

Phylogenetic inference: an overview
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December 11, 2015

This talk will provide an overview of data, models and inference schemes used for constructing evolutionary trees, or phylogenies. Phylogenetic inference has developed into a mature statistical field in recent decades, although many challenges still remain. In the second half of the talk I will describe some of my own research which involves dropping some of the standard assumptions made in phylogenetic models. Specifically, I will cover a model which allows gene sequence composition to evolve over time, and a second model for inferring root positions on trees.