The probability distribution of the reconstructed phylogenetic tree with occurrence data

Ankit Gupta[*]

Department of Biosystems Science and Engineering, ETH Zürich, 4058 - Basel, Switzerland.
Email: ankit.gupta@bsse.ethz.ch

Abstract:

In Epidemiology, stochastic birth-death processes are frequently used to model the underlying population dynamics of infected individuals. In such models, the infection history of extant population naturally gives rise to a phylogenetic tree which can be used to study the historical evolution of the epidemiological process. In this talk, we study the problem of computing the probability distribution of such phylogenetic trees arising from partially sampled birth death processes. We consider observations from three distinct sampling schemes:

1) Individuals can be sampled and removed, through time, and included in the tree.
2) There can be occurrences which are individuals sampled and removed through time but not included in the tree.
3) Extant individuals can be sampled and included in the tree.

The outcome of the process is thus composed of the reconstructed phylogenetic tree spanning all individuals sampled and included in the tree, and a timeline of occurrence events where individuals are not placed along the tree. We derive a formula for computing the joint probability density of this outcome, which can readily be used to perform maximum likelihood or Bayesian estimation of the parameters of the birth-death model. In the context of epidemiology, our probability density enables the estimation of transmission rates through a joint analysis of epidemiological case count data and phylogenetic trees reconstructed from pathogen sequences.

This talk is based on a joint work with Marc Manceau, Timothy Vaughan, Mustafa Khammash and Tanja Stadler.

Keywords: birth-death process; epidemiology; macroevolution; phylogenetics; phylodynamics

References:

1. **Ankit Gupta***, Marc Manceau, Timothy Vaughan, Mustafa Khammash and Tanja Stadler. *The probability distribution of the reconstructed phylogenetic tree with occurrence data*. Journal of Theoretical Biology, Vol. 488, 2020.