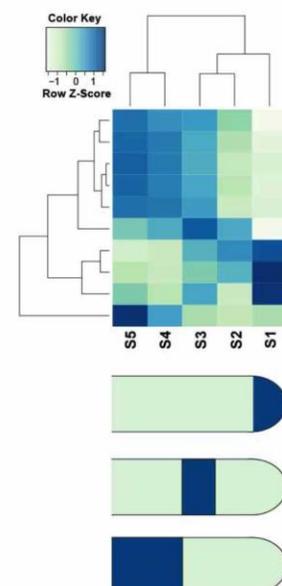
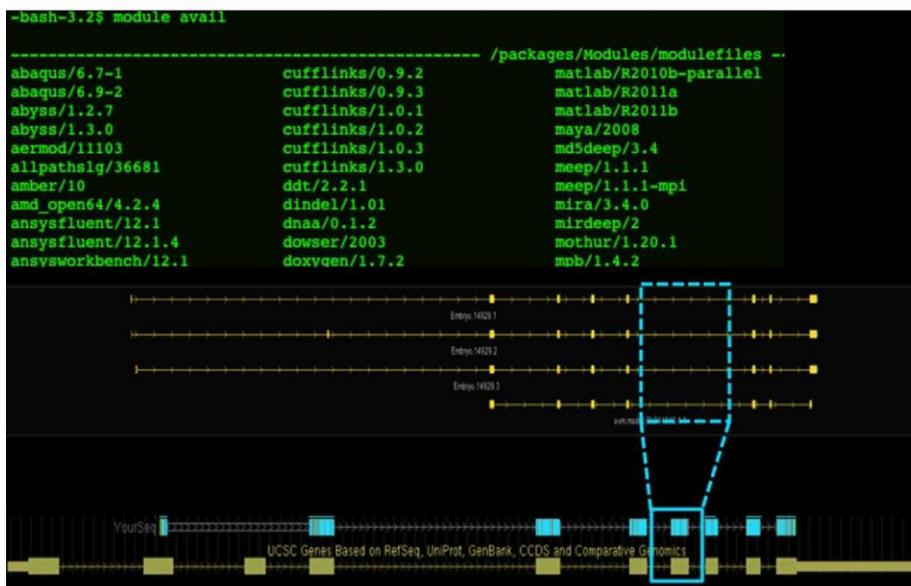


Genomic Approaches to Reptile Regeneration and Conservation

The research of the Kusumi Lab is focused on using genomic and bioinformatic approaches to advance studies of regeneration and the conservation of endangered reptiles.



Project 1: Genomic Approaches to Vertebrate Regeneration

Many vertebrates such as fish, amphibians, and lizards display the ability to regenerate appendages, but in mammals, this ability is lost soon after birth. Our research focuses on identifying the genes that are required for regeneration in two model vertebrate systems: the green anole lizard, *Anolis carolinensis*, and tadpoles of the African clawed frog, *Xenopus laevis*. In both these organisms, they are able to regenerate musculoskeletal and spinal cord tissues to form a new tail after tail loss. Genome sequences of both the green anole and *Xenopus laevis* have been published, and using next-generation transcriptomic sequencing, we have already identified a unique set of genes involved in regeneration in the lizard. SOLUR students will learn and apply bioinformatic techniques, including use of R-based statistical tools, UNIX/Linux-based sequence analysis tools, and Python or PERL scripting languages to analyze these regeneration data. Students who have previous experience in gene expression techniques, particularly quantitative RT-PCR and immunohistological analysis, may also participate in gene expression studies.

Project 2: Desert Tortoise Genome for Conservation

The mission of the Desert Tortoise Genome for Conservation project is the conservation and preservation of the desert tortoise, an icon of the American southwest, for future generations. The Mojave Desert tortoise (*Gopherus agassizii*) is already listed as threatened under the Endangered Species Act, and pressures from habitat loss and disease are pushing the Sonoran Desert tortoise (*G. morafkai*) towards the same fate unless we act now. Preserving the biodiversity of tortoise populations is a critical step to ensure the long-term survival of the tortoise under changing environmental conditions. Deciphering the genome, or complete library of genetic information, for the Sonoran Desert tortoise is a valuable foundation for studying biodiversity to work with our state, federal, and private partners to inform conservation efforts and wildlife management decisions. Further studies of the hybridization zone between the Mojave and Sonoran Desert tortoises will inform decisions on conservation boundaries. Students will learn and apply bioinformatic techniques, including use of R-based statistical tools, UNIX/Linux-based sequence analysis tools, and Python or PERL scripting languages to carry out evolutionary analysis of these genomes. Students who have previous experience with genetic techniques, particularly DNA extraction, sequencing, and PCR, could also participate in genomic studies.

At least a one-year commitment (at 12 hours/week or greater which will primarily be computational work) is required to receive the necessary training to work on these projects. Please contact Dr. Kusumi with any questions.

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Opening date: Fall 2016