

FREGENE datasets: 'Population A'

SUMMARY OF MODELLING ASSUMPTIONS USED TO SIMULATE THE PANMICTIC POPULATION.

Population A mimics the evolution of 10.5K diploid individuals along 200K generations. Each sequence is 1 *Mb* long. Two simulations are available: one neutral (see results in `Output_neutral`) and one with selection (see results in `Output_selected`). Scripts used to generate these simulations are also provided (`fregene_POPNA_neutral.sh` and `fregene_POPNA_sel.sh` respectively). Modelling assumptions are recorded in the input files (in `Input` directory) and summarized below. Finally some R scripts that generate figures describing these simulations can be found in `R_Scripts` together with the corresponding figures (in `Figures`).

General parameters	
Chromosome Length	1 <i>Mb</i>
# Generations	200,000
# Sequences	21,000
Per-site mutation rate	2.3×10^{-8}

Recombination model	
Per site crossover rate:	1.1×10^{-8}
Per site Gene conversion rate:	4.5×10^{-9}
Proportion of recombination events occurring in hotspots	80%
Hotspot length:	2.0 <i>kb</i>
Gene conversion length:	0.5 <i>kb</i>
Mean distance between hotspots:	8.5 <i>kb</i>

Selection parameters (if applicable)	
Prop. of sites under selection:	5×10^{-4}
Proportion of selected sites locally under selection:	0.5
Mean # generations before selected sites are switched off	50,000
selection coefficient:	$s \sim 0.1 \times \mathcal{N}(0.005, 0.005^2)$ $+ 0.9 \times \mathcal{N}(-0.01, 0.005^2)$
dominance coefficient:	$h \sim 0.8 \times \mathcal{N}(0.5, 0.2)$ $+ 0.3 \times \mathcal{N}(1.2, 0.2^2)$
