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***Case Studies in  
Bayesian Phylogenetics***

***Abstract:***

Phylogenetics involves the estimation of evolutionary trees (or phylogenies) from genetic data. The Bayesian approach to phylogenetics, made possible by novel application of Markov chain Monte Carlo computational methods, provides a practical means to coherent statistical inference of evolutionary relationships with easily interpretable measures of uncertainty.

In this talk, I will introduce and discuss recent advances in Bayesian phylogenetics through several case studies: (1) estimation of metazoan (animal) phylogeny on the basis of mitochondrial genome arrangements; (2) molecular evolution of AFLP markers applied to an order of sedges (grass-like plants); and (3) estimation of multiple gene trees from the same species with application to yeast. This talk will emphasize the modeling and computational aspects of Bayesian phylogenetics.

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**Tuesday, September 20<sup>th</sup>, 2005**  
**4:00 p.m.**

Genetics/Biotechnology Center Auditorium  
425 Henry Mall