

The University of Chicago

Department of Statistics

Seminar

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**“Bayesian Inference of Evolutionary Trees
from Mitochondrial Genome Arrangements”**

**Monday, March 3, 2003 at 4:00 PM
133 Eckhart Hall, 5734 S. University Avenue**

ABSTRACT

The estimation of evolutionary relationships is a fundamental problem in evolutionary biology. Genome arrangement data is potentially more informative than DNA sequence data for inferring evolutionary relationships among distantly related taxa. We describe a Bayesian framework for phylogenetic inference from genome arrangement data using Markov chain Monte Carlo methods. We apply the method to assess evolutionary relationships among eight different animal phyla on the basis of mitochondrial genome arrangements.

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