



Science at the Edge Seminar Series

Jointly sponsored by
Quantitative Biology and Modeling
and **Department of Statistics and Probability**

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Population Genetic Inference and Computers: An Embarrassingly Parallel Development

Since the eighties population genetic inference has leaped beyond frequency-based inferences and allows us to estimate parameters of complex population structure models using Bayesian inference based on coalescence theory. These methods have their own difficulties because most often we need to approximate crucial quantities using a Markov chain Monte Carlo algorithm. The talk will give a short overview and introduction of the population genetic background and then show possible improvement on estimates that can be made by using parallel computing of many loci or many replicates. These improvement in speed and accuracy allow comparison of complex population models using likelihood ratio tests or Bayes factors.

Such comparisons will not only help to investigate biological scenarios but will also help to improve our understanding how many data are needed to answer complex questions in biological context.

Tuesday, October 30 at 10:30am
Room 1400 Biomedical and Physical Sciences Bldg.

Refreshments at 10:15