

CALIFORNIA STATE UNIVERSITY, LONG BEACH

THE MATHEMATICS COLLOQUIUM

presents

Dr. Johanna Hardin

Pomona College

speaking on

*Using Robust Measures to Describe Distributions and Similarities of
Microarray Data*

Friday, April 8, 2005

12:00PM-1:00PM

LA5-267

Abstract: One of the difficulties in analyzing microarray data is in knowing what the underlying distribution is. We know how to transform microarray data to deal with symmetry and non-constant variance across different expression levels, but the resulting transformed data have much heavier tails than a normal distribution. We have provided a method of fitting a t-distribution to a data set using a robust estimate of scale. t-distributions arise from scale mixtures of normals as well as from inherently long tailed distributions. Using multiple microarray data sets of different species and technologies, we investigate the source of the variability for genes within a sample and for genes across replicates.