THE UNIVERSITY OF CHICAGO

Department of Statistics

STATISTICS COLLOQUIUM

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Statistical Methods for Analyzing High-throughput Genomic Data

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133 Eckhart Hall, 5734 S. University Avenue

Refreshments following the seminar in Eckhart 110

ABSTRACT

In the burgeoning field of genomics, high-throughput technologies (e.g. microarrays, next-generation sequencing and label-free mass spectrometry) have enabled biologists to perform global analysis on thousands of genes, mRNAs and proteins simultaneously. Extracting useful information from enormous amounts of high-throughput genomic data is an increasingly pressing challenge to statistical and computational science. In this talk, I will present three projects in which statistical and computational methods were used to analyze high-throughput genomic data to address important biological questions. The first part of my talk will demonstrate the power of simple statistical analysis in correcting biases of large-scale protein level estimates and in understanding the relationship between gene transcription and protein levels. The second part will focus on a statistical method called "SLIDE" that employs probabilistic modeling and L_1 sparse estimation to answer an important question in genomics: how to identify and quantify mRNA products of gene transcription (i.e, isoforms) from next generation RNA sequencing data? In the final part, I will introduce an ongoing project where we developed a new statistical measure under a local regression and clustering framework to capture non-functional relationships between a pair of variables. This new measure will have broad potential applications in genomics and other fields.

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