Bait-ER: a Bayesian method to detect targets of selection in Evolve-and-Resequence experiments

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Abstract

For over a decade, experimental evolution has been combined with high-throughput sequencing techniques in so-called Evolve-and-Resequence (E&R) experiments. This allows testing for selection in populations kept in the laboratory under given experimental conditions. However, identifying signatures of adaptation in E&R datasets is far from trivial, and it is still necessary to develop more efficient and statistically sound methods for detecting selection in genome-wide data. Here, we present Bait-ER - a fully Bayesian approach based on the Moran model of allele evolution to estimate selection coefficients from E&R experiments. The model has overlapping generations, a feature that describes several experimental designs found in the literature. We tested our method under several different demographic and experimental conditions to assess its accuracy and precision, and it performs well in most scenarios. However, some care must be taken when analysing specific allele trajectories, particularly those where drift largely dominates and starting frequencies are low. We compare our method with other available software and report that ours has generally high accuracy even for very difficult trajectories. Furthermore, our approach avoids the computational burden of simulating an empirical null distribution, outperforming available software in terms of computational time and facilitating its use on genome-wide data. We implemented and released our method in a new open-source software package that can be accessed at https://github.com/mrborges23/Bait-ER.

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