Package ‘popgen’

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Title Population genetic simulations & numerical analysis

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Imports

Suggests

ZipData no

Description popgen conducts various numerical analyses and simulations in population genetics and evolutionary theory.

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URL `http://faculty.umb.edu/liam.revell/`

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R topics documented:

`founder.event` *Simulation of a founder event*

Description

This function simulates genetic drift with a founding event at time `etime`.

Usage

```
founder.event(p0=0.5,Ne=1000,Nf=10,ttime=100,etime=50,show="p")
```

Arguments

`p0`	Starting frequency for the A allele.
`Ne`	Effective population size at the start of the simulation and after the founding event.
`Nf`	Size of the founding population.
`ttime`	Total time of the simulation.
`etime`	Time for the founding event.
`show`	Two different options for plotting. `"p"` shows the frequency of the A allele through time; `"var"` shows the genetic variation in the population, calculated as p*(1-p). The default is `show="p"`.

Value

The function creates one of two different plots, depending on the value of `show`.

Author(s)

Liam Revell <`liam.revell@umb.edu`>

See Also

`genetic.drift`

Examples

```
founder.event()
founder.event(show="variation")
```

`freqdep` *Numerical analysis of a frequency dependent seletion model*

Description

This function performs numerical analysis of a frequency dependent selection model based on Rice (*Evolutionary Theory*). The fitnesses of the three genotypes in the model are as follows, where f(*XX*) denotes the frequency of the *XX* genotype: w(AA)=1-3*f(Aa)+3*f(aa); w(Aa)=1-s*f(Aa); w(aa)=1-3*f(Aa)+3*f(AA).

Usage

```
freqdep(p0=0.01,s=0,time=100,show="p",pause=0)
```

Arguments

`p0`	Starting frequency for the A allele.
`s`	Parameter that determines the strength of selection against heterozygotes when they are common.
`time`	Number of generations to run the analysis.
`show`	Various options for plotting. `"p"` shows the frequency of A through time; `"surface"` plots the mean fitness as a function of p; `"deltap"` shows the change in p as a function of p; `"cobweb"` creates a cobweb plot showing p(t) by p(t+1). The default is `show="p"`.
`pause`	Pause between generations. `pause=0.01` (for instance) might smooth animation.

Value

The function creates one of several possible plots, depending on the value of `show`.

Author(s)

Liam Revell <`liam.revell@umb.edu`>

See Also

`sexratio`

Examples

```
freqdep(time=100)
freqdep(s=1.5,time=100)
freqdep(s=2,show="cobweb",time=100)
```

`genetic.drift` *Genetic drift simulation*

Description

This function simulates genetic drift at a biallelic genetic locus with no selection and no mutation in a sexually reproducing diploid population or set of populations.

Usage

```
genetic.drift(p0=0.5,Ne=20,nrep=10,time=100,show="p",pause=0.1)
```

Arguments

`p0`	Starting frequency for the A allele.
`Ne`	Effective population size.
`nrep`	Number of replicate simulations.
`time`	Total time, in number of generations, for the simulation.
`show`	Various options for plotting. `"p"` shows the frequency of the A allele through time; `"genotypes"` creates an animated histogram with the frequencies of each of the three genotypes through time; `"fixed"` shows the fraction of populations that have fixed for each allele, a or A; `"heterozygosity"` plots the mean heterozygosity and the expected heterozygosity through time. The default is `show="p"`.
`pause`	Pause between generations. `pause=0.01` (for instance) might smooth animation.

Value

The function creates one of several possible plots, depending on the value of `show`.

Author(s)

Liam Revell `<liam.revell@umb.edu>`

See Also

`founder.event`, `selection`

Examples

```
genetic.drift()
genetic.drift(p0=0.7,show="heterozygosity")
```

`mutation.selection` *Gene frequencies over time under mutation-selection balance*

Description

This function performs numerical analysis of mutation-selection balance with mutation from A to a and selection against (either or both of) Aa and aa.

Usage

```
mutation.selection(p0=1.0,w=c(1,1),u=0.001,time=100,show="q",pause=0,ylim=c(0,1))
```

Arguments

`p0`	Starting frequency for the A allele.
`w`	Fitnesses of the heterozygote (Aa) and homozygote deleterious (aa) genotypes. The fitness of AA is assumed to be 1.0.
`u`	Rate at with A mutates to a.
`time`	Number of generations to run the analysis.
`show`	Two options for plotting. `"q"` shows the frequency of a through time; `"fitness"` plots the mean fitness over time. The default is `show="q"`.
`pause`	Pause between generations. `pause=0.01` (for instance) might smooth animation.
`ylim`	Limits on the y-axis for plotting.

Value

The function creates one of two possible plots, depending on the value of `show`.

Author(s)

Liam Revell `<liam.revell@umb.edu>`

See Also

`genetic.drift`, `selection`

Examples

```
mutation.selection(w=c(1,0),time=100,ylim=c(0,0.1))
```

`rcd` *Simulation of reproductive character displacement in an ecological community*

Description

This function conducts individual-based, genetically explicit numerical simulation of reproductive character displacement in an ecological community. The model is one of multiple species (with fixed relative abundance) competing to utilize the same signal space. There is both stabilizing selection on the signal trait for detectability, as well as (in multi-species simulations) countervailing selection for divergence due to the costs of erroneous mismating attempts.

Usage

```
rcd(nsp=3,nindivs=c(700,400,100),w_t=10,gen=c(500,500),figs="on",pf=100)
```

Arguments

`nsp`	Number of species in the simulation. If `figs="on"`, `nsp` must be 1, 2, or 3.
`nindivs`	A vector of length `nsp` containing the integer number of individuals in each species of the simulation.
`w_t`	Shape parameter of the Gaussian selection surface for the male signalling trait.
`gen`	Vector containing the number of allopatric generations followed by the number of sympatric generations for simulation.
`figs`	Either `"on"` if plotting is turned on, or `"off"` to suppress plotting.
`pf`	Print frequency for the simulation status to screen.

Value

The function returns a list containing the mean male signal trait and the mean female preference over time. It also (optionally) plots these.

Author(s)

Liam Revell <`liam.revell@umb.edu`>

See Also

`genetic.drift`, `selection`

Examples

```
## Not run: X<-rcd(nsp=2,nindivs=c(500,500))
```

`selection` *Numerical analysis of biallelic locus frequency independent selection*

Description

This function performs numerical analysis of a simple biallelic selection model.

Usage

```
selection(p0=0.01,w=c(1.0,0.9,0.8),time=100,show="p",pause=0)
```

Arguments

`p0`	Starting frequency for the A allele.
`w`	Fitnesses for the three genotypes in the following order: AA, Aa, aa.
`time`	Number of generations to run the analysis.
`show`	Various options for plotting. `"p"` shows the frequency of A through time; `"surface"` plots the mean fitness as a function of p; `"deltap"` shows the change in p as a function of p; `"cobweb"` creates a cobweb plot showing p(t) by p(t+1). The default is `show="p"`.
`pause`	Pause between generations. `pause=0.01` (for instance) might smooth animation.

Value

The function creates one of several possible plots, depending on the value of `show`.

Author(s)

Liam Revell <`liam.revell@umb.edu`>

See Also

`freqdep`

Examples

```
selection(w=c(1.0,0.8,0.8),time=500)
selection(w=c(1.0,1.0,0.0),show="surface")
```

`sexratio` *Hypothetical analysis of frequency dependent selection on a sex determining genetic locus*

Description

This function performs numerical analysis of a frequency dependent selection model of a hypothetical diploid sexually reproducing population in which sex is determined by the genotype at a biallelic genetic locus. Genotype AA are male, genotype aa are female, and genotype Aa might be male or female with equal probability.

Usage

```
sexratio(p0=0.01,time=100,show="p",pause=0)
```

Arguments

`p0`	Starting frequency for the A allele. Individuals with AA genotypes are male, while individuals with Aa genotypes are male or female with equal probability.
`time`	Number of generations to run the analysis.
`show`	Two different options for plotting. `"p"` shows the frequency of A through time; `"fitness"` plots the mean fitness through time. The default is `show="p"`.
`pause`	Pause between generations. `pause=0.01` (for instance) might smooth animation.

Value

The function creates one of two possible plots, depending on the value of `show`. Numerical analysis of this model shows how frequency dependent selection should favor alleles that tend to produce the rarer sex in the population.

Author(s)

Liam Revell <`liam.revell@umb.edu`>

See Also

`sexratio`

Examples

```
sexratio(time=100)
```

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