Other - LSU Faculty Candidate Seminar- Interdisciplinary Data Science and Biology Position

Statistical models on Phylogenetic Networks

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Digital Media Center 1034
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Abstract:
Phylogenetic network inference plays an important role in the reconstruction of the tree of life, given the widespread gene flow among different organisms. However, there are many challenges in the inference of reticulate evolution such as network reconstruction and interpretation, and difficulties to summarize network uncertainty. In this talk, I will explain the current difficulties in network statistical inference and present a new scalable method based on pseudolikelihood theory. I will also present extensions of standard trait evolution tools to networks, such as phylogenetic regression or ANOVA, ancestral trait reconstruction, and Pagel's lambda test of phylogenetic signal. All the new tools are implemented in the open-source Julia package PhyloNetworks.

Speaker's Bio:

I am a postdoc at the Department of Human Genetics at Emory University working with professor Michael Epstein on Genome-Wide Association Studies. Last year, I was a postdoc in UW-Madison working with professor Bret Larget on statistical computing methods for Bayesian phylogenetics. I did my PhD in Statistics at the University of Wisconsin-Madison with professor Cécile Ané in the inference of phylogenetic networks to represent the tree of life expanded by extra hybridization edges. I obtained my Master's degree in Mathematics at the University of Wisconsin-Madison with emphasis on probability theory. I am originally from Mexico City where I did my Undergraduate degrees in Actuarial Sciences and Applied Mathematics at ITAM.

This lecture has refreshments @ 02:00 pm

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