

Package ‘HaploVectors’

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Type Package

Title HaploVectors an Integrative Analytical Tool for Phylogeography

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Description Function to extract haplotypic eigenvectors and perform null model-based tests (available at <<https://github.com/vanderleidebastiani/HaploVectors>>).

License GPL (>= 2)

Encoding UTF-8

Depends PCPS (>= 1.0.7)

Imports ape, pegas, reshape

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'pcps.sig.mod.R' 'mutate.names.matrix.p.null.R'
'print.HaploVectors.R'

NeedsCompilation no

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HaploNetDist

*HaploNetDist***Description**

Function to extract haplotypes, compute pairwise distances between haplotypes, build haplotypic networks and compute the frequency of each haplotype per locality.

Usage

```
HaploNetDist(x, pop, dist.model = "N", checkdata = TRUE, ...)
```

Arguments

x	A set of DNA sequences (as an object of class "DNABin" or "haplotype") as used by the function haplotype .
pop	A matrix describing the incidence of each individual (columns) in a given locality (rows).
dist.model	A character string used by the function dist.dna to specify the evolutionary model to be used to compute pairwise distances from DNA sequences (default dist.model = "N").
checkdata	Logical argument (TRUE or FALSE) to check if individual sequences in the pop data follow the same order as in the set of DNA sequences (Default checkdata = TRUE).
...	Additional arguments to the function dist.dna .

Value

A list with:

call	Arguments used.
haplotypes	A list with haplotypes indices that identify each observation sharing the same haplotype.
haplotype.distances	A matrix with pairwise distances between haplotypes.
haplotype.per.locality	A matrix with the frequency of each haplotype per locality (W).
haplotype.network	A matrix with haplotype connections described in the network (D_n).

See Also

[HaploVectors](#)

Examples

```
data(sehv)
HaploNetDist(sehv$sehv.fas, sehv$sehv.pi)
```

HaploVectors

*HaploVectors***Description**

Function to extract haplotypic eigenvectors and perform null model-based tests.

Usage

```
HaploVectors(x, pop, dist.model = "N", log.frequencies = TRUE,
  squareroot.network = TRUE, method = "euclidean",
  squareroot.dis = TRUE, choices = c(1, 2), analysis = "none", FUN,
  envir, choices.analysis, runs = 999, ...)
```

```
## S3 method for class 'HaploVectors'
print(x, ...)
```

Arguments

x	A set of DNA sequences (as an object of class "DNABin" or "haplotype") as used by the function haplotype .
pop	A matrix describing the incidence of each individual (columns) in a given locality (rows).
dist.model	A character string used by the function dist.dna to specify the evolutionary model to be used to compute pairwise distances from DNA sequences (default dist.model = "N").
log.frequencies	Logical argument (TRUE or FALSE) to specify if transformation of natural logarithms plus one in haplotype per locality data must be applied (Default log.frequencies = TRUE).
squareroot.network	Logical argument (TRUE or FALSE) to specify if apply square root on haplotype network (Default squareroot.network = TRUE).
method	Dissimilarity index to apply in matrix P, which describes localities by their haplotypic composition, as accepted by vegdist function in vegan package (Default method = "euclidean").
squareroot.dis	Logical argument (TRUE or FALSE) to specify if use square root of dissimilarity index in matrix P (Default squareroot.dis = TRUE).
choices	Axes for re-scaling. Choices must have length equal to two (Default choices = c(1, 2)).
analysis	Type of analysis, partial match to "none", "haplotypic" or "haplovector" (Default analysis = "none").
FUN	An object of class function to perform the analysis. See Details and Examples.
envir	A matrix with environmental variables for each population, with variables as columns and localities as rows. See Details and Examples.
choices.analysis	Numeric vector to choose the haplo vectors used in analysis. See Details and Examples.
runs	Number of permutations for assessing probability of type I error.
...	Additional arguments to function matrix.p.sig and pcps.sig .

Details

The argument *analysis* specify the type of analysis performed. When *analysis* is equal "haplotypic" the analysis is performed in matrix of haplotypic composition (using `matrix.p.sig` function). The argument *formula* can be specified, where the left hand side gives the resemblance data, right hand side gives the variables. The resemblance data is internally named *p.dist*, thus formula is an expression of the form *p.dist ~ model*. If *analysis* is equal "haplovector" it is performed with haplovector (using `pcps.sig` function). In this case, the argument *formula* can be specified, where the left hand side gives the vectors used, right hand side gives the variables. The vectors are internally named sequentially *haplovector.1*, *haplovector.2*, *haplovector.3* and so on. Thus, formula is an expression of the form *haplovector.1 ~ model*. All functions and methods available in `matrix.p.sig` or `pcps.sig` could be used here, considering the differences mentioned above.

Value

A list with:

<code>call</code>	Arguments used.
<code>haplotypes</code>	A list with haplotypes index that identify each observation that share the same haplotype.
<code>haplotype.distances</code>	A matrix with pairwise distances between haplotypes.
<code>haplotype.per.locality</code>	A matrix with frequency of each haplotype per locality (W).
<code>haplotype.network</code>	A matrix with haplotype connections described in the network (D_n).
<code>vectors</code>	Haplotypic eigenvectors (haplovector).
<code>values</code>	Eigenvalues, relative eigenvalues and cumulative relative eigenvalues.
<code>correlations</code>	Correlations between haplotypic eigenvectors and haplotypes.
<code>P</code>	Matrix of haplotypic composition (P).
<code>scores.haplotypes</code>	Scores for biplots.
<code>model</code>	The observed model returned by FUN.
<code>fun</code>	The funtion used.
<code>statistic.null.site</code>	A matrix with null statistic for site shuffle null model.
<code>statistic.null.taxa</code>	A matrix with null statistic for taxa shuffle null model.
<code>statistic.obs</code>	Observed statistic, F value to predefined function.
<code>p.site.shuffle</code>	The p value for the site shuffle null model.
<code>p.taxa.shuffle</code>	The p value for the taxa shuffle null model.

See Also

[HaploNetDist](#)

Examples

```
data(sehv)

HaploVectors(sehv$sehv.fas, sehv$sehv.pi, envir = sehv$sehv.envir)

HaploVectors(sehv$sehv.fas, sehv$sehv.pi, analysis = "haplotypic", FUN = FUN.ADONIS,
  envir = sehv$sehv.envir, formula = p.dist~R,
  method.p = "euclidean", sqrt.p = TRUE, runs = 99)

HaploVectors(sehv$sehv.fas, sehv$sehv.pi, analysis = "haplotypic", FUN = FUN.ADONIS2.global,
  envir = sehv$sehv.envir, formula = p.dist~R,
  method.p = "euclidean", sqrt.p = TRUE, runs = 99)

HaploVectors(sehv$sehv.fas, sehv$sehv.pi, analysis = "haplovector", FUN = FUN.GLM,
  envir = sehv$sehv.envir, choices.analysis = 1,
  formula = haplovector.1~R, runs = 99)
```

matrix.p.sig.mod

Internal functions

Description

Internal functions with small modifications of [matrix.p.sig](#) and [pcps.sig](#).

Usage

```
matrix.p.sig.mod(comm, phylodist, FUN, runs = 999, parallel = NULL,
  ...)

pcps.sig.mod(comm, phylodist, method = "bray", squareroot = TRUE, FUN,
  choices, runs = 999, parallel = NULL, ...)

mutate.names.matrix.p.null(x, replacement, newname)
```

Arguments

comm	Community data, with species as columns and sampling units as rows.
phylodist	Matrix containing phylogenetic distances between species.
FUN	An object of class function to perform the analysis.
runs	Number of permutations for assessing significance.
parallel	Number of parallel processes or a predefined socket cluster done with parallel package.
...	Other arguments passed to FUN function.
method	Dissimilarity index.
squareroot	Logical argument (TRUE or FALSE) to specify if use square root of dissimilarity index.
choices	Numeric vector to choose the axis used in analysis.
x	An object returned by matrix.p.null .
replacement	A replacement name to matched in object returned by matrix.p.null .
newname	New name to be replaced in object returned by matrix.p.null .

`sehv`*sehv - Simple Example for HaploVectors*

Description

Hypothetical data for running examples.

Usage

```
data(sehv)
```

Format

A list with:

sehv.fas An object of class DNABin with 18 DNA sequences.

sehv.pi A matrix describing the incidence of each individual (columns) in a given locality (rows).

sehv.envir A matrix with one environmental variable describing each locality.

Examples

```
data(sehv)
sehv
```

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