



THE UNIVERSITY OF  
**CHICAGO**

Department of Statistics  
**STATISTICS COLLOQUIUM**

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**Biological Models with Combinatorial Spaces**

**MONDAY, January 14, 2013 at 4:00 PM**

133 Eckhart Hall, 5734 S. University Avenue

*Refreshments following the seminar in Eckhart 110*

**ABSTRACT**

Probabilistic models are common in biology. Many of the successful models have been readily tractable, leaving calculations on models with a combinatorial-sized state space as an open problem. This talk examines two kinds of models with combinatorial state spaces: continuous-time and discrete-time Markov chains. These models are applied to two problems: RNA folding pathways and family genetics. While the applications are disparate topics in biology, they are related via their models, the statistical quantities of interest, and in some cases the computational techniques used to calculate those quantities.

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