Undergraduate Research Symposium   May 17, 2019 Mary Gates Hall

Online Proceedings

1E

ANIMAL BEHAVIOR, ECOLOGY, AND EVOLUTION

Session Moderator: Luke Tornabene, School of Aquatic and Fishery Sciences and the Burke Museum of Natural History and Culture

MGH 231

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Niche Partitioning and Intertidal Habitat Use among Coexisting Gull Species on San Juan Island, Washington
Fiona C Boardman, Senior, Biology (Ecology, Evolution & Conservation)
Mentor: William Breck Tyler, Friday Harbor Labs

Gull species in the genus *Larus* differ in breeding range, habitat use, size, and feeding behavior. During their post-breeding season, however, many species of gulls gather and temporarily occupy the same sites and habitats. Although there is evidence of niche partitioning by gulls in northeastern North America and northwestern Europe, the mechanisms by which gulls coexist in the San Juan Islands of Washington state are poorly studied. To investigate gull coexistence on San Juan Island, WA, we studied the intertidal feeding ecology of Mew Gulls (*Larus canus*), California Gulls (*L. californicus*) and Glaucous-winged Gulls (*L. glaucescens*). Patterns in abundance, behavior, substratum-use, and large prey type (identifiable through spotting scope) were investigated through observational methods at Jackson Beach. Pairwise chi-square tests revealed significant differences in large prey type and substratum use between California and Mew gulls and between California and Glaucous-winged gulls. Patterns in frequency of large prey captured illustrate differences in prey selection among species, with Mew gulls capturing primarily worms, California gulls capturing primarily fish, and Glaucous-winged gulls demonstrating generalist foraging behavior. These findings suggest that during foraging, the gull species use shared habitat differently by specializing in different large prey types. This supports previous evidence of niche partitioning among gulls, and suggests that niche partitioning reduces competition among gull species in the San Juan Islands.

The Evolution of Bone Density in Deep-Sea Snailfishes
Abbey Dias, Junior, Biology, Whitman College
Mentor: Mackenzie Gerringer, Friday Harbor Labs

Maintenance of neutral buoyancy is a challenge to all fishes. In shallow water, this is typically achieved through the use of a swim bladder, though a more favorable mechanism for deep-sea species is through a reduction in skeletal structure. Extreme environmental conditions—low temperature, high pressure, lack of light, limited food availability, and varying oxygen concentrations—exert evolutionary pressures on organisms that inhabit the deep sea. The family Liparidae (snailfishes) span the largest depth range of any marine fishes. Hadal snailfishes, the deepest-living fishes, reside as deep as ˜8,200 meters. With the elimination of swim bladders, a reduction in skeletal structure has become the mechanism by which this family achieves the buoyancy needed to hunt in the water column. We used micro-computed tomography (micro-CT) scanning to study bone density across the full bathymetric range of the Liparidae with representatives across the family tree. Of these specimens, five bones were measured for density: the lower jaw, for purposes of feeding mechanics; the third vertebrae, as a control; the first left pelvic pterygiophore for studying the suction disk; the hypural plate, to study swimming and movement trends, and the sagittal otoliths. Phylogenetic analyses revealed a decrease in bone density with increasing depth. The degree of change in density with depth differed among the structures measured, implying evolutionary effects on the function and performance of bone structures in the deep sea.

Co-Evolution of Cleaning and Morphology in Caribbean Neon Gobies
Jonathan Michael Huie, Senior, Marine Biology, Aquatic & Fishery Sciences
    Levinson Emerging Scholar, Mary Gates Scholar
Mentor: Luke Tornabene, School of Aquatic and Fishery Sciences and the Burke Museum of Natural History and Culture

Cleaning is a mutually beneficial relationship, where the cleaner removes and consumes ectoparasites from its clients.

Among fishes, the cleaning behavior has evolved several times as a juvenile or facultative feeding strategy, and is often lost in adults. However, a minority of taxa clean almost exclusively across their ontogeny (obligate cleaners). The largest radiation of obligate cleaners are the Caribbean neon gobies (*Elacatinus*), that evolved with several congeneric non-cleaners, and in parallel with a closely related lineage of facultative cleaners (*Tigrigobius*). We suspect that obligate cleaning is a specialized trophic ecology tied to an equally specialized feeding morphology that facilitates improved cleaning performance. We coupled micro-CT scanning with the clearing and staining of museum specimens to compare several functional predictors of feeding performance between cleaner gobies and non-cleaners in a phylogenetic context. We also used geometric morphometrics to compare relative changes in head shape and mouth orientation. Obligate cleaning evolved once, and is characterized by a specialized scraping dentition, stouter cranial features, and a more subterminal mouth position relative to non-cleaners. Meanwhile, facultative cleaning evolved at least 2-3 times, and while some species display similar tooth morphologies as the obligate cleaners, they share more in common with non-cleaners. Obligate cleaners also exhibit fewer sexual dimorphic differences, suggesting that the demand for an efficient cleaning morphology trumps sexual selection.

Investigating the Effects of Fine-Scale Homing Behavior on Individual Reproductive Success in Sockeye Salmon (*Oncorhynchus nerka*)

Emily Karen Iversen, Senior, Aquatic & Fishery Sciences
Mentor: Kerry Naish, Aquatic and Fishery Sciences
Mentor: Samuel May, SAFS

Genetic diversity and gene flow are important to long-term viability in wild populations. In migratory species, gene flow (i.e. dispersal between disparate populations) is inherently influenced by the spatial and temporal components of their migrations. Recent findings have revealed the importance of fine-scale population structure in both space and time in Sockeye Salmon (*O. nerka)*. However, the fitness consequences of this fine-scale structure are unclear. Here we evaluate the biological relevance of fine-scale spatial and temporal homing by examining their effects on a quantitative trait, individual lifetime reproductive success. Salmonids are well-known for their extensive journey from the freshwater stream where they hatch, to the ocean, and back to their home stream (i.e. 'homing'). Homing behavior is associated with individual fitness; individuals are locally adapted to their natal streams, and dispersers between non-natal streams can have reduced reproductive success. Population structure within individual streams is generally assumed to be random (panmictic). However, individuals may be locally adapted on a finer scale than previously known, both in space (homing within their natal stream) and return timing. Fine-scale spatial and temporal homing may play a role in individual fitness; therefore, it is important to investigate this relationship. We used zero-inflated negative binomial models and a multi-generation pedigree, reconstructed from two populations of Alaskan Sockeye Salmon, to estimate the impact of homing on individual reproductive success (number of offspring per fish). Our results suggest that fine-scale dispersal in both space and time may reduce lifetime fitness. These results have broad implications for fisheries management and habitat conservation: recognizing the connection between reproductive success and return timing could inform within-season fisheries management, helping maintain the genetic diversity associated with local adaptation; likewise, recognizing the connection between individual salmon success and their habitat may promote maintaining natural heterogeneity in salmon streams.

Birdsong Evolution: Avian Vocalization Frequencies Reflect Adaptation to Habitat Structure

Thomas Meinzen, Senior, Environmental Humanities, Whitman College
Mentor: Johel Chaves-Campos, Study Abroad Program in Tropical Ecology in Monteverde Costa Rica, CIEE
Mentor: Tim Parker, Biology, Whitman College

Acoustic signals are essential for communication, advertisement, and reproduction in a variety of organisms. However, their successful transmission is limited by the environment in which they are produced. My research investigates the acoustic adaptation hypothesis, which proposes that to maximize transmission efficiency, animals evolve vocalizations with characteristics that minimize degradation and attenuation (loss of volume) in their native habitat. This hypothesis predicts that birds of open habitats will exhibit vocalizations with higher frequencies and larger frequency ranges than birds of forest understory habitats, because fewer obstructions and more low-frequency ambient noise in open areas favor successful transmission of higher-frequency signals. I tested this prediction by recording and analyzing the vocalizations of 63 bird species living in open and forested habitats around Monteverde, Costa Rica. I found that on average, bird species of open habitats vocalized at significantly higher and broader ranges of frequencies than birds of forested habitats, suggesting that vocalization transmission efficiency helps shape avian communities and their response to habitat transformations.

Assessing Variation in Reliance of Brown Bears (*Ursus arctos*) on Pacific Salmon as Food in the Lake Aleknagik Ecosystem Using Stable Isotope Signatures

Hyejoo Ro, Senior, Aquatic & Fishery Sciences
Mary Gates Scholar, UW Honors Program
Mentor: Thomas Quinn, Aquatic & Fishery Sciences
Mentor: Aaron Wirsing, Environmental and Forest Sciences
Mentor: Jenny Stern, SAFS

Many environmental factors can influence foraging strategies of predators, such as availability of prey sources. Brown bears feed on many species of animals and plants but Pacific salmon are especially important to their diet. For example, brown bears in the Lake Aleknagik, Alaska ecosystem forage on sockeye salmon as well as other food items. Direct observations and motion-activated cameras have documented bears foraging on salmon but do not reveal variation among individual bears. This study used the distinctive carbon and nitrogen isotope signatures in salmon as a way to assess brown bear diet by processing samples of bear fur collected during the salmon spawning season. As fur sample collection is noninvasive, it provided the opportunity to "resample" bears (individually identified by DNA analysis) multiple times within a season and over the course of multiple seasons. This study demonstrated how various factors, including salmon availability, gender, and location, influence the extent of bear consumption of salmon over time. Understanding the association between brown bear diet and these factors can provide better insight into the importance of both sockeye salmon and alternative food sources to brown bears.

Data Verification of Counts from Automatic Scales: A Case Study of Magellanic Penguins (*Spheniscus magellanicus*) in Punta Tombo, Argentina

Lexi Wachtell, Senior, Environmental Science & Resource Management
UW Honors Program
Mentor: Dee Boersma, Biology

Automatic scales are designed to weigh and count animals when they step on or cross the device. This means that high quantities of data may be collected when researchers cannot be present, with minimal interference to study subjects. However, remote and automated data collection requires verification of the quality of data before analyses. We use automatic scales in Punta Tombo, Argentina to weigh Magellanic penguins (*Spheniscus magellanicus*). Our scales record the time that each penguin crosses, and if certain conditions are met, they record a weight. We verified our data by comparing counts from automated scales with counts from a video recording of penguins crossing the scales. Over twenty hours of video footage were made during a 17-day period where penguins were recorded crossing automatic scales in the morning, midday, and evening on different days. We then counted the number of times a penguin was present in the video and not recorded by the scale. We expect that the proportion of penguins missed will be higher in the morning and evening when more penguins cross the scales, and lower around midday when fewer penguins cross the scales. The scales are designed to record weights when one penguin is present. When several penguins are on the scale or cross rapidly, the scale does not record a weight and may not record the correct number of penguins. Preliminary results support our prediction, with 75% and 78% of birds crossing the scales recorded during the morning and evening respectively, and nearly 100% of birds crossing the scales recorded at midday. By comparing the counts and the times between the scale and the video recording, we can determine how many penguins are missed, count the total number of penguins crossing the scales, and identify when most penguin crossings occur.

A Phylogeographic Approach to the Conservation of the Rough Nose Horned Lizard, *Ceratophora aspera*

Shanelle Ashwini (Shanelle) Wikramanayake, Junior, Biology (General)
Mary Gates Scholar
Mentor: Adam Leache, Biology

High rates of forest conversion and fragmentation have placed many endemic species in the rainforests of Sri Lanka under threat. *Ceratophora* is an endemic and endangered/critically endangered genus of lizards containing five species, and *C. aspera* has the widest distribution spanning four forest regions, making it an ideal candidate species for broader conservation management projects. The goal of this project is to study the phylogeography of *C. aspera* across its range in the forests of southwest Sri Lanka to assess the genetic variability of the remaining populations across two lowland areas, the submontane zone (Sabaragamuwa Hills), and the montane forest zone (Central Hills). Analyses of genetic data are important for understanding the relationships between geography and genetics and to determine where populations are connected and fragmented. During the 2018 and 2019 field seasons, tail clippings were collected from wild lizards. In the University of Washington's Biology Department, DNA sequencing of mitochondrial DNA (ND4 gene) was used to measure genetic diversity within and among populations, and to estimate phylogenetic relationships. Genetic diversity is highest (6%) between the population from Hiyare (lowlands) and the Sabaragamuwa Hills (submontane zone). There is also strong evidence for highland and lowland groups. Populations from Hiyare, Sinharaja and Gilimale show no intra-population variation. Sri Lanka has pledged to reforest 200,000 ha of degraded forest to create forest landscapes under the Bonn Challenge, and to increase forest cover to 30% unde the Paris Climate Agreement. Phylogeographic profiles of endemic species, such as *C. aspera,* are critical for forest restoration strategies as they identify priority areas for reforestation and inform connectivity strategies based on the need to maintain metapopulation structure and genetic diversity.

Behavioral Response of Brown Bears (*Ursus arctos*) to Non-Invasive Hair Collection Methods

Katherine Anne Wold, Senior, Aquatic & Fishery Sciences
Mentor: Thomas Quinn, Aquatic & Fishery Sciences
Mentor: Aaron Wirsing, Environmental and Forest Sciences

The foraging patterns and populations of predators can provide a better understanding of the nutrient dynamics in ecosystems. Brown bears (*Ursus arctos*) are a particularly difficult species to study. However, brown bears are a key predator species to study due to their close relationship with Pacific salmon (*Oncorhynchus spp.*) populations. Noninvasive methods like hair collection and camera traps are emerging as effective ways to study brown bear populations, diet, and behaviors. This study aims to determine whether the use of these methods in the Wood River system (Aleknagik, AK) are unbiased and characteristic of the resident brown bear population. The data used in this study are part of a long-term study (beginning in 2012) taking place in this area involving brown bear predation on sockeye salmon (*Oncorhynchus nerka*) and other population studies. Using video footage from the 2016 field season, this study analyzes brown bear reactions and avoidance of the barbed wire used to collect hair samples. Expected results are a higher frequency of wire avoidance in adult bears, single bears, during daylight, and equal frequency of avoidance between creeks. The results of this study can establish whether these methods of studying bear populations are accurate, or if they need to be modified to collect more inclusive and representative data. Further study is required to develop a comprehensive appreciation for brown bear populations, habitat use, and other behavioral patterns.