

Package ‘HaploVectors’

May 24, 2018

Type Package

Title HaploVectors an Integrative Analytical Tool for Phylogeography

Version 0.0.1

Date 2018-05-24

Author Leandro da Silva Duarte, Jacqueline de Souza Lima, Renan Maestri, Vanderlei Julio Debastiani and Rosane Garcia Collevatti

Maintainer Vanderlei Julio Debastiani <vanderleidebastiani@yahoo.com.br>

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

License GPL (>= 2)

Imports ape, pegas, reshape, PCPS

RoxygenNote 6.0.1

NeedsCompilation no

R topics documented:

HaploNetDist	1
HaploVectors	2
sehv	4
Index	6

HaploNetDist	<i>HaploNetDist</i>
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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

<code>x</code>	A set of DNA sequences (as an object of class "DNABin" or "haplotype") as used by the function haplotype .
<code>pop</code>	A matrix describing the incidence of each individual (columns) in a given locality (rows).
<code>dist.model</code>	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 <code>dist.model = "N"</code>).
<code>checkdata</code>	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 <code>checkdata = TRUE</code>).
<code>...</code>	Additional arguments to the function dist.dna .

Value

A list with:

<code>call</code>	Arguments used.
<code>haplotypes</code>	A list with haplotypes indices that identify each observation sharing the same haplotype.
<code>haplotype.distances</code>	A matrix with pairwise distances between haplotypes.
<code>haplotype.per.locality</code>	A matrix with the frequency of each haplotype per locality (W).
<code>haplotype.network</code>	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", envir, formula, AsFactors = NULL,
  runs = 999, ...)
```

Arguments

<code>x</code>	A set of DNA sequences (as an object of class "DNABin" or "haplotype") as used by the function haplotype .
<code>pop</code>	A matrix describing the incidence of each individual (columns) in a given locality (rows).
<code>dist.model</code>	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 <code>dist.model = "N"</code>).
<code>log.frequencies</code>	Logical argument (TRUE or FALSE) to specify if transformation of natural logarithms plus one in haplotype per locality data must be applied (Default <code>log.frequencies = TRUE</code>).
<code>squareroot.network</code>	Logical argument (TRUE or FALSE) to specify if apply square root on haplotype network (Default <code>squareroot.network = TRUE</code>).
<code>method</code>	Dissimilarity index to apply in matrix P, which describes localities by their haplotypic composition, as accepted by <code>vegdist</code> function in <code>vegan</code> package (Default <code>method = "euclidean"</code>).
<code>squareroot.dis</code>	Logical argument (TRUE or FALSE) to specify if use square root of dissimilarity index in matrix P (Default <code>squareroot.dis = TRUE</code>).
<code>choices</code>	Axes for re-scaling. Choices must have length equal to two (Default <code>choices = c(1, 2)</code>).
<code>analysis</code>	Type of analysis, partial match to "none", "glm", "adonis" (Default <code>analysis = "none"</code>).
<code>envir</code>	A matrix with environmental variables for each population, with variables as columns and localities as rows.
<code>formula</code>	An object of class <code>formula</code> with quotation marks, used in GLM analysis. See Details.
<code>AsFactors</code>	Encode an environmental variable as factor used in GLM analysis. The sequence is the same that in the environmental data matrix. See Details.
<code>runs</code>	Number of permutations for assessing probability of type I error.
<code>...</code>	Additional arguments to function matrix.p.sig and pcps.sig .

Details

The item `formula` is an expression of the form `haplovector.1 ~ envir`. The response term must be the haplovector name, for example, `haplovector.1`, `haplovector.2`, `haplovector.12`, etc.

The item `AsFactors` changes an environmental variable for the class [factor](#). The sequence is the same that in the environmental data matrix, not the order in the formula. Use `c` to combine more than one variable.

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 (haplovectors).
<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>envir.class</code>	The class of each variable in environmental data in glm.
<code>formula</code>	The formula used in glm.
<code>model</code>	The model, an object of class glm or adonis.
<code>statistic.obs</code>	Observed F value.
<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$sehv.pi, envir = sehv$sehv.envir,
             analysis = "glm", runs = 99, formula = haplovector.1~R)
```

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
```

Index

*Topic **datasets**
sehv, [4](#)

c, [3](#)

dist.dna, [2](#), [3](#)

factor, [3](#)

HaploNetDist, [1](#), [4](#)

haplotype, [2](#), [3](#)

HaploVectors, [2](#), [2](#)

matrix.p.sig, [3](#)

pcps.sig, [3](#)

sehv, [4](#)