



BIO
MATH

Ph.D. Dissertation Defense Seminar

Phenotypic Bayesian phylodynamics: hierarchical graph models, antigenic clustering and latent liabilities



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5229 Life Sciences Building

(not the Terasaki Life Sciences building)

ABSTRACT:

Combining models for phenotypic and molecular evolution can lead to powerful inference tools. Under the flexible framework of Bayesian phylogenetics, I develop statistical methods to address phylodynamic problems in this intersection.

First, I present a hierarchical phylogeographic method that combines information across multiple datasets to draw inference on a common geographical spread process. Each dataset represents a parallel realization of this geographic process on a different group of taxa, and the method shares information between these realizations through a hierarchical graph structure.

Additionally, I develop a multivariate latent liability model for assessing phenotypic correlation among sets of traits, while controlling for shared evolutionary history. This method can efficiently estimate correlations between multiple continuous traits, binary traits and discrete traits with many ordered or unordered outcomes. Finally, I present a method that uses phylogenetic information to study the evolution of antigenic clusters in influenza. The method builds an antigenic cartography map informed by the assignment of each influenza strain to one of the antigenic clusters.

Doctoral Committee: Marc Suchard, M.D., Ph.D. (chair), Janet Sinsheimer, Ph.D.,
Kenneth Lange, Ph.D., James Lloyd-Smith, Ph.D., Christina Kitchen, Ph.D.