

# *Colloquium*

UNIVERSITY OF GEORGIA  
DEPARTMENT OF STATISTICS  
INSTITUTE OF BIOINFORMATICS

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## **“Estimating species trees from multilocus data under the coalescent model”**

The desire to infer the evolutionary history of a group of species (species tree) should be more viable now that a considerable amount of multilocus molecular data is available. In this talk, I will introduce three statistical methods for reconstructing species trees under the multispecies coalescent model. The Bayesian method can estimate the topology, species divergence times, and population sizes of the species tree, but involves intensive computation. The other two methods estimate species trees based on summary statistics of gene coalescence times and thus have computational advantages, though the two methods can only estimate the topology of the tree. It can be shown that these methods are statistically consistent in estimating species trees. Empirical and simulation studies suggest that all three methods are useful in understanding the evolutionary history of species.

**Thursday, February 10th, 2011**  
B118 Davison Life Sciences Building  
University of Georgia  
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3:00 pm – Refreshments  
3:30 pm – Talk