Package 'paco'

October 9, 2015

Version 0.2.2

Date 2015-07-13

Title Procrustes Application to Cophylogenetic Analysis

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

Author Juan Antonio Balbuena <j.a.balbuena@uv.es>, Timothee Poisot

<tim@poisotlab.io>, Matthew Hutchinson <matthewhutchinson15@gmail.com>,
Fernando Cagua <fernando@cagua.co>

Maintainer Timothee Poisot <tim@poisotlab.io>

Depends R (>= 3.0.0)

Imports vegan (>= 2.2-0), plyr

Suggests ape, doMC

License MIT + file LICENSE

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

R topics documented:

---

add_pcoord   *Principle coordinate analysis of phylogenies*

Description

Principle coordinate analysis of phylogenies

Usage

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

Arguments

D	A list with objects H, P, and HP, returned by prepare_paco_data
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   *Internal fucntion of add_pcoord performing pricipal coordinate analysis*

Description

Internal fucntion of add_pcoord performing pricipal 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, lingoes, or cailliez)
rn	rownames (optional)

Note

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

---

`gl_links`	*Gopher/lice phylogenies*

Description

Gopher/lice phylogenies

Usage

```
data(gopherlice)
```

`gophertree`	*Gopher phylogeny*

Description

Gopher phylogeny

Usage

```
data(gopherlice)
```

`licetree`	*Lice phylogeny*

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)
```

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

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")
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 proc_analysis
.parallel	if TRUE, calculate the jacknife contribution in parallel using the backend provided by foreach

Value

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

---

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

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, wether the whole residual matrix (matrix) or the residuals per interaction (interaction) is desired

Index