

DEPARTMENT OF
BIOLOGICAL SCIENCES

SEMINAR

MARCH 27

5:00PM

159 IRVINE HALL

Refreshments will be provided



Statistical models on Phylogenetic Networks

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Short 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.



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