Multiple independent introductions in Bayesian phylodynamics

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Bayesian phylodynamics aims to estimate population dynamics using phylogenies that trace genetic relationships. While usually a single phylogenetic tree is inferred with its defining parameters, multiple trees can be estimated jointly to increase statistical power, if genetically distinct entities are characterised by the same or overlapping set of parameters. One example in which this is especially relevant is in infectious disease research, when a pathogen is introduced multiple times independently into the studied population. However, it is poorly understood how phylodynamic methods perform with increasing number and decreasing size of entities. We aim to address this problem in a simulation-based evaluation of an established approach to quantify the dynamic process jointly from multiple independent introductions in a phylodynamic birth-death sampling setup. We find the method to be sensitive to a high percentage of small introductions, as it significantly overestimates the joint birth rate. Through the modelling of the introduction process, however, the birth rate can be robustly inferred.