Speaker: David Siegmund, Stanford University

Title: Detection of Local Signals in Genomics

Abstract:

Several problems of genomic analysis involve detection of local genomic signals. When the data are generated by sequence based methods, the often small and variable number of reads at different positions on the genome suggests point process models involving non-homogeneous Poisson processes, or perhaps negative binomial processes to accommodate excess variability. I discuss a number of examples, and will consider in detail a toy mixture model for detection of deletions inferred from paired end reads. I will also mention a more realistic model for insertions and deletions. Approaches to these problems based on change-point methods are described, with particular attention to the problems of multiple comparisons. The theoretical results are illustrated on simulated data.

This is joint research with Benjamin Yakir and Nancy Zhang.