

Package ‘paco’

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Title Procrustes Application to Cophylogenetic Analysis

Description Procrustes analyses to infer co-phylogenetic matching between pairs of (ultrametric) phylogenetic trees.

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Depends R (>= 3.0.0)

Imports vegan (>= 2.2-0), plyr

Suggests ape, doMC

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URL <http://www.uv.es/cophylpaco/>

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add_pcoord	<i>Principle coordinate analysis of phylogenies</i>
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Description

Principle coordinate analysis of phylogenies

Usage

```
add_pcoord(D, correction = "none")
```

Arguments

D	A list with objects H, P, and HP, returned by <code>prepare_paco_data</code>
correction	Choose the method with which to correct negative eigenvalues ('none', 'cailliez', 'lingoes'). Default is 'none'.

Value

The input list with added objects for the principal coordinates of the objects

Note

Internal function `coordpcoa` is a modified version of `ape::pcoa`, utilising `vegan::eigenvals`

Examples

```
data(gopherlice)
library(ape)
gdist <- cophenetic(gophertree)
ldist <- cophenetic(licetree)
D <- prepare_paco_data(gdist, ldist, gl_links)
D <- add_pcoord(D)
```

coordpcoa	<i>Internal function of add_pcoord performing principal coordinate analysis</i>
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Description

Internal function of `add_pcoord` performing principal coordinate analysis

Usage

```
coordpcoa(D, correction = "none", rn = NULL)
```

Arguments

D A list with objects H, P, and HP, returned by prepare_paco_data
 correction The correction to apply (none, lingoies, or cailliez)
 rn rownames (optional)

Note

Internal function coordpcoa is a modified version of ape::pcoa, utilising vegan::eigenvals

gl_links	<i>Gopher/lice phylogenies</i>
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Description

Gopher/lice phylogenies

Usage

data(gopherlice)

gophertree	<i>Gopher phylogeny</i>
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Description

Gopher phylogeny

Usage

data(gopherlice)

licetree	<i>Lice phylogeny</i>
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Description

Lice phylogeny

Usage

data(gopherlice)

PACo *Performs PACo/procustes analysis*

Description

Performs PACo/procustes analysis

Usage

```
PACo(D, nperm = 1000, seed = NA, method = "r0", symmetric = FALSE,
      correction = "none")
```

Arguments

D	a list with the data
nperm	Number of permutations
seed	Seed if results need to be reproduced
method	The method to permute matrices with: "r0", "r1", "r2", "c0", "swap", "quasiswap", "backtrack", "tswap", "r00". See commsim for details
symmetric	Use symmetric Procrustes statistic
correction	Choose the method with which to correct negative eigenvalues in the internal call of <code>add_pcoord</code> ('none', 'cailliez', 'lingoes'). Default is 'none'.

Examples

```
data(gopherlice)
require(ape)
gdist <- cophenetic(gophertree)
ldist <- cophenetic(licetree)
D <- prepare_paco_data(gdist, ldist, gl_links)
D <- add_pcoord(D)
D <- PACo(D, nperm=10, seed=42, method="r0", correction='cailliez')
print(D$gof)
```

paco_links *Contribution of individual links*

Description

Contribution of individual links

Usage

```
paco_links(D, .parallel = FALSE)
```

Arguments

D	A list returned by <code>proc_analysis</code>
<code>.parallel</code>	if TRUE, calculate the jackknife contribution in parallel using the backend provided by <code>foreach</code>

Value

A list with added object `jackknife`, containing the mean and upper CI values for each link

<code>prepare_paco_data</code>	<i>Prepare the data Simple wrapper to make sure that the matrices are sorted accordingly</i>
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Description

Prepare the data Simple wrapper to make sure that the matrices are sorted accordingly

Usage

```
prepare_paco_data(H, P, HP)
```

Arguments

H	Host distance matrix
P	Parasite distance matrix
HP	Host-parasite association matrix, hosts in rows

Value

A list with objects H, P, HP

Examples

```
data(gopherlice)
library(ape)
gdist <- cophenetic(gophertree)
ldist <- cophenetic(licetree)
D <- prepare_paco_data(gdist, ldist, gl_links)
```

residuals.paco *Get procrustes residuals from a paco object*

Description

Get procrustes residuals from a paco object

Usage

```
## S3 method for class 'paco'  
residuals(object, ...)
```

Arguments

object	a list with the data
...	Used for type, whether the whole residual matrix (<code>matrix</code>) or the residuals per interaction (<code>interaction</code>) is desired

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