

Package ‘skeleSim’

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Type Package

Title Genetic Simulation Engine

Version 0.9.8

URL <https://github.com/christianparobek/skeleSim>

BugReports <https://github.com/christianparobek/skeleSim/issues>

Description A shiny interface and supporting tools to guide users in choosing appropriate simulations, setting parameters, calculating summary genetic statistics, and organizing data output, all within the R environment. In addition to supporting existing forward and reverse-time simulators, new simulators can be integrated into the environment relatively easily.

License GPL-2

LazyLoad Yes

LazyData true

Depends R (>= 3.4.0), igraph, shiny (>= 0.13.0), shinyFiles

Imports adegenet, ape, hierfstat, pegas, markdown, methods, reshape2, rmetasim (>= 3.0.0), strataG (>= 1.0), swfscMisc (>= 1.1)

Suggests knitr, rmarkdown, RJSONIO

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skeleSim-package *Genetic simulation engine*

Description

skeleSim

analysis.funcs	<i>Analysis functions for skeleSim parameter objects</i>
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Description

Run Global, Locus, and Pairwise analyses on results from a single simulation replicate stored in `params@rep.sample#`

Usage

```
analysisFunc(params)
loadResultsMatrix(params, mat, label)
formatOverallStats(g, num.perm.reps)
globalAnalysis(g, num.perm.reps)
locusAnalysisGenotypes(g)
hapSmryFunc(g)
locusAnalysisHaplotypes(g)
calcChordDist(dat)
pairwiseAnalysis(g, num.perm.reps)
```

Arguments

<code>params</code>	a skeleSim.params object.
<code>mat</code>	results matrix to be loaded into params object.
<code>label</code>	analysis type label ("Global", "Locus", or "Pairwise").
<code>g</code>	a gtypes object.
<code>num.perm.reps</code>	number of permutation replicates.
<code>dat</code>	data.frame in hierfstat format (see genet.dist).

fastsimcoal.params-class

fastsimcoal Parameters Class

Description

An S4 class storing parameters specific to fastsimcoal

Slots

fastsimcoal.exec character string for the fastsimcoal command line executable.

pop.info matrix of population sampling information created by the [fscPopInfo](#) function.

hist.ev matrix of historical events created by the [fscHistEv](#) function.

locus.params data.frame specifying loci to simulate created by the [fscLocusParams](#) function.

growth.rate a vector num.pop long giving the growth rate of each population.

sample.times a vector num.pop long giving the time (in generations) that samples are drawn from in population.

fsc.loadScenario

Load skeleSim scenario parameters for fastsimcoal

Description

Load skeleSim scenario parameters for fastsimcoal

Usage

```
fsc.loadScenario(num.pops, pop.size, sample.size, mut.rate, migration = NULL,
  sample.times = NULL, growth.rate = NULL, locus.type = c("dna", "msat",
  "snp"), sequence.length = NULL, num.loci = NULL, transition.rate = NULL,
  gsm.param = NULL, range.constraint = NULL, recomb.rate = NULL,
  chromosome = NULL, num.chrom = NULL, num.gen = NULL,
  source.deme = NULL, sink.deme = NULL, prop.migrants = NULL,
  new.sink.size = NULL, new.sink.growth = NULL, new.mig.mat = NULL,
  fastsimcoal.exec = "fsc252")
```

Arguments

num.pops number of populations.

pop.size a vector giving size of each populaiton.

sample.size a vector giving the number of samples to take from each population.

mut.rate dna, msat: per base pair or locus mutation rate.

migration	a num.pop x num.pop matrix or list of matrices giving the migration rates between each population.
sample.times	a vector giving the number of generations in the past at which samples are taken.
growth.rate	a vector giving the growth rate of each population.
locus.type	a character representation of what type of marker to simulate. Can be "dna", "msat", or "snp".
sequence.length	dna: number of DNA base pairs to use.
num.loci	msat, snp: number of loci to simulate.
transition.rate	dna: fraction of substitutions that are transitions.
gsm.param	msat: Value of the geometric parameter for a Generalized Stepwise Mutation (GSM) model. This value represents the proportion of mutations that will change the allele size by more than one step. Values between 0 and 1 are required. A value of 0 is for a strict Stepwise Mutation Model (SMM).
range.constraint	msat: Range constraint (number of different alleles allowed). A value of 0 means no range constraint.
recomb.rate	recombination rate between adjacent markers.
chromosome	number or character identifying which chromosome the marker is on.
num.chrom	a value giving the number of chromosomes that the locus.params marker specifications should be copied for. If NULL, then chromosome assignment is taken from the chromosome column in locus.params. Any non-NULL integer will cause the chromosome column to be ignored.
num.gen	Number of generations, t, before present at which the historical event happened.
source.deme	Source deme (the first listed deme has index 0)
sink.deme	Sink deme
prop.migrants	Expected proportion of migrants to move from source to sink.
new.sink.size	New size for the sink deme, relative to its size at generation t.
new.sink.growth	New growth rate for the sink deme.
new.mig.mat	New migration matrix to be used further back in time.
fastsimcoal.exec	executable

Value

a [scenario.params](#) object to be loaded into a list in the `scenarios` slot of a [skeleSim.params](#) object.

Note

Vectors for `pop.size`, `sample.size`, `sample.times`, and `growth.rate` will be expanded/recycled to ensure they are as long as `num.pops`.

Depending on the choice of `locus.type`, values for some arguments may be ignored. See argument list above for which arguments are applicable to which `locus.type`.

fsc.run	<i>Run fastsimcoal</i>
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Description

Run fastsimcoal

Usage

```
fsc.run(params)
```

Arguments

params a [skeleSim.params](#) object.

Value

a modified [skeleSim.params](#) object with the results of a fastsimcoal run.

fsc.scenarioCheck	<i>Check parameters for fastsimcoal</i>
-------------------	---

Description

Check parameters for fastsimcoal

Usage

```
fsc.scenarioCheck(params)
```

```
fsc.histEvConverges(hist.ev, pop.size, growth.rate, num.mig.mats = NULL)
```

```
fsc.histEvCheck(hist.ev, pop.size, growth.rate, num.mig.mats = NULL)
```

Arguments

params a [skeleSim.params](#) object.

hist.ev a matrix describing historical events, with one row per event.

pop.size numerical vector giving size of each population.

growth.rate numerical vector giving growth rate of each population.

num.mig.mats number of migration matrices.

fsc.write	<i>Write fastsimcoal files</i>
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Description

Run fastsimcoal

Usage

```
fsc.write(params)
```

Arguments

params a [skeleSim.params](#) object.

Value

a modified [skeleSim.params](#) object with the results of a fastsimcoal run.

getGammaMutRates	<i>Get a Vector of Randomly Chosen Mutation Rates</i>
------------------	---

Description

Get a vector of mutation rates from a gamma distribution by specifying the mean and std. dev. of the distribution

Usage

```
getGammaMutRates(n, gmean = 1e-04, gstd = 1e-05)
```

Arguments

n	Number of loci to select rates for
gmean	Mean of the gamma distribution
gstd	Std Dev of the gamma distribution

Value

a vector of mutation rates (type numeric)

Examples

```
rates = getGammaMutRates(1000,gmean=0.0001, gstd=0.0001)
hist(rates)
rates = getGammaMutRates(1000,gmean=0.0001, gstd=0.00001)
hist(rates)
```

rmetasim.params-class *rmetasim Parameters Class*

Description

An S4 class storing parameters specific to rmetasim

Slots

num.stg a single integer for number of stages
 self.rate a single numeric for selfing rate
 surv.matr a matrix of numerics for survival transitions between stages
 repr.matr a matrix of integers for reproductive (females)
 male.matr a matrix of integers for male contribution (males)
 carrying a single integer for carrying capacity
 init.pop.sizes a vector of integers for initial starting population census sizes (length number of pop'ns)
 num.alleles a vector of integers for number of alleles per locus (length number of loci)
 allele.freq a vector of numerics for initial allele frequencies ???
 num.gen a single integer of number of generations to run

rms.convert *Extract genetic data from landscape object*

Description

Extract genetic data from landscape object

Usage

```
rms.convert(Rland, locus.type)
```

Arguments

Rland a rmetasim landscape object.
 locus.type character giving type of locus (microsat or sequence)

Value

A gtypes object containing genotypes (or sequences)

rms.init.landscape *Initialize a landscape object*

Description

Initialize a landscape object

Usage

```
rms.init.landscape(num.pops = NULL, carrying = NULL, sample.size = NULL,  
mig.rates = NULL, num.loc = NULL, loc.type = NULL, mut.rate = NULL,  
seq.length = NULL, num.stgs = NULL, selfing = NULL, surv.matr = NULL,  
repr.matr = NULL, male.matr = NULL, init.pop.sizes = NULL,  
num.gen = NULL, num.alleles = NULL, allele.freqs = NULL)
```

Arguments

num.pops	number of populations to simulate
carrying	maximum population sizes for each population
sample.size	size of sample to be pulled from each population
mig.rates	a list of among-population migration matrices
num.loc	number of independently segregating loci
loc.type	sequence or microsatellite
mut.rate	per gene mutation rate
seq.length	if simulating a sequence, the length of the molecule
num.stgs	number of demographic stages in a population
selfing	selfing rate (must range from 0 [random mating] to 1 [complete selfing])
surv.matr	within pop survival matrices
repr.matr	within pop reproduction matrices
male.matr	with pop male repro matrices
init.pop.sizes	starting population sizes
num.gen	number of generations to simulate
num.alleles	vector of the number of alleles per locus
allele.freqs	list of allele freqs for each locus (range 0-1)

`rms.init.landscape.func`

Initialize a landscape object

Description

Initialize a landscape object

Usage

```
rms.init.landscape.func(num.pops = NULL, carrying = NULL,
  sample.size = NULL, mig.rates = NULL, num.loc = NULL, loc.type = NULL,
  mut.rate = NULL, seq.length = NULL, num.stgs = NULL, selfing = NULL,
  surv.matr = NULL, repr.matr = NULL, male.matr = NULL,
  init.pop.sizes = NULL, num.gen = NULL, num.alleles = NULL,
  allele.freqs = NULL)
```

Arguments

<code>num.pops</code>	number of populations to simulate
<code>carrying</code>	maximum population sizes for each population
<code>sample.size</code>	size of sample to be pulled from each population
<code>mig.rates</code>	a list of among-population migration matrices
<code>num.loc</code>	number of independently segregating loci
<code>loc.type</code>	sequence or microsatellite
<code>mut.rate</code>	per gene mutation rate
<code>seq.length</code>	if simulating a sequence, the length of the molecule
<code>num.stgs</code>	number of demographic stages in a population
<code>selfing</code>	selfing rate (must range from 0 [random mating] to 1 [complete selfing])
<code>surv.matr</code>	within pop survival matrices
<code>repr.matr</code>	within pop reproduction matrices
<code>male.matr</code>	with pop male repro matrices
<code>init.pop.sizes</code>	starting population sizes
<code>num.gen</code>	number of generations to simulate
<code>num.alleles</code>	vector of the number of alleles per locus
<code>allele.freqs</code>	list of allele freqs for each locus (range 0-1)

rms.run	<i>Run rmetasim</i>
---------	---------------------

Description

Run rmetasim

Usage

rms.run(params)

Arguments

params a [skeleSim.params](#) object.

Value

a modified [skeleSim.params](#) object with the results of a rmetasim run.

rms.scenarioCheck	<i>Check parameters for rmetasim</i>
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Description

Check parameters for rmetasim

Usage

rms.scenarioCheck(params)

Arguments

params a [skeleSim.params](#) object.

skeleSim.checks	<i>Check all simulation parameters</i>
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Description

Check all simulation parameters

Usage

```
overall.check(params)
non.scenario.check(params)
gen.scenario.check(params)
analyses.check(analyses.requested)
```

Arguments

params a [skeleSim.params](#) object.
analyses.requested A named logical vector with elements named Global, Locus, and Pairwise

skeleSim.classes	<i>skeleSim Parameters Class</i>
------------------	----------------------------------

Description

An S4 class storing generic parameters used throughout the workflow

Slots

title a title for the simulation. Used in labelling of output files.
date datestamp for the simulation.
quiet logical determining whether to limit progress reports.
question a single character representing type of analytical question being addressed. Can be one of: (n)ull, p(o)wer, (p)erformance.
simulator.type a single character representing which type of simulator to use. Can be one of: (c)oaescent or (f)orward-time.
simulator a three character code representing which simulator is being run. Currently codes for fastsimcoal(fsc) and rmetasim(rms) exist.
scenarios a list of scenario.params objects.
num.sim.reps number of replicates to run.

`sim.func` a function that runs one replicate of the simulator. Must take and return only a `skeleSim.params` object.

`current.scenario` number of current scenario being run.

`current.replicate` number of current replicate within current scenario being run.

`rep.sample` result of last call to `sim.func`.

`rep.analysis.func` a function that analyzes the results of one simulation replicate.

`num.perm.reps` number of permutation replicates to run for population structure statistics.

`rep.result` result from last call to `rep.analysis.func`.

`analysis.results` a matrix containing result of all replicate analyses.

`sim.summary.func` a function to summarize `rep.analysis`.

`summary.results` a list containign result from call to `sim.summary.func`.

`sim.check.func` a function to check the parameters object prior to running the simualtions

`sim.scen.checks` a matrix containing results of 'checks' on scenario elements (T/F)

`timing` list containing elapsed time for a simulation

`other.checks` a vector containing results of 'checks' on other param object elements

`scenario.reps` a two column matrix describing which iteration matches which scenario/replicate

`analyses.requested` vector of logicals specifying "Global", "Locus", or "Pairwise" analyses have been requested.

`num.pops` number of populations.

`pop.size` a vector `num.pop` long giving size of each population.

`sample.size` a vector `num.pop` long giving the number of samples to take from each population.

`migration` a list of one or more `num.pop` x `num.pop` matrices giving the migration rates between each population.

`locus.type` a character representation of what type of marker to simulate. Can be "dna", "msat", or "snp".

`mig.helper` a list of flags and values that are needed for the shiny interface but are not needed for the simulation itself. Makes it easier to keep track of different ways to specify migration matrices for different scenarios. List elements will include migration model, rows and columns of landscape and distance function.

`num.loci` number of msat or snp loci to simulate.

`sequence.length` number of DNA base pairs to use.

`mut.rate` mutation rate for DNA or msat.

`simulator.params` an object storing simulator-specific parameters. Can be a list or a simulator-specific class.

skeleSim.internals *SkeleSim internal functions*

Description

SkeleSim internal functions

Usage

currentScenario(params)

currentLabel(params)

Arguments

params a [skeleSim.params](#) object.

Value

currentScenario	the parameters for the current scenario.
currentLabel	a character label representing current scenario and replicate.

skeleSimGUI *GUI for skeleSim system*

Description

This function starts the shiny simulation control panel

Usage

skeleSimGUI(launch.browser = TRUE)

Arguments

launch.browser If true, the system's default web browser will be launched automatically after the app is started.

Value

NULL

markdown and shinyFiles import added for shiny app

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