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Abstract

Coalescent simulation is a widely-used tool in population studies of molecular polymorphism. In such simulations a coalescent tree is first produced conditional on a particular demographic model (usually a panmictic constant-size Wright-Fisher population); mutations are then independently spread on this tree conditional on some mutational process, and simulated samples are compared to observed data. Several simulation methods have been proposed for this independent mutational process, the two most popular being either using a fixed mutation rate or using a fixed number of mutations. With a Bayesian approach, we show that these and other methods can lead to statistical errors by radically changing the shape of the simulated trees, especially in non-recombining regions.