

Sexual selection enables long-term coexistence despite ecological equivalence

This document provides basic instructions for compiling and running the model and also provides a description of the parameters used. The included code will run a simulation similar to that presented in Fig. 1d in the manuscript.

The majority of the program is coded in R and can be found in the various `.R` files in the `src_r` directory. Prior to running, the packages `RColorBrewer` and `cubature` will need to be installed. In optimizing the simulation a few basic functions were written in C. These can be found in the `src_c` directory. These must be compiled and then loaded into R before the model can run. In order to compile the C code, through a unix terminal, run the commands provided in the header of `main.R`.

Compiling the C code will create several `.so` files which then need to be loaded into R. The file `main.R` contains all the code necessary to load these files and run a basic simulation (once the file paths have been changed appropriately). Table 1 provides a description of the parameters used in this simulation and default values are given in `main.R`. The local carrying capacity functions we use are also specified in `main.R` as:

- `G.1D`: a local carrying capacity in one dimension with two Gaussian peaks
- `G.2D`: a local carrying capacity in two dimensions with two Gaussian peaks

The model and simulation can, however, handle general landscapes of other forms. For both `G.1D` and `G.2D`, `sigma` specifies the widths of the Gaussian peaks (σ_k in the manuscript) and `K.base` the base height of the landscape to which the Gaussian peaks are added (b in Eq. 1). `K.base`, therefore, determines the level of heterogeneity in the landscape. These carrying capacity functions are later standardized, so only relative differences are important. `p.h` specifies the relative heights of the Gaussian peaks (each peak of height 1 is used as a default). The default parameters specified in `main.R` produce the landscapes used in Fig. 1B (one dimension) and Fig. 1D. (two dimensions).

Name	Description
<code>dimension</code>	The spatial dimension of the model (e.g., 1 or 2).
<code>spatial.model</code>	Set to 1 for a homogeneous local carrying capacity or 2 for a heterogeneous one. If set to 1 the local carrying capacity function provided (see below) will not be used.
<code>genetic.model</code>	Set to 1 for the allelic model or 2 for the quantitative model.
<code>comp.model</code>	Set to 1 for the survival model or 2 for the fecundity model (see SI, Section S2.3 for the latter).
<code>move.model</code>	Set to 1 for the standard movement used throughout the manuscript or 2 for the mating dependent dispersal described in SI, section S2.1.
<code>num.types</code>	The number of distinct mating types present at the beginning of the model run.
<code>num.loci</code>	The number of loci per trait in the allelic model. This has not been used or tested so far and was included primarily to ease future extensions. Thus only a value of 1 should be used.
<code>recomb.rate</code>	The recombination rate between the display and preference traits in the allelic model.
<code>asymmetric.costs</code>	When set to 0, there are no asymmetric costs associated with the display alleles. When set to 1, one of the male display alleles is more costly (the magnitude of this cost is specified by <code>cost.type.1</code> below).
<code>cost.type.1</code>	Strength of asymmetric costs (a).
<code>sigma.s</code>	Spatial competition radius (σ_s).
<code>sigma.f</code>	Female mate-search radius (σ_f).
<code>sigma.m</code>	Movement radius (σ_m).
<code>sigma.p</code>	Preference width in the quantitative model (σ_p).
<code>sigma.r</code>	Mutational distribution in the quantitative model (σ_o).

Table 1: Description of simulation parameters.

Name	Description
<code>N</code>	Total number of offspring produced (N).
<code>K</code>	Total carrying capacity (K).
<code>s0</code>	Free parameter for survival function (s_{\max}).
<code>x.len</code>	Length of spatial x -dimension.
<code>y.len</code>	Length of spatial y -dimension.
<code>fxy</code>	The function specifying the local carrying capacity. Use <code>fxy=G.1D</code> for the one-dimensional model and <code>fxy=G.2D</code> for the two-dimensional model. <code>fxy</code> is then standardized to create $k(x, y)$ in the manuscript.
<code>alpha</code>	Female preference strength (α). A negative value causes complete assortment in the allelic model.
<code>fem.cost</code>	Strength of mate-search costs (m).
<code>male.move</code>	Male diffusion parameters which determine how strongly male movement distances depend on the composition of nearby females (SI, section S2.1 only).
<code>num.gens</code>	Number of generations.
<code>init.spatial.config</code>	The initial spatial distribution of mating types: 1 = random, 2 = pure and spatially segregated patches of P/Q and p/q .
<code>print.every</code>	Number of generations between refreshes while plotting.
<code>file.name</code>	Name of the file to save simulation output to.

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