Package ‘AFLPsim’

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Description This package is developed in the Plant Reproductive Biology Lab (RNM-214) - University of Seville. It contains hybrid simulation functions for dominant genetic data. It also provides several genome scan methods.
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Description

This package is developed in the Plant Reproductive Biology Lab (RNM-214) - University of Seville. It contains hybrid simulation functions for dominant genetic data. It also provides several genome scan methods.

More information on AFLPsim can be found at https://github.com/fbalao/AFLPsim.

To cite AFLPsim, please use citation("AFLPsim")

Details

Package: AFLPsim
Type: Package
Version: 0.3-4
Date: 2013-12-23
License: GPL (>= 2)

Author(s)

Francisco Balao; Juan Luis Garcia-Castaño
Description

This function calls Bayescan program from within R to identifying candidate loci under natural selection from genetic data.

Usage

bayescan(mat, filename, nbp = 20, pilot = 5000, burn = 50000, exec=NULL)

Arguments

mat A matrix with genotypic data to test in hybridsim format
filename a character string giving the name of the output file (without extension)
nbp Number of pilot runs (default is 2)
pilot Length of pilot runs (default is 50)
burn Burnin length (default is 5000)
exec a character string giving the path to BAYESCAN. By default it tries to guess it depending on the operating system (see details).

Details

bayescan tries to guess the name of the executable program depending on the operating system. Specifically, the followings are used: "bayescan_2.1" under Linux and Mac, or "C:/Program Files/BayeScan2.1/binaries/BayeScan2.1_win32bits_cmd_line.exe" under Windows.

Value

Several files with the results and a data.frame with the following variables:

prob The posterior probability for the model including selection
log10.P0. The logarithm of Posterior Odds to base 10
qval q-values for each locus for the model including selection
alpha The estimated alpha coefficient indicating the strength and direction of selection. See Bayescan 2.1 manual
fst The Fst coefficient averaged over populations

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

References


See Also

gscan sim2bayescan
### Description
This model simulates the proportions of parentals, F1, F2, Fx and backcross (on both sides) individuals for each generation and takes into account the initial frequencies of parentals, the assortative mating among taxa as well as fitness differences.

### Usage
```r
demosimhybrid(x, M, F)
```

### Arguments
- **x**: A vector indicating the initial abundances in the population. The vector should sum 1. The order of abundances is: ParentalA, ParentalB, F1, BxA, BxB and Fx.
- **M**: Matrix assortative mating. The size is 6x6 following the same order than vector x. By default random mating (all = 1).
- **F**: A vector indicating the different fecundities of the parentals and hybrids. The vector size is 6 following the same order than vector x. By default equal fecundities (all = 1).

### Details
This function simulate the model of introgressive hybridization of Epifanio and Philipp (2000).

### Value
A object `demosimhybrid`. An matrix of abundances in each generation.

### Author(s)
Francisco Balao `<fbaalo@us.es>`; Marcial Escudero; J.L. García-Castaño

### References
**gscan**

**See Also**

hybridsim  
plot.demosimhybrid

**Examples**

```r
## Example 1. Simulation under parental proportions,
## similar fecundities and random mating
inivalues<-c(0.5,0.5,0,0,0,0)
epi0.5<-demosimhybrid(inivalues)
epi0.5

## Example 2. Simulation under higher frequency of parental B,
## and higher fecundity of parental A and random mating
inivalues2<-c(0.25,0.75,0,0,0,0)
fecundities<-c(1,0.5,0.5,0.5,0.5,0.5)
epi0.75<-demosimhybrid(x=inivalues, F=fecundities)
epi0.75
```

**gscan**

*Genome scan for hybrids*

**Description**

This function fits genomic scan to dominant genotypic data using the method described by *Gagnaire et al (2009)* and the new method by Balao et al (2013; *in preparation*). Significance testing for outlier loci is included.

**Usage**

```r
gscan(mat, type=c("F1","BxA","BxB"), method=c("bal&gar-ca","gagnaire"))
```

**Arguments**

- `mat`:
  - an object of class 'hybridsim' produced by 'hybridsim' or 'hybridize' functions

- `type`:
  - the type of hybrid classes; either "F1", "BxA" or "BxB"

- `method`:
  - a character string specifying the method to test significance of outlier loci; either "gagnaire" or "bal&gar-ca". See Details.
Details

These genome scan methods calculate the null distribution of frequencies under a neutral model.

Gagnaire’s method uses a binomial test to outlier significance. For more conservative and unbiased method, "Bal&gar-car" method calculates the 95% confidence expected hybrid frequencies by the Clopper-Pearson 'exact' procedure (Clopper & Pearson 1934; Brown et al. 2001).

In both methods, the False Discovery Rate (FDR) correction (Benjamini & Hochberg 1995) is used to counteract for multiple comparisons and control the expected proportion of incorrectly rejected null hypotheses.

Value

A list with the following components:

- `pMvalues`: a matrix with P values after False Discovery Rate correction for each loci
- `Outlier`: a vector with outliers

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

References


See Also

hybridsim

Examples

```r
hybrids<-hybridsim(Nmarker=100, Na=30, Nb=30, Nf1=30, type="selection", S=5,Nsel=25, hybrid="F1")
outliers<-gscan(hybrids, type="F1", method="bal&gar-ca")
```
**hybridindex**

**Estimate hybrid index for hybridsim objects**

---

**Description**

This function finds maximum likelihood estimates of hybrid index as described by *Buerkle (2005)* using the packages `introgress`

**Usage**

`hybridindex(data)`

**Arguments**

- `data`: an `hybridsim` object with the profiles of parentals and hybrids.

**Details**

`hybridindex` returns a hybrid index estimate with its 95% confidence interval. See *est.h* and *Buerkle (2005)* for additional details.

**Value**

A data frame with estimates of hybrid index and upper and lower limits of its 95% confidence intervals, which falls within two support units of the maximum-likelihood estimate:

- `lower`: 95% confidence interval lower limit.
- `h`: Maximum-likelihood estimate of the hybrid index.
- `upper`: 95% confidence interval upper limit.

**Author(s)**

F. Balao <fbalao@us.es>; J.L. García-Castaño

**References**


**See Also**

`est.h`
Examples

```r
## simulate parentals and F1 hybrids
hybrids<-hybridsim(Nmarker=50, Na=10, Nb=10, Nf1=10, type="neutral", hybrid="F1")

## estimate hybrid index
hest<-hybridindex(hybrids)
```

---

**Description**

This function simulates AFLP profiles (or other dominant markers) of several hybrid classes (F1 and backcrosses on both parentals) from two parental populations. In addition, selection on several markers can be simulated for the hybrid progeny.

**Usage**

```r
hybridize(pa,pb,Nf1, Nxba = Nf1, Nxb = Nf1, Nf2 = Nf1, type = "selection", hybrid = "all", Nsel = Nmarker * 0.1, S = 0)
```

**Arguments**

- **pa**: AFLP profile of Parental A. A data.frame or matrix.
- **pb**: AFLP profile of Parental B. A data.frame or matrix.
- **Nf1**: number of AFLP profiles for F1.
- **Nxba**: number of AFLP profiles for BxA.
- **Nxb**: number of AFLP profiles for BxA.
- **Nf2**: number of AFLP profiles for F2.
- **type**: type of simulation: 'neutral' or 'selection'.
- **hybrid**: hybrid classes to simulate. By default 'all'. Also 'F1', 'BxA', 'BxB' or 'F2'.
- **Nsel**: number of loci under selection.
- **S**: Selection coefficient (see Details)

**Details**

Simulates F1, F2, Backcross to Parental A (BxA) and Backcross to Parental B (BxB) with and without selection. Parental profiles must be included (individuals in rows and markers in columns). The selection coefficient \( S \) is an integer value from -1 to \( \infty \). This coefficient is 0 when there is no selection (similar to type = "neutral") and it varies following negative and positive directional selection (negative and positive values, respectively).
**Value**

Object `hybridsim` with:

- `PA`: Parental A AFLP profile
- `PB`: Parental B AFLP profile
- `F1`: F1 hybrid AFLP profile
- `F2`: F2 hybrid AFLP profile
- `BxA`: Backcross to Parental A AFLP profile
- `BxB`: Backcross to Parental B AFLP profile
- `Nsel`: Loci under selection (default, under neutral selection)
- `S`: Selection coefficient

**Author(s)**

F. Balao <fbalao@us.es>, J.L. García-Castaño

**References**


**See Also**

`hybridsim`

**Examples**

```r
## AFLP profile Species A
SpeciesA<-read.table(system.file("/files/SpeciesA.txt",package="AFLPsim"),header=TRUE, row.names=1)

## AFLP profile Species B
SpeciesB<-read.table(system.file("/files/SpeciesB.txt",package="AFLPsim"),header=TRUE, row.names=1)

## simulate F1 hybrids
F1hybrids<-hybridize(pa=SpeciesA,pb=SpeciesB, Nf1=30, type="neutral", hybrid="F1")
```
hybridsim

AFLP simulator with selection

Description

This function simulates AFLP profiles (or other dominant markers) of parentals and several hybrid classes (F1 and backcrosses on both parentals). In addition, selection on several markers can be simulated for the hybrid progeny.

Usage

hybridsim(nmarker, Na, Nb, Nf1, Nbxa = Nf1, Nxb = Nf1, Nf2 = Nf1, type = "selection", hybrid = "all", Nsel = nmarker * 0.1, S = 0, apa = 0.5, apb = 0.5)

Arguments

- nmarker: The number of AFLP loci to simulate.
- Na: number of AFLP profiles for Parental A.
- Nb: number of AFLP profiles for Parental B.
- Nf1: number of AFLP profiles for F1.
- Nbxa: number of AFLP profiles for BxA.
- Nxb: number of AFLP profiles for BxB.
- Nf2: number of AFLP profiles for F2.
- type: type of simulation: 'neutral' or 'selection'.
- hybrid: hybrid classes to simulate. By default 'all'. Also 'F1', 'BxA', 'BxB' or 'F2'.
- Nsel: number of loci under selection.
- S: Selection coefficient (see Details)
- apa: value for parameter 1 of the beta distribution
- apb: value for parameter 2 of the beta distribution

Details

Simulate dominant markers (AFLP, RFLP...). Parental allele frequencies are calculated following a beta distribution (Wright 1931). F1, F2, Backcrosses to parental A (BxA) and Backcrosses to parental b (BxB) can be simulated with and without selection. The selection coefficient S is a integer value from -1 to ∞. This coefficient is 0 when there is no selection (similar to type = "neutral") and it varies following negative and positive directional selection (negative and positive values, respectively).
Value

Object hybridsim with:

- PA: AFLP profile parental population A
- PB: AFLP profile parental population A
- F1: AFLP profile F1 hybrid population
- F2: AFLP profile F2 hybrid population
- BxA: AFLP profile Backcrosses to parental population A
- BxB: AFLP profile Backcrosses to parental population B
- Nsel: Loci under selection. NA under neutral selection
- S: Selection Coefficient

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

References


See Also

- hybridize

Examples

```r
hybrids <- hybridsim(Nmarker=100, Na=30, Nb=30, Nf1=30, type="selection", S=10, Nsel=25, hybrid="F1")
```

Description

A *demosimhybrid* object can be plotted using the function `plot.demosimhybrid`, which is also used as the dedicated plot method. This function plots the frequency of parentals and hybrid classes on each generation.

Usage

```r
## S3 method for class 'demosimhybrid'
plot(x, col = c(2, 3, 4, "orange", "orchid", 7), ...)
```
Arguments

- **x**: a `demosimhybrid` object.
- **col**: the colors for the hybrid classes.
- **...**: Arguments to be passed to methods, such as graphical parameters (see `par`).

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

See Also

demosimhybrid

Examples

```r
## Example 1. Simulation under parental proportions,
## similar fecundities and random mating
inivalues<-c(0.5,0.5,0,0,0)
epi0.5<-demosimhybrid(inivalues)
epi0.5
plot.demosimhybrid(epi0.5)

## Example 2. Simulation under higher frequency of Parental B,
## and higher fecundy of Parental A and random mating
inivalues2<-c(0.25,0.75,0,0,0)
fecundities<-c(1,0.5,0.5,0.5,0.5,0.5)
epi0.75<-demosimhybrid(x=inivalues2, F=fecundities)
epi0.75
plot.demosimhybrid(epi0.75)
```

Description

A `hybridsim` object can be plotted using the function `plot.h Hybridsim`, which is also used as the dedicated plot method. This function represents expected hybrid markers frequencies on a neutral sheet.

Usage

```r
## S3 method for class 'hybridsim'
plot(x, hybrid = c("F1", "BxA", "BxB"), col = "lightgreen",
     shade = 0.8, markers = x$SelMarkers, ...)
```
sim2arlequin

Arguments

x A hybridsim object.
hybrid The hybrid classes to simulate: "F1", "BxA" or "BxB".
col A specification for the default plotting color.
shade A specification for the default alpha value.
markers a numeric vector with markers to plot. By default markers under selection by hybridsim function.
... Arguments to be passed to methods, such as graphical parameters (see par).

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

See Also

hybridsim hybridize

Examples

### simulate parentals and F1 hybrids
hybrids<-hybridsim(Nmarker=100, Na=30, Nb=30, Nf1=30, type="selection", S=1, Nsel=25, hybrid="F1")
plot.hybridsim(hybrids, hybrid="F1")

---

**Description**

The function sim2arlequin converts a hybridsim object into a Arlequin input file.

**Usage**

sim2arlequin(x, filename)

**Arguments**

x a hybridsim object
filename a character string indicating the name of the output file

**Value**

Arlequin input file

**Author(s)**

F. Balao <fbalao@us.es>, J.L. García-Castaño
References


See Also

sim2bayescan sim2introgress sim2newhybrids sim2popgene sim2structure

Examples

```r
## simulate F1 hybrids
F1hybrids<-hybridsim(Nmarker=100,Na=100,Nb=100,Nf1=30, type="neutral", hybrid="F1")

## convert to Arlequin input file
sim2arlequin(F1hybrids,filename="F1hybrids_Arlequin.txt")
```

Description

The function sim2bayescan converts a hybridsim object into a Bayescan (Foll & Gaggiotti 2008) input file.

Usage

```r
sim2bayescan(x,filename)
```

Arguments

- `x`  
  a hybridsim object. Only with F1 hybrids
- `filename`  
  a character string indicating the name of the output file

Value

Bayescan input file

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

References

**sim2genind**

**See Also**

`sim2arlequin sim2introgress sim2newhybrids sim2popgene sim2structure`

**Examples**

```r
## simulate F1 hybrids
F1hybrids <- hybridsim(Nmarker=100, Na=100, Nb=100, Nf1=30, type="selection", S=5, Nsel=25, hybrid="F1")

## convert to Bayescan input file
sim2bayescan(F1hybrids, filename="F1hybrids_Bayescan.txt")
```

---

**Description**

The function `sim2genind` converts a `hybridsim` object into a `genind` object of the package `adegenet`. It is wrapper of the function `df2genind`

**Usage**

```r
sim2genind(x)
```

**Arguments**

- `x` a `hybridsim` object

**Value**

A `genind` object

**Author(s)**

F. Balao `<fbalao@us.es>`, J.L. García-Castaño

**See Also**

`genind df2genind`

**Examples**

```r
## simulate F1 hybrids
F1hybrids <- hybridsim(Nmarker=100, Na=100, Nb=100, Nf1=30, type="neutral", hybrid="F1")

## convert to genind object
F1gen <- sim2genind(F1hybrids)
```
Description

The function sim2introgress converts a hybridsim object into an introgress input file. It is a wrapper to the function `prepare.data` of the package `introgress`.

Usage

```r
sim2introgress(x)
```

Arguments

- `x` a `hybridsim` object

Value

a list returned by the function `prepare.data` of the package `introgress`

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

References


See Also

`prepare.data` `sim2arlequin` `sim2bayescan` `sim2newhybrids` `sim2popgene` `sim2structure`  

Examples

```r
## simulate hybrids
hybrids<-hybridsim(Nmarker=100,Na=100,Nb=100,NF1=30, type="selection", hybrid="all")

## convert to introgress input file
hybrids2<-sim2introgress(hybrids)
```
Function \texttt{sim2newhybrids} converts a \texttt{hybridsim} object into a NewHybrids input file.

\begin{verbatim}
Usage
  sim2newhybrids(x, filename)

Arguments
  x   a \texttt{hybridsim} object
  filename a character string indicating the name of the output file

Value
  a NewHybrids input file

Author(s)
  F. Balao <fbalao@us.es>, J.L. García-Castaño

References

See Also
  \texttt{sim2arlequin sim2bayescan sim2introgress sim2popgene sim2structure}

Examples
  ## simulate hybrids
  hybrids <- hybridsim(Nmarker=100, Na=30, Nb=30, Nf1=30, type="neutral", hybrid="all")

  ## convert to NewHybrids input file
  sim2newhybrids(hybrids, filename="newhybridsinput.txt")
\end{verbatim}
sim2popgene  

Converting hybridsim object to a PopGene input file

Description

The function `sim2popgene` converts a hybridsim object into a PopGene input file.

Usage

```r
sim2popgene(x, filename)
```

Arguments

- `x`: a `hybridsim` object
- `filename`: a character string indicating the name of the output file

Value

a PopGene input file

Author(s)

F. Balao <fbalao@us.es>, J.L. García-Castaño

References


See Also

`sim2arlequin` `sim2bayescan` `sim2introgress` `sim2newhybrids` `sim2structure`

Examples

```r
## simulate F1 hybrids
F1hybrids <- hybridsim(Nmarker=100, Na=100, Nb=100, Nf1=30, type="neutral", hybrid="F1")

## convert to genepop input file
sim2popgene(F1hybrids, filename="F1hybrids_Popgene.txt")
```
**sim2structure**

*Convert a hybridsim object to a STRUCTURE input file*

**Description**

The function `sim2structure` converts a hybridsim object into a Structure 2.3 input file.

**Usage**

```r
sim2structure(x, filename)
```

**Arguments**

- `x`  
a hybridsim object
- `filename`  
a character string indicating the name of the output file

**Value**

a Structure input file

**Author(s)**

F. Balao <fbalao@us.es>, J.L. García-Castaño

**References**


**See Also**

`sim2arlequin` `sim2bayescan` `sim2introgress` `sim2newhybrids` `sim2popgene`

**Examples**

```r
## simulate F1 hybrids
F1hybrids<-hybridsim(Nmarker=30,Na=30,Nb=100,NF1=30, type="neutral", hybrid="F1")

## convert to STRUCTURE input file
sim2structure(F1hybrids, filename="F1hybrids_Structure.txt")
```
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