar level of intake $101 \pm 4 \text{ g} \cdot \text{kg}^{-0.75} \cdot \text{d}^{-1}$ after restriction. Food intake was $147 \pm 6 \text{ g} \cdot \text{kg}^{-0.75} \cdot \text{d}^{-1}$ during 11 days of restriction in lactating females, which was similar to the intakes of control females without calves ($136 \pm 8 \text{ g} \cdot \text{kg}^{-0.75} \cdot \text{d}^{-1}$). Food intakes of the restricted group were similar before ($182 \pm 8 \text{ g} \cdot \text{kg}^{-0.75} \cdot \text{d}^{-1}$) and after ($192 \pm 9 \text{ g} \cdot \text{kg}^{-0.75} \cdot \text{d}^{-1}$) restriction, which suggests that mothers were unable to increase intakes to compensate for lost feeding time. Pregnant caribou used fat stores slowly to tolerate a reduction in food intake in winter. Lactating caribou continued to sustain the growth of their calves during restriction and maintained body mass even though body fat stores were low. Female caribou probably saved energy by reducing resting metabolism to tolerate reductions in food availability by 25-50%, which would allow wild animals to move to better foraging areas.

150^F: Biting mechanics of rabies vectors: exploring the link between cranial morphology and infectious disease control

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The striped skunk (*Mephitis mephitis*) is unresponsive to the oral rabies vaccination programs in the US that utilize baits containing sachets filled with liquid vaccine. Because the baits must be bitten and the vaccine subsequently ingested, we aim to elucidate potential biomechanical differences between skunks and raccoons (*Procyon lotor*) that may contribute to the observed differences in oral immunization success. We compare natural bite forces at different gapes in live animals to assess the effect of muscle stretch and bite location (i.e., tooth position) on bite performance. The force produced by skunks at the premolar position at a 2 cm gape was higher than at the 1 cm gape, suggesting that they have a fiber architecture and length that helps them maintain bite force at wider gapes. In contrast, raccoons had lower bite forces at the carnassial/molar at the 2 cm gape compared with the 1 cm. This means that despite being larger than skunks, muscle stretch is affecting their ability to bite on more distal teeth. Maximum bite forces did not differ when biting on the premolars or carnassial/molars. Skunks had significantly higher bite forces at the canines. This means that the ability of the animal to puncture vaccine sachets is likely not the cause of differential immunization success and factors related to chewing and swallowing need to be considered.

151: Nutritive composition of bamboo culm, leaves, and shoots selected by two captive giant pandas

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Giant pandas consume a nearly-exclusive bamboo diet containing high levels of indigestible plant structural components, despite retaining the gastrointestinal physiology of a carnivorous species. Seasonal dietary shifts, defined by the part of bamboo that is consumed, may facilitate the species utilization of this feed source. We evaluated bamboo selection by two captive giant pandas in relation to variations in plant part and nutrient composition over four months (January, March, May, October). Despite apparent higher nutritive value in leaf (crude protein [CP] >12%, acid detergent fiber [ADF] <40%), culm (CP <5%, ADF >59%) was the predominant plant part consumed by giant pandas during the majority of trials. Maximum bamboo culm intake (> 80% total DMI) coincided with times of culm starch of > 6% and culm hemicellulose >25% (January and March). However, starch and hemicellulose concentrations in culm were relatively low during May and October (culm starch < 4%; culm hemicellulose < 22%), when giant pandas consumed the highest observed levels of shoots or leaves. Bamboo shoots were preferentially consumed when available (May), likely due to their low proportion of plant structural compounds (ADF = 42%) and relatively high CP (11%) content. Rather than selecting a diet that is nutritionally consistent year-round, giant pandas apparently forage for potentially digestible carbohydrates, resulting in shifting plant part preferences throughout the year in response to nutrient fluctuations in bamboo.

152^F: Is snow cover an adequate predictor of suitable habitat for wolverines?

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In the conterminous United States, wolverines (*Gulo gulo*) occupy semi-isolated patches of sub-alpine habitat in low densities. For years, research has indicated that persistent spring snow is vital for wolverine denning and kit survival. Explanations for why adult reproduction and kit survival are dependent on snow include thermal constraints, food caching, and protection from predators. Some scientists argue that suitable wolverine habitat can be modeled and predicted based primarily, or solely, on persistent spring snow cover. Due to the species' likely reliance on persistent snow cover and the small population size of wolverines in the conterminous U.S. (less than 300 individuals), the wolverine is currently a candidate T&E species under the Endangered Species Act (ESA). The wolverine has been considered as a candidate for listing several times since 1994 but has rejected each time due to uncertainty in the scientific information indicating that listing is warranted. In recent years, based on both emerging research and previous rejections to list wolverines as a T&E species, there has been speculation that snow cover alone may not be an adequate predictor of wolverine habitat suitability. Preliminary results indicate that

factors such as human land-use and forest cover are also likely key predictors for suitable wolverine habitat.

153^F: Cortisol levels in *Pekania pennanti*: relationship between home range disturbance and physiological stress.

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Cortisol is an energy mobilizing hormone that can serve as an indicator of stress in mammals. By collecting fisher (*Pekania pennanti*) hair and measuring an individual's cortisol level, we were able to examine the physiological response of the animal to disturbance in their home range. Chronic stress is known to lead to serious health problems in mammals such as suppressed immune function and reduced reproductive output. My study focused on an isolated fisher population in the central Sierra Nevada Mountains, California. We examined the influence of disturbance (e.g., human activities, habitat fragmentation, forest management actions) within an individual fisher's home range on physiological stress as measured by cortisol concentrations in the hair. By collecting fisher hair and measuring an individual's cortisol level over time, we evaluated the physiological response of the animal to disturbance in their home range. We have compared the entire home range (95% isopleth) of the animal to the core (30% isopleth) where the majority of their time is spent. We have also examined survival rates and initial kit counts of each female during the denning season to determine the impact that high cortisol levels may have on vital rates of fishers in this population.

154: Rapid evolution and the genetics of disease resistance in Tasmanian devils

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Although cancer rarely acts as an infectious disease, a recently emerged transmissible cancer threatens the persistence of Tasmanian devils (*Sarcophilus harrisii*). Devil facial tumor disease (DFTD) has swept across nearly the entire species range, causing a population decline of 80 percent in just 20 years. Using high-throughput genomic sequencing approaches, we have detected evidence for rapid evolution in response to DFTD as well as a genetic basis for variation in disease-related traits. First, we applied a genome scan approach in three populations for which we have devil samples from both before and after DFTD outbreak, and we identified two genomic regions showing strong signatures of rapid parallel response to selection. Both regions contain candidate genes with immune and cancer-related functions. We have expanded this list of candidate loci under selection by targeting regions of the genome across several more independent populations. Further, we have conducted genome-wide association mapping of disease-related phenotypic traits across several populations. Key traits, including time of survival with disease and tumor growth rate, show a significant genetic basis and association with a relatively small number of major-effect loci. Our results suggest the presence of standing genetic variation that could facilitate the evolution of resistance and/or tolerance to DFTD in devil populations, providing hope for the persistence of devil populations in the face of this devastating disease.

155: Understanding and predicting habitat for Canada lynx conservation at the range periphery

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Canada lynx (*Lynx canadensis*) are a federally threatened species within the contiguous US. Thus, understanding and predicting habitat for lynx is essential for effective and efficient recovery, conservation, and management. Here, we used a 15-year dataset incorporating 86 radio-marked lynx to understand habitat use, habitat selection, and functional responses in habitat use. Additionally, we developed multi-scale and scale-integrated predictions of habitat at the landscape-level, which is relevant for many land-management applications. Our analyses revealed that across scales and seasons, lynx use more mature and spruce-fir forests than any other structure stage or species. However, at the landscape-level, intermediate snow depths and the distribution of snowshoe hares (*Lepus americanus*) were the strongest predictors of where lynx placed their home ranges. Within home ranges, female and male lynx increasingly selected advanced regeneration forest structures as they became more available. These patterns supported the bottom-up mechanisms regulating Canada lynx in that advanced regeneration generally provides abundant snowshoe hares, while mature forest is where lynx hunt efficiently. In contrast, lynx exhibited decreasing use of stand initiation structures. Managers can apply the relative proportions of forest structure classes along with our lynx response curves to inform landscape actions (e.g., logging) targeted at facilitating the forest mosaic used and selected by Canada lynx. Collectively, our work provides insight that informs conservation and management efforts aimed at Canada lynx habitat.

156^E: Characterizing adaptations in Tasmanian devil (*Sarcophilus harrisii*) populations in the face of a transmissible cancer

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The Tasmanian devil (*Sarcophilus harrisii*), is threatened with extinction by a contagious cancer - devil facial tumor disease (DFTD). DFTD has spread ~95% of the way across Tasmania, causing localized declines exceeding 90% and an overall reduction of devil population size by 80%. Despite epidemiological model predictions of species' extinction, devils persist in regions of long-term infection. Inconsistencies between model-based extinction predictions and observed persistence necessitate further research characterizing the adaptive potential of devil populations across Tasmania. In this study, we tested whether patterns of adaptive genetic diversity varied across the geographic range of the Tasmanian devil. To assess genetic variation, we designed a RAD capture array (Rapture) and genotyped 8,000 SNPs from 3,500 individuals. We then tested the extent to which spatial variation in genetic diversity was generated by selection imposed by abiotic variables chosen *a priori* based on devil ecology or DFTD. We used differentiation outlier tests and genetic-environment association studies to test for candidate loci under divergent selection across the landscape pre- and post-DFTD emergence. Prior to disease arrival, we found strong evidence for adaptation to abiotic variables in the local environment in Tasmanian devil populations. However, following DFTD arrival, few of these candidate loci were maintained, suggesting local adaptation to abiotic environmental variables was overcome by the strong selection imposed by DFTD.

157^E: The ectoparasite diversity of New England cottontails (*Sylvilagus transitionalis*) and habitat when non-native species are present

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Historically common throughout the northeastern United States, the New England cottontail (*Sylvilagus transitionalis*) has experienced declines throughout its range. Loss of early successional habitat and competition with the eastern cottontail (*Sylvilagus floridanus*), introduced in the early 1900s, limit the New England cottontail population. Parasitism may also play a role in limiting New England cottontails, as high numbers of ectoparasites occur at certain times of the year. Parasite mediated competition may be

occurring between the two cottontail species. To investigate this, we compared ectoparasite species of New England cottontails among sites with different proportions of eastern cottontails. In addition, we evaluated the proportion of tick species and the tick abundance found on New England cottontails and those found on eastern cottontails and compared it to the proportion found in the environment. We analyzed the relationship between tick density and the different vegetation types, season using Bayesian regression, and time within season. Preliminary findings suggest no significant difference in tick abundance among four habitat types; however, tick density was much lower at our mostly native-vegetation site than the other sites. Ticks decreased over the spring and declined over the fall. Results from this study will provide insight the parasite mediated competition between the two cottontail species, and the potential role of parasites as a limiting factor for New England cottontail.

158: Forest structure influences bushy-tailed woodrat and northern flying squirrel density in the eastern Cascade Range

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Land managers face substantial challenges balancing forest restoration and northern spotted owl (*Strix occidentalis caurina*) habitat conservation management objectives in fire-prone dry forest landscapes on the east side of the Cascade Range in Washington and Oregon. Northern flying squirrels (*Glaucomys sabrinus*) and bushy-tailed woodrats (*Neotoma cinerea*) are the primary prey for northern spotted owls in this landscape. Understanding forest structure characteristics correlated with the density of these prey species will be important for managers trying to balance competing management objectives. From 2011 through 2014, we used live-trapping mark-recapture techniques and spatially explicit capture-recapture models to estimate flying squirrel and woodrat density and forest structure correlates within three study sites. Trapping was conducted prior to implementation of three dry forest restoration projects on USFS lands: 1) the Lookout Mountain Project, Crescent Ranger District, Deschutes N.F., OR, 2) the Westside Project, Klamath Falls Ranger District, Fremont-Winema N.F., OR and 3) the Swauk-Pine Project, Cle Elum Ranger District, Okanogan-Wenatchee N.F., WA. Post-treatment sampling at these study sites will be conducted in 2017 to 2018.

159: Comparing the effectiveness of RADseq and microsatellites for parentage and sibship assignment in mammal populations

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Microsatellites currently are the most widely used genetic markers for parentage and sibship assignment in wildlife populations. However, the development of next-generation sequencing (NGS) technologies is leading to a dramatic increase in the use of single nucleotide polymorphisms (SNPs) across the field of genetics by facilitating fast, cost-effective SNP discovery and genotyping. For wildlife populations, restriction-site associated DNA sequencing (RADseq) has become a widely used NGS-based method for generating SNP data because it requires no prior genomic resources and is minimally affected by ascertainment bias. We compared the effectiveness of microsatellite versus RADseq markers for parentage and sibship assignment in two wildlife populations that have low genetic diversity: bighorn sheep in Oregon, and Mexican gray wolves in New Mexico and Arizona. Our bighorn analyses used 15 microsatellite loci for samples collected from 43 lambs from five cohorts (2011-2015) and about 90% of possible mothers in the population, and our wolf analyses used 22 microsatellite loci for 32 pups from one cohort (2004) and about 90% of possible parents. We generated data from several thousand RADseq SNPs from the same samples. We evaluated the minimum number of RADseq markers required to achieve high assignment power, and assessed the feasibility of using RADseq data for developing assays with a small number of highly variable SNPs for inexpensive, high-throughput genotyping of low-quality genetic samples, such as fecal samples.

160: Natal dispersal of tree sloths in a highly modified landscape: Implications for tropical biodiversity conservation

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Conversion of tropical forests for agriculture results in both a reduction of habitat and an increase in fragmentation. Both have particularly important consequences for mammalian habitat specialists, especially those with low dispersal power. Tree sloths are Neotropical forest obligates that feature a sedentary lifestyle strategy. Consequently, habitat loss and fragmentation should have a disproportionate effect on their natal dispersal ability. Taking advantage of a radio-tracking dataset of three- (*Bradypus variegatus*) and two-toed sloths (*Choloepus hoffmanni*) at our long-term study site in northeastern Costa Rica, we aimed to describe the patterns of natal dispersal, and quantify survival and transition probabilities using multi-state mark-recapture models. We found that independence and dispersal time were shorter in three-toed sloths, but did not detect differences in the dispersal distances between species. Moreover, we found that monthly survival probabilities were lower for three-toed compared to two-toed sloths, and were lowest during the independent stage for both species. Despite being sedentary species, all monitored young dispersed for both species, possibly as consequence of high connectivity in the area. Our work highlights important species-level differences between these groups of tree sloths and has implications for their persistence in increasingly altered landscapes of Central America.

161^E: Glucocorticoid changes over pregnancy in mammals: similarities and differences among and within orders

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Glucocorticoids (cortisol, corticosterone) are stress hormones that have essential functions during pregnancy. However, out of the 5,400 species of extant mammals in 19 different orders, our understanding of the dynamics of glucocorticoids and their carrier protein, corticosteroid-binding globulin (CBG), during pregnancy is based only about 10 clinical model species in 3 main orders. From each of these models, generalizations have been made about the functions of glucocorticoids during pregnancy and the mechanisms driving changes in maternal secretion. We review the published evidence in mammals to assess whether this generality holds up by comparing the patterns of change in glucocorticoids and CBG over pregnancy across taxa. Overall, unbound glucocorticoids tend to increase as pregnancy proceeds, but there are exceptions, and there is no clear pattern in total glucocorticoid and CBG secretion. Contradictions in glucocorticoid changes across taxa reveal that some the classic functions of these hormones do not hold up across species. In addition, increases in both in maternal glucocorticoids and CBG during pregnancy cannot be generally attributed to changes in estrogen, progesterone, or fetal production of hormones. Thus there are profound differences amongst orders and within orders in the pattern of glucocorticoid changes over pregnancy.

162^E: Temperature and food quality influence selection of food patches and diets by small mammalian herbivores

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Temperature plays an important role in the time and energy budgets of small mammals and can influence their selection of food patches and diets. The objective of this study was to examine preferences for temperature in food patches, and the effect of temperature on diet selection, intake, digestion, passage rate, and metabolism in two species, pygmy rabbits (*Brachylagus idahoensis*) and mountain cottontail rabbits (*Sylvilagus nuttallii*). In a series of feeding experiments, we investigated 1) perceived riskiness of food patches that varied in temperature, 2) effects of temperature on selection of the plant secondary metabolite 1,8 cineole and plant fiber in their diet, 3) effects of temperature on daily intake, digestion and

passage of food, and 4) effects of 1,8 cineole and plant fiber on resting metabolic rate. Both species generally chose to feed in patches that were relatively colder, and this effect was greater for the larger cottontails. Both species also chose to eat more total food and a greater proportion of high fiber food when the temperature was colder. Food quality affected dry matter digestibility, but not resting metabolic rate of the rabbits. Understanding how the interactions between temperature and food quality affect selection of food patches and diets by small mammalian herbivores, and the physiological mechanisms governing these choices, will be useful for predicting how these species might respond to climate change.

163: When the ball is in the female's court: the role of male testosterone in the scramble-competition mating system of the North American red squirrel

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Male reproductive success in most mammals is determined by their success in direct inter-male competition through aggression and conflict, resulting in female-defense mating systems being predominant. This is linked to male testosterone levels and its dynamics. However, in certain environments, a scramble-competition mating system has evolved, where female reproductive behavior takes precedence and male testosterone dynamics are unlikely to be related to inter-male competition. We studied the North American red squirrel (*Tamiasciurus hudsonicus*), using a hormonal challenge protocol to assess their stress response, condition, energy mobilization, and indices of immune function. Testosterone levels at the base bleed were high in breeding males and virtually absent in non-breeding males. Breeding males were in better condition, but a similar ability to mobilize energy compared with non-breeding males. Though total cortisol was higher in non-breeding males, free cortisol was twice as high in breeding males, as their corticosteroid binding globulin levels were half as high. Testosterone and components of the stress axis functioned in a profoundly different manner in male red squirrels, with their scramble-competition mating system, than in males of mammals with female-defense mating systems. There are four interrelated reasons for these adaptations in male red squirrels: the marginal benefits of each mating, the constraints of mate searching away from their own resource-based territories, energy mobilization in a harsh environment, and a long lifespan.

164: The trap-happy trap-shy dilemma: trappability is not always a proxy for personality

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Behavioral tendencies vary consistently among individuals and this variation is known as personality. Previous studies have found that personality traits measured through standardized behavioral tests predict trappability (i.e. trap-happy and trap-shy individuals). However, the nature of this relationship is unclear since it has been explored only within single-species and never across environments. This is problematic because trappability is a labile characteristic that can vary between seasons, environments etc. It is essential to understand this link because there is great potential for the use of trappability as a proxy for personality. For example, if trappability reflects personality this would allow researchers to extract personality data from long-term capture-mark-recapture datasets. To clarify this relationship, we designed a large-scale field experiment to measure both personality and trappability in five small mammal species and across four distinct forest types. With an open-field test, we quantified behavior in 189 deer mice (*Peromyscus maniculatus*), 170 Southern red-backed voles (*Myodes gapperi*), 42 American red squirrels (*Tamiasciurus hudsonicus*), 53 woodland jumping mice (*Napaeozapus insignis*), and 70 Northern short-tailed shrews (*Blarina brevicauda*). We identified personality in four of our target species and through mixed-effects modelling we showed that personality traits did not predict trappability. Furthermore, trappability was inconsistent within individuals from all species. Our results suggest that trappability is not reflective of personality and thus cannot be used as a proxy for personality.

165: Subtle social structure in eastern grey kangaroos revealed through association indices and lagged association rates

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Eastern grey kangaroos *Macropus giganteus* are gregarious, with females mostly philopatric and most males dispersing. Females are thus assumed to form kin clusters, but details of associations among different sex-age classes are largely unknown. We observed 153 marked kangaroos at Wilsons Promontory National Park, Australia, on 122 days over a period of 9 months. We examined relationships within and between six different sex-age classes using half-weight indices and lagged association rates. We found subtle social structure. Mean half-weight indices were similar within compared to between different sex-age combinations. For adult females, there was a weakly positive relationship between pairwise relatedness and dyadic half-weight indices but this effect disappeared after controlling for geographic distance or spatial overlap. Lagged association rates decreased exponentially only for adult males with adult females accompanied by young-at-foot in the breeding season. Most other lagged association rates decreased slightly in a linear fashion and few were constant. Although females without young-at-foot appeared to be more social than females with young-at-foot, all associations among individuals were weak. Contrary to expectations, the social structure of kangaroos was not based on female relatedness at high density under strong fission-fusion dynamics.

166: Seasonal body condition and space use of urban raccoons in the Chicago Metropolitan Area

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While urbanization poses challenges to wildlife, it also provides anthropogenic resources that can be exploited by some human-tolerant species. One species that is adept at using urban resources is the raccoon (*Procyon lotor*). Commonly found throughout cities in North America as well as parts of Europe and Asia, raccoons are able to use refuse to supplement their natural diets and human structures (e.g., attics, garages) as resting sites. To examine how urban resources may influence the body condition and behavior of urban-adapted wildlife, we trapped 192 (120 male, 72 female) adult raccoons from three sites across Chicago's urbanization gradient between October 2014 and January 2017. Lengths and weights of the raccoons were used to calculate individual body mass indices (BMIs). Additionally, 19 of the raccoons were tracked via GPS (n=7) or VHF (n=12) radiocollars. While male and female BMIs varied seasonally ($p < 0.01$), only female BMIs varied by location ($p < 0.001$). Male and female home range sizes were similar on average, but males included more unnatural space in their home ranges than females ($p < 0.05$). Regardless of how much unnatural space was used, however, raccoons remained within 500m of a green space (e.g., wooded river's edge). Close proximities to more "natural" habitats suggest that, while they do use anthropogenic resources, urban wildlife still rely on green spaces for persistence.

167: Indirect effects of wolf presence on moose behavior in Minnesota

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Wolves (*Canis lupus*) have increased in Minnesota due to legal protection and the increased availability of white-tailed deer (*Odocoileus virginianus*), which serve as prey. Simultaneously, moose (*Alces alces*) have experienced dramatic population declines. Predators can affect prey populations directly through lethal encounters, and indirectly through behavioral modifications, which reduce encounter rates (at the expense of foraging efficiency). We used first-passage times (FPTs = time required for an individual to move beyond a pre-specified radius), applied to moose GPS-locations in northeastern Minnesota (NE) and Voyageurs National Park (VNP), to test hypotheses regarding moose behavioral responses to changes in wolf predation risk. Larger FPTs were assumed to be associated with rest/foraging behaviors and shorter FPTs with travel/fleeing. We hypothesized that: (1) moose FPTs would be shorter in areas

selected by wolves, and that the relationship between moose FPTs and wolf habitat selection would be (2) stronger in NE, where moose make up a larger percentage of wolf diet, and (3) during times of day when wolves were more active. Moose FPTs were ~30% smaller in areas strongly avoided or selected for by wolves, and FPTs were more highly correlated with wolf habitat selection in NE than VNP. The relationship between FPTs and wolf resource selection did not show consistent patterns with time of day. These findings highlight the potential non-consumptive role wolf presence plays in moose behavior.

168^{HTA}: Regional landscape connectivity for recolonizing populations of American black bears (*Ursus americanus*)

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Landscape connectivity is vital for species conservation in human-modified landscapes. Although large carnivore recolonizations are globally uncommon, in southcentral USA American black bears (*Ursus americanus*) populations are increasing and expanding, yet the potential movement pathways are unknown. We used electronic circuit theory to develop a regional (Mississippi, Louisiana, Arkansas, Missouri, and eastern Texas) connectivity model. We estimated landscape resistance to movement using GIS-based features (1-km res.): land cover, distance to major rivers, road density, and highway presence. We selected national forests and wildlife refuges as patches among which to model movement pathways. Using citizen-reported bear sightings from Mississippi and Missouri, we validated our model comparing current density between sightings and random locations, and evaluated land cover selection at fine and coarse scales. Recolonizing bears choose both habitat and non-habitat for coarse scale movement, yet strongly avoided areas of human disturbance at a finer scale. Bear sightings occurred in areas of higher current density ($p < 0.001$), suggesting our model had good performance characterizing areas bears would use at a coarse scale. Contiguous forested areas and riparian corridors along major rivers appeared most likely to facilitate movement. Highways appeared as semi-permeable barriers to movement that intersected several connectivity bottlenecks. Management to maintain or improve connectivity in identified areas, including forest retention, preservation of riparian buffers, and highway mitigation techniques, may facilitate bear recolonization and aid broader conservation objectives.

169^F: Status and distribution of the plains spotted skunk (*Spilogale putorius interrupta*) in Texas

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Research of rare or understudied species often include novel approaches. The potentially endangered plains spotted skunk (*Spilogale putorius interrupta*) is an uncommon mephitid historically distributed throughout much of Texas. While museum data were sufficient to create a historical species distribution model, current data are lacking. To assess the status of the skunk, we collected presence data using both field surveys and crowd source methods. Field surveys were conducted throughout the state using live traps, trail cameras, and track plates. Presence data were also compiled from academic, wildlife, and citizen scientists' groups. Cumulatively, 103 observations in 25 counties were recorded using both methods. Fifteen skunks were detected during field surveys while 88 verified observations, from 2003 to present, were recorded using crowd source methods. During surveys, skunks were predominately found in either native prairie or juniper forest habitats. Spotted skunk presence data were used to create a MaxEnt species distribution model. The model predicts that the plains spotted skunk is still widely distributed in Texas. Survey and crowd source results indicate that the skunk has low localized abundance, but there are at least two populations with high local abundance: in the coastal prairies northwest of Houston and in juniper forests at Fort Hood in the Cross Timbers ecoregion of east-central Texas.

170^{E,HTA}: Population genetic structure of recolonizing American marten in the northeastern United States

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American marten (*Martes americana*) are patchily distributed at the southeastern periphery of their distribution in the northeastern United States. Populations have persisted in Maine and New York since European arrival, and are recovering after 20th century extirpations in New Hampshire and Vermont. We used molecular techniques to determine the source population(s) of two Vermont populations, and to estimate genetic structure throughout the northeast. Genetic data were obtained from 11 microsatellite loci and a 320 bp D-loop fragment from individuals from New York, southern Vermont, northern Vermont, New Hampshire, and Maine. Variation in allele and genotype frequencies, and estimates of *F*_{st} based on both microsatellite and mtDNA data suggest that the population in southern Vermont is remnant of a reintroduction that had previously been deemed unsuccessful, whereas the population in northeastern Vermont was colonized by dispersers from New Hampshire. Genetic clustering based on microsatellite data suggests that the population in New York is distinct from the remaining populations. Genetic clustering based on mtDNA data suggests further substructure within the two larger genetic clusters detected by microsatellite data, with a stronger contribution by individuals from New York to the founding of the southern Vermont population. These differences in genetic structuring likely result from male-biased dispersal and female philopatry. Our results highlight the importance of using multiple source populations and extensive monitoring programs in reintroduction efforts.

171: Preliminary results of an acoustic bat survey at Camp Gruber Training Center, Braggs, Oklahoma

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Acoustic detection coupled with ultrasonic analysis is an emerging field that has revolutionized the way that bat ecology is studied in recent years. I present results of a preliminary acoustic survey at Camp Gruber Training Center (CGTC), a military facility in Braggs, Oklahoma. The goals of this survey were to (1) estimate diversity of bat species living in or near the facility and (2) determine if any threatened or endangered species were present. I deployed Anabat Express acoustic detectors at 10 sites throughout CGTC during the summer of 2016. Collected bat call files were analyzed using three bat call identification software programs: Echoclass, Bat Call ID, and Kaleidoscope. These programs assign species identifications to call files based on characteristics of the echolocation calls produced by bats. Although the programs generally agreed on which species were most commonly detected, they differed in the proportions of those species. I will perform a physical (mist netting) survey in the summer of 2017 to test how well these programs represent the actual occurrence of species at CGTC.

172^F: Reconstructing the mechanisms behind the decline of snowshoe hare via translocation

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Climate change alters the geographic range boundaries of species, leading to local extirpations and novel community assemblages. Snowshoe hares (*Lepus americanus*) have experienced a significant range contraction in the northern Great Lakes region. Heightened mortality due to phenological mismatch between snow conditions and coat color change is a likely mechanism for the range contraction, but regional empirical evidence is lacking. To test the phenological mismatch hypothesis, we translocated 96 snowshoe hare from a site where they are currently abundant to a neighboring site in central Wisconsin where they have recently become functionally extirpated and monitored their persistence. Post-release, hares were monitored daily for survival via radio-telemetry and mortality events were immediately examined for evidence of predator-specific mortality using sign and genetic analysis of saliva. We obtained visual observations of translocated hares weekly, and documented their habitat use, local site snow conditions and hair coloration. We observed high mortality during snow-free periods when hares were white, with terrestrial carnivores (e.g. bobcat, coyote) being the primary predators. Our preliminary findings support the hypothesis that increased predation resulting from phenological mismatch and snow

cover attenuation can result in local extirpation, and help to reveal how climate change can interact with biotic forces to reshape the geographic range of historically abundant species.

173^F: Modeling the influence of landscape connectivity on dispersal movements of the northern flying squirrel

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Landscape connectivity is a fundamental component of successful wildlife dispersal. Evaluation of landscape connectivity may be accomplished using landscape characteristics or by examining wildlife dispersal behavior. Individual-based models allow for evaluation of landscape connectivity by simulating the interaction between species-specific dispersal behavior and landscape features. Our objective was to use a spatially-explicit IBM to evaluate how landscape connectivity influenced dispersal movements of northern flying squirrels (*Glaucomys sabrinus griseifrons*) under alternative forest management scenarios. We simulated timber harvests of various sizes and locations that increased heterogeneity and potentially influenced connectivity, and quantified landscape connectivity for flying squirrels of each harvest scenario. We evaluated the link between landscape connectivity and flying squirrel movement. Landscapes with greater connectivity exhibited longer flying squirrel dispersal distances, more sinuous dispersal paths, and a greater total area of landscape utilization. However, landscapes with greater overall habitat loss did not always exhibit the lowest level of connectivity. Our IBM demonstrated the importance of behavior in conjunction with landscape features to influence the movement of dispersing individuals. The spatially-explicit IBM provided a framework to evaluate the connectivity of the landscape, which could be a useful tool when evaluating the influence of landscape heterogeneity, stochastic behavior, and habitat management on wildlife movement and dispersal.

174^F: Accounting for species-specific biogenic fractionation of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ in hair and bone collagen

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Stable isotope analysis (SIA) is a useful tool for quantifying important characteristics of an animal's niche and estimating the contribution of potential food sources to an animal's diet. However, stable isotope enrichment factors (SIEFs) and tissue discrimination values (TDVs) must be considered when applying SIA to niche estimation: a SIEF is the difference in isotopic signal between the dietary resource and focal animal tissue, resulting from biogenesis, while TDVs are the differences in signal between tissue types, which arise due to differences in fractionation during biogenesis. In mammals, controlled feeding studies in a limited number of taxa have been used to estimate both SIEFs and TDVs, which are now regularly applied across a range of taxonomic groups. Use of these generalized values may produce inaccurate diet estimates or confound interspecific niche comparisons, especially when multiple tissue types are used. We measured the species-specific differences in $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ between hair and bone collagen for 7 Great Basin rodent species to evaluate their variability, within and among species. We found that hair-bone collagen TDVs are variable both across and within species. Furthermore, diet estimates made with collagen stable isotope values adjusted by species-specific vs. generalized TDVs obtained from the literature yield ecologically relevant differences. Thus, as SIA continues to develop as an analytical tool for ecologists, ongoing evaluation of our assumptions in its application is essential.

175^F: Unmanned aerial systems measure structural habitat quality for pygmy rabbits across multiple scales

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Assessing habitat quality is a primary goal of ecologists, however, evaluating habitat parameters at organism-relevant resolutions across management-relevant extents is challenging. Unmanned aerial systems (UAS) provide an avenue for bridging the gap between field-based habitat measurements and satellite-based remote sensing. Our goal in this study was to evaluate the potential for UAS technology to estimate several dimensions of habitat quality that provide security from predators and forage for pygmy rabbits (*Brachylagus idahoensis*) in a sagebrush-steppe environment. At the plant and patch scales, we compared UAS-derived estimates of vegetation height, volume, and concealment from aerial predators to field-based measurements and estimates from terrestrial laser scanning (TLS), another remote sensing technique. Then, we mapped habitat structure across two sagebrush landscapes in Idaho, USA. The UAS-derived estimates matched those from TLS for height ($r^2 = 0.85$), volume ($r^2 = 0.94$), and aerial concealment ($r^2 = 0.68$). However, there was less agreement with field-based measurements of height ($r^2 = 0.67$), volume ($r^2 = 0.31$), and aerial concealment ($r^2 = 0.29$). We suggest that the relatively poor fit of UAS to field-based data is likely driven by the coarse level of detail of field-based measurements compared with hundreds of measurements per plant by TLS and UAS. This work illustrates an approach for garnering fine-resolution habitat data across broad landscapes for use in studies of animal ecology, conservation, and land management.

176: Small mammals of Yacuri National Park, Loja Province, Ecuador

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In July 2016, a mammal survey was conducted in Yacuri National Park, Loja province, Ecuador. Yacuri National Park is located on the western slope of the Andes (4° 42'42"S, 79° 26'25"W). The survey area included a páramo bog 1 (3,393 m elevation), a páramo bog 2 (3,422 m elevation) a forest near the cabin (3,226 m elevation), a lower páramo (3,183 m elevation), a páramo lagoon (3,401 m elevation), a secondary forest (3,077 m elevation), and a mountain ridge (3,454 m elevation). Sherman traps, pitfall traps, and mist nets were used in collecting the specimens. 213 specimens were caught. A total of 10 species were collected including *Thomasomys cinereus*, *T. caudivarius*, *T. taczanowskii*, *Microryzomys altissimus*, *Caenolestes caniventer*, *Marmosops impavidus*, *Akodon mollis*, *Akodon sp.*, *Sturnira erythromos*, and *Anoura geoffroyi*. Two additional species were observed and photographed *Lycalopex culpaeus*, and *Sylvilagus brasiliensis*. This study also compared the effects of elevation on Ecuadorian rodent diversity at the taxonomic level of tribe.

177^{E,HTA}: Comparison of trapping techniques for *Glaucomys volans* in a bottomland hardwood forest in central Louisiana

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A variety of methods exist to survey southern flying squirrels. When trapping, the use of traps affixed to trees is generally recommended (e.g., Risch and Brady 1996). In my study, traps were positioned on trunks of trees approximately 1.5m above the ground. Traps were placed horizontally or vertically and baited with pecans, white-stripe sunflower seeds, or peanut butter and rolled oats. I investigated if any combination of trap orientation and bait type resulted in greater trap success.

Forty-seven individual flying squirrels were captured a total of 115 times over nearly 2,900 traps nights. Both horizontal and vertical traps baited with pecans had greater captures than expected, and all other treatments had less captures than expected based on availability. No preference for either vertically- or horizontally-oriented traps was observed. However, non-target captures were much more frequent in horizontal traps. I found no mention in the literature of either pecans as bait for flying squirrels, or traps being placed vertically on the trunks of trees. Based on my results, I recommend using vertically-placed traps baited with pecans in regions where pecans are native in order to maximize flying squirrel captures and minimize non-target captures.

178: Locomotor performance in the striped skunk (*Mephitis mephitis*)

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The striped skunk (*Mephitis mephitis*) is an ambulatory carnivore that has exchanged speed and active predation for omnivory and chemical defense against predators. Previous cost-of-transport research in Mustelidae suggests that specialized adaptations for exploiting a resource or environment tend to decrease efficiency during mammalian quadrupedal locomotion at lower speeds and improve energy economy at higher speeds. This study evaluated locomotor performance in the striped skunk and compared these results to those previously observed in more closely related Mustelidae. Using open-flow respirometry and a variable-speed treadmill, I measured oxygen consumption to estimate energy use and cost of transport and analyzed videos of the exercise trials to evaluate gait characteristics. At all speeds greater than a slow walking pace, striped skunks were less efficient than predicted by allometric equations. Striped skunks only used two gaits, walking and bounding, and unlike many mammals, never employed an intermediate trotting gait. These results suggest that unlike semi-arboreal *Mustela caurina*, and semi-aquatic mink and river otters, morphological adaptations in the striped skunk may increase their energy costs during locomotion at most speeds.

179: Comparative microbiomes of feeding generalist *Sciurus niger* and specialist *S. aberti*

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We compared the gastrointestinal microbiomes of Abert's squirrels (*Sciurus aberti*) and fox squirrels (*S. niger*) to evaluate interspecific and intraspecific microbial community composition. We hypothesized that dietary and gastrointestinal (GI) morphological differences between the two species would result in uniquely different communities and abundance of gut bacteria. Abert's squirrels exhibit a specialized diet consisting predominately of ponderosa pine (*Pinus ponderosa*) structures while fox squirrels exhibit a generalist diet. Four females of each species were collected (n=8) from a ponderosa pine-Gambel oak (*Quercus gambelii*) forest. We collected tissue samples from the stomach, small intestine, cecum, and large intestine, in addition to a fecal sample. Bacterial DNA samples were isolated and the V4 region of the 16s rRNA was used for sequence alignment. Operational taxonomic units (OTUs) were assigned using the workflow provided by QIIME. Results showed that microbial communities form distinct clusters in both species, but also within the upper and lower regions of the gastrointestinal tract. At the GI locations and species level, *Prevotella copri* and *Prevotella* spp. were the most important features for machine learning analysis. Abert's squirrels exhibited less variation in microbial communities between individuals than fox squirrels, which may be explained by their specialist diet. There were also functional differences identified from intraspecific comparisons of GI tract region using a PICRUST analysis.

180: Mineral phenology of forages available for migratory caribou in Alaska

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Productivity and movement of migratory ungulates can be influenced by the demand for energy, N and minerals. We collected 1296 samples of seven forages through the summer ranges of the central arctic and western arctic caribou herds between ordinal days 149 and 273 from 2011 to 2014. Minimum dietary concentrations of minerals required by lactating caribou (*Rangifer tarandus*) were estimated by combining published requirements for production in domestic ungulates with measures of food intake, mass change and milk yield of female caribou. Concentrations of available energy and N increase during early lactation and decline through the summer. Minerals do not follow the same temporal pattern as energy and N in caribou forages. In all forage species, concentrations of Ca and Mn increased over summer while those of P, K and Cu declined. Woody browse contained more Ca than graminoids especially in late summer.

Concentrations of P in all forages were below estimated requirements after mid-summer, especially in the central arctic range. Concentrations of Na in all forages were below dietary requirements except for some graminoids and the forb *Pedicularis spp.* on the coastal plain. Caribou may vary their movements to maximize net uptake of Na and P with N in early summer and balance Ca with P supplies in late summer.

181: The rest of the story: black bears' bed sites in northern Minnesota

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All mammals must sleep but where and why they sleep there is not always known. Based on the literature and previous experience, we hypothesized that black bears (*Ursus americanus*) would choose sites with overhead cover (to keep cool) in lowland areas (to avoid people) with a big tree nearby (that a bear could climb) compared to random sites. We hypothesized that females with cubs, compared to females without cubs, would choose bed sites close to big trees with coarse bark, which young cubs can climb easily, and with big horizontal limbs, on which mothers could wait. The most common trees in our study site that meet these requirements are white pines (*Pinus strobus*). We hypothesized that females with cubs would become less choosy of rest sites as summer progressed and cubs became more mobile. We used 4 hours of GPS locations clustered within the 25 m field error for our collars to identify nearly 400 potential bed sites. We chose 100 of these sites at random to visit and paired each potential bed site with a site 100 m in a random direction. We found bed sites at nearly every cluster site. Bed sites did differ from random sites, females with cubs did choose bed sites differently than females without cubs, and females with cubs did become less choosy as summer progressed.

182^F: Seasonal roost networks of southeastern myotis in an old-growth bottomland hardwood forest

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Little is known about the roosting habits of southeastern myotis, *Myotis austroriparius*, in Coastal Plain forests. Our objective was to examine the roost networks of southeastern myotis in Congaree National Park, an old-growth bottomland hardwood forest in the Upper Coastal Plain of South Carolina during winter (November-March) 2015-16 and summer (May-August) 2015 and 2016. We located roosts through opportunistic cavity searches and by tracking radio-tagged bats. Of roosts used by transmitted bats, 77.8% were used only during one season, 19.4% were used during two seasons, and 2.7% were used during all three seasons. To examine roost network structure, we calculated the number of primary connections between roosts which we defined as the number of bat-trips between two roosts. Single-season roosts had an average of 2.4 ± 0.3 primary connections to other roosts, two-season roosts had an average of 5.0 ± 2.0 connections to other roosts, and the three-season roost had 9 primary connections to other roosts. Using the network mapping program Gephi, we analyzed the structure of the roost network by season using roosts as nodes and connections as edges. Network analysis revealed that southeastern myotis used distinctly different roost networks in winter and summer. Analysis of seasonal variation in roost networks may be important for informing management decisions and lead to greater understanding of disease and parasite transmission as well as social organization.

183: New species of cottontails (Leporidae: *Sylvilagus*) from northern South America illuminate previously concealed regional biodiversity

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Of the 19 currently recognized species of *Sylvilagus* Gray, 1867, 15 inhabit North America, and only 5 are recognized in South America: *S. brasiliensis* Linnaeus, 1758 (throughout most of the continent); *S. varynaensis* Durant and Guevara, 2001, restricted to the southern lowlands of Venezuela (states of Barinas, Portuguesa, and Guarico); *S. andinus* (Thomas, 1897) from the Andean páramos of Ecuador

and potentially in a sporadic manner to the Colombian and Venezuelan Páramos; and *S. tapetillus* Thomas, 1913, from the coastal plain in the region of Rio de Janeiro. In addition to these, putative subspecies of *S. floridanus*, primarily a North American taxon, nominally are recognized from the grassland plains areas of northwestern South America east of the Andes. While *S. varynaensis* and *S. tapetillus* are monotypic, *S. brasiliensis* contains at least 37 named taxa in synonymy, distributed in various habitats; *S. andinus* requires further study. As a result of the recent description of a neotype for *S. brasiliensis*, it is now possible to assess species limits and begin the process of illuminating formerly obscured biological diversity in South American cottontails. Here, I describe a new species of *Sylvilagus* from the lowlands of western Suriname, and excise *S. sanctaemartae* Hershkovitz, 1950 from synonymy with *S. brasiliensis*. While some species of South American *Sylvilagus*, such as *S. sanctaemartae*, may be relatively widespread, other taxa, including *S. brasiliensis*, appear to be much more restricted in range. I explore some potential factors in an attempt to explain the evolutionary history and distribution of species in *Sylvilagus*.

184: Small mammal responses to climate change in the Colorado Rocky Mountains

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Many small mammals in North America are responding to anthropogenic climate change, particularly those with larger body sizes and at higher elevations. Here we assess current small mammal distributions across four elevational transects in Colorado—two in the southwestern San Juan Mountains and two in the northeastern Front Range Mountains. Average Colorado temperatures have increased by ~2°F with regional evidence that warming has been greatest at mid-elevations. At each of the 32 sites, we conducted live-trapping (1500 trap-nights), pitfall trapping (3600 trap-nights), and repeated visual surveys. We compare current elevational distributions to historical, pre-climate change distributions based on ~35,000 georeferenced specimens, which are partitioned between the two mountain ranges and pre- and post-1970s. Robustness of detected range shifts is assessed using both contemporary population sizes and counts of historical specimens across the sampled ranges. Upward shifts and upper limit expansions as well as a few downward shifts in elevation are detected on both mountain ranges. As in most multi-species studies, some species have no detectable response, in this case typically the common, wide-ranging species. A few species were historically detected across a broad elevational range, but in contemporary surveys were rare and more narrowly detected. Additionally, the temperature-range shift response is reinforced by the significant trend of higher elevational range limits in the warmer San Juan Mountains compared to the Front Range for shared species.

185: Whither Climate Change in the Kluane Boreal Forest Ecosystem?

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The boreal forest is the largest forest ecosystem in North America. Since 1973, we have documented major changes in the dynamics of the vertebrate food web in the southwestern Yukon, an area little affected by humans but strongly affected by climate change. Plant growth has been increasing, particularly visible in the shrub layer. Changing predator-prey dynamics are associated with colonization by new prey species and new predators. We have documented snowshoe hares over five 9-10 year cycles and cyclic peaks have been steadily diminishing. The dynamics of the hare cycle are explained by direct predation and the fear of predators. Every predator in the system eats hares with lynx, coyotes, and great horned owls the major ones. Climate affects hares by its impact on snow depth and hardness and coat-color mismatch, which affect predator hunting success, particularly of coyotes. Vole cycles have increased in amplitude with increased primary productivity, and the overall increase in vole density has allowed an increase in predator populations of marten and weasels. Voles are now responsible for more of the energy flow in this part of the boreal forest than are snowshoe hares and red squirrels. Arctic

ground squirrels, formerly abundant, have disappeared from the forest since 2000 and are in a predator pit. Future trends for small mammals in this ecosystem depend upon climate change and increased human intrusion.

186: Climate forcing, abundance-occupancy relationships, and diet specialization in an African small-mammal community

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Abundance-occupancy relationships (AORs) are widespread in nature: species with expansive distributions tend to be locally abundant, whereas those with restricted distributions tend to be locally rare. The ubiquity of AORs has been hypothesized to reflect differences in resource requirements among species, such that those species that are able to use a broad array of resources should occur at more sites, and be relatively abundant in the sites that they occupy. This prediction of the resource breadth hypothesis has proven challenging to test, because resource preferences (which are flexible) often are conflated with resource requirements (which are fixed). We tested the resource-breadth hypothesis in a guild of small, herbivorous mammals exposed to shifts in resource availability driven by a short but steep rainfall gradient and exclusion of ungulates. Through a combination of repeated sampling of individuals, blood plasma carbon isotopes, and reconstruction of diet profiles through meta-barcoding of fecal DNA, we show that diet generalism arises within and among individuals in a population, and manifests either as individuals adjusting resource use in the face of shifting availability through time, or resource use in proportion to availability within a home range. Rare, restricted species tended to be specialists whose resource use was related weakly to availability. Quantifying species differences in resource use relative to availability should reveal mechanisms underlying AORs and responses to changing climates.

187: Responses of Australian desert mammals to extreme climatic events: past, present, and future

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Arid Australian environments are characterized by long periods of rainfall deficit and heavy but infrequent rains and broad-scale flooding. Rodents respond to these events by showing dramatic 'boom' and 'bust' dynamics, as do some of their mid-sized marsupial predators; small insectivorous marsupials, by contrast, show idiosyncratic responses. Although large rainfalls herald pulses of productivity, these events are exploited also by introduced predators such as the European red fox (*Vulpes vulpes*) and feral cat (*Felis catus*). Wildfires frequently burn large areas the year after large rainfall events, removing all above-ground vegetation. The high activity of introduced predators and lack of cover at these times expose small mammals to intense predation; populations may become locally extinct or retreat to unburned refuges. We quantify these patterns, using data on four focal species (two rodents, two dasyurid marsupials) studied for 27 years at multiple sites over a large (8000 square kilometer) area in Australia's most extreme arid region, the Simpson Desert. We show that a canid predator, the dingo (*Canis dingo*) can mitigate the effects of foxes and cats on native small mammals by suppressing their activity, and also quantify the importance of small refuge sites for small mammal persistence. Past trends and future predictions indicate that the boom and bust cycle will intensify due to climate change, potentially exacerbating the threats faced by small native mammals.

188: Variation in femora of Late Pleistocene muskrats (*Ondatra zibethicus*) from Darke County, Ohio

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Excavations at the Carter Bog site near Ansonia in Darke County, Ohio in the early 1970s produced hundreds of fossilized bones of Late Pleistocene (Wisconsinan-aged) animals, including major deposits of giant beaver (*Castoroides ohioensis*), Jefferson's ground sloth (*Megalonyx jeffersonii*), American mastodon (*Mammuth americanum*), stagmoose (*Cervalces scotti*), and muskrat (*Ondatra zibethicus*). Despite the potential wealth of information to be gained from these specimens, most of this material has remained unexamined since its recovery. Muskrats, in particular, are represented by hundreds of postcranial elements (including humeri, tibiofibulae, and femora). Here we report preliminary findings of analyses of more than 200 muskrat femora excavated from 3 different strata that have been radiocarbon dated to between 11,700 and 14,700 years before present. Our initial results indicate a possible shift in body size (from smaller to larger individuals) within the Carter Bog muskrat population over this timeframe. We also outline our goals for future studies that take advantage of the large numbers of fossil elements of muskrats and other taxa that are available from this site. Using these elements as proxies for body size will allow us to shed light on variation in muskrat populations through time during the late Pleistocene, when the climate of North America was changing.

189^F: Usage of a major North Dakota river as a corridor by migratory bats

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The devastating spread of White-Nose Syndrome has led to an increasing body of work on hibernating bats; yet, we still lack basic information about the migratory ecology of most species, such as the specific corridors or land features used during migration. North Dakota is a state not abundantly equipped with natural hibernacula; hence, most summer residents presumably migrate to southerly sites for the winter months. Previous work suggests that rivers may be important migratory corridors for bats, but this has rarely been quantified or studied in detail. The goal of this work was to assess the importance of a major river corridor in central ND as a migratory corridor for bats. In Summer 2016, ultrasonic detectors with two microphones each were placed along the southward-flowing Missouri River in central ND. Microphones at each site were arranged parallel to the river and positioned 10m apart. Directionality (northward/southward flight) or nondirectionality of recorded bats was determined by analysis of the resulting stereo files in which calls were sequentially detected by both microphones. Directionality patterns varied over time and between species, likely due to species-specific migratory patterns and behaviors. The results of this study will help us better understand the migratory ecology of bats in the Northern Great Plains.

190: Morphometric analysis and geographical-climatic distribution of endemic rodents in the “*Peromyscus megalops*” species group

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Deer mice of the *Peromyscus megalops* species group are endemic to Mexico and they mainly occur in montane cloud forests, one of the most threatened ecosystems in the country. Species in this group are less studied than other *Peromyscus* species, and many of the biological characters shared between them are not well-defined. We analyzed geographic variation in the three species of the *Peromyscus megalops* species group using morphometric analyses and ecological niche modeling. We examined specimens of *P. megalops*, *P. melanurus*, and *P. melanocarpus* housed in Mexican collections, collecting measurements for 16 cranial characters. We gathered occurrence records for each of the species, which were used together with bioclimatic layers in MaxEnt for ecological niche modeling. We find important variation between the species, evident in the length of the maxillary tooth row and the interorbital and frontal breadths, where variation in dental features might suggest that these species differ in their feeding habits. Examining the bioclimatic niches of the three species, the most important ecological variables were those related to precipitation. *P. melanurus* and *P. megalops* had significantly similar niches, with *P. melanocarpus* occurring in areas with colder and more humid climates. These results suggest that morphological divergence has not accompanied niche divergence in this group.

191^F: The role of the Andean rivers in the speciation of Sigmodontinae: an approach from *Oligoryzomys*

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The species *Oligoryzomys andinus* and *O. destructor* are distributed along the Central Andes, which is dissected by three main rivers: Marañon, Huallaga, and Apurimac. These rivers have been regarded as physical boundaries of areas of endemism and proposed to act as barriers for Andean biota, promoting divergences dated between ~3.5 and ~2.3 Mya, and hypothesized might have driven the speciation within the Andes. Our aim is to evaluate the role of these Andean rivers on the diversification of *Oligoryzomys* spp. by assessing different scenarios across the rivers: a) allopatric barrier, b) preexisting barrier with independent colonization events, c) preexisting barrier with colonization from one side to the other of the river by founder effect, and d) non-allopatric barrier. In order to assess these scenarios four loci (one mitochondrial and three nuclear) were sequenced, phylogeographic analyses with a coalescent approach were implemented, and taxonomic revisions were conducted. Results show: 1) the diversity of Central Andean *Oligoryzomys* is greater than is currently known; 2) three lineages of *Oligoryzomys* invaded the Central Andes from the lowlands; 3) the most likely scenario accounting for the differentiation between populations (from one lineage of *Oligoryzomys*) across the Apurimac river is one where the river acted as a preexisting barrier with a single colonization event from the southern toward northern side of the river ~1 Mya, without current gene flow.

192: Influence of trap modifications and environmental predictors on capture success of southern flying squirrels

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Sherman traps are the most commonly used live traps in studies of small mammals and have been successfully used in the capture of arboreal species like the southern flying squirrels (*Glaucomys volans*). However, southern flying squirrels spend proportionately less time foraging on the ground, which necessitates above-ground trapping methods and modifications of capture protocols. Further, quantitative estimates of factors affecting capture success of flying squirrel populations has focused solely on effects of trapping methodologies. We developed and evaluated the efficacy of a portable Sherman trap design for capturing southern flying squirrels. We used logistic regression to quantify potential effects of time-dependent and time-independent factors on capture success of southern flying squirrels. We recorded a total of 165 capture events (119 females, 44 males, 2 unknown) using our modified Sherman trap design. Probability of capture success decreased 0.10 per 1° C increase in daily maximum temperature and by 0.09 per unit increase in wind speed (km/hr). Conversely, probability of capture success increased by 1.2 per 1° C increase in daily minimum temperature. Probability of capturing flying squirrels was negatively associated with trap orientation. Our modified trap design is a safe, efficient, and cost-effective capture method when moderate weather (temperature, wind speed) conditions prevail. Further, strategic placement (northeast side of tree) of traps and quantitative information on site-specific characteristics could increase southern flying squirrel capture success.

193: Preliminary data on the genetic structure of puma (*Puma concolor*) populations in Argentina.

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Genetic isolation due to habitat fragmentation and the consequent loss of landscape connectivity is considered a major threat to wildlife conservation, especially for wide-ranging carnivores, such as puma. In this work we investigated puma genetic diversity and population structure in Argentina, increasingly affected by habitat loss, using 40 puma samples including scats, dead animals and museum specimens. We analyzed a set of 30 microsatellite loci displaying between 3 and 13 alleles. Across all samples and 29 loci (missing value < 5%), the average observed heterozygosity was $H_o=0.61$, average expected heterozygosity was $H_e=0.70$ and average number of alleles per locus was $N_a=5.83$. Population structure analysis of 22 samples revealed two distinct genetic subdivisions in central-southern Argentina corresponding to Buenos Aires and Chubut Provinces. This preliminary result suggests the potential presence of a genetically structured population between two areas only 343 km apart. Future work will include the analyses of a comprehensive dataset throughout almost the entire country combining recent and historical samples to confirm the observed population structure and estimate genetic diversity and gene flow across populations. Moreover, it will allow inferences on possible demographic events of puma population in Argentina and on the presence of barriers to puma dispersion. Maintaining landscape connectivity may be necessary for the conservation of viable puma populations, mostly for a species living in a fragmented landscape and under heavy hunting pressure.

194^F: Determining patterns of community assembly using species distribution models and Late Quaternary fossil assemblages

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The importance of neutral and non-neutral processes on the composition of communities is often debated. The relative importance of different processes can vary depending on the scale of the study, species pool size, and the nature of climate or habitat change experienced by a community. However, it is difficult to predict which processes are important under specific scenarios, making it challenging to determine how species will assemble into communities as they respond to future climate change. In this study we assess the importance of climate in facilitating the assembly of small mammals at Samwell Cave over the previous 18,000 years. We built species distribution models to generate climate-based predictions of community composition at fourteen past time periods. The predicted communities were compared to the fossil communities found at Samwell Cave in each of the time periods; matches and mismatches were attributed to climate, interactions, or other processes. Preliminary results suggest that the presence of some species in the community can be attributed to climate but mismatches for other species suggest that climate is not the only factor determining the composition of communities. Further, the importance of climate filtering on the community assembly process is not correlated with the amount of climate variation observed between two time periods. These results suggest that projections of future mammalian communities will need to include factors in addition to climate.

195^F: Phylogeography of *Sciurus carolinensis*: can museum specimens say anything new? yes.

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Museum specimens can potentially provide largely unexploited phylogeographic data, especially for species that are abundant or well-studied. We investigated this potential by assembling (onsite and online) geographic and temporal data for 1928 adult *Sciurus carolinensis* (American grey tree squirrel) from 27 museums. Subspecies was specified for 1159 specimens: 273 *S. c. carolinensis*, 59 *S. c. extimus*, 72 *S. c. fuliginosus*, 58 *S. c. hypophaeus*, 697 *S. c. pennsylvanicus*. Collection localities were converted to latitude and longitude. The data generally clustered geographically by subspecies with notable curiosities. First, the geographical range of *S. c. pennsylvanicus* branched in two distinct directions from a central point on the east coast (~42°N, 72°W). One branch went directly west along the

~42oN latitude and one branch headed southwest. Second, although *S. c. carolinensis* has a distinct cluster in the southeast near northern Florida, it has a wide, sporadic distribution further to the west and north (~75-95oW, 32-40oN). Finally, specimens without an associated subspecies geographically cluster in two distinct groups. One cluster matches the distribution of *S. c. pennsylvanicus*, but the other cluster (collected primarily from 1960-2000) has a western distribution that is not clearly part of the distribution of the named subspecies. Our investigations reveal that even a broad-based, somewhat-coarse use of specimen data from museums can yield novel information on phylogeographic distributions.

196: Impacts of long-term predation risk on stress response and behavior in the rodent, *Octodon degus*

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Glucocorticoids are secreted in response to stressors across a wide range of taxa. One common stressor experienced by animals is encounters with predators. Chronic predation risk is linked to elevated levels of baseline and stress-induced glucocorticoids as well as poor negative feedback efficacy. Separately, animals in areas with higher predation risk display more bold behavior. Furthermore, a negative correlation exists between glucocorticoid levels and boldness behavior. To date, no studies have examined the interplay between predation risk, stress response, and behavior. It remains unexplained why chronic predation risk is linked to elevated glucocorticoid levels as well as bolder behavior, and yet glucocorticoid levels are negatively correlated with boldness. Here, we assess these links in the degu (*Octodon degus*), a rodent endemic to Chile. Work was carried out in Fray Jorge National Park from July-November 2016 in four plots that exclude aerial and terrestrial predators and four control plots. Degus were trapped, baseline and stress-induced blood samples were obtained, a dexamethasone challenge was performed, and a final blood sample was taken to determine negative feedback efficacy. Boldness and exploratory behavior were assessed using an open-field test. All data is being analyzed and when completed this study will be the first to report on the interaction between predation risk, stress response, and behavior, thus filling in current gaps in knowledge.

197^F: Habitat associations of small mammals along an extensive elevation gradient

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Habitat associations and preferences interact with competitive interactions to play an important role in determining the composition and structure of small mammal community assemblages. These associations can mediate responses to climate change and can change across space and through time, so there is a need for complete studies spanning an entire gradient. To improve our understanding of this relationship, we are completing a comprehensive assessment of species composition and habitat associations across a 2,500 m elevation gradient spanning 8 distinct habitats in southern California. Moreover, we are integrating this with previous work to assess how small mammal communities and their associations have changed since a similar survey in the 1960s. We are using 10x10 trapping grids (15-m spacing) with 12" Sherman live traps to survey heteromyid and cricetid rodents in paired sites at 8 elevations along this gradient. I will apply canonical correspondence analysis, a form of constrained ordination, to analyze the relationship between community assemblages and habitat metrics. In the face of climate change and anthropogenic desertification, deeper understanding of community structure and habitat associations along such gradients is fundamental to our ability to predict the response of small mammal communities to climate change.

198: Irregular annual cycles in captive Southern Idaho Ground Squirrels (*Urocitellus endemicus*)

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The southern Idaho ground squirrel (*Urocitellus endemicus*) is one of two mammal species endemic to Idaho. It is active above ground from January or February until May or June; it is normally inactive underground in torpor for the remainder of the year, but the annual cycle has not been studied in detail. *U. endemicus* was a Candidate species from 2001 until 2015; in 2002, a captive population was established at Zoo Boise. We monitored activity of a population of 26 captive-born southern Idaho ground squirrels at Zoo Boise over a period of one year (March 2016 to February 2017) using a Biomark™ Multiplexing Antenna Pit Tag Reading System with 8 antennae. The pen had 8 feeding stations with one antenna at each. Activity of individual squirrels varied from 63 to 211 (mean 132) days per year. Although Zoo Boise is climatically similar, and attempted to emulate natural availability of food and water, the annual cycle of captive animals was seriously out of phase that of wild squirrels. We documented high levels of activity during fall and early winter. Some individuals showed idiosyncratic periods of activity, alternating days to months of activity and inactivity; one adult male was active in fall only. These results have implications for managing captive breeding populations of a hibernating species.

199^F: A diversity assessment of small mammals and their ectoparasites in south Texas

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Texas is a geographically variable state containing a large diversity of plants and animals. Due to widespread private land ownership, organismal biodiversity is poorly known across the southern portion of the state. We investigated the diversity of small mammals and their ectoparasites on private properties owned by the East Foundation in an effort to document and better understand vertebrate and invertebrate biodiversity across South Texas. Small mammals (primarily rodents) were captured and carefully inspected for ectoparasites, and genetic differentiation of widespread mammal species was assessed using the mitochondrial ND2 gene. In total, 337 individual mammals representing 18 species were retained and examined for ectoparasites. Of the widespread mammal species, genetic differentiation was generally low (although there were some exceptions). Sixteen mammal species and 273 individuals (81%) were parasitized by approximately 2,200 individuals of mites, lice, ticks, and/or fleas. Mites, ticks, lice, and fleas parasitized 16, 9, 9, and 7 mammal species, respectively. Most host associations have already been documented in the literature, although a new association of a hoplopleurid louse parasitizing the northern pygmy mouse (*Baiomys taylori*) was noted. Our work will aid in broadening the knowledge of general biodiversity in this area, including possibly discovering new species and associations for South Texas.

200^F: Are elephant shrews more like elephants, or shrews? Quantifying life-history and demographics of *Elephantulus rufescens*

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Across orders of mammals, life history strategies often fall along a fast-slow continuum. Typically, “fast-living” mammals have short periods of gestation and lactation, mature quickly, produce many altricial offspring, and are short-lived and small-bodied. “Slow-living” mammals tend toward opposite patterns. The rufous elephant shrew (*Elephantulus rufescens*) is a small (35 – 65 g) Afrotherian with life history characteristics from both sides of the fast-slow continuum (short time-to-weaning and lifespan; small litters of precocial young). To assess how this unusual life history interacts with environmental variation to shape population size and growth, we examined 7 years of demographic data in the UHURU (Ungulate Herbivory Under Rainfall Uncertainty) experiment in central Kenya. Using robust design mark-recapture methods, we estimated survival, recruitment, and population size to project population growth as a function of environmental covariates (rainfall, vegetation community). To quantify how the unusual life history of *E. rufescens* manifests as population-level responses to seasonal shifts in rainfall and vegetative cover, we compared demographic sensitivities between *E. rufescens* and more “typical” small

mammals with which it co-occurs: the fringe-tailed gerbil (*Gerbilliscus robustus*), Hinde's bush rat (*Aethomys hindei*), and the northern pouched mouse (*Saccostomus mearnsi*). Where mammals deviate from life-history expectations, population responses to environmental variation can reveal the costs and benefits associated with particular combinations of life-history characteristics, especially when contrasted with those of typical mammals with which they co-occur.

201^E: Immunogenetic variation in a declining native species and its introduced congener

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Evaluating immunogenetic variation in wild populations can provide valuable insights into the maintenance of functionally significant genetic diversity. This information is particularly valuable for species facing ecological challenges widely relevant to other taxa, such as population decline, habitat loss and fragmentation, or species invasion. Here, we investigate immunogenetic diversity in two New England mammals: a declining native species that is part of an ongoing reintroduction effort (the New England cottontail; NEC; *Sylvilagus transitionalis*) and an introduced congener that is thriving regionally (the eastern cottontail; EC; *S. floridanus*). We utilize a candidate gene approach coupled with next-generation sequencing to capture immunogenetic variation 1) across naturally-occurring NEC populations, 2) within the NEC captive breeding and reintroduction program, and 3) across ECs within their introduced New England range. Initial sequencing efforts target major histocompatibility complex (MHC) class II genes, which are involved in parasite/pathogen defense. Preliminary results support historical positive selection acting on NEC MHC genes, limited contemporary diversity within and across populations, and that MHC diversity within the NEC captive breeding program is reflective of naturally-occurring variation. Analyses of additional immune genes and of ECs are forthcoming. Knowledge of how immunogenetic variation is maintained across NEC and EC populations is of direct value to ongoing conservation efforts and also enhances our understanding of how non-neutral genetic diversity is maintained across ecological and demographic challenges of global relevance.

202: Fisher (*Pekania pennanti*) reproductive parameters in the southern Sierra Nevada relative to the broader range

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The fisher (*Pekania pennanti*) is an elusive forest carnivore of conservation concern that reaches the southernmost limit of its distribution in the southern Sierra Nevada of California. Data on fisher reproduction in this region are limited and applicability of parameters from other areas uncertain. To address this, we reviewed literature on fisher reproduction over the species' range, and compare this with data collected over 7 years in the southern Sierra Nevada; we emphasize 1) the proportion of females reproducing, 2) parturition date, and 3) litter size. On average across its range, 71% of adult females reproduced (range, 40 – 100%; $n = 16$), parturition occurred on 25 March (total range, 3 March – 17 April; $n = 16$), and litter size was 2.5 (total range, 1 – 4; $n = 16$). In our study area, we tracked 42 adult female fishers, 35 of which used 257 reproductive dens; 0.86 (range, 0.79 – 1.0) of females attempted denning and 0.75 (range across years, 0.64 – 1.0) were successful. Mean parturition date was 30 March (range 17 March – 12 April; $n = 69$), and mean litter size was 1.57 (range, 1 – 3; $n = 75$). Female fishers in the southern Sierra Nevada reproduced at a rate comparable to or higher than elsewhere in North America, gave birth at similar or later dates, but had the lowest litter size reported for the species.

203: Environmental factors and population demography of the big-eared woodrat in coastal-central California

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The effects on small mammal populations of changing weather patterns are notably lacking for California's 3 million ha of oak woodland (*Quercus* spp.). To begin to fill this information gap, we applied Pradel's temporal symmetry models to a 20-year biannual capture-mark-recapture (CMR) dataset (1993-2014) collected in oak woodland of coastal-central California. We estimated capture probability (p), apparent survival (Φ), recruitment rate (f) and realized population growth rate (λ) of the big-eared woodrat (*Neotoma macrotis*), and tested for the effects of temperature and rainfall on the woodrat's vital rates. Monthly λ was 0.999, indicative of a stable population, although it varied over time (from 0.848 to 1.189). Monthly Φ was 0.937, higher for females (0.942) than males (0.930), and higher in spring (0.941) than in fall (0.934). Monthly f was 0.063, with the highest f among males in the fall (0.127). Rainfall and temperature (with a one-season lag) strongly influenced Φ and f but in opposite directions; high rainfall increased Φ but decreased f , whereas high temperature decreased Φ but increased f . Although some populations of big-eared woodrat in marginal habitats may be threatened by predicted weather patterns, the thermal modification provided by woodrat dwellings and phenotypical adjustment of a litter to future environmental conditions (i.e., bet-hedging) may buffer climate change effects.

204: Hybridization of deer in Texas utilizing a sperm-egg fusion protein called zonadhesin

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White-tailed Deer (*Odocoileus virginianus*) and Mule Deer (*Odocoileus hemionus*) are known to hybridize across the United States and Canada. In Texas, hybridization between these two species occurs in the Trans-Pecos region and along the edges of the Llano Estacado. Although these two taxa are recognized as biological species, some studies have shown that local hybridization may be as high as 24%. To detect intraspecific hybridization such as this, it is often necessary to use molecular methods that can target genes presumably involved in isolating mechanisms. Herein, we examine a gene (zonadhesin, ZAN) involved in post-mating isolation. This gene codes for a sperm protein that is crucial in species-specific binding of the spermatozoa with the zona pellucida of the egg during fertilization. It is thought that ZAN is a possible isolating mechanism between closely related species by controlling gamete binding across species boundaries. When hybridization occurs, this crucial isolating barrier presumably fails. It may be that the divergence time is so recent between these species that this barrier is not yet established. Testes, muscle, and liver tissues from six Mule Deer and five White-tailed Deer individuals were harvested by hunters and Texas Parks and Wildlife employees from Cottle and Kerr counties. In addition, cytochrome-*b* and retinoid binding protein gene both will be utilized to determine a background genotype on individuals used in this study.

205: Population ecology of mule deer in northeastern Oregon: understanding the fundamental role of nutrition

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Since the 1960's, western North America has experienced a decline in mule deer populations throughout their historic range, and the factors contributing to this decline have been a source of substantial debate among both scientists and managers. Reduced quality and quantity of habitat and competition with other ungulates have been implicated, but a mechanistic understanding of the relative importance of these factors remains elusive. Habitat loss or degradation may impose nutritional constraints on deer that can lead to malnutrition, starvation, disease, or increased risk of predation. Such effects also may interact with density-dependence, resulting in the manifestation of density dependent feedbacks on body condition, fecundity and survival at smaller population sizes. Additionally, it has been hypothesized that mule deer

and elk compete for resources, and that to mitigate the negative impacts of competition and facilitate coexistence, mule deer may avoid elk in space or time, and/or use alternative resources. Our research focuses on three main objectives: 1) assess the degree to which mule deer are nutritionally limited; 2) determine the degree to which nutritional limitation is a direct result of habitat quality, an indirect result of competition, or a combination of these; and 3) determine if elk behavior affects performance of mule deer by limiting access to high-quality forage, thereby influencing the degree of nutritional stress experienced by deer.

206^F: Documenting the interactions of leopards (*Panthera pardus*) and anthropogenic landscape features on a livestock ranch in central Kenya

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Understanding the behavior and ecology of large carnivores in human-dominated landscapes is important for developing sustainable land use strategies that are capable of meeting the needs of humans and wildlife. Throughout their geographical range, leopards (*Panthera pardus*) come into conflict with humans when they threaten safety and livelihoods, but their behavior and ecology are poorly documented because of this species' stealth and elusive nature. My research attempts to overcome past limitations by combining high-resolution GPS and accelerometer data collected from free-ranging leopards with recent computational and statistical methods from the field of movement ecology. For this presentation, I will demonstrate how I use stochastic simulations of animal movement, called random walks, to examine how leopards alter their habitat preferences across gradients of anthropogenic disturbance. I will also show how I use a Bayesian state-space statistical model to infer the latent behavioral state of individual leopards at each observed location. Combined, these techniques allow me to elucidate the behavioral and environmental correlates of human-leopard interactions on a livestock ranch in Laikipia, Kenya.

207: Effects of forest management techniques on bat habitat use at Fort Indiantown Gap, Pennsylvania

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Bats in the eastern United States currently face a host of threats, including white-nose syndrome. Several species are being evaluated for threatened or endangered status due to dramatic population declines. Recent research suggests that conservation of summer habitat may be one of the most effective conservation strategies for these populations. This approach will require a clearer understanding of how forestry practices affect bat communities. The objective of this study was to assess the impacts of forest management techniques on use of summer bat habitat. We focused on the bat community at Fort Indiantown Gap, a military installation in Pennsylvania, where data on forest composition, management treatments, and bat species presence have been collected since 2003. We collected additional data by mist-netting and acoustic monitoring during summer 2016, which we compared to historical data to examine changes in the bat community by forest treatment over time. We hypothesized that bat habitat use will positively correlate with higher burning rates from prescribed fire, and higher rates of mechanical thinning. Both techniques are expected to reduce clutter and increase insect abundance, which are generally beneficial to bat species. Investigating these relationships can further our understanding of bat habitat use, and better inform land managers of best practices to manage bat summer roosting and foraging habitats.

208^F: Development of a y-maze visual assay for *Peromyscus leucopus* and *Sigmodon hispidus*

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Rodent responses to light stimuli are important in determining many aspects of their behavior such as foraging ecology, predator avoidance, and habitat choice. Retinal damage has been observed by other investigators in laboratory rodents exposed to lead. Vision in wild mammals may be impacted by Pb and others contaminants in the environment. We developed a y-maze assay for use in measuring initial response to light stimuli in white-footed mice (*Peromyscus leucopus*) and hispid cotton rats (*Sigmodon hispidus*). Our goals were to determine usefulness of this device in assessing response to light stimuli in these species and to establish baseline responses in wild animals not exposed to environmental contaminants. We used light (40 – 45 lux) in a randomly selected arm of the y-maze as our stimulus and recorded whether animals chose the lighted arm or the dark arm of the y-maze. Both species readily ran through the y-maze. *Peromyscus leucopus* chose the dark arm 80% of the time ($n = 20$, $p = 0.01$) but *Sigmodon hispidus* chose the dark arm only 67% of the time ($n = 12$, $p = 0.39$). Based on these data, this apparatus shows promise for determining response to light stimulus in wild rodents. Next, we will use this device to investigate effects of environmental Pb on vision in these species.

209^E: Effects of domestic dog scent on nocturnal small mammal foraging

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To better understand how domestic dogs affect native wildlife, we tested whether dog scent decreases nocturnal foraging by small mammals in oak-woodland habitat. We set eight North-South oriented transects in the oak-woodlands of the University of California Fort Ord Natural Reserve in Marina, California. We placed trays containing a mix of seed and sand at 5-m intervals along each transect, as well as a dog urine scent station at one end of each transect and a control (i.e., water) scent station at the other end. We measured Giving Up Densities (i.e., GUD; the density of seed remaining when animals give up foraging) with distance from dog scent by weighing the seed remaining in each tray after each of six nights of foraging. To account for variation in foraging related to vegetative cover, we also measured the distance from each seed tray to vegetation above it. We found GUD decreased with time, but did not vary with distance to either dog scent station or vegetative cover. Our preliminary results suggest small mammal perception of risk does not vary with either distance from dog urine scent or height of vegetative cover, but decreases as small mammals become accustomed to visiting seed trays each night. Thus, the scent of domestic dogs may not negatively affect foraging of native nocturnal small mammals in oak-woodland habitats.

210: Intraspecific space use in *Peromyscus polionotus*

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Sociality in rodents varies along a continuum from completely solitary, except when mating, to obligate communal living. In the genus *Peromyscus*, some species (*P. leucopus* and *P. maniculatus*) exhibit sociality at certain times and in certain environmental conditions, while other species (e.g., *P. californicus*) are socially monogamous. *Peromyscus polionotus*, is a common member of communities in the southeastern U.S. that is found on sandy soils where it constructs burrows. This species is also monogamous. Monogamy should be reflected in space use where males and females share overlapping home ranges, and home range size is equal. In this study, we examined home ranges and burrow use of 38 individuals using radio telemetry in winter of 2014-2015, spring of 2015, and summer of 2015. Home range size ranged from 1306 m² - 1532 m² and did not differ between sexes or seasons. Home ranges of males and females overlapped, and there was a pattern of site fidelity. Burrows were clustered spatially and the location of burrows persisted over time. Burrows were used by multiple combinations of mice, including all types of pairs and trios. Over the course of the study, groups of mice used multiple burrows. Groups included both reproductive and non-reproductive individuals. Our results support monogamy in this species, and a higher level of sociality than is found in other members of the genus.

211: Abundance, activity patterns and interactions among ocelots, bobcats, cattle, nilgai, feral hog, and javelinas

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In southern Texas, ocelots (*Leopardus pardalis albescens*) are located in two small populations on private and public lands in Willacy and Cameron counties. East El Sauz Ranch of the East Foundation, in Willacy County, has the largest known population of ocelots in the United States. Research on ocelot interactions with other carnivores and prey species have been previously studied across their geographic range, however interactions with cattle (*Bos taurus*) and game species on private lands has not been examined. This study analyzes photographic data from 2011-2017 to examine differences in abundance, activity patterns and interactions among ocelot, bobcat (*Lynx rufus*), cattle, and three game species, nilgai (*Boselaphus tragocamelus*), feral hogs (*Sus scrofa*), and javelina (*Pecari tajacu*). We will focus on use of trails and occurrences within dense thornshrub by the target species. Patterns showed that the two smaller game species, hog and javelina, had greater overlap of activity. They used areas that were secluded and isolated, similar to behavior observed by ocelots. Nilgai was not related to ocelot movement or activity. Information derived from this study will assist management of cattle, game species, bobcat and ocelot coexistence. Furthermore, these results will benefit future ocelot recovery and conservation on private lands in southern Texas.

212: Recovery of an imperiled swamp rabbit metapopulation following the Bird's Point Levee breach

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In an effort to prevent flooding in Cairo, Illinois during spring of 2011, the U.S. Army Corps of Engineers activated the Bird's Point-New Madrid Floodway. This event resulted in scouring of the floodway, with an immediate effect on established populations of swamp rabbits. In this study, we assess the recovery of the swamp rabbit metapopulation within the floodway. We used occupancy data from 3 statewide surveys for swamp rabbits (1992, 2001, and 2011) to estimate parameters for a spatial patch occupancy model. Beginning in 2011, we conducted yearly surveys of habitat patches within and along the New Madrid Floodway. The parameterized occupancy model was then used to simulate potential responses to the flooding event. Both the model and occupancy data are in broad agreement, and show a recovery of the metapopulation.

213: Interaction networks of bats, their blood-feeding parasites, and the microbiome

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The transmission of vector-mediated diseases is not well understood in most wildlife systems. Previous research indicates that the structure of host-parasite communities may impact their susceptibility to novel pathogens. In the case of bats, little is known about the role blood-feeding arthropods play in transmitting and maintaining diseases in bat populations. We examine the interactions between bats and their arthropod parasites using two network-based analyses to assess the potential disease transmission routes in bat communities. In addition, we test the impact of bacterial diversity in the microbiome of arthropod parasites of bats on the structure of the host-parasite community to better inform models of disease transmission. The microbiome of arthropods impacts their ability to vector pathogens, and we expect the bacterial diversity in the arthropods of bats to correlate with host bat association and host bat ecology. Our preliminary findings indicate that bat flies and ticks are highly host-specific and form highly structured community networks. Highly structured networks may lead to ease of novel pathogen transmission due to fewer steps required to reach all hosts in a community. By examining the network

structure of bats and their parasites, we will broaden scientific understanding of this understudied system and improve disease transmission models for bats.

214: ASM Systematic Collections Committee 2017 Resurvey of the Mammal Collections of the Western Hemisphere

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The American Society of Mammalogists Systematic Collections Committee (ASM SCC) serves the Society by handling all matters related directly or indirectly to systematic collections of mammals. Among its primary responsibilities are the maintenance of a directory of mammal collections and conducting a survey of existing collections approximately once each decade. The 2017 resurvey provides data for approximately 400 mammal collections located in the western hemisphere. As in past surveys, we provide a comprehensive directory of collections, document the nature and extent of holdings in these collections, and assess trends in collection growth and institutional support for collections. Beyond those metrics we evaluate the current level of web-based accessibility of collection data, growth of frozen tissue collections, and assess whether current collection infrastructure and methods are able to meet the rapidly evolving needs of current and future research in mammalogy and environmental change.

215: Morphological and genetic variation in southwestern chickarees (Genus *Tamiasciurus*)

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In the American Southwest, multiple disjunct populations of coniferous forests on mountaintops harbor a predictable mammalian fauna. Unfortunately, we still know relatively little about geographic variation in ecological and evolutionary features and biogeographic history for many species. For example, recent phylogenetic analyses question existing taxonomy of red squirrels (chickarees, Genus *Tamiasciurus*) and shows exceptionally high phylogeographic structure among regional, disjunct populations of the American Southwest. Consequently, in this study we revisit morphologically based geographic variation of southwestern chickarees to evaluate taxonomy and test competing hypotheses of ecogeographic variation. We used morphometric analyses for 12 cranial measurements and four external measurements across >300 specimens. Using spatially weighted multivariate analyses we detect strong correspondence between morphological variation and individual montane regions predicted by phylogeographic patterns, but is incompletely captured by taxonomy. Consequently, taxonomic revision may be warranted in this system. Next steps of this project are to quantify ecophenotypic variation using geometric morphometrics combined with phylogeographic patterns and niche modeling to determine how ecological and evolutionary factors have led to diversification in this system, which may result in insights for other co-distributed species.

216: Use of "cover" in habitat ecology: a framework for operationalizing the concept

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The concept of cover is used generally in ecological studies to refer to structural habitat features that provide one or more functions, such as reducing thermal stress or enhancing security. Despite extensive use, the concept remains loosely defined in the ecological literature. Our objectives were to assess how ecologists are using the term cover in the context of habitat studies, and to develop a functional framework to operationalize the concept in animal-habitat relationships. We conducted a literature review across ecological journals, and synthesized use and measurement of cover. Papers published during 1995-2015 were selected using the Web of Science by searching the words "cover" and "habitat". This returned 1,112 articles, and we randomly selected half for review. We evaluated each study to identify if the following were defined or measured: 1) functions of cover; 2) properties that provided specific functions; 3) habitat features that created cover; and 4) methods for measuring cover. Protection from predators was the most common function attributed to cover, however, few studies measured or even defined properties that provided that function. We contend that cover should be defined explicitly by the

function(s) that it serves, and that it should be measured as *functional properties* of the habitat. A more precise framework will help to advance understanding of animal-habitat relationships and increase our ability to predict responses habitat changes.

217^E: Hearing sensitivities of sympatric grasshopper mice (genus *Onychomys*)

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Grasshopper mice (genus *Onychomys*) are predatory rodents of the western United States that produce long-distance vocalizations to find potential mates and mark territory boundaries. Call fundamental frequencies are species-specific where all three species (*O. arenicola*; 14.9 kHz, *O. leucogaster*; 11.6 kHz, and *O. torridus*; 13.5 kHz) occur in sympatry in southwestern New Mexico. The “matched filter hypothesis” predicts a strong correspondence between acoustic signals of senders and hearing sensitivity of receivers to maximize signal detection. In this study, we measured auditory brainstem responses, a physiological measure of hearing sensitivity, in all three species in the laboratory. We broadcast frequencies between 8-17 kHz (at 1 kHz steps) to anesthetized animals in a soundproof chamber. Our preliminary data (n =2/species) indicate that males of all three species are broadly sensitive to frequencies between 10-16 kHz, suggesting selection for species recognition in the context of interspecific territoriality. In contrast, we predict that females will have tighter matched filters to minimize costs associated with mismating.

218^E: Small mammalian herbivores decrease herbaceous plant cover in shrub-invaded grassland

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Shrub encroachment in southwestern grasslands has negatively impacted ranching, soil conservation, and grassland dependent species. Past research has cited overgrazing, altered fire regimes, and climate change as potential causes of shrub encroachment, but a potential driver of this ecological shift that is ubiquitous and understudied is herbivory pressure from native mammals. On a 10.92 ha sub-watershed within the USDA-ARS Walnut Gulch Experimental Watershed near Tombstone, Arizona, cattle were removed over 50 years ago, yet the intershrub area remains devoid of an herbaceous layer. We hypothesized that at this site, herbivory pressure of native mammals is significant enough to suppress the reestablishment of an herbaceous strata, further contributing to the displacement of grasslands by native shrubs. We constructed herbivore exclosures with 5 treatment levels to assess herbivory pressure among size classes of mammalian herbivores, which we defined as small (e.g. kangaroo rats [*Dipodomys merriami*]), medium (e.g. desert cottontails [*Sylvilagus audubonii*]), and large (e.g. mule deer [*Odocoileus hemionus*]). Preliminary results show a significant effect of cage type on herbaceous cover. Average cover in cages where small and medium sized mammals were allowed access was significantly lower than in other cage types. This pattern suggests that the presence of small and medium sized herbivores can impede the re-establishment of grasslands following shrub encroachment.

219^E: Identification and characterization of SNP markers for the Columbia Basin pygmy rabbit (*Brachylagus idahoensis*)

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The pygmy rabbit (*Brachylagus idahoensis*) is the smallest rabbit in North America and is unique among rabbits due to its ability to consume sagebrush. Loss and fragmentation of habitat due to agricultural conversion has led to the near extirpation of the disjunct pygmy rabbit population in the Columbia Basin (CB), Washington (WA) State. In 2001, the CB pygmy rabbit was listed as a distinct population segment under the Endangered Species Act. Sixteen CB rabbits were taken from the last remaining population in Sagebrush Flats, WA to start a captive breeding program, and 111 rabbits from other states were added for genetic rescue. Rabbits were moved to semi-wild breeding enclosures at Sagebrush Flats, and since

2012, approximately 1900 mixed ancestry rabbits have been released into the wild. Currently, microsatellites are being used to examine genetic diversity and estimate CB ancestry in the captive and wild populations. To provide further insight into genomic diversity, we have used a single digest RADseq (restriction site associated DNA sequencing) protocol on 114 pygmy rabbit samples from the source populations to generate the first genome-wide set of single nucleotide polymorphism (SNP) markers. These markers will allow us to assess ancestry, test for adaptive variation, and genetically monitor captive and wild populations of CB pygmy rabbits to guide strategies for conservation and management.

220: A survey of the mammals of Refugio Nacional de Vida Silvestre Curú, Costa Rica

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The Curú National Wildlife Reserve is located on the southern tip of the Nicoya Peninsula of Costa Rica. Despite its small size (84 ha), Curú is home to a rich and diverse mammalian fauna and serves as an important protected area for biodiversity on the peninsula. Despite being the oldest National Wildlife Reserve in Costa Rica (established by special decree in 1983), no previous comprehensive mammal surveys have been conducted at Curú. From visits in 2010, 2012, 2015, and 2017, we conducted short-term but comprehensive surveys of mammalian species at Curú. Surveys included early morning and evening hikes through the reserve, mist-netting for bats, and small mammal trapping. We found 41 mammalian species representing 7 Orders (Didelphimorphia, Pilosa, Chiroptera, Primates, Rodentia, Carnivora, Artiodactyla). Bats were by far the most common mammals at Curú, with 18 species mist-netted, and one additional species found on a building. The known bat fauna is particularly rich at Curú, making up >50% of all mammalian species there. Procyonids, agoutis, white-tailed deer, white-faced capuchin monkeys, and bats such as the Jamaican fruit bat were particularly common at Curú. Felids and marsupials were found to be quite scarce but are known to occur at Curú. Future mammal surveys will involve the addition of camera traps and hair snares, and further mist-netting and small mammal trapping will be conducted.

221: Landscape correlates of small mammal communities along an urban-rural gradient in Xinjiang, China

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One of the most recent, rapid urbanizations has been in far western China. The city of Shihezi went from approximately 50 people to greater than 1,000,000 in just over 50 years. Extending from the urban zone is an agricultural matrix dominated by vineyards and cotton fields, with small towns and non-agricultural vegetated areas embedded within this matrix. Beyond the agricultural zone is desert. Using snap traps along standardized transects, we sampled urban parks, vineyards, grasslands, and deserts for small mammal species composition and abundance. A GIS database was developed to relate small mammal populations to landscape-level patterns, including human density, degree of urbanization, industry, residential areas, agricultural intensity, and natural areas. Eleven different species were captured. Two species, (*Microtus arvalis* and *Rattus rattus*, both in low abundance, were found in urban areas. The agricultural landscape had slightly higher rodent diversity and abundance than the urban zone, although still rather low. The grassland, although not natural, reflected the greatest landscape diversity which was correlated with the greatest small mammal diversity. Although the desert had relatively low rodent diversity, it had moderately high abundance and the greatest biomass, primarily *Meriones meridianus*. As is often the case with vertebrates, small mammal abundance was correlated with landscape diversity along an urban-rural gradient. This frequently occurs midway along the gradient, even in cases of extremely rapid urbanization.

222^E: Can prey gut microbiome predict stress response in predator-prey interactions? A wolf-livestock study

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Understanding the relative importance of prey state due to stress responses caused by predator presence (trait-mediated effects) will help predicting the total effect of predator on prey populations beyond direct consumption (density-mediated effects). Quantitative measure of trait-mediated effects of wolves on livestock fitness will help promoting wolf conservation in increasingly human dominated landscapes. The analysis of fecal glucocorticoid (GCM) is widely used to measure stress response. However, GCM provide inconclusive results when applied to fine-scale resolution of spatio-temporal variation in predation risk. We investigated with a controlled experiment on 5 cows, 1) if the gut microbiome metabolome can better predict stress response compare to GCM, and 2) if differences in the metabolome before and after a stressful event are correlated to changes in the bacterial communities of the gut. Our results show that stress caused changes in the composition and structure of the gastrointestinal tracts of cattle. Moreover, these changes are correlated to the changes in the metabolome, but not with the changes in the levels of GCM. These findings demonstrate that the metabolomic analysis of the cattle microbiome can better predict acute stress response. We present also preliminary results of our field study to investigate cattle stress response after encounters with wolves. Both wolves and cows were fit with GPS collars with proximity sensors.

223^E: Home range and survival of bobcats in an agriculturally dominated landscape

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Increased understanding of space use requirements and mortality of bobcats (*Lynx rufus*) across fragmented midwestern landscapes is a prerequisite to successful management programs, particularly as it relates to population dynamics and the role of population models in adaptive species management. To our knowledge, previous investigations of bobcat population ecology in Illinois are limited to the southern region of the state. Thus, quantitative information on bobcat population demographics in other regions of the state is needed. We studied home range use and survival of bobcats across fragmented landscapes of west-central Illinois. We calculated seasonal home range sizes and annual survival from 22 bobcats (13 males, 9 females) captured from January 2016 to March 2017. Because home range and survival data are currently limited to a single year, comparisons between sexes were not conducted. Nevertheless, mean annual home range and core area sizes were 104.9 km² (SE = 52.2) and 19.0 km² (SE = 10.4), respectively. We documented 3 deaths, all of which were human-related; annual survival was 0.625 (95% CI = 0.443–0.807). Our study will provide Illinois wildlife managers with region-specific annual and seasonal survival and home range estimates that were previously unknown, thus aiding in harvest management decisions and development of non-invasive protocols for abundance estimation.

224^E: Effects of hunting pressure by humans on survival and habitat selection by elk (*Cervus elaphus*)

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Human activity can influence the survival and distribution of individuals within populations. Pursuit by hunters may shape patterns of movement and resource selection for game species like elk (*Cervus elaphus*). Our objective was to determine the effects of hunting pressure on population dynamics and distribution of elk on the landscape, specifically the relative use of public vs. privately owned lands. We captured 320 cow and 42 bull elk along the Wasatch Range of Utah and fitted each individual with a GPS transmitter during the winters of 2015-16 and 2016-17. Location of each individual was recorded twice daily. When we received a mortality signal, we located the deceased animal and determined cause of death within 48 hours. We determined the distribution of elk on private versus public lands throughout the

year. Annual survival of collared elk was 84% during the first year of study. Hunter harvest accounted for 81% of all deaths. Elk altered their habitat use patterns in response to harvest pressure, selecting private land 60% of the time in during the hunting season compared to only 25% two months prior to the hunting season. We suggest that hunting pressure is a driving force influencing habitat use among elk. A more thorough understanding of the impact of hunting pressure on game species will lead to a better understanding of population dynamics and more effective management practices.

225^E: Relationship between specific gravity, osmolarity, and creatinine in giant panda urine

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Urine samples from exotic species often are of high value and/or low volume, thus creatinine, a destructive assay, is inadequate for normalizing urine water content variability. To address this problem, we hypothesized that specific gravity and osmolarity may be used as accurate, rapid, minimally destructive and reliable techniques for normalization of urine in place of the creatinine chemical assay. To test our hypothesis, giant panda (*Ailuropoda melanoleuca*) urine samples were obtained from six (n=3 male; n=3 female) individuals. Samples (n=10/individual) were measured for specific gravity (SG), osmolarity (OS), and creatinine (CR). Values were obtained using an ATAGO digital hand-held refractometer, vapor pressure osmometer, and colorimetric biochemical assay, respectively. Predicted models were calculated using linear regression analysis at the individual, gender and full model level. Correlation coefficients (R^2) ranged from 0.85–0.96 in SG and 0.83–0.95 in OS among individuals. Gender analysis displayed greater male correlations with coefficients of 0.87 (SG) and 0.86 (OS), compared to female coefficients ($R^2=0.79$ and $R^2=0.67$). With an R^2 value of 0.81, the SG full model represented the highest correlation overall compared to OS coefficient of 0.74. Regression models at the individual level are the best CR predictors, yet remain strong across gender and full model levels. Overall, SG and OS are potential alternatives to CR correction for the normalization of dilution variability in giant panda urine.

226: Alternative methods to evaluate plant part selection by the giant panda

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Giant pandas historically thrived on diets primarily comprised of bamboo, a grass characterized by its tall, woody structure, and evergreen foliage. Earliest reports of giant panda ecology described seasonal transitions in bamboo plant part selection, which have since been confirmed in numerous groups of free-ranging and captive giant pandas. Describing plant part selection by giant pandas is difficult, as differences in water content and bamboo intake rate between bamboo plant parts preclude behavioral observations from accurately predicting actual dry matter consumed. We concluded that sampling of offered and rejected bamboo provided a more realistic assessment of plant part intake by giant pandas. To address the discrepancies between measurement of plant part intake by feeding trial and foraging behavior observations, we proposed image analysis of fecal samples to evaluate leaf consumption by giant pandas. Image analysis of giant panda feces at different levels of leaf intake revealed that feces greenness was strongly correlated to leaf dry matter intake for two giant pandas ($P < 0.01$; $r^2 = 0.91$; $n = 9$), and has potential field applications as a non-invasive, simple procedure to evaluate giant panda feeding behavior.

227: Resolving rodent ecology using 3D dental shape descriptors

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Laser-scanning, microcomputed tomography (μ CT), and high-throughput computing have facilitated the modern explosion of functional morphology-based studies. We μ CT-scanned crania and mandibles for more than 200 extant North American rodent species to correlate fine-scale ecology with functional tooth morphology. We created idealized tooth models by extracting enamel and dentin isosurfaces for lower cheek teeth and cropping meshes to the functional crown. We collected hundreds of quantitative dental measures per individual including Dirichlet normal energy (DNE), orientation patch count (OPC), relief index (RFI), hypsodonty indices (HI), and several novel measures. We employed step-wise discriminant function analysis to determine which of these myriad variables actually best predict diet. We also measured intraspecific dental variation among nine focal species and consistency between the same variables computed by different software. We correctly classified more than 90% of 153 species between six diet categories (rootivory, folivory, granivory, invertivory, omnivory, and frugivory) by jackknife cross-validation. "Misclassified" species usually plotted within in the categories of documented fallback foods. Volumetric enamel-dentin ratio was the best diet predictor while relief, complexity, and curvature measures were of more middling power. We observed very low intraspecific dental variation across variables and mostly consistent results across software packages. Ultimately, this work aims to optimize dental ecomorphological analysis, elucidate how natural selection shapes morphology, and serve as a calibration dataset for reconstructing diet from tooth morphology in other mammals.

228: An undergraduate course to prepare students to optimize their experience at a national conference

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Scientific conferences provide professional, academic, and social opportunities for undergraduate students. However, most undergraduate students do not attend conferences. Students who attend often express anxiety associated with presenting research, networking, or unfamiliarity with the environment. To address these concerns, we developed an undergraduate course aimed at optimizing the experience of attending professional conferences. Prior to the conference we held face-to-face meetings to discuss expectations and prepare for the meeting. Students completed assignments including identifying interesting presentations, creating a schedule, and identifying networking opportunities. During the conference daily, informal meetings were held to discuss experiences and meet with guest speakers. Student work completed during the conference included networking and asking questions, among others. After the conference, a final face-to-face meeting was held to discuss experiences and submit a reflective essay. To assess the effectiveness of the course, we distributed a pre- and post-survey to students. Thirteen students enrolled and attended the conference. Student participation during the conference exceeded our expectations. Student feedback was unanimously positive and indicated the conference experience enhanced through the course. Content analysis of reflective essays indicated that progress in professional, academic, and social abilities was made. Survey results indicated an increase in student interest in attending graduate school. Formal preparation for attendance of a national scientific conference maximizes the potential for students to benefit from their experience.

229^E: Resource selection in desert bighorn sheep (*Ovis canadensis nelsoni*): tradeoffs associated with recruitment

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Selection of resources that effect the development of a fetus and increase probability of survival for neonates is essential for maintaining viable populations in large ungulates. Therefore, it is essential that biologists understand how species select resources across gestation to increase their ability to manage recruitment. Desert bighorn sheep (*Ovis canadensis nelsoni*) populations have dwindled across their range over the last several decades and translocations have been a key management strategy for recolonizing areas. When selecting translocation sites, it is essential that biologists select areas with habitat types that positively influence recruitment. To increase understanding of sheep resource selection

during gestation and following parturition, we captured and collared 30 adult, female sheep on Lone Mountain, of which 15 were translocated to the Garfield Hills range. In addition to receiving collars, all individuals were given vaginal implant transmitters to provide parturition timing information. Following captures, we monitored parturition events, adult resource selection, and neonate survival. We used mixed effects logistic regression to identify habitat selection during gestation, following parturition events, and following the mortality of neonates. Our results indicated that adults shifted resource selection from areas with higher nutritional availability to more precipitous terrain immediately following parturition events. In addition, our results indicated that females shifted resource selection to areas with higher quality vegetation and reduced terrain ruggedness following the mortality of a neonate.

230: A summary for the African Graduate Student Research Fund Committee of the American Society of Mammalogists, 2013-2017

The African Graduate Student Research Fund committee (V. Apkenas*, B. Buttler, T. Demos, A. Ferguson, J. Goheen, L. Helgen, A. Hodge, A. Linzey, M. McDonough, P. Moehlman, R. Norris, B. Patterson, C. Rodrigues, R. Rose, D. Schlitter, and P. Webala)

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In 2013, the African Graduate Student Research Fund (AGSRF) was formed to support work by African nationals conducting graduate research on wild mammals in Africa. As of 2016, the AGSRF has supported work by six individuals from five countries (Cameroun, Kenya, Madagascar, Morocco, and Rwanda), contributing to 11 peer-reviewed articles, theses, and dissertations on a diversity of mammalian species, including aoudad (*Ammotragus lervia*), chimpanzees (*Pan troglodytes*), and Madagascan flying foxes (*Pteropus rufus*). Individuals supported by the AGSRF continue to contribute to the field of mammalogy through on-going graduate research (n=3), working as heads of field research for conservation organizations (n=2), and wildlife veterinary work (n=1). This poster will provide an update on the six individuals funded by the AGSRF.

231^F: Quantifying prey selection for mountain populations of leopard and hyenas using DNA metabarcoding, traditional hair microscopy, and camera traps

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While a fair amount of information exists for hyena and leopard diet in savannah ecosystems, little data is available for montane populations, thereby limiting conservation information for these declining apex carnivores. To understand prey diversity and dietary overlap for large carnivores in the Mt. Kenya ecosystem, we combined morphological and DNA metabarcoding techniques on scats for prey identification as well as camera trapping for estimating prey availability. We confirmed the presence of striped hyena (*Hyena hyena*), spotted hyena (*Crocuta crocuta*), and African leopard (*Panthera pardus*) on the mountain. *Panthera pardus* and *C. crocuta* were detected in montane forest (2300-2700m a.s.l.), bamboo forest (2700-3100m), transition forest (3100-3500m), subalpine moorland (3500-4300m), and alpine moorland (4300-4700m) vegetation zones. *Crocuta crocuta* was camera-detected in all zones

except transition forest and subalpine moorland, unlike morphological scat analysis which detected them in all zones, fully overlapping *P. pardus*. *H. hyena* was only camera-detected in forest plantation at the foot of the mountain, where *P. pardus* was absent. Small mammals (shrews, rodents) and antelopes were detected in their diet. Whereas morphological and DNA scat analysis were accurate for prey identification, the former was weak in identifying scat host species. Application of camera traps was useful for detecting potential prey and predators, allowing us to determine dietary preferences. Combining three techniques helped to elucidate the trophic ecology of apex predators on Mt. Kenya.

232^E: Variation in disease prevalence of a contagious cancer across the geographic range of Tasmanian devils

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The world's largest carnivorous marsupial species, the Tasmanian devil (*Sarcophilus harrisii*), is threatened with extinction by a unique cancer known as devil facial tumor disease (DFTD). DFTD is an infectious, clonal, neoplasia that evades immune response through epigenetic regulation. It has caused significant population size declines. First discovered in Northeastern Tasmania in 1996, it has since spread across most of Tasmania, leaving few uninfected populations. Here we tested whether environmental heterogeneity across the species' range played any role in disease spread. Previous studies have shown frequency-dependent transmission. However, none of these studies have explicitly modeled the influence of devil abundance and environmental variables on disease prevalence. Using mark-recapture data collected over the past 12 years, we calculated the relative abundances of populations across Tasmania using two different approaches: minimum number alive and catch per unit effort. Using these abundance data with disease status, we estimated the proportion of devils with DFTD in a population. Preliminary findings revealed that some populations take longer to decline compared to others once disease arrives. To determine if environmental variation played a role in these differences in disease prevalence across devil populations, we will test for correlations between environmental variation and disease prevalence. Our results will provide additional insight into understanding the dynamics of disease transmission and allow us to improve models regarding future spread of disease.

233^{E,HTA}: Optimizing detection of a desert carnivore at scent stations

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Kit fox (*Vulpes macrotis*) are a species of concern in the western United States, and an efficient protocol to detect and monitor populations would benefit conservation efforts. A recent method for monitoring wildlife involves lures and remote cameras in an occupancy-modeling framework. However, the utility of occupancy modeling is dependent on the optimization of "capturing" individuals at camera stations. Different lures have been used to attract foxes; however, their efficacy and durability have not been evaluated. Additionally, relocating scent stations during mid-sampling may increase rates of visitation. Our objective was to identify the optimal lure and relocation procedure to maximize visits and recapture rate of foxes. We placed remote cameras at 660 random locations throughout nine study regions in three geographical regions in Utah. Each location was randomly assigned one of three methods to broadcast scent: Plaster of Paris tablet, cotton swabs, or hollowed golf ball. After seven days, half of the scent stations were relocated 100 meters while others remained in place. Stations were then monitored for an additional week. Detection of kit foxes did not vary by scent but did vary by method of scent deployment, with cotton swabs yielding the highest rate of visitation. Recapture rates did not increase when scent

stations were relocated. We suggest that the use of cotton swabs maximizes captures and improves the predictive power of occupancy modeling.

234: Winter bait stations as a multi-species survey tool

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Winter bait stations consisting of a carcass attractant, remote camera, and hair snare are becoming a commonly used technique for multi-species inventory and monitoring. Lacking is a technical evaluation of their effectiveness. From 2010-14, we conducted 563 sampling sessions at 497 bait stations stratified in 453 5x5 km cells in northern Idaho and adjoining mountain ranges. We detected 29 species of mammals ($n = 25$) and birds ($n = 4$). We evaluated the effectiveness of cameras and DNA collection to detect species and individual animals, factors affecting DNA viability, the effectiveness of re-visiting stations, and the influence of elevation, seasonality, and latency on detections. Length of deployment time and elevation increased genetic species ID success, but individual ID success rates were increased only by collecting hairs earlier in the season. Re-visiting stations did not change camera or genetic species detection results but did increase the number of individual genotypes identified. Marten (*Martes americana*) and fisher (*Pekania pennanti*) were detected quickly while bobcat (*Lynx rufus*) and coyote (*Canis latrans*) showed longer latency to detection. Seasonality significantly affected coyote and bobcat detections but not marten, fisher, or weasel (Genus: *Mustela*). We provide specific study design recommendations for researchers developing bait station surveys.

235^{HTA}: Coyote dominance and urban avoidance in the occupancy of gray foxes

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Habitat and interspecific interactions are two of the major factors that influence the composition of mammalian carnivore communities. Human development has changed the habitat and thus the abundance and prevalence of species in these communities. The loss of many large predators has facilitated rise of species who tolerate urbanization. In such landscapes, coyote (*Canis latrans*) have become an abundant and dominant member of the carnivore community. Gray foxes (*Urocyon cinereoargenteus*) share habitat with coyote, but are present less frequently. Differences in body size and empirical observations of intraspecific predation suggest that coyote may reduce the range of gray foxes due to competitive exclusion. To explain differences in detections of coyote and gray fox, we model the occupancy of each species based on habitat and interspecific interactions. We use camera trapping at 132 sites in the Appalachian region to generate detection histories of each species. Using single species occupancy models, we relate habitat covariates to the detection histories of each species. Additionally, we use two species occupancy models to determine the impacts of coyote occupancy and detection on gray fox occupancy. Our findings suggest that gray fox occupancy is positively correlated to forest cover, and negatively to urbanization. Additionally, intense presence of coyote has a negative impact on gray foxes, suggesting that interspecific interactions, not just habitat, affects the presence of gray fox.

236: Pictures, predators, and prey: camera data and community dynamics after a fisher reintroduction

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Researchers are often concerned with how reintroduced organisms fare in their new environments, but often cannot document how the reintroduced organisms affect their new communities. Fishers (*Pekania pennanti*) are a model mammalian carnivore that has been translocated >40 times across its range in North America. Fishers are generalists that consume many types of medium- to small-sized mammals. Understanding how predators forage for and change the abundance and distributions of prey is important

for management and conservation. Subsequent to the reintroduction of 40 fishers over 3 years (2009-2012) to their former range in northern California, we placed trail cameras at over 600 locations (yearly = 100 ± 41) for diverse reasons including to estimate fisher reproduction and evaluate the spatial distribution of fishers through time. We deployed both baited and un-baited cameras for an average of $42.4 \pm 33-52$ days, distributed across years and seasons. We quantified the naïve occupancy rates of key prey species through time. *Tamiasciurus douglasii* (0.53 ± 0.16) had the highest naïve occupancy rate followed by *Sciurus griseus* (0.41 ± 0.14 ;) and *Glaucomys sabrinus* (0.08 ± 0.06). Occupancy estimates were highly variable in time and space but indicated that fishers did not negatively affecting them after release. We will further evaluate specific habitat metrics for each of these species to evaluate how these overlap with habitat and prey selection by fishers.

237: Trophic traps: Inferring species relationships from camera trap imagery

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Camera traps are a widely-used tool in wildlife management, with applications for long-term monitoring of species occurrence over broad spatial scales. Relative to many other survey methods (DNA, collaring, capture-recapture), camera traps allow the simultaneous documentation of more than one species. This multi-species approach has been used to assess factors affecting single species and the co-occurrence of species across the landscape. Less well appreciated is the potential for this multi-species approach to capture the intimate relationships between organisms that give rise to critical ecological processes: fear, herbivory, predation. Here, I draw on examples of how camera traps have been used to assess species interactions at wildlife crossing structures in Banff National Park and fear-structured patterns of herbivory in an African savanna. While not a perfect solution to quantifying animal behaviour, camera traps offer a powerful tool to help gain novel insights on the hidden trophic relationships in nature.

238: Interspecific comparison of hantavirus prevalence in *Peromyscus* from a fragmented agro-ecosystem in Indiana

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Hantaviruses are rodent borne pathogens that are the causative agents for hantavirus pulmonary syndrome (HPS) in humans and their prevalence in rodent host populations varies spatially and temporally. Comparatively little is known about hantavirus prevalence within rodent populations from the Midwestern United States, where two species of native mice (prairie deer mice [*Peromyscus maniculatus bairdii*] and white-footed mouse [*P. leucopus noveboracensis*]) are dominant members of rodent communities. We sampled both species in central Indiana and tested individuals for presence of hantavirus antibodies to determine whether seroprevalence (% of individuals with antibodies reactive to SNV antigen) differed between species, or among different habitat types within fragmented agro-ecosystems. Prevalence of hantavirus antibodies varied significantly between species, with seroprevalence in prairie deer mice (21.0%) being nearly 4 times higher than white-footed mice (5.5%). Seroprevalence was almost 8 times higher within the interior of row-crop fields (37.7%) occupied solely by prairie deer mouse populations, relative to field edges (5.2%) where species occurred syntopically or adjacent forest habitat (6.1%) occupied solely by white-footed mice. Understanding species- or habitat-specific differences in hantavirus prevalence in rodents is important for informing human disease risk and management programs. In the fragmented Midwestern agro-ecosystem of this study, prairie deer mice appear to be the dominant hantavirus reservoir with particularly high seroprevalence in populations within the interior of row-crop fields.

239: Does urbanization ameliorate the effect of endoparasite infection in Merriam's kangaroo rat (*Dipodomys merriami*)?

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Urban development can fragment and degrade remnant habitat. These habitat alterations can have profound impacts on wildlife populations, including parasite infection status and body condition of animals living in urban and suburban areas. We investigated the influence of urbanization on populations of Merriam's kangaroo rat (*Dipodomys merriami*) and their parasites. We predicted that urban development would affect infection status and body condition of kangaroo rats in urban versus wildland areas. We live trapped kangaroo rats at 5 urban and 5 wildland sites in and around Las Cruces, NM from 2013-2015, and collected fecal samples from 209 kangaroo rats. Endoparasite presence was determined using fecal flotation and molecular barcoding. Seven parasite species were detected, although only two, parasitic worms *Mastophorus dipodomis* and *Pterygodermatites dipodomis*, occurred frequently enough to allow for statistical analysis. We found an effect of the interaction between urbanization level and infection status on body condition in kangaroo rats infected with *P. dipodomis*, but not with *M. dipodomis*. Wildland animals infected with *P. dipodomis* had lower body condition scores than infected animals in urban areas or uninfected animals in either habitat. This result suggests that living in an urban environment may buffer Merriam's kangaroo rats from some detrimental impacts of endoparasite infection. Possible mechanisms of this effect may be increased availability of anthropogenic resources, alterations to intermediate host abundance, or behavioral differences between populations.

240: Bat behavioral responses to white-nose syndrome and implications for resistance and tolerance

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When pathogens are introduced into naïve mammalian populations, they may impose novel selective pressures that cause strong negative effects upon hosts. For instance, white-nose syndrome (WNS), an emerging infectious disease (EID) of hibernating bats, continues to spread at an alarming rate across North America, with millions of bats killed in the last decade. When pathogens maintain high virulence, population persistence may depend upon host populations' ability to adjust behaviorally or physiologically, either through adaptation or phenotypic plasticity. In the context of WNS, it remains unclear to what extent behavioral changes in affected bats are adaptive, and whether they vary with previous exposure to the disease and across generations. Using infrared video recordings, we systematically compared behavioral changes in response to WNS in juvenile and adult hibernating little brown bats (*Myotis lucifugus*) that had been captured from colonies with different WNS experience. Preliminary analysis suggests all groups of infected bats initially exhibited increased grooming and overall activity relative to controls, but contrary to bats from naïve colonies, bats from colonies with long experience with WNS reduced overall activity in late winter. These behavioral differences may represent adaptive changes by experienced bats to reduce infection loads while maximizing energy conservation. Investigating how these variables relate to infection severity, WNS mortality, and physiological variables affecting host susceptibility will clarify the influence of behavior on host responses to EIDs.

241: Speak of the devil: communication in the endangered Tasmanian devil

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The endangered Tasmanian devil, *Sarcophilus harrisii*, produces a unique vocalization, the 'arff', during feeding events. Using 30 adult Tasmanian devils, we tested the hypotheses that: 1) arffs have signature characteristics, 2) devils discriminate between different devil's arffs, and 3) arffs are associated with reduced aggression, increased feeding success and/or cooperation during group feeding events at carcasses. We classified 90-91% of arffs to the correct individual (using PIC, PCA and multinomial logistic regression), demonstrating that signature characteristics exist in arffs. Habituation-dishabituation

playback experiments revealed that devils discriminated between other individual devil's arffs in 75% of the cases. In group-feeding experiments, increased utterances of arff calls were associated with decreased aggression ($P = 0.009$), increased feeding success ($P = 0.019$) and increased cooperation during feeding ($P < 0.001$). We also suggest that the transmission of Devil Facial Tumor Disease, a contagious cancer driving the species to extinction, may be exacerbated by the inability of infected devils to produce arff calls with recognizable signature characteristics, which may lead to increased aggression and biting on the part of conspecifics and disease transfer from bitten to biter.

242: Prevalence of hantaviruses in rodent assemblages from sylvan and disturbed habitats in Mexico and Texas

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Hantaviruses (Family Bunyviridae) are zoonotic pathogens in North America that occur in close association with reservoir hosts of the Family Cricetidae. Assemblage structure and species richness are likely strong drivers for the maintenance and spread of Hantavirus infections in wild rodents. Hantavirus prevalence has been proposed to be negatively correlated with increased assemblage species diversity (i.e., dilution effect). Presumably, anthropogenic habitat degradation that reduces rodent diversity would be tied to increased Hantavirus seroprevalence. We captured and tested a total of 2,406 rodents from 20 sites in Mexico and Texas distributed along a latitudinal gradient that spans the Nearctic and Neotropic transition zones. We sampled sylvan and disturbed habitats at each site to compare assemblage composition, structure and Hantavirus seroprevalence. Average assemblage seroprevalence was 5.65% with a wide range of 0 to 33.8%. Among all sites we found no differences in abundance, species richness, evenness, and seroprevalence between habitat types. However, the geographical distribution of seroprevalence was highly heterogeneous with seven sampling transects deviating from the average expectation of seroprevalence, with four above and three below this value. Our results do not support a relationship between habitat degradation, rodent diversity and Hantavirus seroprevalence. Biotic homogenization likely prevented any differences at the scales we studied. Large geographical differences in seroprevalence are likely more tied to variance of assemblage composition that include or not Hantavirus reservoir hosts.

243: Effects of age and colony experience on bat responses to white-nose syndrome

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White-nose syndrome has led to severe regional declines in several North American bat species, though remnant populations persist. The response of survivor individuals and their offspring to continued exposure to the pathogenic fungus *Pseudogymnoascus destructans* that causes white-nose syndrome will largely determine whether these remnant populations can persist or recover over time. In this study, we sought to understand how bat responses to pathogen exposure varied with age and colony experience with the disease. We hypothesized that juvenile and naïve bats would fare worse than other bats when exposed to the pathogen. We captured juvenile and adult little brown myotis (*Myotis lucifugus*) from colonies that were naïve to (Wisconsin) or experienced with white-nose syndrome (New York). In a

controlled laboratory experiment, we inoculated bats with the pathogen, then tracked bat responses overwinter. Results were not always consistent with expectations: naïve juveniles had longer torpor bouts than other bats, and experienced and naïve adults did not respond differently. However, juveniles generally responded more poorly to the disease than adults: naïve juveniles had a higher fungal load than other bats and experienced juveniles had a shorter survival duration. These results suggest adults may not improve response to white-nose syndrome with experience, and juvenile bats may be particularly susceptible to the disease. Thus, mortality may remain high well after the initial invasion, and juvenile recruitment may be limited.

244^{E,HTA}: Genetic structure and differentiation within the eastern spotted skunk (*Spilogale putorius*): a microsatellite analysis

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Microsatellites are used extensively to assess a variety of population-level parameters including gene flow, structure, dispersal patterns, and heterozygosity. Because these genetic markers are capable of amplifying homologous sequences in related taxa, thus eliminating the need for species-specific markers, they are especially useful when researching rare and understudied organisms. One such species, the plains spotted skunk (*Spilogale putorius interrupta*), has recently declined range-wide, lacks any information pertaining to its genetic variability, and is currently being considered for listing as an endangered species. In order to assess the levels of genetic diversity and structure of this subspecies, tissues obtained from field surveys and museum collections ($n = 28$) were analyzed across 12 cross-species microsatellite loci. Additionally, tissue samples from the Appalachian (*S. p. putorius*; $n = 13$) and Florida (*S. p. ambarvalis*; $n = 18$) spotted skunks were analyzed to enable genetic comparisons among the 3 subspecies, as well as to test the validity of the subspecies designations. Structure analyses indicated the presence of 3 clusters commensurate with morphological subspecies designations. An overwhelming presence of private alleles and a strong degree of genetic differentiation ($F_{ST} > 0.261$) of the plains subspecies from the Appalachian and Florida subspecies highlights a lack of gene flow beyond the plains subspecies range, potentially suggesting the need to consider *S. p. interrupta* as a unique evolutionarily significant unit.

245: Comparative population genomics of New England cottontail (*Sylvilagus transitionalis*) and eastern cottontail (*S. floridanus*)

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The New England cottontail (*Sylvilagus transitionalis*) is a species of greatest conservation need. One possible cause for the decline of New England cottontail is competition with non-native eastern cottontail (*S. floridanus*). Hundreds of thousands of eastern cottontail were introduced east of the Hudson River starting in the early 1900s. New England cottontail is an obligate early successional species, whereas eastern cottontail is considered a habitat generalist. Because of their more limited habitat, New England cottontail should have more restricted gene flow than sympatric eastern cottontail. We used a double-digest Restriction-site Associated DNA (ddRAD) approach to develop genomic markers to identify single nucleotide polymorphisms (SNPs) for both cottontail species. We analyzed the population genomic structure of each species at the regional scale of the northeast US (New England cottontail $n=248$; eastern cottontail $n=275$) and at the scale of Cape Cod, MA (New England cottontail $n=108$; eastern cottontail $n=73$). We identified nearly 9,000 SNPs for New England cottontail and over 10,000 SNPs for eastern cottontail. At a regional scale, the clustering of New England cottontail samples matched previously identified geographic groups. Eastern cottontail samples, however, formed clusters that gradually transitioned into other clusters from different geographic areas. At a smaller ecological scale the pattern for the two species was the opposite on Cape Cod. Our research will help inform management decisions to conserve New England cottontail.

246: Getting the scoop from poop: telling the story of the expanding wolf population in Oregon

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Genetic monitoring is a powerful tool for conservation and management of mammal populations. When combined with field data it has the potential to provide nuanced data about recolonizing and expanding populations. Gray wolves (*Canis lupus*) first reestablished a breeding pack in Oregon in 2008. The population has grown to a minimum count of 110 wolves in 12 packs as of December 2015. Oregon Department of Fish and Wildlife collected genetic samples from all captures and from noninvasive sources like scat and hair where potential wolf sign was located. Multi-locus microsatellite genotypes were generated and gray wolf ancestry was confirmed using program Structure. Genotype data was then used to determine familial relationships between individuals and packs using a combination of relatedness, parentage and Bayesian cluster analysis. A total of 157 noninvasive samples were collected between 2011 and 2017 from which 42 individuals were initially identified. An additional 58 individuals were sampled from capture or mortalities. Genetic analysis showed since 2012, seven packs were formed by members of existing packs while four packs were formed by one member of existing packs and an individual not born in Oregon. Thus, genetic data indicate that although Oregon was initially recolonized from the NRM population the expanding wolf population in Oregon was comprised primarily of individuals born in Oregon packs rather than dispersers from Idaho.

247: Determining distribution boundaries of Oklahoma pocket gophers (*Geomys*) using microsatellite and mitochondrial markers

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The goals of this research are to utilize genetic markers (microsatellites, mitochondrial DNA) to identify the distribution boundaries of *Geomys bursarius* (plains pocket gopher) and *G. breviceps* (Baird's pocket gopher) in central Oklahoma, and determine if the range of *G. jugossicularis* extends into the Oklahoma panhandle. Previously, cranial measurements were used to identify species and propose a boundary between *G. bursarius* and *G. breviceps* in central Oklahoma. Additionally, a contact zone between the 2 species was confirmed in Norman, Oklahoma. Recent research has suggested a 3rd species of pocket gopher, *G. jugossicularis*, occurs in the Oklahoma panhandle. Genetic analyses will be used to reevaluate the proposed boundary line and known contact zone between the central Oklahoma 2 species, as well as confirm the identity of samples collected from the panhandle. Furthermore, genetic data will be used to assess the possibility of hybridization within contact zones across the state. Preliminary data was used to identify 3 distinct clusters of pocket gophers, 2 in central Oklahoma and a 3rd in the panhandle. Admixture has been detected between the 2 central Oklahoma clusters, and between the western Oklahoma and panhandle clusters, suggesting the possibility of hybridization in 2 separate contact zones.

248: Comparing SNPs and microsatellites for sibship analysis in grey wolves (*Canis lupus*)

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The successful reintroduction and recovery of grey wolves (*Canis lupus*) in the Northern Rocky Mountain distinct population segment resulted in their delisting in 2008, shifting their subsequent management from federal to state agencies. The Idaho Department of Fish and Game has subsequently monitored grey wolves to maintain populations at recovery levels while permitting regulated harvest. To this end, managers would like to estimate a minimum count of breeding pairs and identify the number of packs with harvested pups. These metrics can be obtained through genetic sibship reconstruction of harvested pups. Wolves harvested from May 2014 - April 2015 were identified to age class by tooth analysis, and nuclear DNA microsatellite genotypes were generated at 18 loci for 98 pups. Likelihood methods implemented in the program COLONY identified 23 sibgroups of 2-4 pups and 42 individuals that could not be placed into any sibgroup. These single individuals may represent additional packs or could be an artifact of low power to define sibgroups. Thus, we are currently generating RADseq data for these samples to identify thousands of single nucleotide polymorphism (SNP) loci that can be used to repeat the sibship analyses

and compare results and statistical power between SNP and microsatellite loci. The shift to SNPs is expected to increase statistical power, decrease uncertainty in likelihood analyses, and improve comparability among and within laboratories.

249: Genetic origins of US feral swine populations

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Feral swine (*Sus scrofa*) are a long-established invasive species in the United States with mainland populations dating back to the mid-1500s. Despite their long history, feral swine largely remained restricted to the southeast, California, and Hawaii until the 1980s but have since expanded dramatically with populations established in >40 states. We used molecular tools to gain a greater understanding of the origins of both historic and newly emerging populations and elucidate the processes driving range expansion. Specifically, we used principal component analysis to compare high density single nucleotide polymorphism genotypes (29,383 loci) of 3436 feral swine sampled across the invaded US range to a comprehensive reference set of 2968 domestic pigs and wild boar, representing 152 distinct genetic groups. Historic populations were genetically intermediate to US/European pigs and European wild boar, consistent with documented history in which feral populations were established through the intentional and unintentional release of domestic pigs and subsequently augmented with wild boar to improve hunting appeal. Several newly emerging populations (i.e., Michigan, Colorado, and Indiana) had a far higher wild boar genetic composition than historic populations suggesting a novel source was used in the establishment of these populations. Future work with genetic clustering algorithms will allow us to increase the precision in which we can quantify genetic composition and will improve our ability to identify the sources of new populations.

250^E: Life at the edge: genetic and ecological interaction across a woodrat hybrid zone

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Forecasting organismal response to changing environmental conditions is a principal concern for biologists, and range shifts are expected to be one biotic response. Understanding ecological and demographic dynamics occurring at range boundaries is fundamental to predicting future response. Here, we present data regarding a contact zone between two species of woodrat in the genus *Neotoma* that each meet their respective range edges in Kern Co., CA. We studied *N. lepida* and *N. bryanti* at a site characterized by two distinct communities: western Mojave desert scrub and coastal oak woodland. We also conducted 2-way choice cafeteria experiments to quantify differences in dietary preference between these two herbivorous species for two plants common in each of the adjacent habitats: *Prunus fasciculata* (Desert almond) and *Rhamnus californica* (Coffeeberry). We find the two woodrat species are hybridizing at the site and that the species are spatially segregated and largely associated with distinct plant communities. Two-way choice trials showed a difference in dietary preference for *Rhamnus* sp. (associated with hill habitat) and *Prunus fasciculata* (associated with flat habitat) among individuals of each genotypic class. As environmental change continues to reshape ecological communities, it is critical to understand ecological relationships at species boundaries and the nature of the adaptive potential of these range-edge populations.

251: Density responses of small mammals to timber harvesting for oak regeneration

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Disturbance induced by forest management aimed at oak regeneration alters environmental conditions that have consequences for forest organisms. Small mammals such as eastern chipmunks (*Tamias*

striatus), white-footed mice (*Peromyscus leucopus*), and short-tailed shrews (*Blarina brevicauda*) respond at the population level to changes in microhabitat following timber harvesting. We modelled density (or relative abundance) as a function of habitat type (matrix, harvest opening, opening edge, and shelterwood) and examined the relationship between density and distance to harvest boundary with spatially explicit capture-recapture models. Chipmunks responded positively to all harvest openings and increased in density following the second stage of a shelterwood harvest. White-footed mouse density decreased following a poor mast year, and both mouse and chipmunk densities were elevated in the summer following a relatively good mast year. We observed distance-dependent density relationships for both white-footed mice and chipmunks in which both species tended to exhibit higher densities near harvest boundaries relative to forest matrix. Structural complexity created at the edge of harvest openings offers benefits to species associated with edge habitat, especially 6-8 years after harvest. Short-tailed shrews responded negatively to all harvest treatments, especially clearcuts, relative to controls, but shrew use of openings appears to have increased 6-8 years post-harvest. We discuss our results in terms of the implications of oak regeneration silviculture for short- and long-term responses of small mammals.

252: Population ecology of the California mouse in a semi-arid oak-woodland

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The California mouse (*Peromyscus californicus*) inhabits the 3 million ha of semi-arid California oak (*Quercus* spp.) woodland. The impact of predicted climate change on its populations has not been studied. To collect needed demographic information, we conducted capture-mark-recapture (CMR) sampling from 1993 to 2014 in essentially undisturbed oak woodland in coastal-central California. Using Pradel's temporal symmetry models, we estimated population growth rate (λ) and its components, apparent survival (ϕ) and recruitment (f), and tested for the effects of temperature and rainfall on these vital rates. During the 20-year study, overall monthly λ was 1.001 ± 0.009 (estimate \pm SE), pointing to a stable population; however, λ exhibited strong temporal variation. Overall ϕ was 0.856 ± 0.005 , but varied temporally and by sex between 0.485 and 0.977. Monthly f averaged 0.146 ± 0.005 and ranged from zero to 0.556. Rain strongly increased recruitment, there being little or no recruitment during intense drought. Rainfall also improved ϕ and λ , but cold temperature had little effect on California mouse vital rates, likely a result of paternal care in this socially monogamous rodent. Although a changing climate threatens to intensify and lengthen drought periods, our results favor the cautious conclusion that the monogamous mating system of this species predisposes resilience and persistence in a changing California oak woodland.

253: Bat response to prescribed fire frequency in oak-dominated forests

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Prescribed fire has become a popular management tool, providing a means to reduce fuel loads and stimulate oak regeneration. Previous studies indicate fire may also be beneficial to bats by reducing understory clutter and creating snags for roosting. Our objective was to assess impacts of prescribed fire frequency on bat activity within oak-dominated forest stands at Fort Indiantown Gap (FIG), a military training facility in Pennsylvania. FIG foresters have used prescribed fire extensively since 2004, with burn frequencies that range from never-burned to annually-burned, providing the opportunity to test the effects of a wide range burn frequencies. We hypothesized that bat activity would increase with burn frequency. We used Pettersson D500x acoustic detectors to passively record bat echolocation call sequences in 110 forest stands from May through September 2016. Bat call sequences were identified to species using SonoBat 4.0.7 identification software. Big brown bats (*Eptesicus fuscus*) and eastern red bats (*Lasiurus*

borealis) comprised 97% (N = 5,362 of 5,523) of identified call sequences. We used Akaike Information Criterion to evaluate generalized linear models of bat call data for each species using burn frequency and other ecological predictor variables. Our analyses contribute to the understanding of the relationship between bats and prescribed fire by determining whether bat activity continues to increase with fire frequency, or reaches an upper limit where habitat suitability declines.

254: Dominant, generalist species of small mammals and forestry management practices in northern California

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Studies on the effects of forestry management practices on small mammal communities emphasize the effects of short-term logging (specifically clearcutting) to specialist species that are the most vulnerable to disturbance. Generalist species, which can dominate small mammal communities, occur in diverse locations and are important consumers and prey species. Generalist species are associated with forested stands with high canopy cover and ground-level structural elements (e.g., downed logs). We hypothesized that dominant, generalist small mammals would have reduced population sizes in stands without vegetative elements including downed wood debris and shrub cover as well as high overhead canopy. We tested our hypothesis by estimating both catch per unit effort (CPUE) and minimum numbers of animals alive (MNA) of deer mice [*Peromyscus spp.*] and woodrats [*Neotoma spp.*] in forests that were never clear cut, clearcut < 20 years ago, and clearcut > 20 years ago. In concordance with previous studies, we found that deer mice and woodrats increased in both CPUE and MNA shortly after stands have been clear cut. Yet, stands that were clearcut >20 years ago had reduced CPUE and MNA for deer mice and woodrats. Our results indicate that the relative abundances of dominant, generalist species are negatively associated with moderately aged plantations that had high canopy closure and moderate tree size, but that lacked structural elements including large downed wood debris and shrubs.

255: Patterns of genetic variation in the pygmy rabbit (*Brachylagus idahoensis*) in California and Nevada, USA

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Pygmy rabbits (*Brachylagus idahoensis*) are extreme habitat and dietary specialists restricted to the big sagebrush communities of the Great Basin. Here, we report on the geographic distribution of genetic variation across 14 pygmy rabbit populations from throughout their range in Nevada and California. Our aim was to identify patterns of diversity and differentiation across this portion of the range, and determine whether patterns of population structure correspond with potential biogeographic barriers. We genotyped 194 individuals at 13 microsatellite loci using DNA extracted from fresh fecal pellets. We find that populations in the Mono Basin of California show high genetic differentiation from the remainder of the sampled range. The Mono Basin lies about 160 km from the nearest known contemporary pygmy rabbit populations in Nevada and are separated by inhospitable habitat from the remainder of the range. Across their range in Nevada, we find modestly differentiated genetic clusters that are spatially widespread and overlapping. Throughout their range pygmy rabbits face increasing pressures from habitat loss leading to greater fragmentation of populations. Our work will contribute to understanding the genetic and evolutionary consequences of this landscape change and contribute to ongoing efforts to ensure sustainable management of pygmy rabbit.

256: Heat dissipation limit theory: from laboratory mice to Svalbard reindeer

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Evidence is growing that maximal rates at which animals can acquire and expend energy may frequently be limited intrinsically (by an individual's physiology) rather than extrinsically (by food supply). The nature of these limits is central to understanding many aspects of animal performance, including reproductive output, foraging behavior and thermoregulatory capabilities, which shape species distribution patterns, population dynamics and ecosystem processes. There is an ongoing debate whether intrinsic constraints act "centrally" (capacity of alimentary tract to process the ingested food), "peripherally" (capacity of peripheral organs to perform work) or through the "heat dissipation limit" (HDL, capacity to dissipate body heat to avoid hyperthermia). Attempts to distinguish between these three ideas have focused on lactation in small mammals. By monitoring food intake, litter growth and milk production in laboratory mice, we demonstrated that animals with experimentally enhanced capacity to dissipate body heat (*via* exposure to low ambient temperatures or fur removal) ate more food, produced more milk and weaned heavier litters than mice lactating at high ambient temperatures or those with intact fur. Both empirical evidence and theoretical considerations have led us to postulate that endotherms are limited in their performance by the capacity to dissipate body heat. The implications of the HDL theory for large-bodied animals will be discussed in the context of rapidly warming Arctic and its effects on Svalbard reindeer (*Rangifer tarandus platyrhynchus*).

257: Ecosystem engineering by subterranean insects buffers large mammals against climate warming

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Tropical savannas support the most diverse assemblages of large-bodied mammals on earth, and also are commonly occupied by colonies of mound-building termites. These subterranean insects concentrate nutrients and water, which leads to dense, nutrient-rich vegetation on and/or around mounds. In addition to serving as "resource hotspots," nest structures and associated vegetation generate heterogeneity in the thermal landscape that may be important for buffering large, heat-sensitive mammals against the energetic costs of rising environmental temperatures. We used a mechanistic model of heat and mass transfer to evaluate the importance of termite mounds as thermal refugia under current and future climate scenarios for three congeneric antelope species that varied five-fold in body size. Rates of evaporative water loss necessary to maintain homeothermy were significantly higher in matrix habitat than on mounds for all three species. However, the proportional reduction in water loss conferred by using mounds increased with body size. Similarly, under simulated climate-warming scenarios, the cost of using matrix habitat increased more rapidly than the cost of using mounds, but this discrepancy was most pronounced for larger species. Our results suggest that the importance of termite mounds as thermal refugia will increase considerably as global temperatures rise, but that the benefits of using mounds will accrue disproportionately to larger-bodied species. This could have important implications for competition and niche partitioning in size-structured communities of large mammals.

258: The physiological limits to foraging in pinnipeds: ability to respond to a changing world

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Large mammals are constrained in their ability to respond to environmental change. The aerobic dive limit (ADL) an important determinant of diving ability scales with body size. We compare the ADL of pinnipeds with respect to their foraging behavior to determine when body size is important and when other physiological adjustments come into play and when physiological capacity is reached. We compared the physiological determinants of ADL in all 6 extant species of sea lions. ADL was estimated from measurements of total body oxygen stores and estimates of metabolic rate. Overall, animals that forage near the ocean floor have a greater tendency to approach or exceed their ADL compared to animals that forage near the surface. Physiological capacity of each group was closely matched with their diving behavior, suggesting that sea lions may be able to increase their diving capacity in response to greater physiological need through "conditioning". It was surprising that the largest sea lion were the shallowest divers, while some of the smaller sea lions dove deepest and had the greatest physiological capability to

dive for prolonged periods. Some species that operate at or near maximum diving performance will be less capable of responding to reductions in food availability due to climate change (El Nino, global warming) and/or fishery interactions.

259: Limitations of large body size in determining polar bear responses to sea ice loss

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Polar bears (*Ursus maritimus*) are the largest and most carnivorous of all ursids. They have evolved to hunt lipid-rich marine mammals on sea ice which provides a high energy food resource to support their large body size. Climate change has resulted in substantial loss of summer sea ice in many parts of their range altering their distribution and impacting both energetics and feeding behavior. Polar bears have been documented to be feeding less in the late summer and autumn, traveling further, using lower quality habitats, and spending more time on land where there have been increasing reports of terrestrial feeding. We review recent studies that have investigated limitations of food resources and energetic costs relative to polar bear body size and those of other large mammals and carnivores, to their ability to respond to sea ice loss. Feeding and energetic studies of ursids suggest that polar bears are limited in using terrestrial foods to meet energetic requirements, unable to lower metabolic rate in response to seasonal food deprivation, and constrained by high energetic costs associated with locomotion. These physiological limitations will define long-term responses of polar bears to sea ice loss while also determining how polar bears may balance food intake, diet composition, and activity levels to maintain body condition and thereby reproduction and survival in the short-term.

260: The shrew from Palawan

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A survey of small mammals on Mt. Matalingahan (2086 m elevation), southern Palawan Island, Philippines, in 2007 obtained specimens of a distinctive, apparently previously unknown shrew (Soricidae). Unlike the previously known native shrew that occurs sympatrically, *Crocidura palawanensis*, which has a slender body, slender fore- and hind feet, and a long, thin tail with a few long vibrissae, this apparently new species has a stout body, broad forefeet, and a short tail covered by short, dense fur. The dental formula traditionally used would result in assignment to *Suncus*, but a genetic analysis using Ultra-Conserved Elements shows the new species to be phylogenetically distant from *Suncus murinus* (the type species of *Suncus*) and to not be assignable to any recognized genus. The new species was common on Mt. Mantalingahan from 1550 m to 1950 m (near the peak), but was not detected from 700 m to 1300 m elevation. In contrast, *Crocidura palawanensis* occurs from sea level to the peak. Of 22 captures, 20 were on the ground and two were less than 0.5 m above the ground, whereas 8 of 30 *Crocidura palawanensis* were captured above ground, up to 2 m above the ground surface. Preliminary data suggest that *Suncus ater*, currently known only from the holotype captured on Mt. Kinabalu, Sabah, Borneo, is similar to the new shrew from Palawan, and may be its sister-species.

261: Central America and its squirrel of many colors: phylogeography of *Sciurus variegatoides*

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Central America is a region filled with an incredible amount of species within its relatively small area. Unfortunately, many such species in this region, including many mammals, have drastically little known about them or their relationship to Central America's constant geologic upheaval. One such species is the variegated squirrel (*Sciurus variegatoides*), which exhibits multiple, distinct pelage patterns across its range from southern Mexico to central Panama. Hypotheses for the variable pelage of *S. variegatoides* include possible adaptations to primary habitat and/or consequences of the variable climatic ranges seen in the region. Despite this, no studies have investigated this variation or these hypotheses using morphological or molecular means. In fact, the last revision of this species in 1937 identified 15 subspecies based solely on pelage differences. Given this, we undertook a phylogeographic assessment of this species using both molecular and morphological methods. Mitochondrial genomes were collected from museum specimens using capture hybridization, and cranial shape differences between subspecies and localities were assessed using two-dimensional geometric morphometrics. Preliminary morphological and molecular data posits that there is less variation among subspecies than the intriguing pelage patterns would suggest. Understanding the evolutionary patterns in this species will add to the current, sparse literature of Central American mammal evolution and increase our understanding of the biogeographic patterns affecting species in this region.

262: Climate change may adversely affect Dall sheep populations through variation in snow extent

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Northern alpine ecosystems are especially vulnerable to climate change because they occur at high latitudes and high elevations, but knowledge about the specific impacts of climate change on these systems is lacking. Dall sheep are an iconic species endemic to northern alpine ecosystems, and recent population declines have been attributed to harsh weather conditions. We investigated the effect of snow extent on Dall sheep recruitment using 16 years of range-wide remote sensing and Dall sheep survey data collected from 2000-2015. Annual recruitment increased with higher snowline elevations on May 15 (the peak of the lambing season) and decreased with later snow-off dates as well as higher snow cover frequencies. Our best-supported linear mixed model included an interactive effect of snow-off date and latitude. This model predicted that the negative effect of snow-off date on recruitment was strongest at high latitudes, and increasingly weaker at lower latitudes. Predictions from this model indicated that, compared to mean weather conditions, population growth would decrease by 2% in years with a late snow-off date at intermediate northern latitudes, and by 4% at high latitudes. These results demonstrate that the timing and frequency of snow cover affect Dall sheep throughout their range, and indicate that climate change could adversely affect the population dynamics of this iconic northern species.

263: Biotic and abiotic factors predicting the global distribution and population density of an invasive large mammal

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Biotic and abiotic factors are increasingly acknowledged to synergistically shape broad-scale species distributions. However, the relative importance of biotic and abiotic factors in predicting species distributions is unclear. In particular, biotic factors, such as predation and vegetation, including those resulting from anthropogenic land-use change, are underrepresented in species distribution modeling, but could improve model predictions. Using generalized linear models and model selection techniques, we used 129 estimates of population density of wild pigs (*Sus scrofa*) from 5 continents to evaluate the relative importance, magnitude, and direction of biotic and abiotic factors in predicting population density

of an invasive large mammal with a global distribution. Incorporating diverse biotic factors, including agriculture, vegetation cover, and large carnivore richness, into species distribution modeling substantially improved model fit and predictions. Abiotic factors, including precipitation and potential evapotranspiration, were also important predictors. The predictive map of population density revealed wide-ranging potential for an invasive large mammal to expand its distribution globally. This information can be used to proactively create conservation/management plans to control future invasions. Our study demonstrates that the ongoing paradigm shift, which recognizes that both biotic and abiotic factors shape species distributions across broad scales, can be advanced by incorporating diverse biotic factors.

264: Modeling range dynamics of montane rodents to evaluate climate tracking over time

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Mountain systems provide opportunities for studying biogeographic dynamics along gradients in climate and habitat. The Toiyabe Range and the Ruby Mountains represent closely situated, but isolated, mountain ranges of the North American Great Basin, that share similar climates and small mammal faunas. Previous work, however, suggests that over the past century, range dynamics of some species have been dissimilar across these two mountain ranges. One hypothesis is that species are tracking climate, but shifts in climate suitability differ between mountains. An alternative hypothesis is that species are responding to other factors that shape the geographic range, such as changing land use practices and interspecific interactions, which may differ between mountains. We employed high quality historic (pre 1950) and modern (post 1980) museum records and climate reconstructions to create species distribution models, and tested whether a suite of rodents conserved their climatic niche over time. If species were simply tracking climate, we predicted fidelity between the historic and modern models in each mountain range. However, we found mismatch between historic and modern models for some species, suggesting other factors are at play besides climate.

265: A test of three habitat suitability indexes for black bears in northeastern Minnesota

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We tested 3 habitat suitability index models developed for black bears (*Ursus americanus*) living in northern forests: the southern Appalachian Region, the Upper Great Lakes Region and the conifer-deciduous forests of New England. Between 2010 and 2013 we followed 13 collared female black bears in northeastern Minnesota, amassing 6798 ± 1770 GPS locations per bear per year (mean \pm SD). We constructed values for the variables included in each model from geographic information systems (GIS) data sets, in-situ measurements and *a priori* from the literature and tested the models in a geographic information system (GIS) at both the population and individual level. All three models predict habitat selection by the bears successfully and the New England model showed the strongest positive correlation between habitat selection and index values. The results suggest that our northeastern Minnesota study area offers poor habitat for black bears due to a lack of hard mast fall foods, an abundance of logging roads and few old growth stands.

266: Cryptic and sympatric: untangling *Sylvilagus* spp. in western North Carolina

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Cryptic species present unique challenges to the conservation community. Such species are particularly perplexing to manage and protect when one species of a cryptic complex is a common game species

often dubbed a pest, while another is a relatively rare species of conservation concern. One such species pair can be found in the mountains of western North Carolina. The eastern cottontail (*Sylvilagus floridanus*) is widely distributed, preferring disturbed, open habitat; the Appalachian cottontail (*Sylvilagus obscurus*) is a poorly understood, high elevation, early successional spruce-fir specialist. Though declining in much of its range and listed as Near Threatened by IUCN, the status of *S. obscurus* in North Carolina is not known. We sought to collect information on range overlap for these two species through field surveys, molecular techniques, and ecological niche modeling. We conducted live trapping and fecal surveys at Roan Mountain Highlands, NC in 2016. Following molecular species identification of tissue and scat samples, occurrence records were combined with georeferenced museum records to predict distributions for each species using MaxEnt. Eastern cottontails were more common at Roan Highlands than Appalachian cottontails, despite extensive surveys of spruce-fir habitat in the area. While ecological niche modeling indicates distinct habitat preferences for these two species, habitat loss, fragmentation and climate change may be facilitating encroachment of *S. floridanus* into this and other high elevation *S. obscurus* habitat.

267: Historical biogeography of mustached bats (genus *Pteronotus*)

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The genus *Pteronotus* is a clade of insectivorous bats widely distributed in the Neotropical Region and has recently gone through a taxonomic update which increased more than twice its diversity. Using molecular data of 15 *Pteronotus* lineages, we reconstructed a time-calibrated tree and estimated range evolution across phylogeny to investigate the biogeographic processes related to the origin and current patterns of distribution of this group. The origin of the genus *Pteronotus* occurred approximately 16 million years ago (Ma), with initial cladogenesis events being evenly distributed across the phylogeny. Divergence between most closely related species is recent, falling in the Pleistocene period less than 2.6 Ma. Mainland lineages present congruent patterns of north versus south continent splitting while insular clades differ in their time of arrival in the Caribbean Islands. Temporal and geographic range estimates for early nodes of *Pteronotus* phylogeny suggest a central role of Neogene tectonic reorganizations of Central America in the group diversification process. Also, South American colonization by *Pteronotus* occurred early in the genus history. Founder-event speciation was an important mode of lineage splitting in *Pteronotus*, with two independent dispersal jumps having occurred to the Greater Antilles. Finally, Pleistocene sea-level variation and climatic oscillations are possibly associated with divergence between sister-species and recent ages of MRCA for *Pteronotus* species.

268^F: Modeling distribution and connectivity of recovering American marten populations in Vermont using expert elicitation techniques

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American marten (*Martes americana*) were considered extinct in Vermont by the 1950s and unsuccessfully reintroduced in the early 1990s. Recently, two small populations were detected, one in far southern Vermont where the reintroduction occurred and the other in far northern Vermont. Mapping connectivity between populations represents a management priority. However, little information exists on marten in the state due to their rarity. We developed an occupancy model for marten using an expert-opinion approach, then used the model to map connectivity between populations. We elicited opinions on marten occupancy from experts (n = 16) in the region, including biologists, managers, trappers and researchers, using an online survey to develop the model. The survey allowed experts to estimate occupancy probability at several sites and accounted for uncertainty in their estimates. We examined multiple candidate models that included the influence of 15 habitat-related covariates on responses and used model selection techniques to estimate the best model in the set. We then applied the top model on

a pixel-by-pixel basis to map potential distribution and used a circuit theory approach to identify corridors and movement flow between populations. Our results provide a quantitative measure of how landscape conditions influence occupancy that can be updated over time with empirical data. Maps of connectivity reveal potential pathways of movement that can inform conservation planning for marten recovery in the state.

269^F: Integrating step-selection functions with movement states to investigate black bear habitat selection

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As animals traverse the landscape, intrinsic and extrinsic factors influence their behavioral state, which in turn influences how and where they move across the landscape. Incorporating behavioral state into step-selection functions could provide a better understanding of an animal's habitat requirements. We investigated the movements of 16 black bears (*Ursus americanus floridanus*) (6 females, 10 males) in a fragmented area of Florida using bi-hourly GPS data collected from 2011 to 2014. Our framework allowed bears to switch between two behavioral states: we used hidden Markov models to estimate distributions of step-lengths and turning-angles in each state and probabilities of switching between states. We applied the Viterbi algorithm to assign a most probable state to each bear observation. For the step-selection function, we randomly selected alternate locations for each observed location based on the bears' (estimated) behavioral state. We compared each location with the alternate locations using conditional logistic regression. Preliminary results suggest that the two states best explaining bear movements were a "resting" state with short step-lengths (average: 12.76 ± 8.80 m) and greater turning-angles (average: $177.04 \pm 0.0^\circ$), and a "traveling" state with long step-lengths (average: 515.97 ± 61.27 m) and smaller turning-angles (average: $1.58 \pm 17.19^\circ$). Forested wetlands and urban areas were the most and least selected land covers, respectively. These results demonstrate the usefulness of investigating movement patterns along with habitat selection.

270: Characteristics associated with tree cavities used by female fishers (*Pekania pennanti*) as reproductive dens

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Tree cavities are important natural resources used by wildlife species worldwide; they provide animals with physical and thermal protection and are often of high value during reproduction. Female fishers (*Pekania pennanti*) use tree cavities as reproductive den microsites; females give birth in natal dens and typically move kits to ≥ 1 maternal den during a den season. Few studies have characterized attributes of tree cavities used by reproductive females including the spatial distribution of trees with cavities used during a single season (i.e., den cluster). We located reproductive dens of 45 radio-collared female fishers between 2008 – 2015, then measured physical and thermal attributes at a subset of previously used den cavities. Physical measurements were similar for natal and maternal den cavities, with the exception that natal den entrances were smaller. Data from temperature loggers deployed inside and outside den cavities suggest that they provided good insulation from cold temperatures; natal den cavity interiors experienced a smaller proportion of days below 5° C relative to maternal dens. Mean distance between dens used by a female during a den season averaged $364 \text{ m} \pm 314 \text{ SD}$ (range 0 – 1,894 m), while distance among all dens averaged $930 \text{ m} \pm 650 \text{ SD}$ (range 0 – 2,718 m). Characteristics of den clusters may provide guidance for conservation of potential den trees at a spatial scale relevant to fisher

reproduction.

271: Impact of linear features on boreal caribou and moose distributions with implications for apparent competition

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Anthropogenic disturbances are implicated as the root cause of boreal caribou (*Rangifer tarandus*) population declines. In northeast BC, linear features (roads and seismic lines), resulting mainly from natural gas development, may exacerbate the effects of apparent competition between caribou and moose (*Alces alces*) by altering moose densities or distributions, thus increasing wolf (*Canis lupus*) presence in caribou ranges. We explored the potential for linear features to affect moose distributions, increase moose-caribou overlap, and increase predation risk from wolves. We used resource selection functions developed for radio-collared caribou (154) and moose (61) to quantify responses to linear features and to estimate caribou-moose overlap by predicting the relative probability of moose use within caribou home ranges and at caribou mortality locations attributed to wolves. We then evaluated the influence of linear features on overlap and the relationship between overlap and locations of wolf-killed caribou. Moose and caribou responses to roads and seismic lines varied. Linear features frequently corresponded to higher overlap between moose and caribou and overlap was positively associated with caribou mortalities during some seasons. The magnitude of these responses, however, was small. The impact of linear features on caribou survival via changes in moose distributions is likely secondary to alternative mechanisms by which linear features and other disturbances decrease caribou survival, such as increases in moose and wolf densities and increases in wolf hunting efficiency.

272: Low survival, high predation pressure present conservation challenges for an endangered endemic forest mammal

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Peripheral populations are often ecologically distinct and of conservation concern due to isolation, low numbers, and climatic extremes. Targeted management programs are informed via fine-scale analyses of demographic processes in such populations. Population survival rate could be more important than fecundity in species that do not have highly reproductive life histories. The Mount Graham red squirrel (MGRS; *Tamiasciurus fremonti grahamensis*), the southernmost population of North American red squirrel, is restricted to one mountain range in southeastern Arizona, USA. The population has been monitored intensively, and individuals marked and radio-tagged since 2002. Although MGRS reproduction is similar to congeners, little to no population growth is observed. Here we estimate the survival rates and mortality hazard in MGRS to understand the impact of natural mortality on survival and population function. We estimated survival for 381 marked MGRS and a subset of 135 known-fate individuals using Cormack-Jolly-Seber models. We used hazard models and competing risks regression to assess cause-specific mortality by age class and sex. Across sex and juvenile and adult age classes, individuals had an approximately 10% chance of dying in any given month and a 63% chance of dying each year (annual survival estimate = 0.37). Avian predators were responsible for >65% of all known mortality events. Low juvenile and adult survival and multiple raptor species of conservation concern complicate management for population growth and recovery.

273^F: Evaluation of non-invasive fecal sampling for monitoring bobcats and ocelots in South Texas

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Field research methods to monitor the endangered ocelots (*Leopardus pardalis*) in South Texas include live-trapping and camera stations. However, months of trapping efforts often result in the capture of only a few individuals, and camera stations cannot gather genetic information for population monitoring. Bobcats (*Lynx rufus*) and other carnivores are known to defecate along roads and trails within their home ranges. Thus, it may be possible to incorporate non-invasive scat sampling as an additional monitoring tool for ocelots, with added benefits such as the acquisition of DNA. We evaluated the feasibility of collecting felid scats along ranch roads adjacent to known ocelot habitat to determine abundance of ocelots and bobcats where the two species co-occur. We extracted DNA from 172 samples and confirmed species of origin through mitochondrial DNA sequencing. We were able to identify 70 bobcat samples and 0 ocelot with an 88.4% amplification success rate. Abundance estimates from closed mark-recapture using microsatellite genotypes will be compared to data from a grid of 26 camera stations within the same study areas. Scat sampling is an efficient way to acquire genetic material from bobcats. However, our lack of ocelot detections suggests that ocelots do not prefer to use roads for moving and scat marking as other carnivores do, or that the event is rare and did not occur during our surveys.

274: Are North American populations of migratory tree-roosting bats declining?

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As concerns over environmental impacts of fossil fuels grow, wind energy is increasingly popular. However, large numbers of bats are killed at some wind energy facilities and this raises concerns about cumulative impacts on bat populations. An estimated 0.84 and 1.7 million bats have been killed in the U.S. and Canada from 2000-2011, and this increases by over 500,000 fatalities annually, 78% of which are of three species of migratory tree-roosting bats. Given these estimates, there are worries that the population viability of bats may be threatened. Although population estimates are lacking for migratory tree-roosting bats, recent population modelling derived from expert elicitation suggests that for hoary bat populations to persist, the mean annual population growth rate must be substantially higher than what appears “most likely” and that current fatality levels could cause a 91% decrease in the population size of hoary bats within 50 years. We examined how acoustic detections, capture rates, rabies submission rates, and wind-energy related fatality rates of migratory tree-roosting bats change through time to look for evidence of population declines. If all these metrics consistently show declines, then this may indicate declining populations. We found multiple signs of population declines in all three species examined. Our analyses highlight the need for effective policy and mitigation strategies that embrace adaptive and flexible management and address cumulative impacts.

275: Estimating winter habitat quality of New England cottontail with a focus on diet and nutrition

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The New England cottontail (NEC) (*Sylvilagus transitionalis*) is found only in small fragmented portions of its former range, was formerly a candidate for listing under the federal Endangered Species Act, and currently is listed as a species of concern in Rhode Island. Since 2012, captive-bred individuals have been released on Patience Island (PI) in Narragansett Bay to establish an experimental population with the ultimate goals of reintroduction to mainland Rhode Island and establishment of self-sustaining wild populations. Recent genetic surveys of NEC on PI provide evidence of a self-propagating population, which suggests the presence of suitable habitat. Therefore, PI provides an optimal study site for an investigation of diet and nutrition. Primary factors limiting population growth must be identified for successful implementation of a future reintroduction program; however few studies have addressed how habitat quality affects NEC fecundity and persistence. Habitat quality data was obtained by investigating the components of NEC diets and determining the nutritional values of vegetative species consumed. Nutritional data were compared with diet composition and vegetation availability to determine which nutritional components are driving NEC forage selection. The results of this study can be employed for

future research focusing on the nutritive values of reintroduction sites and will inform the decision-making processes related to the conservation and management of this declining species.

276^{HTA}: Use of cooler microclimates by herbivores challenged with dietary plant toxins

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Increasing ambient temperatures, as predicted by climate change, pose a new threat to herbivorous mammals. Higher temperatures interact with mammalian physiology in such a way that poisonous compounds become more potent. This phenomenon is known as temperature-dependent toxicity (TDT). While the mechanism and effects of TDT have been previously documented, it remains unknown whether mammalian herbivores can behaviorally mitigate TDT. We investigated use of cooler microclimates by desert woodrats (*Neotoma lepida*) from the Mojave Desert that feed on chemically defended leaves of creosote bush (*Larrea tridentata*). Utilization of cooler microclimates and the influence of microclimate access on food intake and body mass maintenance were determined in a laboratory-based experiment. Woodrats were either given access to 21°C and 29°C microclimates or prevented access to 21°C, and fed diets with or without creosote toxins. We predicted that woodrats would use cooler microclimates when provided and show improved performance compared to woodrats held at 29°C. Regardless of diet, woodrats used cooler microclimates when provided. Access to 21°C did not affect total food intake but did buffer against body mass loss compared to woodrats without access. These results suggest that cooler microclimates could provide a means to mitigate TDT through improved body mass maintenance. Understanding how mammalian herbivores interact with their environment is imperative to advance the field of plant-herbivore interactions and to further elucidate impacts of climate change.

277^{E,HTA}: The influence of social context on call amplitude in grasshopper mice (*Onychomys*)

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Acoustic communication plays an important role in the social lives of many animals. Modulation of vocal parameters such as duration and frequency can often reveal a sender's motivational state, status, or social context. However, sound amplitude is often overlooked because of technical challenges associated with microphone calibration and controlling for distance from the sound source. In this study, we systematically measured vocalizations produced by grasshopper mice (*Onychomys*) to explore how vocal parameters change in relation to social context. We found that males produce spectrally-similar vocalizations when spontaneously advertising in an upright posture and while prone in the physical presence of a potential mate. However, spontaneous calls were about 30 dB louder than the softer mating calls. Mechanistically, empirical measures of the spontaneous calls align with the observed posturing and theoretical models of sound amplification from a flared mouth opening, derived from horn acoustics and loudspeaker design. Functionally, higher call amplitudes in spontaneous contexts reflect the need for animals to advertise to potential mates and competitors over long-distances.

278: Comparative liver metabolism between juniper specialist *Neotoma stephensi* and generalist *Neotoma albigula*

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While herbivory is a common dietary strategy in mammals, they rarely specialize on a single plant species, likely because of limitations in detoxifying high levels of plant secondary compounds. To explore metabolic advantages of dietary specialists, we analyzed the livers of a juniper specialist, *Neotoma stephensi* (consumes >85% juniper), and its sympatric generalist, *N. albigula* (consumes ≤30% juniper), for cytochrome P450 2B (CYP2B) content and microsomal turnover of α-pinene, the most abundant terpene in one-seeded juniper (*Juniperus monosperma*). In both *Neotoma* species, transition from a

juniper-free (0%) to 30% juniper diet increased CYP2B expression (2-3 fold) and α -pinene turnover rates (4-fold). In *N. stephensi*, higher levels of dietary juniper (60% and 85%) further induced CYP2B and increased α -pinene turnover rates. Although no species-specific differences in feeding behavior or α -pinene turnover rates were observed at 30% dietary juniper, CYP2B levels were 1.7-fold higher in *N. stephensi* than in *N. albigula* ($p < 0.01$). Because *N. albigula* does not consume more than 30% juniper, it is unknown whether this species lacks the ability to further increase expression of either CYP2B or other enzymes that metabolize α -pinene. However, the increased CYP2B expression and α -pinene turnover rates in *N. stephensi* exposed to 60% or 85% juniper suggest that CYP2B enzymes support this species' consumption of high α -pinene levels.

279^F: The comprehensive visual system of Ord's kangaroo rat (*Dipodomys ordii*) and the potential for UV-communication

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Communication in the UV-spectrum is known in insects, plants, fish, amphibians, reptiles, birds, and few mammal species. UV-communication requires both signaling mechanisms and perception mechanisms. Signaling mechanisms include UV-reflective morphological characteristics such as hair, feathers, skin, and flowers. Such reflection of UV for communication is only known to occur between 350-400nm (UV-A). For such signaling to serve as a means of communication, the visual system of the intended signal recipient must be able to perceive light wavelengths as short as 350nm. Here we used UV photography and photospectrometry to determine UV-reflection by body markings of the kangaroo rat that could be used in UV-communication. We also analyzed the visual system using immunohistochemical labeling (IHC), quantitative and qualitative transmission methods, and microscopy to determine the UV-sensitivity of the visual system of the kangaroo rat (*Dipodomys ordii*). Our results show UV-reflective body markings that contrast with background pelage and could be used in communication. We also determined a UV-sensitive visual system and a visual system that resembles that of a crepuscular/diurnal species as well as that of a nocturnal species, as expected. Visual acuity in low light might be associated with known avoidance of activity during high moonlight intensity; we propose that the species could easily compensate for loss of foraging due to high moonlight nights by foraging during crepuscular or diurnal periods.

280^F: Immunity and growth trade-offs vary with elevation in a hibernating small mammal

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Identifying the ecological factors that shape the evolution of life histories has been a topic of great interest for several decades. Populations of the same species can express important differences in life history traits, often apparent when comparing populations along an elevational gradient, where differences in phenology, reproduction, survival, and growth exist. However, trade-offs between such fitness traits and immunity have rarely been studied in the wild. We live-trapped Uinta ground squirrels (UGS, *Urocitellus armatus*) to examine the relationship between immunocompetence (measured by a bacterial killing assay) and growth in two UGS populations located 600 m. apart in elevation while accounting for age and sex. Higher elevation yearlings/adults emerged with lower body mass, but compensated by increasing their investment in growth, entering estivation at the same body mass as lower elevation individuals. This compensatory growth came at a cost, as immunocompetence decreased more rapidly in individuals at the higher elevation, indicating a trade-off between growth and immunity. These trade-offs were not detected in juveniles, which had similar growth rates and immunocompetence across elevations. However, higher elevation juveniles emerged lighter than lower elevation individuals and remained lighter through estivation. We hope to quantify the consequences of such trade-offs on survival to predict the ability of UGS populations that inhabit different elevations to adapt to an increasingly variable climate.

281^F: Life history trade-offs within an artificially selected species

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Artificial selection has been used to increase the expression of desirable traits in the lab mouse. Associated with this procedure, hundreds of well-characterized phenotypic variants (strains) are now available for use in research. Although these strains are typically used in biomedical research models, we propose that data from these mice can be used to identify patterns of life history variation. We used the publicly available Mouse Phenome Database by the Jackson Laboratory to investigate correlations among life history traits and between these traits and physiological variables. We used fitness-related variables in a principal component analysis, which resulted in two principal components (breeding frequency and reproductive strategy) that describe the variance in reproductive performance. Scores from this analysis were then regressed against other life-history traits (body mass and lifespan) and physiological variables associated with metabolism. Interestingly, we found that reproductive performance and longevity were not significantly correlated, as we had initially hypothesized. Further, reproductive performance was not correlated with adult body mass nor metabolic variables. We did find, however, that adult insulin-like growth factor 1 (IGF-1) concentration was significantly related to breeding frequency. Our analysis supports the hypothesis that IGF-1 may contribute to variation in reproductive performance. Together, these results help understand what drives individual variation in life history, as well as the phenotypic and physiological correlates that accompany this variation.

282^{F}: Variation in body fat along an elevational gradient in the deer mouse (*Peromyscus maniculatus*)**

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Body composition (percent fat and lean mass) is frequently used to assess fitness in wild populations because it is closely linked to reproductive output. Body composition is also important to thermoregulation in endotherms, as fat can provide both insulation and fuel to power heat production. Although percent body fat varies seasonally in some mammals, little is known about how it differs between populations in different environments. The insulative properties of fat may be especially important to thermoregulatory performance at high elevations, where the ability to maintain a stable body temperature via aerobic thermogenesis is constrained by hypoxia. We tested whether body composition varies along an elevational gradient in the deer mouse (*Peromyscus maniculatus*). Deer mice were collected along six transects spanning 2,500 meters of elevation in the Colorado Front Range during the summers of 2015 and 2016. Following collection, body composition was measured via quantitative magnetic resonance. Preliminary results suggest that body fat increases with elevation in both relative and absolute terms. Additionally, individuals from higher elevations carried relatively more intrascapular brown adipose tissue. Relative lean mass decreased with elevation, although absolute lean mass did not vary between sites. Further work is needed to determine whether these differences are the result of intrinsic, population-level variation in lipid biosynthesis or dietary factors. This research was supported by a 2015 Student Grant-in-Aid awarded to Cole Wolf.

283: Seasonal nutrient utilization by two captive giant pandas consuming a bamboo-based diet

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Giant pandas exhibit distinctive seasonal preferences in bamboo plant part selection as a foraging strategy to meet nutrient requirements while consuming a poorly-utilized diet. We examined digestibility of macronutrients in two captive giant pandas consuming bamboo-based diets across four months (January, March, May, October), which encompassed culm-, shoot-, and leaf-consumption seasons. Giant pandas have a limited ability to utilize diets primarily comprised of mature bamboo culm and leaves, with total dry matter (DM) digestibility being less than 30%. Though the majority of bamboo's dry biomass is plant-structural compounds (dietary fiber), giant pandas can apparently utilize some fiber and non-fiber nutrients, such as hemicellulose (HC), starch, and crude protein (CP), to a greater extent (apparent

digestibility ranges: 33 - 56%, 47 - 88%, 34 - 58% for HC, starch, CP, respectively). When bamboo shoots were included in the diet (May), giant pandas achieved higher digestion rates for DM, organic matter, neutral detergent fiber, acid detergent fiber, HC, and gross energy (apparent nutrient digestibility > 40%). We propose that the basis of giant panda foraging strategy is maximization of digestible energy intake, often from carbohydrate sources, which has applications in areas of giant panda conservation and management of animals in captive scenarios.

284: Mountain goat: Montana's bipolar alpine ungulate

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Among the four states and four Canadian provinces and territories inhabited by native populations of mountain goats, Montana is unique. More than 75 years ago, the state wildlife agency began transplanting mountain goats (495 animals to 27 locations) into previously unoccupied mountain ranges. We gathered and synthesized available harvest and population data for all native and introduced populations across the state. Supplementing these data with responses to a questionnaire we sent to the 18 Montana Fish, Wildlife and Parks' biologists that manage goats, we assessed past trends and current status of Montana's mountain goats. As introduced populations have generally prospered—numbering 2,525 or 69% of the statewide population—native populations (outside Glacier National Park) have declined from an estimated 4,100 during the 1940s to about 1,160 (31%) of the statewide population in 2016. Many populations are small and potentially demographically isolated. Whereas native herds sustained 80–90% of public harvest 50 years ago, introduced populations have produced about 85% of the statewide harvest in recent years. Total harvest has declined over that period from 300–500 to ~210 goats annually. Our survey of biologists identified likely causes of population changes and a wide range of management and research needs that would benefit mountain goat management. We have recommended development of a statewide plan for the species' long-term management and conservation.

285^E: Winter ecology of prairie deer mice (*Peromyscus maniculatus bairdii*) in cultivated habitats and implications for agricultural ecosystem services

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Prairie deer mice (*Peromyscus maniculatus bairdii*) are permanent residents of row-crop fields in the Midwestern United States, and may provide ecosystem services by regulating weed seed and waste grain populations. Seed predation is especially critical in the months of highest seed availability following crop harvest, and is dictated by population density and individual patterns of diet choice. We used a combination of spatial mark-recapture demographic and stable isotope dietary analyses to investigate the ecology of prairie deer mice during this critical over-winter period within corn and soybean agro-ecosystems of west-central Indiana. Winter prairie deer mouse populations were robust (typically > 13 individuals/ha) in the row-crop habitats we sampled. Apparent survival of individuals varied throughout winter (57–79% monthly survival rate), and mean over-winter (December–April) survival of adults was 21%. Winter diets were dominated by waste grain, with corn and soybean contributing 55% and 77% of diet for mice sampled in corn and soybean fields, respectively. Based on our results and published field metabolic rates, we estimate that prairie deer mice consume 6.3 kg/ha of waste corn and 7.1 kg/ha of waste soybean seeds during the non-growing season. Collectively, our results suggest that prairie deer mice make meaningful contributions to reducing waste-grain populations during winter in post-harvest row-crop fields, during a time of year when most other seed predators are inactive.

286: Effects of prolonged immunocontraception on the breeding behavior of American bison

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In late 2009 the Catalina Island Conservancy began using the immunocontraceptive vaccine porcine zona pellucida (PZP) as a means of controlling fertility, and thus population size, of an introduced herd of American bison (*Bison bison*) on the island. Although PZP application successfully slowed population growth, lingering questions remained about the long-term effectiveness of PZP to manage large, free-ranging wildlife populations. We sought to determine the reversibility of PZP by ceasing the annual application in a subset of cows and monitoring for subsequent calf arrival, and to document changes in the timing and length of the breeding season in response to PZP by recording breeding behavior and assessing fecal progesterone (FP) levels in all cows on the island over a 13-month period. To date, no new calves had been observed on the island, suggesting that, following repeated applications of PZP, bison cows may not resume normal reproduction for at least three years. Based on behavioral observations and FP levels, cows consistently displayed estrous cycles throughout the study period, indicating that bison may ovulate continuously when conception is blocked. Because there is little evidence that an extended breeding season will negatively impact the health of bulls or result in large numbers of out-of-season births, PZP appears to be a highly effective tool for maintaining a stable population of bison on Catalina Island.

287: Impacts of range seedings on a keystone species: Piute ground squirrel diets in southwestern Idaho

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Piute ground squirrels (*Urocitellus mollis*) are keystone species in shrub-steppe habitats in southwestern Idaho. After wildfires, rangeland seedings (mostly exotic grasses) are commonly used for rehabilitation, but without data on whether or not native herbivores can subsist on the species seeded. Our objective was to determine if seeded plants were being utilized in Piute ground squirrel diets. We selected two established seedings with similar ground squirrel populations. Kuna Butte was dominated by cheatgrass (*Bromus tectorum*), native Sandberg bluegrass (*Poa secunda*), seeded Siberian wheatgrass (*Agropyron fragile*) and Anatone bluebunch wheatgrass (*Pseudoregnaria spicatum*). Initial Point was dominated by invasive bur buttercup (*Ranunculus testiculata*), seeded forage kochia (*Brassia prostrata*) and Siberian wheatgrass, and remnant Sandberg bluegrass. Both sites had exceptionally low plant species diversity. In 2014, we live-trapped Piute ground squirrels and collected fecal pellet samples (n=120). We determined diet composition using a microhistological technique. At Kuna Butte, cheatgrass and Sandberg bluegrass constituted 87% of the diet. At Initial Point, Sandberg bluegrass, forage kochia, Siberian wheatgrass, and cheatgrass comprised 99.7% of the diet. Seeded grasses were less utilized than remnant grasses. This is troubling because ground squirrels typically eat more forbs than less-digestible grasses; cheatgrass and Sandberg bluegrass desiccate early in drought years; and forage kochia is a purposely introduced, invasive species. Low dietary diversity in seedings may not provide adequate long-term nutrition for Piute ground squirrels.

288: Survival and cause-specific mortality of American pronghorn in western South Dakota

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Limited information exists on survival and cause-specific mortality of pronghorn (*Antilocapra americana*) inhabiting sagebrush-steppe regions within the Dakotas. Objectives of our study were to provide additional estimates of survival and cause-specific mortality for adult (>18 months), yearling (6-18 months) and fawn (<6 months) pronghorn in South Dakota. Additionally, we wanted to evaluate exposure of pronghorn to novel diseases including Epizootic Hemorrhagic Disease (EHD), West Nile Virus (WNV), Blue Tongue Virus (BTV), Bovine Viral Diarrhea Virus (BVDV), Neospora, and Parainfluenza-3 (PI-3). From 2015 to 2016, we monitored 69 adult, 34 yearling and 92 fawn pronghorn within and surrounding Butte County, South Dakota. Overall survival rates for adults and yearlings was 0.89 (95% CI, 0.82 – 0.95) and 0.77 (95% CI, 0.61 – 0.93), respectively. Primary mortality causes for adults were unknown at

36%, while predation on yearlings comprised 83%. Survival rates for fawns pooled across years was 0.66 (95% CI, 0.54 – 0.78) with predation (n=15) as the leading cause of mortality. In 2015, we collected blood samples and extracted serum from 50 (40 adult, 10 yearling) radio-collared pronghorn. Disease exposure was variable and ranged from 5% for BTV and BVDV to 67.5% for WNV; EHD (60%), PI-3 (40%), and Neospora (10%) were intermediate relative to exposure. Our study provides information on an historical population of pronghorn previously used to reestablish populations throughout the northeast region of the distribution.

289: Effects of silvicultural herbicides on the nutritional ecology of Columbian black-tailed deer

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Black-tailed deer (*Odocoileus hemionus columbianus*) depend on abundant and nutritious understory vegetation found in early-seral forests. Thus, intensive forestry practices, such as the use of herbicides to decrease vegetation competition with conifers, may affect the nutritional ecology of black-tailed deer in the Pacific Northwest. We compared nutrient intake of black-tailed deer between stands that received herbicide treatments paired with those that did not, and investigated how these responses changed as forests aged from early seral stages (≥ 2 years post-harvest) to canopy closure (≤ 20 years post-harvest). Using hand-raised tractable black-tailed deer, bite count methods and behavioral observations, we measured diet composition, diet quality and nutrient intake within each paired stand. Additionally, we measured vegetation biomass and overstory characteristics for each stand. We found herbicide use decreased the amount of understory biomass and biomass of plants useable to deer. Foraging deer were able to collect diets of equal quality (digestible energy) between treatments. However, because of a greater abundance of plants offering large bite masses (e.g., shrubs), deer were able to consume forage faster in non-sprayed plots, particularly in the 1-3 age class, resulting in higher digestible energy intake in non-sprayed plots. As stands aged, abundance of forage declined, as did the quality of diets deer consumed and regardless of herbicide spray, open canopy stands provided more, high quality forage for deer than closed canopy stands.

290^E: Follow the bear: expanding understanding of black bear ecology across variable densities and landscapes

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The relationships and interactions between species space use and the environment they occupy directly impact species distributions, genetic diversity, the spread of disease, human-wildlife conflict, and therefore conservation and management planning. As a result, animal resource selection behavior and its drivers have been a focus of ecological research for decades. Yet many aspects of these patterns remain unclear, due in part to the dynamic nature of the behavioral processes driving this phenomenon. For instance, in the Lower Peninsula of Michigan, black bear occurrence has increased in previously uninhabited southern regions. This southern region of the Lower Peninsula features significantly more agricultural and urban areas than are typical of the past distribution of bears in Michigan. It is unclear how bears will use and navigate such an abruptly altered and highly variable landscape. Thus, our objective was to improve understanding of the behavioral processes driving black bear resource selection in the southern extent of their range in the Lower Peninsula. We applied step-selection analyses to a GPS dataset of 15 radio-collared bears to address our objective. Our results highlight the roles local bear density, temperature, and landscape configuration play in black bear use of heterogeneous landscapes. These insights expand our knowledge of these fundamental, yet complex, interactions between black bears and their environment.

291: Of the Northwest wind: Pine marten science and politics in forest planning

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The history of land management decisions across the United States is often at odds with scientific investigations regarding the biological diversity and conservation status of individual species. As US National Forests across the nation complete land management plan revisions, new information about species assemblages, diversification, and populations' responses to climate change can influence management actions and forest policy into the future. We use recent research with American pine marten (*Martes americana*, and *Martes caurina*) as a case study to examine the use of science in land management planning through the lens of conservation genomics, and land management planning revision strategies in Montana and Alaska. We use pine marten to examine two questions regarding biological diversity and conservation science in forest planning, 1) What are the scientific and political mechanisms by which genomic or morphological species-specific information can be interpreted in forest planning rules, and 2) does the natural diversity of landscape reflect the diversity of both species-specific investigations, as well as the land management planning that governs these species' distributions? Preliminary findings suggest that all land management policies tend to focus on species-level diversity through the mechanism of the US Endangered Species Act, but that regionally, or locally, forest planning processes are beginning to incorporate more genomic-level information about species in forward-thinking planning practices. Some of this research was supported by a Grants-In-Aid to Natalie Dawson in 2006.

292: The evolution of intelligence in mammalian carnivores

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Intelligence should evolve to help animals solve problems posed by the environment, but it remains unclear how environmental complexity or novelty facilitates evolutionary enhancement of cognition, or whether domain-general intelligence evolves in response to domain-specific selection pressures. The social complexity hypothesis, which posits that intelligence evolved to cope with the labile behavior of group-mates, has been strongly supported by work on the socio-cognitive abilities of primates and other animals. I review the remarkable convergence in social complexity between old-world primates and spotted hyenas, and describe our tests of the social complexity hypothesis in regard to both cognition and brain size in hyenas. Behavioral and morphological data indicate remarkable convergence between primates and hyenas with respect to their abilities in the domain of social cognition. However, social complexity failed to predict either brain volume or frontal cortex volume in a larger array of mammalian carnivores. To inquire whether social complexity can explain the evolution of domain-general intelligence, we presented simple puzzles to members of 39 zoo-housed carnivore species, and found that species with larger relative brain size were better at solving the problem. However, social complexity failed to predict success in this task. Although social complexity appears to enhance social cognition, there are no clear causal links between social complexity and either brain size or performance in problem-solving tasks outside the social domain in mammalian carnivores.

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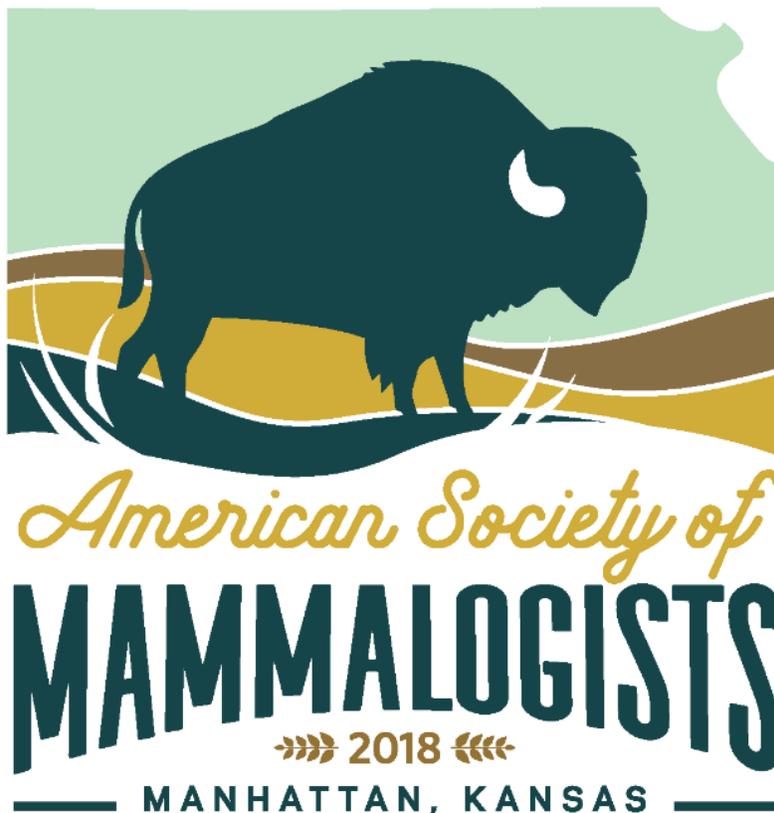
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SAVE THE DATE!!!

**98TH ANNUAL MEETING OF THE AMERICAN
SOCIETY OF MAMMALOGISTS**



Please join us June 25-29, 2018, in Manhattan, Kansas for the 98th Annual Meeting of the American Society of Mammalogists. The conference will be held on the campus of the Kansas State University, located in the Flint Hills of Kansas, in the Southern Tallgrass Prairie Region of the Central Plains. Learn about the latest advances in the study of mammals and interact with researchers and educators specializing in these fascinating animals. Come and enjoy everything this grassland region has to offer!

On-campus housing will be available and hotel blocks will be made available for meeting attendees. Detailed conference and registration information will be made available on the conference website (www.mammalmeetings.org).

The scientific program will include contributed oral and poster presentations as well as symposia, plenary speakers, and workshops. A full social agenda is planned including the opening mixer at the Flint Hills Discovery Center, an awards social at the KSU Alumni Center, picnic on the Konza Prairie Biology Station, the annual Run-for-Research, and fieldtrips. Details for these events will be made available on the conference website.

For more information about the 2018 meeting, contact the chair of the Program Committee, Cody Thompson, University of Michigan Museum of Zoology (734-615-2810, mammal.meetings@gmail.com), local co-hosts from the Kansas State University, Adam Ahlers (785-532-0875, aahlers2@k-state.edu), Andrew Hope (785-532-6347, ahope@k-state.edu), Drew Ricketts (785-532-1949, arickett@k-state.edu), and Elmer J. Finck from Fort Hays State University (785-628-4269, ejfinck@fhsu.edu), or Tony Ballard, Kansas State University Conference Services (785-532-2402, tballard@k-state.edu).

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