

**STANFORD UNIVERSITY**  
**DEPARTMENT OF STATISTICS**  
**JOINT STATISTICS AND BIOSTATISTICS SEMINAR**

4:15 p.m., Wednesday, November 10, 1999  
Sequoia Hall Rm. 200  
(Cookies at 3:45 in 1st Floor Lounge)

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**The use of bioinformatics for  
analyzing and interpreting biomolecular sequence data**

I will describe bioinformatics methods for the analysis of a protein family using information based on evolutionary relationships (multiple sequence alignments), mutation studies, protein structure (three dimensional crystal structure of some members of the protein family) and function (results from biochemical and physiological experiments). I illustrate the analysis and interpretations on the RecA protein family (major recombination/repair protein), on the heat shock protein 60 (HSP60) family (corrects misfolded proteins), on the heat shock protein 70 family (chaperone and translocase). Each of these protein families has one to three structures available and more than 100 sequence homologues from diverse species. In this context, bioinformatics concepts and techniques can combine function, structure, and evolution information to extract insights, model mechanisms, and suggest experiments.

Please note that this seminar is on Wednesday instead of the usual Tuesday.