



The Chinese University of Hong Kong
Department of Statistics

Seminar

Analysis of Genome-scale Datasets - Opportunities and Challenges

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Abstract

High throughput experimental methods based on microarrays and deep sequencing have created many types of genome-wide datasets. While these large-scale datasets have greatly facilitated the study of complex interactions between biological objects, they could also lead to misleading results if not properly processed. Signal values could be biased by factors such as intrinsic genomic contents, experimental protocols and reagents, to name but a few. In this talk I will use some of my recent work as examples to illustrate some challenges in whole-genome data analysis, and briefly describe the current approaches to dealing with them. Most of the work described in this talk was done in collaboration with members of the Gerstein Lab at Yale University.

Date: September 21, 2010
Time: 2:00 p.m. - 3:00 p.m.
Place: William M W Mong Engineering Building, Room 407
The Chinese University of Hong Kong