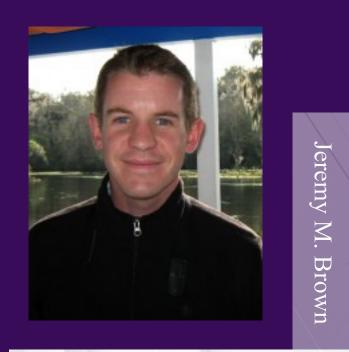
Computational Biology Seminar Series for Undergraduates

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

Jeremy M. Brown Louisiana State University

September 9, 2013 5:30 p.m. A101 Life Sciences Building Annex Reception begins at 5:00 p.m



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. 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.

BIO:

Jeremy M. Brown is a computational evolutionary biologist and an assistant professor. 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.



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