

University of California, Irvine
Foundations of Statistics Seminar Series

*Gaussian process-based Bayesian nonparametric inference of
population trajectories from gene genealogies*

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Monday, November 7, 2011
4:00 – 5:00 PM
Donald Bren Hall - Room 2011
(Bldg. #314 on campus map)

Changes in population size influence genetic diversity of the population and, as a result, leave imprints in genomes of individuals in the population. We are interested in an inverse problem of reconstructing past population dynamics from genomic data. We start with a standard framework based on the coalescent, a stochastic process that generates genealogies connecting randomly sampled individuals from the population of interest. These genealogies serve as a glue between the population demographic history and genomic sequences. It turns out that times at which genealogical lineages coalesce contain all information about population size dynamics. Viewing these coalescent times as a point process, estimation of population size trajectories is equivalent to estimating a conditional intensity of this process. Therefore, our inverse problem is similar to estimation of an inhomogeneous Poisson process intensity function. We demonstrate how recent advances in Gaussian-based nonparametric inference for Poisson processes can be extended to nonparametric estimation of population size dynamics under the coalescent. Using simulations, we show that our new method is more accurate and precise than a competing Gaussian Markov random field smoothing approach. We conclude with analyses of population dynamics of hepatitis C and human influenza viruses.

This is joint work with Julia Palacios.

For directions please refer to <http://www.ics.uci.edu/about/visit/>
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