

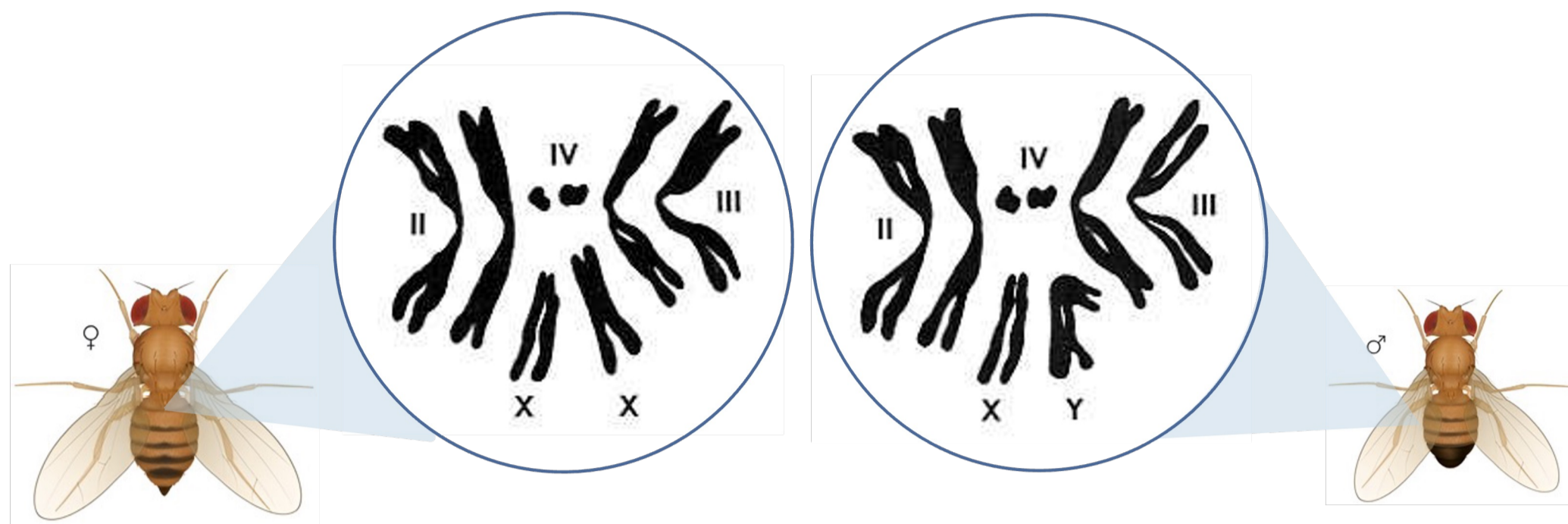
The evolution of sexually antagonistic variation in fruit flies

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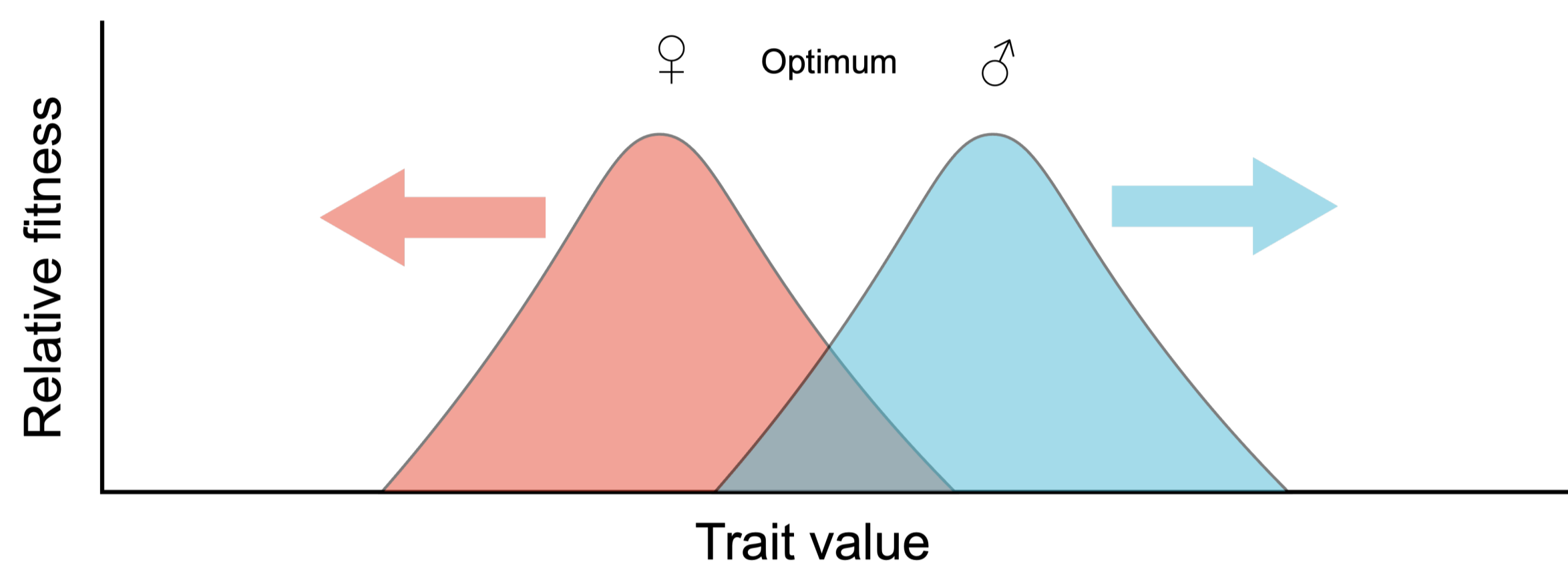
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Introduction



Shared genomes but opposing trait optima



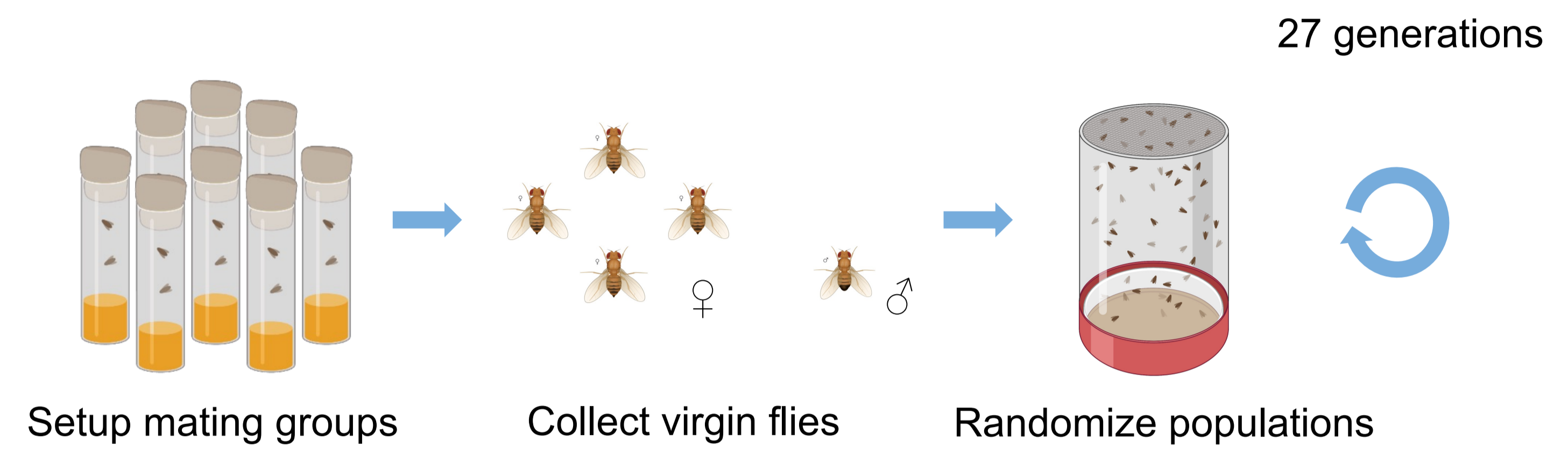
Sexual antagonism: a genetic conflict where one allele confers a benefit to one sex but a detriment to the other sex

What is the genetic basis of sexually antagonistic variation?

Methods

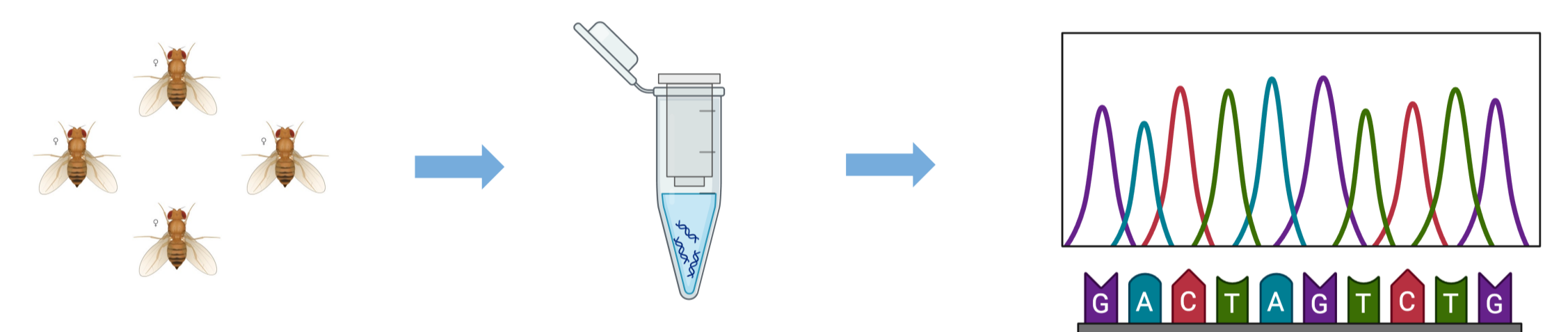
1 Experimental evolution under sex-limited selection

allows beneficial allele to rise in one sex without counter-selection in another

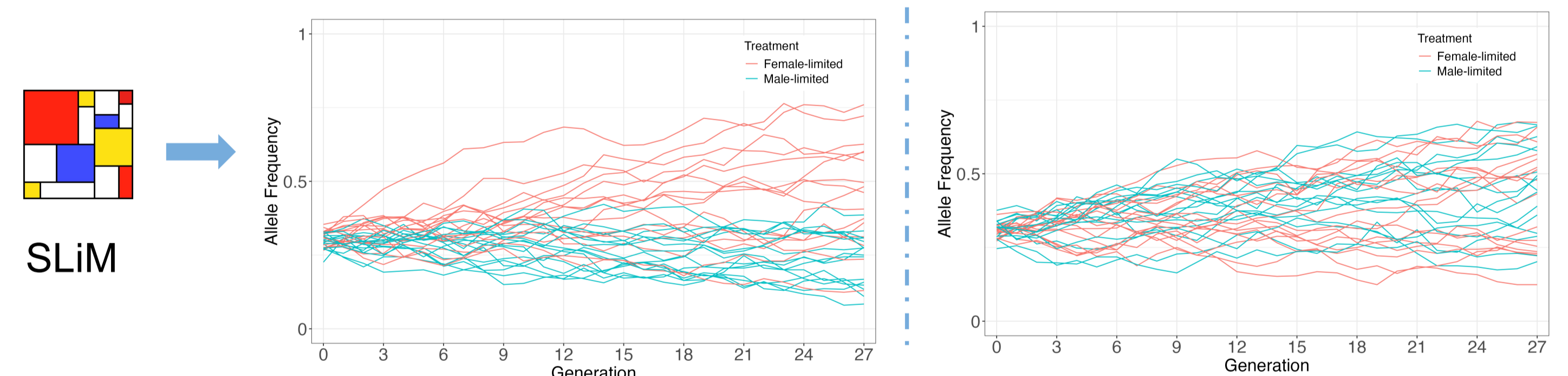


2 Identification of sexual-antagonistic variants with Approximate Bayesian Computation

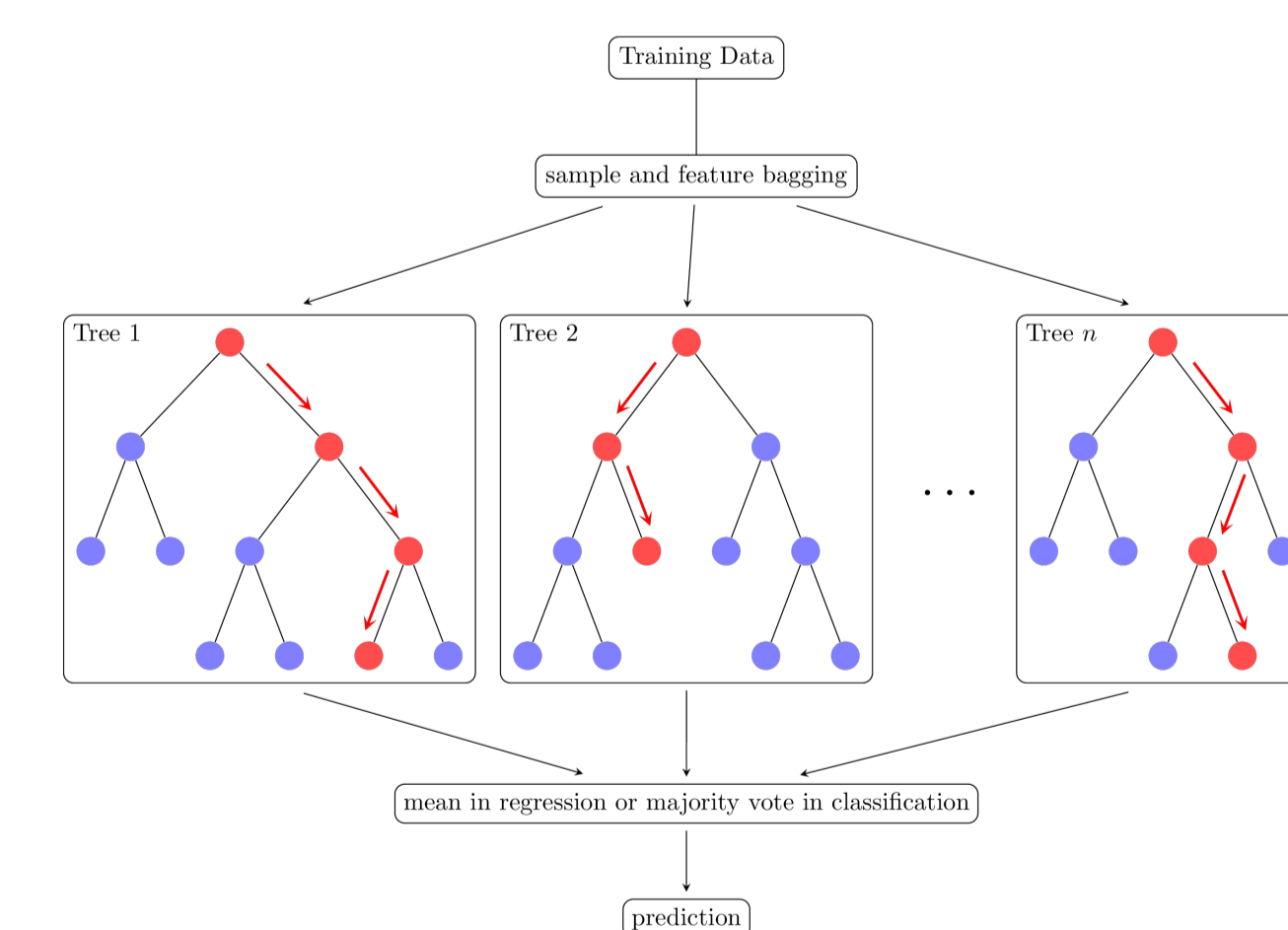
Experimental data → Pool-Seq allele frequency estimates every 3 generations



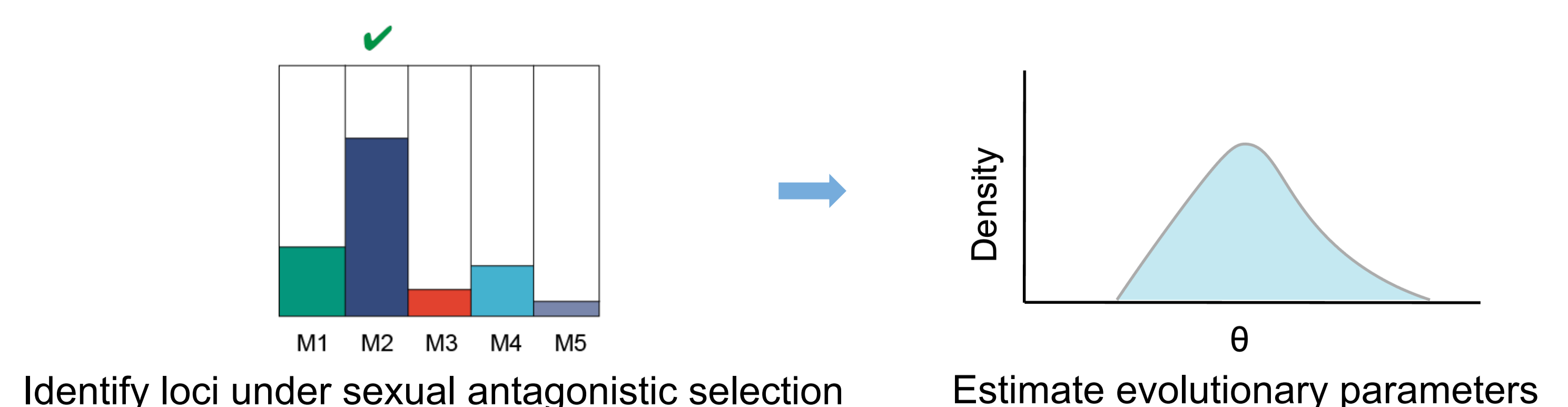
Simulate allele frequencies replicating experimental setup under different selection models



Train random forests on summary statistics from simulations



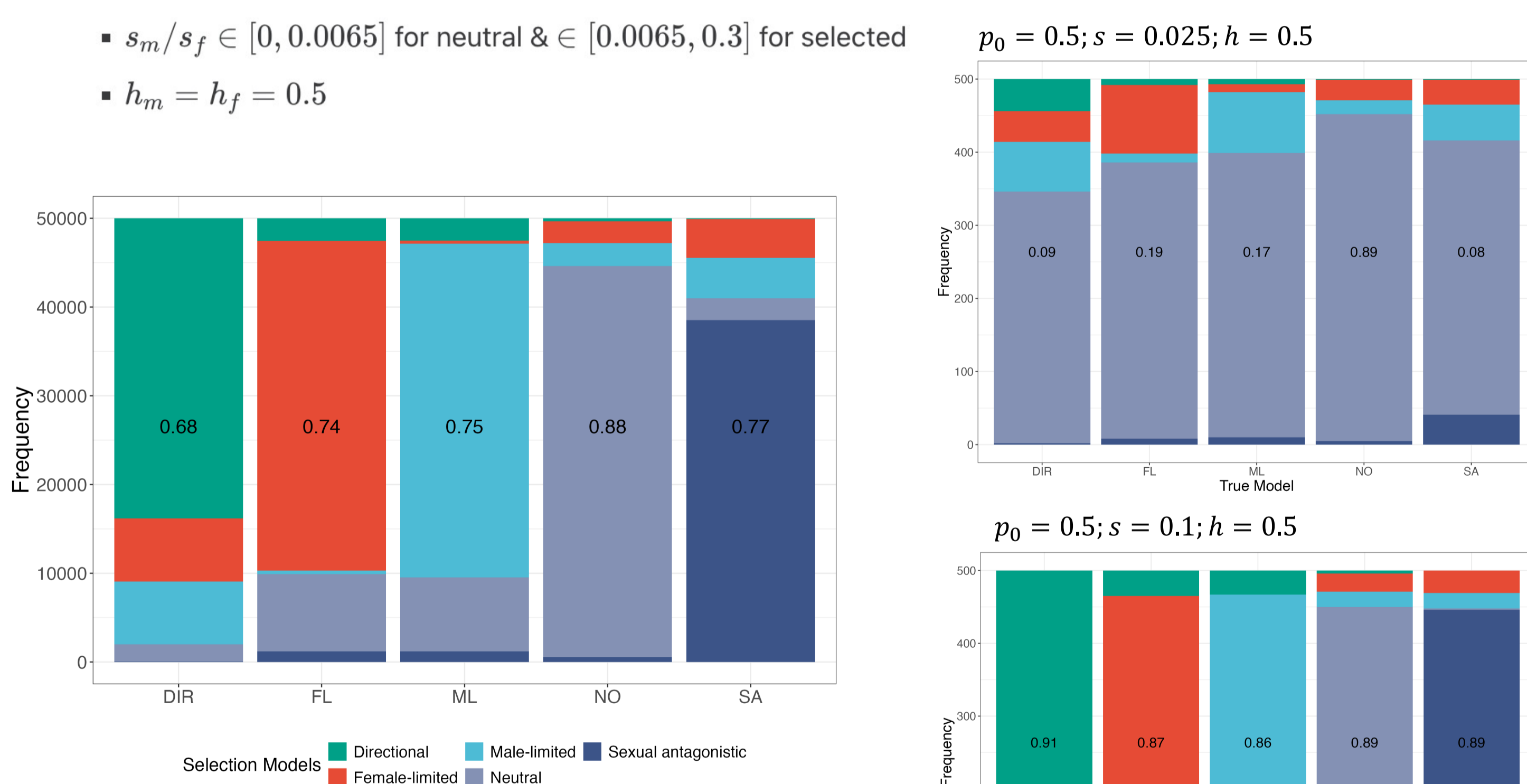
Make predictions on experimental data



Results

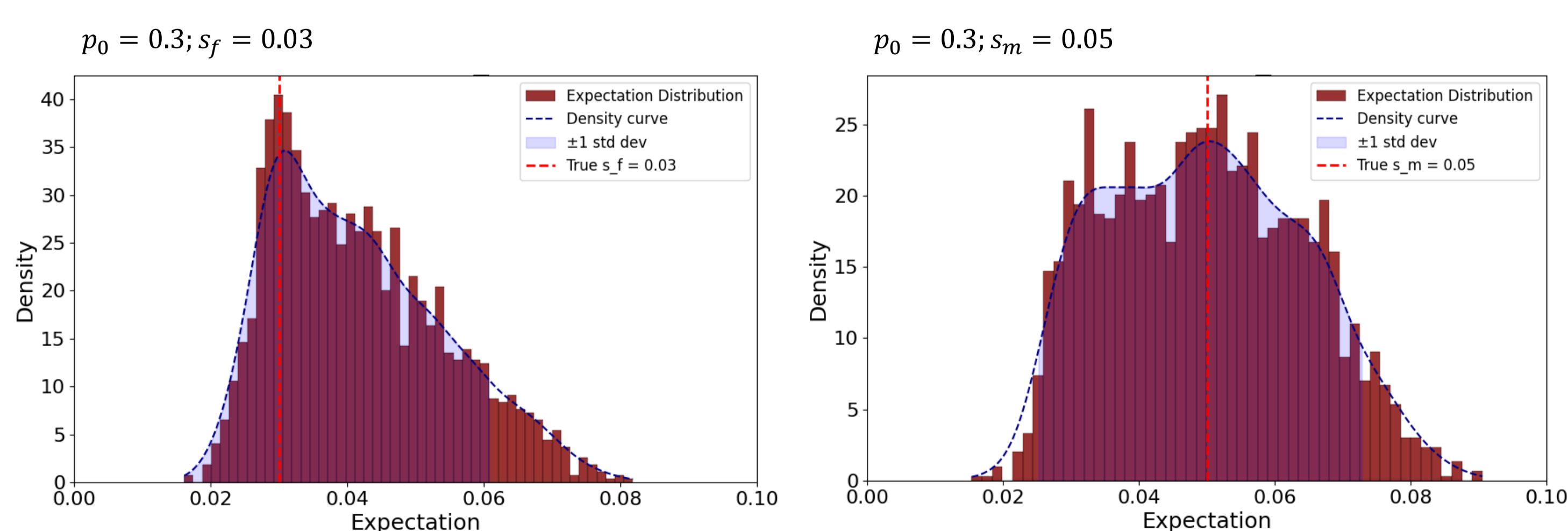
Random Forests were trained on 50000 simulations for each of the five selection models with the following parameters

- $p_0 \in [0.1, 0.9]$
- $s_m/s_f \in [0, 0.0065]$ for neutral & $[0.0065, 0.3]$ for selected
- $h_m = h_f = 0.5$



Model selection works well for strong selection ($s = 0.1$) but performs poorly for weak selection ($s = 0.025$)

Representative parameter estimation predictions



Parameter inference models work well for both s_m and s_f



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