Statistics Seminar Series

Statistical Challenges in the Post-Genome Era

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Thursday, November 14, 2002, 4:00-5:00pm
Mathematics and Computer Science (MCS) Building, Room 149
111 Cummington Street, Boston

Tea and Cookies at 3:30pm in MCS 153

Abstract: On February 12, 2001 leaders of the Human Genome Project announced the completion of a sequence draft of the human genome. The result of these efforts is a map of the human genes, and because about 50genes have known functions, the challenge now is to annotate this map, by discovering the functions of genes, and their interplay with proteins and the environment to create complex, dynamic living systems. This is the goal of functional genomics. The modern approach to functional genomics takes advantage of the new technology of microarrays to observe the genome of an entire organism in action by simultaneously measuring the level of expression of thousands of genes under the same experimental condition. Microarray technology is used in simple comparative experiments, when the goal is to identify the genes that are differentially expressed in cells of the same tissue in two different conditions. More ambitious experiments try to discover gene functions or gene interactions from temporal or multifactor experiments. The design and analysis of these experiments require the development of new modeling and computational techniques, and this talk will describe some of the recent methodology we developed for the analysis of microarray data.

For directions and maps, please see *http://math.bu.edu/research/statistics/statseminar.html*. For other information, please contact Eric Kolaczyk (*kolaczyk@math.bu.edu*) or the main department office at (617)353-2560.