

## **Analyzing Phylogenetic Treespace**

### **Abstract:**

Evolutionary histories, or phylogenies, form an integral part of much work in biology. In addition to the intrinsic interest in the interrelationships between species, phylogenies are used for drug design, multiple sequence alignment, and even as evidence in a recent criminal trial. A simple representation for a phylogeny is a rooted, binary tree, where the leaves represent the species, and internal nodes represent their hypothetical ancestors. This talk will focus on some of the elegant questions that arise from assembling, comparing, summarizing, visualizing, and searching the space of phylogenetic trees.