

The Math Colloquium Department of Mathematics San José State University



Susan Holmes Stanford University

Computational Tools for Evaluating Phylogenetic and Hierarchical Clustering Trees NOVEMBER 3, 2010, MH320

Abstract: Inferential summaries of tree estimates are useful in evolutionary biology, bioinformatics, psychometrics and data mining. I will present applications of the Billera, Holmes, Vogtman (2001) distance on trees to inferential problems. I will compare the tree of trees representation to the Euclidean approximations of treespace made available through Multidimensional Scaling of the matrix of distances between trees, and I will also provide applications to microarrays and the evolution of metagenomic data of bacteria in the gut. (Joint work with John Chakerian.)

Background: Students should know Euclidean geometry and a little about what a statistical confidence interval is.

About the speaker: Susan Holmes is a Professor of Statistics at Stanford. She works in Computational Statistics and applications of mathematical ideas to biology. She is part of Stanford's Bio-X group, is Director of the Mathematical and Computational Sciences undergraduate degree, and Director of the Stanford Statistics VIGRE program.

SNACKS IN MH331B AT 2:30 PM TALK STARTS AT 3 PM

For more information, see our full schedule at:

http://www.math.sjsu.edu/~hsu/colloq/