

### File S3

**SelSim** is a program for Monte Carlo simulation of SNP data for a recombining region within which a single bi-allelic site has experienced natural selection. It allows simulation from either a fully stochastic model of, or deterministic approximations to, natural selection within a coalescent framework.

The simulated data generated with SelSim and invertFREGENE under the neutral model produce slightly different distributions of the iHS statistic. The two software were run under the same parameter settings (effective population size, mutation rate and recombination map) and therefore the observed differences can be attributed to the different underlying models used in the two methods. invertFREGENE simulates genetic data forward-in-time while SelSim performs backward-in-time simulation.