

Presentation title:

Distance, likelihood, and Bayesian approaches to phylogenetics and phylogenetic uncertainty

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Abstract:

There are many methods that can be used to estimate phylogenetic trees from DNA sequence data. Different methods will often result in different phylogenetic trees, and different estimates of the confidence we can have in those trees (phylogenetic uncertainty). If we want to make good inferences from DNA sequence data, we need to understand how different methods treat the data. In this lecture, I will focus on the three most commonly used approaches in molecular phylogenetics – distance, Likelihood, and Bayesian methods. I will discuss the theoretical underpinnings and practical uses of each method, including their similarities, differences, assumptions, benefits, and shortcomings. I will finish by describing how each method can be used to estimate and/or account for phylogenetic uncertainty.