Package 'qgsim'

March 14, 2025

Type Package

Title Simulate quantitative trait evolution on dynamic adaptive landscapes

Version 1.0

Date 2024-01-11

Description This package was developed for educational purposes. It can be used to simulate quantitative trait evolution on dynamic adapative landscapes for multiple populations. Two traits are modeled and these evolve by selection, drift and gene flow.

License GPL (>= 3)

Encoding UTF-8

Depends R (>= 3.4.0), mnormt (>= 2.0.0)

Imports

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

R topics documented:

---

qgsim-package   *The 'qgsim' package.*

Description

This package was developed for educational purposes. It can be used to simulate quantitative trait evolution on dynamic adapative landscapes for multiple populations. Two traits are modeled and these evolve by selection, drift and gene flow.

1

Author(s)

Maintainer: Zachariah Gompert <zach.gompert@usu.edu> (ORCID)

Authors:

- Ethan Dayley <ethan.dayley@usu.edu>

---

qgsim_func   *Simulate evolution*

Description

This function simulates evolution for a pair of quantitative traits using a quantitative genetic model. Evolution occurs by selection, drift and migration. Simulations can be for any number of populations and can involve various forms of adaptive peak movement.

Usage

```
qgsim_func(
  npops = 2,
  mig = 0,
  Ne = 500,
  theta0 = 0,
  z0 = 0,
  h2 = 0.5,
  Gcor = 0.2,
  omega11 = 1,
  omega22 = 1,
  omegaCor = 0,
  model = "Brownian",
  ngens = 100,
  tsd = 0.02,
  tmn = 0.01
)
```

Arguments

npops	number of populations to simulate.
mig	the migration rate, this is the total proportion of individuals in each population made up of migrants from the other populations.
theta0	this specifies the initial optimal value for the traits, you can supply a single value (applied to both traits), one value per trait, or a matrix with one value per population (row) and trait (column).
z0	this specifies the initial trait values, you can supply a single value (applied to both traits), one value per trait, or a matrix with one value per population (row) and trait (column).

h2	the trait heritabilities, assumed to be the same for both traits (must be between 0 and 1).
Gcor	the genetic correlation between the pair of traits (must be between -1 and 1).
omega11	denotes the intensity of selection (curvature of the adaptive landscape) with respect to trait 1, larger values result in weaker selection default = 1.
omega22	denotes the intensity of selection (curvature of the adaptive landscape) with respect to trait 2, larger values result in weaker selection default = 1.
omegaCor	denotes the strength of correlational selection, larger values denote stronger selection for combinations of trait 1 and trait 2 (must be between -1 and 1, 0 denotes independent selection on each trait) default = 0.
model	denotes the model for adaptive peak movement, must be one of the following: "Brownian", "Uncorrelated", or "Trend"; detailed descriptions are provided below.
ngens	number of generations to simulate default = 100.
tsd	standard deviation for peak movement, larger values denote larger (random) jumps in adaptive peak locations (must be a positive number).
tmn	average direction shift in the location of the adaptive landscape, only relevant for the "Trend" model (can be negative or positive, but must be a single value for both traits).

Details

With the Brownian motion peak shift model, a random normal deviation with standard deviation tsd is added to the peak location each generation. With the Uncorrelated peak shift model, the peak location is follows a normal distribution with independent peak locations each generation. The peak location for each trait is specifically drawn from a normal distribution with mean 0 and standard deviation tst. Finally for Trend, the peak location shifts by a random normal deviation each generation with a mean tmn and standard deviation tsd. In all cases, peak shifts occur independently in each population.

Value

A list with two objects, the mean trait values (z) and adaptive peak locations (theta). Each of these is itself a list with one matrix per population. The population matrixes have two columns, one per trait, and one row per generation.

---

qgsim_plot_bivar *Generate a bivariate plot*

Description

This function takes the output of qgsim and some specifiers and generates a bivariate plot

Usage

```
qgsim_plot_bivar(qgsim_res, populations, vars, type = "p", pch = 16)
```

Arguments

`qgsim_res`	the results of a qgsim function call.
`populations`	either a single number indicating a population to plot, or a vector with two values indicating populations to plot against each other.
`vars`	either a single value or a vector of with two values indicating the z/theta values to plot against each other (can be z1, z2, theta1, or theta2).
`type`	same as for base R plot() function
`pch`	same as for base R plot() function

Value

the output of an r plot() function displaying the required bivariate plot

---

`qgsim_repl`	*Simulate evolution (with replicates and summaries)*

Description

This function is a wrapper for the gqsim function which lets you run replicates and get summaries. The summaries currently available include: mean rate of evolution ('mean_evol_rate', average change in each trait across populations and generations), evolutionary lag ('mean_evol_lag', average distance in bivaraiate trait space between the optimal phenotypes and z), correlations in evolution between traits ('mean_traitwise_corr', averaged over time and populations), correlations in evolution across populations ('mean_popwise_corr', averaged over time and traits), and the variance in mean trait values across populations in the final generation ('end_phenotypic_variance', averagec over traits).

Usage

```
qgsim_repl(
  nreps = 1,
  summaries = c(),
  npops = 2,
  mig = 0,
  Ne = 500,
  theta0 = 0,
  z0 = 0,
  h2 = 0.5,
  Gcor = 0.2,
  omega11 = 1,
  omega22 = 1,
  omegaCor = 0,
  model = "Brownian",
  ngens = 100,
  tsd = 0.02,
  tmn = 0.01
)
```

Arguments

nreps	number of replicates to run
summaries	a vector of strings containing any summaries to be included in the results
npops	number of populations to simulate.
mig	the migration rate, this is the total proportion of individuals in each population made up of migrants from the other populations.
theta0	this specifies the initial optimal value for the traits, you can supply a single value (applied to both traits), one value per trait, or a matrix with one value per population (row) and trait (column).
z0	this specifies the initial trait values, you can supply a single value (applied to both traits), one value per trait, or a matrix with one value per population (row) and trait (column).
h2	the trait heritabilities, assumed to be the same for both traits (must be between 0 and 1).
Gcor	the genetic correlation between the pair of traits (must be between -1 and 1).
omega11	denotes the intensity of selection (curvature of the adaptive landscape) with respect to trait 1, larger values result in weaker selection default = 1.
omega22	denotes the intensity of selection (curvature of the adaptive landscape) with respect to trait 2, larger values result in weaker selection default = 1.
omegaCor	denotes the strength of correlational selection, larger values denote stronger selection for combinations of trait 1 and trait 2 (must be between -1 and 1, 0 denotes independent selection on each trait) default = 0.
model	denotes the model for adaptive peak movement, must be one of the following: "Brownian", "Uncorrelated", or "Trend"; detailed descriptions are provided below.
ngens	number of generations to simulate default = 100.
tsd	standard deviation for peak movement, larger values denote larger (random) jumps in adaptive peak locations (must be a positive number).
tmn	average direction shift in the location of the adaptive landscape, only relevant for the "Trend" model (can be negative or positive, but must be a single value for both traits).

Details

With the Brownian motion peak shift model, a random normal deviation with standard deviation tsd is added to the peak location each generation. With the Uncorrelated peak shift model, the peak location is follows a normal distribution with independent peak locations each generation. The peak location for each trait is specifically drawn from a normal distribution with mean 0 and standard deviation tst. Finally for Trend, the peak location shifts by a random normal deviation each generation with a mean tmn and standard deviation tsd. In all cases, peak shifts occur independently in each population.

Value

A list with two objects, the mean trait values (z) and adaptive peak locations (theta). Each of these is itself a list with one matrix per population. The population matrixes have two columns, one per trait, and one row per generation.

---

var_covar_mat_vis   *Visualize variance/covariance matrices*

Description

Visualize the G and omega variance/covariance matrices generated in qgsim

Usage

```
var_covar_mat_vis(h2 = 0.5, Gcor = 0.2, omega11 = 1, omega22 = 1, omegaCor = 0)
```

Arguments

h2	the trait heritabilities, assumed to be the same for both traits (must be between 0 and 1).
Gcor	the genetic correlation between the pair of traits (must be between -1 and 1).
omega11	denotes the intensity of selection (curvature of the adaptive landscape) with respect to trait 1, larger values result in weaker selection default = 1.
omega22	denotes the intensity of selection (curvature of the adaptive landscape) with respect to trait 2, larger values result in weaker selection default = 1.
omegaCor	denotes the strength of correlational selection, larger values denote stronger selection for combinations of trait 1 and trait 2 (must be between -1 and 1, 0 denotes independent selection on each trait) default = 0.

Value

The plot showing 95% CI for both generated matrices

Index