



The University of Chicago
Department of Statistics

Seminar Series

XIAOWEI WU

Department of Statistics
Rice University

Bayesian Analysis of Array CGH Data

THURSDAY, July 16, 2009, at 12:00 PM
110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

We propose a Bayesian approach to analyze array comparative genomic hybridization (CGH) data. Different from most currently available methods, this new approach builds a Bayesian hierarchical model for the data and use a reversible jump Markov chain Monte Carlo (MCMC) algorithm for posterior sampling. The estimated parameters are used to identify copy number changes (gains/losses) in the target DNA sequence. This method is computationally efficient and is flexible to model various covariance structures of the data. Moreover, it also has great advantage in analyzing recurrent copy number alterations (CNAs) in multiple arrays. Simulation study shows a good performance of the proposed method. As a real data analysis example, we apply the method to publicly available Corriel cell lines data and obtain satisfying results.

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