

## **Inferring demography along the phylogeny**

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The influence of population size on population genetics is crucial, affecting the stochastic nature of evolution and the overall efficiency of mutation and selection. Previous studies inferred demography along phylogenies using various methods, but often relied on strong assumptions about demographic processes or can only detect variations in the population size. Here, we expand the polymorphism-aware phylogenetic models to accommodate fluctuating demography. Our theoretical approach involves simulating the mutation-drift dynamics observed in the effective population within a smaller population composed of only a few individuals. By operating in this reduced state-space, our models provide computationally efficient means to infer demography. We demonstrate that our method can accurately estimate one effective population size per branch and the divergence times of all ancestral nodes in the phylogeny. To showcase its practical application, we apply our method to genomic data from great apes.