



The University of Chicago  
Department of Statistics

FOURTH YEAR PHD PRESENTATION

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**A Coalescent-based Method for Inferring Migration Rates from Large-scale Genetic Data**

**THURSDAY, November 3, 2011, at 3:00 PM**

110 Eckhart Hall, 5734 S. University Avenue

**ABSTRACT**

We consider the problem of inferring the presence of barriers and corridors (or more generally, inferring migration rates) from genetic data.

Habitat heterogeneity leaves its mark on genetic variation by impacting gene flow. In a habitat with uniform migration, the genetic differentiation between individuals from the same species is positively correlated with the Euclidean distance between their origin. In a heterogeneous habitat, genetic variation will be structured differently from its expectation under uniform migration. For example, individuals separated by a barrier will be less closely related, and therefore less genetically similar, than if the barrier were absent.

We work with a class of demographic models, parametrized in terms of migration rates between neighboring locations, that predict equilibrium genetic structure. More precisely, given a population graph and a set of migration rates, we compute the expected times to coalescence (a measure of expected relatedness) by solving a large system of linear equations. From the expected coalescence times, we derive a likelihood for the observed genetic data and perform Bayesian inference for the migration rates.

We discuss how the model addresses the inference problem of estimating migration rates from observed genetic differentiation, and we use simulated genotype data to illustrate its performance in the case of a two-dimensional habitat under several models of migration.

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