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Phylogenetic inference of multiscale selection pressures using a continuous state birth-death process

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Phylogenetic inference of multiscale selection pressures using a continuous state birth-death process

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Abstract

In host-pathogen systems, pathogen strains can have varying levels of fitness at the within host and between host scales. This can be presented through changes in the ability to compete at the within host scale or through variation in the host's ability to transmit. Here we develop a method to perform inference on the magnitude and direction of selection pressures within and between hosts along with other relevant parameters like effective population size. Hosts in this model are assigned to a value that is an element of some closed and bounded set. In the context of a host-pathogen system, allele frequency or a measure of genetic distance can be used. Given a phylogeny with continuous-valued tip states, we can perform maximum-likelihood inference utilizing a continuous state birth-death branching process.