8-7 SLEVIN, MC*; FRESIN, W; CANNATARO, G; ANDERSON, RC; Florida Atlantic University; *mslevin2018@fau.edu*
Smarts and Symbiosis: Elucidating the Relationship between the Microbiome and Cognitive Performance in Birds
Recent years have seen a surge of research on the link between an individual's cognitive ability and its gut microbiome. With recent advances in understanding avian cognition, songbirds are an ideal system for investigating this relationship. In a captive Zebra Finch (*Taeniopygia guttata*) population of 42 adults, I quantified individual variation in performance on cognitive tasks (novel foraging, color association, and color reversal) that measure motor learning and memory, recording the number of trials needed to pass each task and error rate per trial. I sampled the gut microbiome via cloacal swab immediately prior to testing, sequenced the bacterial taxa present, and assessed diversity and relative abundance in each sample using Qiime2. There was high individual variation in cognitive performance, ranging from 22 to 80 trials needed to complete all three tasks (mean = 15.1 ± 1.4 trials for novel foraging, 9.4 ± 0.8 for color association, and 16.2 ± 0.9 for color reversal), with no sex difference for any task (all $P > 0.18$). Color association and reversal performance were correlated ($r = 0.3$, $P = 0.03$), but neither task was correlated with novel foraging performance ($r = -0.02$, $P = 0.9$). Finally, the slope of the per-trial error rate over the course of each color task was significantly correlated with the number of trials needed to complete the task ($r = 0.4$, $P = 0.003$). I will relate each bird's cognitive performance to its microbiome characteristics to test for evidence of a gut-brain axis. Our results from this model songbird species will build a foundation for future research, including understanding the microbiome during critical developmental stages (e.g., song learning) and in wild populations.

17-4 SMEDLEY, GD*; SERB, JM; Iowa State University; *gdsmedley13@gmail.com*
Molluscan Transcriptomes Suggest a More Complex Visual Cycle Homologous to Vertebrates
Photoreceptive organs have evolved as many as 65 times over the course of evolutionary history. Interestingly, nearly all light sensitive structures function via the same pathway of phototransduction. Phototransduction is a two step process which causes a conformational change of the photopigment upon light absorption and then requires resetting by reuptake or recycling of the bound retinal isomer. The latter half of the phototransductive pathway is known as the retinoid visual cycle. The molluscan visual cycle functions via retinochrome which photoisomerizes all-*trans* to 11-*cis* retinal by absorbing a photon and a shuttle protein transports the retinal isomers between the photoisomerase and the opsin. In vertebrates, retinal is recycled using shuttle proteins to transport the retinal between cell lines and through a well-characterized complex of enzymes for phototransduction or storage. Insects possess bistable opsins allowing retinal recycling within the opsin; however, recent studies have shown the enzymes of insects are homologous to those found in the vertebrate visual cycle. Changes in the understanding of the insect visual cycle and lack of a described non-light dependent molluscan visual cycle leads one to challenge the current simplicity of the molluscan visual cycle. To investigate this pathway in molluscs, published transcriptomes were searched for proteins involved in vertebrate or insect visual cycles. The results show the presence of RPE65, CRALBP, RDH5, and RDH12, in molluscan species, suggesting 1) molluscs possess a more complex visual cycle and 2) the origin of the retinoid visual cycle is before the protostome-deuterostome split.

122-3 SMITH, MG*; WESTGATE, AJ; KOOPMAN, HN; Harvard University, UNC Wilmington; *mollygablersmith@gmail.com*
Adipose tissue in diving animals: measuring the potential for gas exchange
Diving tetrapods are a biologically diverse group; however, they are all under similar constraints: oxygen limitation and increased hydrostatic pressure at depth. Adipose tissue is an interesting tissue to study, due to its physiologically important roles (e.g. metabolic energy storage, regulation of energy balance and thermoregulation) and because nitrogen (N_2) is 5 times more soluble in fat than in blood, creating a potential N_2 sink in animals consistently diving to depth. We examined the adipose tissue of diving tetrapods (3 species of seabirds, 3 sp. of sea turtles, 3 sp. of pinnipeds and 10 sp. of cetaceans), focusing on how adipose tissue structure allows these animals to cope with the physiological demands of diving. Adipose tissue microvessel density and diffusion distance were used to evaluate the comparative potential for aerobic activity (i.e. O_2 delivery). Long duration divers (i.e. beaked whales, > 120 min.) had relatively lower microvessel density (2.6 ± 0.5%) and greater diffusion distances (44.0 ± 13 µm), compared to short duration divers (e.g. eider ducks, < 2 min.; 4.4 ± 1.7% and 24.7 ± 9.9 µm). We hypothesize that beaked whale adipose tissue characteristics may function to minimize energetic costs during diving. Previous research indicates that lipid composition (lipid classes and short chained fatty acids [FA]) in some whales is an important factor determining N_2 solubility. However, there was no relationship between FA profile and N_2 solubility in the animals studied; species with similar FA profiles had different N_2 solubility values. The 3D structure of intact lipid molecules may elucidate the complex interactions between O_2, N_2 and lipid. Future studies should consider these interactions to better understand the physiological adaptations in diving animals.

84-4 SMITH, SM*; ANGIELCZYK, KD; KERBIS PETERHANS, JC; Field Museum of Natural History, Chicago, IL; *smsmith@fieldmuseum.org*
Vertebral number and spinal regionalization in large shrews (Soricidae)
In addition to having unique extra articulations on its vertebrae, the hero shrew (*Scutisorex*) is unusual in having almost twice as many lumbar vertebrae as other shrews of its size. Other than being noted in descriptive literature, this increase in vertebral number has received little attention; there has been no investigation of how it might reflect the elusive function of the highly modified *Scutisorex* spine. Comparisons of individual vertebrae and whole-column characteristics between *Scutisorex* and other large shrews are also lacking, despite the fact that such studies could give insight into i) function of particular vertebral regions in shrews with and without external vertebral modifications, and ii) developmental patterns driving regional proportions. We collected µCT scans and linear measurements of cervical, thoracic, and lumbar vertebrae in two species of *Scutisorex* and three other species of large shrews. We compared a variety of linear vertebra measurements, and trabecular bone characteristics of each centrum, across species. Further, using this combined suite of measurements, we executed principal coordinates analysis and segmented regression to detect unique vertebral regions in each taxon. Our results show that relative to other large shrews, *Scutisorex* has a shorter thoracic region and longer lumbar region, and, despite having more dorsal vertebrae than other species, does not have a proportionally longer body length. Regionalization signals vary within and across the five species, but generally suggest that functional regions may not correspond exactly with traditionally recognized anatomical regions of the column, and that the extended lumbar region in *Scutisorex* may afford it an additional functional region.