Statistics Seminar

A Flexible Bayesian Framework to Study Viral Trait Evolution

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Friday, October 25
12:00 DERR 122

Abstract: During the course of an epidemic, many viral pathogens are known to evolve rapidly, leaving an imprint of the pattern of spread in their genomes. Uncovering the molecular footprint of this transmission process is a key goal of phylodynamic inference. Less focus has been put on the evolution of quantitative traits of viruses, such as geographical location or virulence. The goal of Phylogenetic Comparative Methods is to account for a shared evolutionary history among a set of non-independent samples. Conditioning on such a history, the observed traits can be seen as the result of a stochastic process running on the branches of a phylogenetic tree. We propose a Bayesian inference framework for the study of this flexible model. Using a MCMC based method, it relies on the efficient sampling of the constrained parameters of the model, and takes advantage of the tree structure for fast likelihood computations. It encompasses a wide family of Gaussian processes, allowing for fine-grained modelling of trait evolution of various biological systems. We implemented this new approach in the phylogenetic software BEAST, and applied it to the study of heritability of virulence in HIV.

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