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Computational Biology Seminar Series for Undergraduates

Models, Genomes, and Trees: Computational Inferences of Evolutionary History

Jeremy M. Brown, LSU Department of Biological Sciences

Assistant Professor

Life Sciences Building Annex A101
September 09, 2013 - 05:30 pm

Abstract:

Evolutionary biologists are driven by a desire to understand the staggering diversity of life on Earth, its history of change through time and the processes that have driven such change. DNA sequences are the fundamental material upon which evolutionary change is wrought and each organism's genome carries the legacies of its evolutionary history. By sequencing the genomes of different organisms, we can use their similarities and differences to reconstruct historical relationships, known as phylogenies, and to test hypotheses about the evolutionary past. Phylogenies are of fundamental importance to fields as diverse as conservation, behavior, forensics, agriculture, and medicine. However, reconstructing phylogenies can be a very difficult and time-consuming task. Many genomes are enormous, genes can evolve in wildly different ways, and the number of possible shapes to the Tree of Life is beyond astronomical (literally). Therefore, modern phylogenetic analyses require serious computational power. In this talk, we will explore how phylogenies can help solve crimes of intentional disease transmission, uncover the ancient and hidden world in the soils of Amazonian rainforests, and resolve the 'turtle identity crisis'. We will also talk about how none of this would be possible without biologists who are also interested in mathematics, programming, and who have access to really big computers.

http://lbrn.lsu.edu/events/comp-bio/brown.html

Speaker's Bio:

Jeremy M. Brown is a computational evolutionary biologist and an assistant professor in LSU's Dept. of Biological Sciences. A native of Indianapolis, IN, he did his undergraduate studies in biology at Indiana University. There, he spent much of his free time chasing reptiles and amphibians and even more of his time in a research lab watching female bugs care for their offspring. Attempting to become a herpetologist, Jeremy chose to pursue his Ph.D. in Ecology, Evolution, and Behavior at the University of Texas – Austin, where he instead became interested in methods for reconstructing the Tree of Life from gene sequences (a field known as phylogenetics). After leaving Texas in 2009, he moved to California, where he was a National Science Foundation Postdoctoral Fellow at UC-Berkeley. As a postdoc, he started thinking about ways to use massive 'next-generation' sequencing datasets to infer phylogenies and learn about how evolution causes genomes to change over time. Along the way, he learned how to write computer code and use large computing clusters. In 2011, Jeremy joined the faculty of LSU's Dept. of Biological Sciences and started one of the department's first entirely computational labs. Research in his lab is primarily split between developing new statistical approaches and software for estimating phylogenetic trees, and using these trees to understand the evolution of organisms as varied as HIV, turtles, and the 'Ant from Mars' – which actually lives in Brazil. His work has been covered by various news outlets including the New York Times, MSNBC, Fox News, 20/20, National Geographic, Oprah and even featured in a recent book by Jane Goodall. He finally became a real herpetologist after starting a field project on chorus frog hybridization here in Louisiana.

This lecture has refreshments @ 05:00 pm
This lecture has a reception @ 05:00 pm