Scripts

Two python scrips are included (CreateCGenomeSimInputDist.py and PassCGenomeSim.py). They are specifically designed to create and process the data for the paper, they are not general-purpose scripts.

CreateCGenomeSimInputDist.py

Creates input files for QLTSim, drawing parameters from the distributions specified in the paper. Running the program produces 15,000 input files outputs the parameters as a table. For a description of the parameters please see the QTLSim manual.

PassCGenomeSim.py

Summarizes the output from QTLSim, it takes the output from QTLSim and produces a summary, the columns are described below.

Output variables: label in parentheses corresponds to the column name in the supplementary data file

(eq) GenotypeVar end: Directional selection is introduced at generation 4999 of a simulation (the first generation is denoted "0"). This column records the generation number following the onset of directional selection at which the genotype variance reached its equilibrium value (see below). A "-1" in this column indicates that the genotype variance was at or below the eventual equilibrium variance prior to the onset of directional selection. This can occur either because of genetic drift or when selection is weak. A blank in this column indicates that the population went extinct.

(eq95) GenotypeVar 95% end: the number of generations required for the genetic variance to reach 95% of its equilibrium value.

(gvstart) GenotypeVar start: the genotypic variance at the point that directional selection is introduced (at generation 4999). Note that owing to neutral drift this will typically differ from the genetic variance at the start of the simulation, calculable from heritability times the phenotypic variance.

* (gveq) GenotypeVar end mean: The mean of the genotypic variance in the final 500 generations of directional selection. This is the equilibrium genetic variance.

* (gvslope10) GenotypeVar 10 slope: the slope of the line relating the genetic variance to the generation number, measured over the first ten generations following the introduction of directional selection.

* (pmslope10) Phenotype 10 slope: the slope of the line relating the mean phenotype to generation number, measured over the first ten generations following the introduction of directional selection.

* (pend) Phenotype End slope: the slope of the line relating the phenotypic mean to generation number for the final 500 generations of the model (that is, during its equilibrium phase)

* (spmslope10) Phenotype Ratio 10 slope: as above for pmslope10 but scaled by the running phenotypic standard deviation.

* (spend) Phenotype Ratio End slope: as above for the phenotype "end" measures but scaled by the running standard deviation of the phenotype mean. This measures the long-term number of standard deviations of phenotypic change per generation.

* (west) W End Mean: an estimate obtained from the data of the theoretical population-genetic parameter ω.

* (sc=selection coefficient) Surviving Slope End Mean: the slope of the line relating the value of the trait to fitness, calculated within the subset of the population that survives selection.

* ssc (standardised selection coefficient) Surviving Standardised Slope End Mean: as above but scaling the phenotype value by its standard deviation. This is the standardised selection coefficient.

* (surviv) Surviving Population End Mean: the mean number of survivors following selection calculated over the final 500 generations. Population size is set within QTLSim.