



The Math Colloquium  
Department of Mathematics  
San José State University



Glenn Tesler  
UC San Diego

*Reconstructing the Genomic Architecture of  
Ancestral Mammals*

APRIL 29, 2009, MH320

**Abstract:** In addition to frequent single-nucleotide mutations, mammalian and many other genomes undergo rare and dramatic changes called *genome rearrangements*. Although analysis of genome rearrangements was pioneered by Dobzhansky and Sturtevant in 1938, we still know very little about the rearrangement events that produced the existing varieties of genomic architectures. Recovery of mammalian rearrangement history is a difficult combinatorial problem that I will cover in this talk. Our data sets have included sequenced genomes, as well as radiation hybrid maps of additional mammals.

*Background:* Students should be familiar with basic concepts from discrete math, such as permutations and the basics of graph theory.

*About the speaker:* Glenn Tesler is a professor in the Department of Mathematics and a core faculty member in the interdisciplinary programs in bioinformatics at UCSD. He received his Ph.D. in Mathematics from MIT in 1995, in the area of Algebraic Combinatorics. He studies computational and algorithmic aspects of genomics.

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/>