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Title:

PoMo via RevBayes: Inferring Phylogenies, Disentangling GC-bias and Balancing Selection

Abstract:

The interplay between mutation, genetic drift, directional and balancing selection shapes the diversity of populations, however, it can be highly complex and challenging to disentangle. To address this, sophisticated models with a high degree of flexibility and the ability to handle multi-individual data are required. We have developed a set of polymorphism-aware phylogenetic models called PoMos. These models are based on the Moran model and have recently demonstrated their effectiveness in inferring species trees, as well as capturing mutational effects, fixation biases, and GC-bias rates. To enhance accessibility, we have implemented these models in the open-source Bayesian inference framework RevBayes. The framework offers several advantages, including its graphical model environment and the capability to compute coverage frequencies for validation analysis. In this study, we further expanded the capabilities of PoMos to investigate neutral, GC-bias, and for the first time, balancing selection. The novel aspect of our approach in studying balancing selection lies in PoMos' ability to account for ancestral polymorphisms and incorporate parameters that measure frequency-dependent selection. We evaluated our new method by conducting tests on a set of simulated data using the popular evolutionary framework Slim, along with a custom Moran model simulator implemented in RevBayes. Furthermore, we examined real sequences from *Drosophila* populations to gain insights into the evolutionary history of genomic regions known to be subject to frequency-dependent balancing selection, which leads to sex-limited colour dimorphism.