

Package ‘HaploVectors’

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Type Package

Title HaploVectors an Integrative Analytical Tool for Phylogeography

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

License GPL (>= 2)

Imports ape, pegas, reshape, PCPS

RoxygenNote 6.0.1

NeedsCompilation no

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HaploNetDist	<i>HaploNetDist</i>
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Description

Function to extracts the haplotypes, computes pairwise distances between haplotypes, haplotypic network and computes 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 specifying the evolutionary model to be used to computes pairwise distances from DNA sequences (default <code>dist.model = "N"</code>).
<code>checkdata</code>	Logical argument (TRUE or FALSE) to check if individual sequence in the pop data follows the same order as the set of DNA sequences (Default <code>checkdata = TRUE</code>).
<code>...</code>	Additional arguments to function dist.dna .

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).

See Also

[HaploVectors](#)

Examples

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

HaploVectors

HaploVectors

Description

Function to extracts haplotypic eigenvectors and performing 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 specifying the evolutionary model to be used to computes pairwise distances from DNA sequences (default <code>dist.model = "N"</code>).
<code>log.frequencies</code>	Logical argument (TRUE or FALSE) to specify if apply transformation of natural logarithms plus one in haplotype per locality data (Default <code>log.frequencies = TRUE</code>).
<code>squareroot.network</code>	Logical argument (TRUE or FALSE) to specify if use square root in 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 locality as rows.
<code>formula</code>	An object of class formula 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 significance.
<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`.

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.

haplotype.per.locality	A matrix with frequency of each haplotype per locality (W).
haplotype.network	A matrix with haplotype connections described in the network (D_n).
vectors	The haplotypic eigenvectors (haplovectors).
values	The eigenvalues, relative eigenvalues and cumulative relative eigenvalues.
correlations	Correlations between haplotypic eigenvectors and haplotypes.
P	Matrix of haplotypic composition (P).
scores.haplotypes	Scores for biplot graphics.
envir.class	The class of each variable in environmental data in glm.
formula	The formula used in glm.
model	The model, an object of class glm or adonis.
statistic.obs	Observed F value.
p.site.shuffle	The p value for the site shuffle null model.
p.taxa.shuffle	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
```

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