The Hong Kong Polytechnic University
Department of Applied Mathematics

Seminar

On

A Reversible Jump Markov Chain Monte Carlo Approach for Repeats Analysis

by

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Abstract

Trans-dimensional model selection problems often occur in Bioinformatics. Although the reversible jump Markov chain Monte Carlo (RJMCMC) algorithm introduced by Green (1995) is theoretically capable of solving trans-dimensional problems, its slow convergence limited its application to simple model selection problems. We explored the techniques to improve the mixing rate of RJMCMC. The basic guideline is to pilot the trans-dimensional move by one-step forward estimation. The improved RJMCMC is successfully applied in tandem repeats detection, which is a classical NP hard DNA sequence analysis problem.

Date : **March 30, 2012 (Friday)**

Time : **2:30 p.m. – 3:30 p.m.**

Venue : **HJ610, The Hong Kong Polytechnic University**

* * *   ALL ARE WELCOME   * * *