

## QTLSim

QTLSim models the evolution of a quantitative trait locus (QTL) in a population under stabilising or directional selection. The QTL comprises genetic and environmental effects. Population size, the strength of selection, heritability, the size of the input (target) phenotypic variance and the size of the per generation mutational variance can all be set by the user. Haploid and a limited diploid modes are available.

QTLSim does not model the genome or multiple genetic loci directly. For a more comprehensive, general purpose and flexible simulation package, see SLiM (<https://messerlab.org/slim/>). For a detailed description of the simulations, please see the accompanying paper.

## Running the program

QTLSim is run from the command line and takes a configuration file as a parameter. An example configure file is given below. The commands can be found in Example1.txt.

## Building QTLSim

QTLSim is written in C and requires the GSL – GNU Scientific Library (<https://www.gnu.org/software/gsl/>).

A basic CMake file is provided for Linux systems, the program can be built with

```
cmake CMakeLists.txt && make
```

or directly

```
gcc ./Src/*.c -oQTLSim -lgsl -lm -O3
```

the code can also be built using Visual Studio 2022.

## License

QTLSim is open source and is released under GNU General Public License V3.0 (<https://www.gnu.org/licenses/gpl-3.0.en.html>)

## Commands

Command	Help
Purpose	Prints a help message
Parameters	None
Example	Help

Command	Sample
Purpose	Set the frequency at which the population information is printed
Parameters	Integer
Example	Sample 1

Command	PopSize
Purpose	Sets the size of the population
Parameters	Integer
Example	PopSize 10000

Command	NoQTL
Purpose	Sets the number of quantitative trait loci (QTL) to simulate
Parameters	Integer
Example	NoQTL 2

Command	Ploidy
Purpose	Sets the ploidy number of the individuals in the simulation
Parameters	Integer, 1 or 2
Example	Ploidy 2

Command	Drift
Purpose	Toggle drift on or off, drift is off by default
Parameters	None
Example	Drift

Command	MutationScalar
Purpose	Sets the mutational variance, expressed as a scalar of the environmental variance, typically $1/1000^{\text{th}}$ of the environmental variance.
Parameters	Float
Example	MutationScalar 0.001

Command	Generations
Purpose	Sets the number of generations to run the simulation
Parameters	Integer
Example	Generations 10000

Command	ChangeFitnessSD
Purpose	Changes the standard deviation of the fitness function on a specific generation. The new SD is used for the rest of the simulation.
Parameters	Integer and float
Example	ChangeFitnessSD 5000 0.1
Command	MoveFitnessSD
Purpose	Specify what generation to start moving the fitness function. The fitness function is moved by the specified SD and according to the OptimumMoveType.
Parameters	Integer and float
Example	MoveFitnessSD 2500 1.5
Command	Seed
Purpose	Set the random number seed used in the simulation. If no seed is specified, one is created based on the date / time and process ID.
Parameters	Integer
Example	Seed 52423368
Command	PhenotypeVar
Purpose	Set the phenotype variance
Parameters	Float
Example	PhenotypeVar 0.01
Command	Heritability
Purpose	Set the genetic heritability
Parameters	Float (0,1)
Example	Heritability 0.5
Command	OptimumMoveType
Purpose	Determines how the fitness function mean moves each generation when the MoveFitnessSD command is used. There are three move types, fitness, phenotype and continuous.

OptimumMoveType	Fitness function mean
Fitness	$X + (\text{FitnessFunctionSD} \times \text{MoveFitnessSD})$
Phenotype	$X + (\text{sqrt}(\text{PhenotypeVar}) \times \text{MoveFitnessSD})$
Continuous	Fitness function mean + MoveFitnessSD

Where X is the mean phenotype of the current population. MoveFitnessSD is the SD supplied to the MoveFitnessSD command.

The continuous move type will continuously increase the mean of the fitness function without respect to the population's current fitness. This often leads to scenarios where the entire population dies. In these cases, the simulation will end.

Parameters	A string, Fitness, Phenotype, or Continuous
Example	OptimumMoveType Phenotype

## Example

Below is an example set of commands, which can be found in Example1.txt.

Generations 6500

Sample 1

PopSize 10000

NoQTL 1

Ploidy 2

Heritability 0.5

PhenotypeVar 0.01

MutationScalar 0.001

ChangeFitnessSD 5000 0.170000

MoveFitnessSD 5000 2.0

OptimumMoveType Phenotype

This simulation runs for 6500 generations and prints the population every generation. It has a population size of 10000 individuals, with one QTL each with two chromosomes (Ploidy 2). Heritability is set to 0.5, and the phenotype variance is 0.01. The amount of mutation that is applied each generation is set to  $1/1000^{\text{th}}$  of the environmental variance, using the MutationScalar command. On the  $5000^{\text{th}}$  generation, the fitness function is set to have a SD of 0.17 and sets the mean of the of fitness function 2 SDs larger than the mean phenotype (see above).

## Command Table

Command	Parameter	Example
Help	None	Help
Sample	Integer	Sample 1
PopSize	Integer	PopSize 1000
NoQLT	Integer	NoQLT 10
Ploidy	Integer, 1 or 2	Ploidy 1
Drift	None	Drift
MutationScalar	Float	MutationScalar 0.001
Generations	Integer	Generations 10000
ChangeFitnessSD	Integer and Float	ChangeFitnessSD 5000 0.1
MoveFitnessSD	Integer and Float	MoveFitnessSD 2500 1.5
Seed	Integer	Seed 52423368
PhenotypeVar	Float	PhenotypeVar 0.01
Heritability	Float (0,1)	Heritability 0.4

## Output

QTLSim prints the output using a tab delimiter format. The output consists of the simulation options, a header, and the stats of the population. The ">" can be used to redirect the output from the screen to a specified file. The columns of output are detailed below.

Column header	Information
Generation	The generation number
Phenotype Mean	The phenotype mean
Phenotype Ratio	The mean phenotype / sqrt(phenotype variance)
Genotype Var	The genotype variance
P Survived	The number of individuals which survived
Heritability	Genotype variance / (Genotype variance + environmental variance)
Fitness Function Mean	The mean of the fitness function
Fitness Function SD	The standard deviation of the fitness function
Surviving Slope	The slope, and Standardised Slope for the surviving members of the population, where x is the individuals' phenotype and y is the fitness of the individuals. If phenotype is greater than the mean of the fitness function, it is reflected. The standardised slope is the slope multiplied by the standard deviation of the phenotypes.
Surviving Standardised Slope	
w	Sqrt(GenotypeVar <sup>2</sup> / Mutational variance )