Likelihood Estimation of Large Species Trees
Using the Coalescent Process

A species tree is a weighted tree-graph that represents the order and the magnitude of separation between a given set of species. Statistical estimation of trees is an integral part of studying species trees. Although various likelihood and Bayesian estimators of species trees are available, none of these methods are fast enough to estimate very large species trees under a certain commonly used model (the coalescent). This problem is especially relevant today because there has been a recent influx of large amount of genomic data. Here I will present an approach of fast likelihood estimation of species trees, exploiting a certain special structure of the tree space. Using this approach, one will be able to estimate larger species trees than previously possible in a reasonable time.

Refreshments will be served following the seminar in 1181 Comstock Hall.