

## Signature-Informed Selection Detection: A Novel Method for Multi-Locus Wright-Fisher Models with Recombination

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In this research, we introduce a novel Bayesian framework for detecting selection in Wright-Fisher models, deploying a signature-based kernel method for likelihood approximation. By extracting a set of signatures from the trajectories of allele frequencies, our approach captures the higher-order dynamics embedded within the data. Given the computational intractability of likelihood, we utilize the extracted signatures to estimate the likelihood, which in turn facilitates the Bayesian inference of selection forces that have shaped the observed data. We further employ a Bayesian generalized posterior coupled with a Population Monte Carlo (PMC) algorithm to generate posterior samples of selection coefficients. This powerful combination leverages the strictly proper nature of the signature kernel scoring rule, enabling us to infer selection dynamics efficiently even in complex high-dimensional and temporal data settings. We demonstrate the efficacy of our methodology through comprehensive simulations and application to real-world datasets. Notably, our approach effectively detects selection not just in univariate, but also in multivariate Wright-Fisher models, inclusive of 2-locus and 3-locus models with recombination. The added complexity from recombination, which produces mixed signals between loci, makes the inference of selection challenging, yet our methodology skillfully navigates these intricacies. This novel technique provides a promising path for further understanding the complex mechanisms of evolution, enriching our insights into the dynamics of genetic selection across various evolutionary scenarios.