



Inference of transmission network structure from HIV phylogenetic trees

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Abstract

Phylogenetic inference is an attractive mean to reconstruct transmission histories and epidemics. As the interest lies in how HIV-1 spread in a human population, many previous studies have ignored details about the evolutionary process of the pathogen. Because phylogenetics investigates the evolutionary history of the pathogen rather than the spread between hosts per se, we first investigated the effects of including a within-host evolutionary model in epidemiological simulations. In particular, we investigated if the resulting phylogeny could recover different types of contact networks. To further improve realism, we also introduced patient-specific differences in infectivity across disease stages, and on the epidemic level we considered incomplete sampling and the age of the epidemic. Second, we implemented an inference method based on approximate Bayesian computation (ABC) to discriminate among three well-studied network models and jointly estimate both network parameters and key epidemiological quantities such as the infection rate. Our ABC framework used both topological and distance-based tree statistics for comparison between simulated and observed trees. Overall, our simulations showed that a virus time-scaled phylogeny (genealogy) may be substantially different from the between-host transmission tree. This has important implications for the interpretation of what a phylogeny reveals about the underlying epidemic contact network. In particular, we found that while the within-host evolutionary process obscures the transmission tree, the diversification process and infectivity dynamics also add discriminatory power to differentiate between different types of contact networks. We also found that the possibility to differentiate contact networks depends on how far an epidemic has progressed, where distance-based tree statistics have more power early in an epidemic. Finally, we applied our ABC inference on two different outbreaks from the Swedish HIV-1 epidemic.

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