Package ‘adephylo’

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### adephylo-package

The adephylo package

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**Description**

This package is devoted to exploratory analysis of phylogenetic comparative data. It re-implements and extends phylogenetic procedures from the ade4 package (which are now deprecated).

Comparative data (phylogeny+traits) are handled as **phylo4d** objects, a canonical class implemented by the **phylobase** package. Trees are handled as **phylo** objects (from the ape package) or as **phylo4** objects (**phylobase**’s extension of **phylo** objects).

Main functionalities of adephylo are summarized below.

---

### TOPOLOGICAL INFORMATION

Several functions allow one to retrieve topological information from a tree; such information can be used, for instance, as a basis to compute distances or proximities between tips.

- **listDD**: lists the direct descendants from each node of a tree.
- **listTips**: lists the tips descending from each node of a tree.

- **.tipToRoot**: finds the set of nodes between a tip and the root of a tree.

- **sp.tips**: finds the shortest path between tips of a tree.

- **treePart**: defines partitions of tips reflecting the topology of a tree. This function can output non-independent dummy vectors, or alternatively an orthonormal basis used by the orthogram procedure.

=== PHYLOGENETIC PROXIMITIES/DISTANCES ===

Several phylogenetic proximities and distances are implemented. Auxiliary function easing the computation of other distances/proximities are also provided:

- **distRoot**: computes different distances of a set of tips to the root.

- **distTips**: computes different pairwise distances in a set of tips.

- **proxTips**: computes different proximities between a set of tips.

=== MEASURES/TESTS OF PHYLOGENETIC AUTOCORRELATION ===

Several procedures allow one to measure, and/or test phylogenetic signal in biological traits:

- **abouheif.moran**: performs Abouheif’s test, designed to detect phylogenetic autocorrelation in a quantitative trait. This implementation is not based on original heuristic procedure, but on the exact formulation proposed by Pavoine et al. (2008), showing that the test is in fact a Moran’s index test. This implementation further extends the procedure by allowing any measure of phylogenetic proximity (5 are proposed).

- **orthogram**: performs the orthonormal decomposition of variance of a quantitative variable on an orthonormal basis as in Ollier et al. (2005). It also returns the results of five non parametric tests associated to the variance decomposition.

- **moran.idx**: computes Moran’s index of autocorrelation given a variable and a matrix of proximities among observations (no test).

=== MODELLING/INVESTIGATION OF PHYLOGENETIC SIGNAL ===

Rather than testing or measuring phylogenetic autocorrelation, these procedures can be used for further investigation of phylogenetic signal. Some, like **me.phylo**, can be used to remove phylogenetic autocorrelation. Others can be used to understand the nature of this autocorrelation (i.e., to ascertain which traits and tips are concerned by phylogenetic non-independence).

- **me.phylo/orthobasis.phylo**: these synonymous functions compute Moran’s eigenvectors (ME) associated to a tree. These vectors model different observable phylogenetic signals. They can be
used as covariables to remove phylogenetic autocorrelation from data.

- **orthogram**: the orthogram mentioned above also provides a description of how biological variability is structured on a phylogeny.

- **ppca**: performs a phylogenetic Principal Component Analysis (pPCA, Jombart et al. 2010). This multivariate method investigates phylogenetic patterns in a set of quantitative traits.

=== GRAPHICS ===
Some plotting functions are proposed, most of them being devoted to representing phylogeny and a quantitative information at the same time.

- **table.phylo4d**: fairly customisable way of representing traits onto the tips of a phylogeny. Several traits can be plotted in a single graphic.

- **bullseye**: an alternative to table.phylo4d based on fan-like representation, better for large trees.

- **scatter.pppca, screeplot.pppca, plot.pppca**: several plots associated to a phylogenetic principal component analysis (see pppca).

=== DATASETS ===
Several datasets are also proposed. Some of these datasets replace former version from ade4, which are now deprecated. Here is a list of available datasets: carnii9, carnii70, lizards, maples, mjrochet, palm, procella, tithonia, and ungulates.

To cite adephylo, please use the reference given by citation("adephylo").

**Details**

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**Author(s)**

Thibaut Jombart <tjombart@imperial.ac.uk>
with contributions Stéphane Dray <dray@biomserv.univ-lyon1.fr>.
Parts of former code from ade4 by Daniel Chessel and Sébastien Ollier.

**See Also**

The ade4 package for multivariate analysis.
Description

The test of Abouheif (1999) is designed to detect phylogenetic autocorrelation in a quantitative trait. Pavoine et al. (2008) have shown that this test is in fact a Moran’s I test using a particular phylogenetic proximity between tips (see details). The function `abouheif.moran` performs basically Abouheif’s test for several traits at a time, but it can incorporate other phylogenetic proximities as well.

Note that the original Abouheif’s proximity (Abouheif, 1999; Pavoine et al. 2008) unifies Moran’s I and Geary’s tests (Thioulouse et al. 1995).

`abouheif.moran` can be used in two ways:
- providing a data.frame of traits (`x`) and a matrix of phylogenetic proximities (`w`)
- providing a `phylo4d` object (`x`) and specifying the type of proximity to be used (`method`).

Usage

```r
abouheif.moran(x, W=NULL, 
    method=c("oriAbouheif", "patristic", "nNodes", "Abouheif", "sumDD"), 
    a=1, nrepet = 999, alter=c("greater", "less", "two-sided"))
```

Arguments

- `x` a data frame with continuous variables, or a `phylo4d` object (i.e. containing both a tree, and tip data). In the latter case, `method` argument is used to determine which proximity should be used.
- `W` a `n` by `n` matrix (`n` being the number rows in `x`) of phylogenetic proximities, as produced by `proxTips`.
- `method` a character string (full or unambiguously abbreviated) specifying the type of proximity to be used. By default, the proximity used is that of the original Abouheif’s test. See details in `proxTips` for information about other methods.
- `a` the exponent used to compute the proximity (see `proxTips`).
- `nrepet` number of random permutations of data for the randomization test
- `alter` a character string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two-sided"

Details

`W` is a squared symmetric matrix whose terms are all positive or null.
$w$ is firstly transformed in frequency matrix $A$ by dividing it by the total sum of data matrix:

$$a_{ij} = \frac{W_{ij}}{\sum_{i=1}^{n} \sum_{j=1}^{n} W_{ij}}$$

The neighbouring weights is defined by the matrix $D = \text{diag}(d_1, d_2, \ldots)$ where $d_i = \sum_{j=1}^{n} W_{ij}$.

For each vector $x$ of the data frame $x$, the test is based on the Moran statistic $x^T Ax$ where $x$ is D-centred.

**Value**

Returns an object of class `krandtest` (randomization tests from ade4), containing one Monte Carlo test for each trait.

**Author(s)**

Original code from ade4 (gearymoran function) by Sébastien Ollier
Adapted and maintained by Thibaut Jombart <tjombart@imperial.ac.uk>.

**References**


**See Also**

- `gearymoran` from the ade4 package
- `Moran.I` from the ape package for the classical Moran’s $I$ test.

**Examples**

```r
if(require(ade4) && require(ape) && require(phylobase)){
  ## load data
  data(ungulates)
  tre <- read.tree(text=ungulates$tre)
  x <- phylod(tre, ungulates$tab)

  ## Abouheif's tests for each trait
  myTests <- abouheif.moran(x)
  myTests
  plot(myTests)

  ## a variant using another proximity
  plot(abouheif.moran(x, method="nNodes") )

  ## Another example
  data(maples)
  tre <- read.tree(text=maples$tre)
  dom <- maples$tab$Dom
```
## Abouheif's tests for each trait (equivalent to Cmean)

```r
W1 <- proxTips(tre, method="oriAbouheif")
abouheif.moran(dom, W1)
```

## Equivalence with moran.idx

```r
W2 <- proxTips(tre, method="Abouheif")
abouheif.moran(dom, W2)
moran.idx(dom, W2)
```

---

**bullseye**  
*Fan-like phylogeny with possible representation of traits on tips*

### Description

This function represents a phylogeny as a fan, using circles to provide a legend for distances and optionally colored symbols to represent traits associated to the tips of the tree. This function uses and is compatible with ape’s `plot.phylo`.

### Usage

```r
bullseye(phy, traits=NULL, col.tips.by=NULL, col.pal=spectral,
    circ.n=6, circ.bg=transp("royalblue", .1), circ.unit=NULL,
    legend=TRUE, leg.posi="bottomleft", leg.title="", leg.bg="white",
    traits.inset=1.1, traits.space=0.05, traits.pch=19, traits.cex=1,
    alpha=1, axis=TRUE,...)
```

### Arguments

- **phy**  
  a tree in `phylo`, `phylo4` or `phylo4d` format.

- **traits**  
  an optional data.frame of traits.

- **col.tips.by**  
  an optional vector used to define colors for tip labels; if unnamed, must be ordered in the same order as `phy$tip.label`.

- **col.pal**  
  a function generating colors according to a given palette; several palettes can be provided as a list, in the case of several traits; the first palette is always reserved for the tip colors; this argument is recycled.

- **circ.n**  
  the number of circles for the distance annotations.

- **circ.bg**  
  the color of the circles.

- **circ.unit**  
  the unit of the circles; if NULL, determined automatically from the data.

- **legend**  
  a logical specifying whether a legend should be plotted; only one legend is displayed, with priority to tip colors first, and then to the first trait.

- **leg.posi, leg.title, leg.bg**  
  position, title and background for the legend.
traits.inset inset for positioning the traits; 1 corresponds to the circle crossing the furthest tip, 0 to the center of the plot.

traits.space a coefficient indicating the spacing between traits.

traits.pch, traits.cex
type and size of the symbols used for the traits; recycled if needed.

alpha alpha value to be used for the color transparency, between 0 (invisible) and 1 (plain).

axis a logical indicating whether an axis should be displayed.

... further arguments to be passed to plot methods from ape. See plot.phylo.

Author(s)
Thibaut Jombart <tjombart@imperial.ac.uk>

See Also
table.phylo4d for non-radial plots.

The phylo4d class for storing phylogeny+data.

plot.phylo from the ape package.

dotchart.phylog.

Examples
if(require(ape) && require(phylabor) && require(adegenet)){

data(lizards)
tre <- read.tree(text=lizards$hprA) # make a tree

## basic plots
bullseye(tre)
bullseye(tre, lizards$traits)

## customized
par(mar=c(6,6,6,6))
bullseye(tre, lizards$traits, traits.cex=sqrt(1:7), alpha=.7,
legend=FALSE, circ.unit=10, circ.bg=transp("black",1),
edge.width=2)
}


Description

This data set describes the phylogeny of carnivora as reported by Diniz-Filho et al. (1998). It also gives the body mass of these 19 species.

Usage

data(carni19)

Format

carni19 is a list containing the 2 following objects:

tre is a character string giving the phylogenetic tree in Newick format.
bm is a numeric vector which values correspond to the body mass of the 19 species (log scale).

Note

This dataset replaces the former version in ade4.

Source


Examples

```r
## Not run:
if(require(ape) & require(phylode)){
  data(carni19)
  tre <- read.tree(text=carni19$tre)
  x <- phylo4d(tre, data.frame(carni19$bm))
  table.phylo4d(x, ratio=.5, center=FALSE)
}
## End(Not run)
```
Description

This data set describes the phylogeny of 70 carnivora as reported by Diniz-Filho and Torres (2002). It also gives the geographic range size and body size corresponding to these 70 species.

Usage

data(carni70)

Format

carni70 is a list containing the 2 following objects:

- **tre** is a character string giving the phylogenetic tree in Newick format. Branch lengths are expressed as divergence times (millions of years)
- **tab** is a data frame with 70 species and two traits: size (body size (kg)); range (geographic range size (km)).

Note

This dataset replaces the former version in ade4.

Source


Examples

```r
## Not run:
if(require(ape) && require(phylobase)){

data(carni70)
rownames(carni70$tab) <- gsub("_", ".", rownames(carni70$tab))
tre <- read.tree(text=carni70$tre)
x <- phylo4d(tre, carni70$tab)
table.phylo4d(x)

par(mar=rep(.1,4))
table.phylo4d(x,cex.lab=.5, show.n=FALSE, ratio=.5)

## transform size in log and test for a phylogenetic signal
size <- log(carni70$tab[,1])
names(size) <- row.names(carni70$tab)
```
orthogram(size, tre)

## transform range and test for a phylogenetic signal
yrange <- scale(carni7@tab)[,2]
names(yrange) <- row.names(carni7@tab)
orthogram(yrange, tre)
}

## End(Not run)

---

**Distance-Based Assignment**

**Description**

These functions are under development. Please do not use them unless asked by the author.

**Usage**

```r
## S3 method for class 'phylo'
dibas(x, grp, method = c("default", "leaveOneOut"),
    fromRoot=FALSE, metric = c("Abouheif", "nNodes", "patristic","sumDD"),
    n.items=NULL, ...)

## S3 method for class 'matrix'
dibas(x, grp, method = c("default", "leaveOneOut"), ...)

## S3 method for class 'dist'
dibas(x, grp, method = c("default", "leaveOneOut"), ...)

## S3 method for class 'vector'
dibas(x, grp, method=c("default","leaveOneOut"),
    n.items=NULL, ...)
```

**Arguments**

- **x**
  a phylo object, or a symmetric matrix of pairwise distances of class matrix or dist.
- **grp**
  a factor indicating the groups of observations.
- **method**
  a character string indicating the method to be used for estimating the distribution of pairwise distances within groups. The default method ("default") uses all observations, while the "leaveOneOut" estimates separate group distributions for each individual, leaving this one out in the estimation process.
- **metric**
  a character string matching "nNodes", "patristic", "Abouheif", or "sumDD" indicating the distance measure to be used. See `distTips` for more information. Note that patristic distances should be avoided in presence of one or more highly diverse group because of the 'hand fan' syndrome (see example).
fromRoot

a logical indicating if distances from the root, rather than between groups, should be used.

n.items

a vector of integers of the same length as x, stating how many times each items in 'x' should be repeated; used to take into account differences in abundances of the different items (e.g. sequences in multiple copies).

..."further arguments passed to other methods. Can be used to provide arguments to table.phylo4d in plot method.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

Examples

```R
## Not run:
if(require(ape)){
    ### SIMPLE SIMULATED DATA ###
    ## 50 variables, 2 groups, 30 indiv
dat <- simDatGroups(k=2, p=50, n=c(15,15), mu=c(0,1))
names(dat)

    ## make a tree
tre <- nj(dist(dat$dat))
plot(tre,type="unr", tip.col=c("blue","red"),as.integer(dat$grp)],
     main="simulated data - tree")

    ## use dibas method
res <- dibas(tre, dat$grp, metric="nNodes")
res

    barplot(t(res$prob), main="group membership probabilities")

    ### NON-PARAMETRIC TEST BASED ON MEAN SUCCESSFUL ASSIGNMENT ###
    ## use dibas method
distHo <- replicate(100,
        dibas(tre, sample(dat$grp), metric="patristic")$mean.ok)
pval <- mean(res$mean.ok<=c(distHo,res$mean.ok))
pval

    hist(c(distHo,res$mean.ok), col="grey",
         main="Mean successful assignement - permuted values")
abline(v=res$mean.ok, col="red")
mtext(side=3, text="Observed value in red")

    ### HAND FAN SYNDROME ###
    ## 50 variables, 2 groups, 30 indiv
dat <- simDatGroups(k=2, p=50, n=c(15,15), mu=c(0,1), sigma=c(2,4))
names(dat)
```
## Make a Tree

```
## make a tree

tre <- nj(dist(dat$dat))
plot(tre, type="unr", tip.col=c("blue","red")[as.integer(dat$grp)],
     main="simulated data - tree")

text(side=3, text="hand-fan syndrome")
```

## Use Dibas Method

```
## use dibas method

res.patri <- dibas(tre, dat$grp, metric="patristic")
res.patri$grp.tab # poor results
plot(table(res.patri$groups), main="Group assignment - dibas patristic")

res <- dibas(tre, dat$grp, metric="nNodes")
res$grp.tab # results OK
plot(table(res$groups), main="Group assignment - dibas nNodes")
```

### More Complex Dataset ###

```
### MORE COMPLEX DATASET ###

if(require(adegenet)){

    dat <- simDatGroups(k=5, p=50, n=c(5,10,10,30,60), mu=sample(1:5, 5,
                    replace=TRUE), sigma=sample(1:5)/2)
    names(dat)

    ## make a tree

    tre <- nj(dist(dat$dat))
    plot(tre, type="unr", tip.col=fac2col(dat$grp), main="simulated data - tree")

    ## use dibas method

    res <- dibas(tre, dat$grp, metric="Abouheif")
    res

    plot(table(res$groups), main="Group assignment - dibas Abouheif")

}
```

## End(Not run)
**Description**

The function `distRoot` computes the distance of a set of tips to the root. Several distances can be used, defaulting to the sum of branch lengths.

**Usage**

```r
distRoot(x, tips, method=c("patristic","nNodes","Abouheif","sumDD"))
```

**Arguments**

- `x`: a tree of class `phylo`, `phylo4` or `phylo4d`.
- `tips`: A vector of integers identifying tips by their numbers, or a vector of characters identifying tips by their names.
- `method`: a character string (full or abbreviated without ambiguity) specifying the method used to compute distances; possible values are:
  - `patristic`: patristic distance, i.e. sum of branch lengths
  - `nNodes`: number of nodes on the path between the nodes
  - `Abouheif`: Abouheif’s distance (see details)
  - `sumDD`: sum of direct descendants of all nodes on the path (see details)

**Details**

Abouheif distance refers to the phylogenetic distance underlying the test of Abouheif (see references). Let \( P \) be the set of all the nodes in the path going from \( \text{node1} \) to \( \text{node2} \). Let \( \text{DDP} \) be the number of direct descendants from each node in \( P \). Then, the so-called 'Abouheif' distance is the product of all terms in \( \text{DDP} \).

\( \text{sumDD} \) refers to a phylogenetic distance quite similar to that of Abouheif. We consider the same sets \( P \) and \( \text{DDP} \). But instead of computing the product of all terms in \( \text{DDP} \), this distance computes the sum of all terms in \( \text{DDP} \).

**Value**

A numeric vector containing one distance value for each tip.

**Author(s)**

Thibaut Jombart <tjombart@imperial.ac.uk>

**References**


**See Also**

distTips which computes the same phylogenetic distances, but between tips.
Examples

```r
if(require(ape) & require(phylobase)){
  ## make a tree
  x <- as(rtree(50),"phylo4")
  ## compute 4 different distances
  met <- c("patristic","nNodes","Abouheif","sumDD")
  D <- lapply(met, function(e) distRoot(x, method=e) )
  names(D) <- met
  D <- as.data.frame(D)

  ## plot these distances along with the tree
  temp <- phylo4d(x, D)
  table.phylo4d(temp, show.node=FALSE, cex.lab=.6)
}
```

**distTips**  
*Compute some phylogenetic distance between tips*

**Description**

The function `distTips` computes a given distance between a set of tips of a phylogeny. A vector of tips is supplied: distances between all possible pairs of these tips are computed. The distances are computed from the shortest path between the tips. Several distances can be used, defaulting to the sum of branch lengths (see argument `method`).

An option (enabled by default) allows computations to be run using compiled C code, which is much faster than pure R code. In this case, a matrix of all pairwise distances is returned (i.e., `tips` argument is ignored).

**Usage**

```r
distTips(x, tips, method=c("patristic","nNodes","Abouheif","sumDD"), useC=TRUE)
```

**Arguments**

- `x`: a tree of class `phylo`, `phylo4` or `phylo4d`.
- `tips`: A vector of integers identifying tips by their numbers, or a vector of characters identifying tips by their names. Distances will be computed between all possible pairs of tips.
- `method`: a character string (full or abbreviated without ambiguity) specifying the method used to compute distances; possible values are:
  - `patristic`: patristic distance, i.e. sum of branch lengths
  - `nNodes`: number of nodes on the path between the nodes
  - `Abouheif`: Abouheif’s distance (see details)
  - `sumDD`: sum of direct descendants of all nodes on the path (see details)
- `useC`: a logical indicating whether computations should be performed using compiled C code (TRUE, default), or using a pure R version (FALSE). C version is several orders of magnitude faster, and R version is kept for backward compatibility.
Details

Abouheif distance refers to the phylogenetic distance underlying the test of Abouheif (see references). Let P be the set of all the nodes in the path going from node1 to node2. Let DDP be the number of direct descendants from each node in P. Then, the so-called 'Abouheif' distance is the product of all terms in DDP.

sumDD refers to a phylogenetic distance quite similar to that of Abouheif. We consider the same sets P and DDP. But instead of computing the product of all terms in DDP, this distance computes the sum of all terms in DDP.

Value

An object of class dist, containing phylogenetic distances.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

References


See Also

distTips which computes several phylogenetic distances between tips.

Examples

```r
if(require(ape) & require(phylobase)){
## make a tree
x <- as(episode(10), "phylo4")
plot(x, show.node=TRUE)
axisPhylo()

## compute different distances
distTips(x, 1:3)
distTips(x, 1:3, "nNodes")
distTips(x, 1:3, "Abouheif")
distTips(x, 1:3, "sumDD")

## compare C and pure R code outputs
x <- rtree(10)
all.equal(as.matrix(distTips(x)), as.matrix(distTips(x, useC=FALSE)))
all.equal(as.matrix(distTips(x, meth="nNode")),
  as.matrix(distTips(x, meth="nNode", useC=FALSE)))
all.equal(as.matrix(distTips(x, meth="Abou")),
  as.matrix(distTips(x, meth="Abou", useC=FALSE)))
all.equal(as.matrix(distTips(x, meth="sumDD")),
  as.matrix(distTips(x, meth="sumDD", useC=FALSE)))
```
## compare speed

```r
x <- rtree(50)
tim1 <- system.time(distTips(x, useC=FALSE)) # old pure R version
tim2 <- system.time(distTips(x)) # new version using C
tim1[c(1,3)]/tim2[c(1,3)] # C is about a thousand time faster in this case
```

### listDD

- **List direct descendants for all nodes of a tree**

### Description

The function `listDD` lists the direct descendants from each node of a tree. The tree can be of class `phylo`, `phylo4` or `phylo4d`.

### Usage

```r
listDD(x, nameBy=c("label","number"))
```

### Arguments

- **x**
  - A tree of class `phylo`, `phylo4` or `phylo4d`.
- **nameBy**
  - a character string indicating whether the returned list must be named by node labels ("label") or by node numbers ("number").

### Value

A list whose components are vectors of named nodes (or tips) for a given internal node.

### Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

### See Also

- `listTips` which lists the tips descending from each node.
- `treePart` which defines partitions of tips according to the tree topology.

### Examples

```r
if(require(ape) & require(phylobase)){
  ## make a tree
  x <- as(rtree(20),"phylo4")
  plot(x,show.node=TRUE)
  listDD(x)
}
```
listTips  

List tips descendings from all nodes of a tree

Description

The function listTips lists the tips descending from each node of a tree. The tree can be of class phylo, phylo4 or phylo4d.

Usage

listTips(x)

Arguments

x  A tree of class phylo, phylo4 or phylo4d.

Value

A list whose components are vectors of named tips for a given node.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

See Also

listDD which lists the direct descendants for each node.

treePart which defines partitions of tips according to the tree topology.

Examples

if(require(ape) & require(phylobase)){
## make a tree
x <- as(rtree(20),"phylo4")
plot(x,show.node=TRUE)
listTips(x)
}

Description

This data set describes the phylogeny of 18 lizards as reported by Bauwens and Díaz-Uriarte (1997). It also gives life-history traits corresponding to these 18 species.

Usage

data(lizards)

Format

lizards is a list containing the 3 following objects:

- traits is a data frame with 18 species and 8 traits.
- hprA is a character string giving the phylogenetic tree (hypothesized phylogenetic relationships based on immunological distances) in Newick format.
- hprB is a character string giving the phylogenetic tree (hypothesized phylogenetic relationships based on morphological characteristics) in Newick format.

Details

Variables of lizards$traits are the following ones: mean.L (mean length (mm)), matur.L (length at maturity (mm)), max.L (maximum length (mm)), hatch.L (hatching length (mm)), hatch.m (hatchling mass (g)), clutch.S (Clutch size), age.mat (age at maturity (number of months of activity)), clutch.F (clutch frequency).

Note

This dataset replaces the former version in ade4.

References


Examples

```r
## Not run:
if(require(ape) && require(phylobase)){

## see data
data(lizards)
liz.tr <- read.tree(tex=lizards$hprA) # make a tree
liz <- phylo4d(liz.tr, lizards$traits) # make a phylo4d object
```
table.phylo4d(liz)

## compute and plot principal components
if(require(ade4)){
liz.pca1 <- dudi.pca(lizards$traits, cent=TRUE, 
scale=TRUE, scannf=FALSE, nf=2) # PCA of traits
myPC <- phylo4d(liz.tr, liz.pca1$li) # store PC in a phylo4d object
varlab <- paste("Principal \(\text{component}\) ", 1:2) # make labels for PCs
table.phylo4d(myPC, ratio=.8, var.lab=varlab) # plot the PCs
add.scatter.eig(liz.pca1$eig,2,1,2, posi="topleft", inset=c(0,.15))
title("Phylogeny and the principal components")

## compute a pPCA ##
## remove size effect
temp <- lapply(liz.pca1$tab, function(e) residuals(lm(e~1+liz.pca1$li[,1])))
temp <- data.frame(temp)
row.names(temp) <- tipLabels(liz)

## build corresponding phylo4d object
liz.noSize <- phylo4d(liz.tr, temp)
ppca1 <- ppca(liz.noSize, method="Abouheif", scale=FALSE, scannf=FALSE)
plot(ppca1)
}

## End(Not run)

maples

\textit{Phylogeny and quantitative traits of flowers}

\section*{Description}
This data set describes the phylogeny of 17 flowers as reported by Ackerly and Donoghue (1998). It also gives 31 traits corresponding to these 17 species.

\section*{Usage}
data(maples)

\section*{Format}
tithonia is a list containing the 2 following objects: - tre: a character string giving the phylogenetic tree in Newick format.
- tab: a data frame with 17 species and 31 traits.

\section*{Note}
This dataset replaces the former version in ade4.
Misc utils

Source

Data were obtained from the URL http://www.stanford.edu/~dackerly/acerdata.html (no longer maintained).

References


Examples

## Not run:
if(require(ape) && require(phylobase)){

data(maples)

## see the tree
tre <- read.tree(text=maples$tre)
plot(tre)
axisPhylo()

## look at two variables
dom <- maples$tab$Dom
bif <- maples$tab$Bif
plot(bif,dom,pch = 20)
abline(lm(dom~bif)) # a strong negative correlation ?
summary(lm(dom~bif))
cor.test(bif,dom)

## look at the two variables onto the phylogeny
temp <- phylo4d(tre, data.frame(dom,bif, row.names=tre$tip.label))
table.phylo4d(temp) # correlation is strongly linked to phylogeny

## use ape's PIC (phylogenetic independent contrasts)
pic.bif <- pic(bif, tre)
pic.dom <- pic(dom, tre)
cor.test(pic.bif, pic.dom) # correlation is no longer significant
}

## End(Not run)

Misc utils

Low-level auxiliary functions for adephylo

Description

These hidden functions are utils for adephylo, used by other functions. Regular users can use them as well, but no validity checks are performed for the arguments: speed is here favored over safety.
Most of these functions handle trees inheriting \texttt{phylo4} class.

\texttt{.tipToRoot} finds the set of nodes between a tip and the root of a tree.

\textbf{Usage}

\texttt{.tipToRoot(x, tip, root, include.root=FALSE)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} A valid tree of class \texttt{phylo4}.
  \item \texttt{tip} An integer identifying a tip by its numbers.
  \item \texttt{root} An integer identifying the root of the tree by its number.
  \item \texttt{include.root} a logical stating whether the root must be included as a node of the path from tip to root (\texttt{TRUE}), or not (\texttt{FALSE}, default).
\end{itemize}

\textbf{Value}

\texttt{.tipToRoot}: a vector of named integers identifying nodes.

\textbf{Author(s)}

Thibaut Jombart \texttt{<tjombart@imperial.ac.uk>}

\textbf{Examples}

\begin{verbatim}
if(require(ape) & require(phylobase)){
  ## make a tree
  x <- as(rtree(20),"phylo4")
  plot(x, show.node=TRUE)

  ## .tipToRoot
  root <- rootNode(x)
  .tipToRoot(x, 1, root)
  lapply(1:nTips(x), function(i) .tipToRoot(x, i, root))
}
\end{verbatim}

\begin{verbatim}
Phylogeny and quantitative traits of teleos fishes
\end{verbatim}

\textbf{Description}

This data set describes the phylogeny of 49 teleos fishes as reported by Rochet et al. (2000). It also gives life-history traits corresponding to these 49 species.
Usage

data(mjrochet)

Format

mjrochet is a list containing the 2 following objects:

- **tre** is a character string giving the phylogenetic tree in Newick format.
- **tab** is a data frame with 49 rows and 7 traits.

Details

Variables of `mjrochet$tab` are the following ones: tm (age at maturity (years)), lm (length at maturity (cm)), l05 (length at 5 per cent survival (cm)), t05 (time to 5 per cent survival (years)), fb (slope of the log-log fecundity-length relationship), fm (fecundity the year of maturity), egg (volume of eggs \(mm^3\)).

Note

This dataset replaces the former version in ade4.

Source

Data taken from:

Summary of data - Clupeiformes: [http://www.ifremer.fr/maerha/CLUPE.html](http://www.ifremer.fr/maerha/CLUPE.html)
Summary of data - Argentiniformes: [http://www.ifremer.fr/maerha/ARGENTIN.html](http://www.ifremer.fr/maerha/ARGENTIN.html)
Summary of data - Atheriniformes: [http://www.ifremer.fr/maerha/ATHER.html](http://www.ifremer.fr/maerha/ATHER.html)
Summary of data - Perciformes: [http://www.ifremer.fr/maerha/PERCI.html](http://www.ifremer.fr/maerha/PERCI.html)
Summary of data - Pleuronectiformes: [http://www.ifremer.fr/maerha/PLEURO.html](http://www.ifremer.fr/maerha/PLEURO.html)
Summary of data - Scorpaeniformes: [http://www.ifremer.fr/maerha/SCORPA.html](http://www.ifremer.fr/maerha/SCORPA.html)

References


Examples

```r
## Not run:
if(require(ape) && require(phylobase)){

data(mjrochet)
tre <- read.tree(text=mjrochet$tre) # make a tree
traits <- log((mjrochet$tab))

## build a phylo4d
```
mjr <- phylo4d(tre, traits)

## see data
table.phylo4d(mjr, cex.lab=0.5, show.node=FALSE, symb="square")

## perform Abouheif’s test for each trait
mjr.tests <- abouheif.moran(mjr, nrep=499)
mjr.tests
}
## End(Not run)

---

**Moran’s eigenvectors**  
*Computes Moran’s eigenvectors from a tree or a phylogenetic proximity matrix*

**Description**

The function `orthobasis.phylo` (also nicknamed `me.phylo`) computes Moran’s eigenvectors (ME) associated to a tree. If the tree has 'n' tips, (n-1) vectors will be produced. These vectors form an orthonormal basis: they are centred to mean zero, have unit variance, and are uncorrelated. Each vector models a different pattern of phylogenetic autocorrelation. The first vectors are those with maximum positive autocorrelation, while the last vectors are those with maximum negative autocorrelation. ME can be used, for instance, as regressors to remove phylogenetic autocorrelation from data (see references).

ME can be obtained from a tree, specifying the phylogenetic proximity to be used. Alternatively, they can be obtained directly from a matrix of phylogenetic proximities as constructed by `proxTips`.

**Usage**

```r
me.phylo(x=NULL, prox=NULL, method=c("patristic","nNodes","oriAbouheif","Abouheif","sumDD"), a=1)
orthobasis.phylo(x=NULL, prox=NULL, method=c("patristic","nNodes","oriAbouheif","Abouheif","sumDD"), a=1)
```

**Arguments**

- `x`  
  A tree of class `phylo`, `phylo4` or `phylo4d`.

- `prox`  
  A matrix of phylogenetic proximities as returned by `proxTips`.

- `method`  
  A character string (full or abbreviated without ambiguity) specifying the method used to compute proximities; possible values are:
  - `patristic`: (inversed sum of) branch lengths
  - `nNodes`: (inversed) number of nodes on the path between the nodes
  - `oriAbouheif`: original Abouheif’s proximity, with diagonal (see details in `proxTips`)
Moran's eigenvectors

- Abouheif: Abouheif's proximity (see details in proxTips)
- sumDD: (inversed) sum of direct descendants of all nodes on the path (see details in proxTips).
  
  a the exponent used to compute the proximity (see ?proxTips).
  
Value

An object of class orthobasis. This is a data.frame with Moran's eigenvectors in column, with special attributes:
- attr(.,"values"): Moran’s index for each vector - attr(.,"weights"): weights of tips; current implementation uses only uniform weights

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

References


See Also

- proxTips which computes phylogenetic proximities between tips.

- treePart which can compute an orthobasis based on the topology of a phylogeny.

Examples

```r
if(require(ape) && require(phylobase)){

  ## SIMPLE EXAMPLE ##
  ## make a tree
  x <- rtree(50)

  ## compute Moran's eigenvectors
  ME <- me.phylo(x, met="Abouheif")
  ME

  ## plot the 10 first vectors
  obj <- phylo4d(x, as.data.frame(ME[,1:10]))

```

Moran's index

Computes Moran's index for a variable

Description

This simple function computes Moran's index of autocorrelation given a variable and a matrix of proximities among observations.

Usage

moran.idx(x, prox, addInfo=FALSE)
Moran’s index

Arguments

- `x`: a numeric vector whose autocorrelation is computed.
- `prox`: a matrix of proximities between observations, as computed by the `proxtips`. Off-diagonal terms must be positive or null, while diagonal terms must all equal zero.
- `addInfo`: a logical indicating whether supplementary info (null value, minimum and maximum values) should be returned (TRUE) or not (FALSE, default); if computed, these quantities are returned as attributes.

Value

The numeric value of Moran’s index.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

References


See Also

- `proxtips` which computes phylogenetic proximities between tips of a phylogeny.

Examples

```r
## Not run:
## use maples dataset
data(maples)
tre <- read.tree(text=maples$tre)
dom <- maples$tab$Dom
bif <- maples$tab$Bif

## get a proximity matrix between tips
W <- proxtips(tre, met="Abouheif")

## compute Moran’s I for two traits (dom and bif)
moran.idx(dom, W)
moran.idx(bif, W)
moran.idx(rnorm(nTips(tre)), W)

## build a simple permutation test for ‘bif’
sim <- replicate(499, moran.idx(sample(bif), W)) # permutations
```
orthogram

**Orthogonal decomposition of variance**

**Description**

This function performs the orthogonal decomposition of variance of a quantitative variable on an orthonormal basis. It also returns the results of five non-parametric tests associated to the variance decomposition. It thus provides tools (graphical displays and tests) for analysing phylogenetic patterns in one quantitative trait. This implementation replaces the (deprecated) version from the ade4 package.

Several orthonormal bases can be used. By default, basis is constructed from a partition of tips according to tree topology (as returned by `treepart`); for this, the argument `tre` must be provided. Alternatively, one can provide an orthonormal basis as returned by `orthobasis.phylo`, or a proximity matrix from which an orthonormal basis based on Moran’s eigenvectors will be constructed (argument `prox`).

**Usage**

```r
orthogram(x, tre=NULL, orthobas = NULL, prox = NULL,
          nrepet = 999, posinega = 0, tol = 1e-07, cdot = 1.5,
          cfont.main = 1.5, lwd = 2, nclass,
          high.scores = 0, alter=c("greater", "less", "two-sided"))
```

**Arguments**

- `x` a numeric vector corresponding to the quantitative variable
- `tre` a tree of class `phylo`, `phylo4` or `phylo4d`
- `orthobas` an object of class ‘orthobasis’
- `prox` a matrix of phylogenetic proximities as returned by `proxTips`
- `nrepet` an integer giving the number of permutations
- `posinega` a parameter for the ratio test. If posinega > 0, the function computes the ratio test.
- `tol` a tolerance threshold for orthonormality condition
The function computes the variance decomposition of a quantitative vector \( x \) on an orthonormal basis \( B \). The variable is normalized given the uniform weight to eliminate problem of scales. It plots the squared correlations \( R^2 \) between \( x \) and vectors of \( B \) (variance decomposition) and the cumulated squared correlations \( SR^2 \) (cumulative decomposition). The function also provides five non-parametric tests to test the existence of autocorrelation. The tests derive from the five following statistics:

- \( \text{R2Max} = \max(R^2) \): It takes high value when a high part of the variability is explained by one score.
- \( \text{SkR2k} = \sum_{i=1}^{n-1} (iR^2_i) \): It compares the part of variance explained by internal nodes to the one explained by end nodes.
- \( \text{Dmax} = \max_{m=1,...,n-1} (\sum_{j=1}^{m} R^2_j - \frac{m}{n-1}) \): It examines the accumulation of variance for a sequence of scores.
- \( \text{SCE} = \sum_{m=1}^{n-1} (\sum_{j=1}^{m} R^2_j - \frac{m}{n-1})^2 \): It examines also the accumulation of variance for a sequence of scores.
- \( \text{ratio} \): depends on the parameter \( \text{posinega} \). If \( \text{posinega} > 0 \), the statistic ratio exists and equals \( \sum_{i=1}^{\text{posinega}} R^2_i \). It compares the part of variance explained by internal nodes to the one explained by end nodes when we can define how many vectors correspond to internal nodes.

**Value**

If \( \text{high.scores} = 0 \), returns an object of class `krandtest` (randomization tests) corresponding to the five non-parametric tests.

If \( \text{high.scores} > 0 \), returns a list containing:

- \( \text{w} \): an object of class `krandtest` (randomization tests)
- \( \text{scores.order} \): a vector which terms give labels of vectors that explain the larger part of variance

**Note**

This function replaces the former version from the ade4 package, which is deprecated. Note that if ade4 is not loaded BEFORE adephylo, then the version from ade4 will erase that of adephylo, which will still be available from adephylo::orthogram. In practice, though, this should never happen, since ade4 is loaded as a dependence by adephylo.
**Author(s)**

Original code: Sébastien Ollier and Daniel Chessel.

Current maintainer: Stéphane Dray <dray@biomserv.univ-lyon1.fr>

**References**


**See Also**

`orthobasis.phylo`

**Examples**

```r
## Not run:
if(require(ape) && require(phylobase)){

## a phylogenetic example
data(ungulates)
tre <- read.tree(text=ungulates$tre)
plot(tre)

## look at two traits
afbw <- log(ungulates$tab[,1])
neonatw <- log((ungulates$tab[,2]+ungulates$tab[,3])/2)
names(afbw) <- tre$tip.label
names(neonatw) <- tre$tip.label
plot(afbw, neonatw) # relationship between traits
lm1 <- lm(neonatw~afbw)
resid <- residuals(lm1)
abline(lm1)

## plot the two traits and the residuals of lm1
x <- phylo4d(tre, cbind.data.frame(afbw, neonatw, residuals=resid))
table.phylo4d(x) # residuals are surely not independant

## default orthogram for residuals of lm1
orthogram(resid, tre)

## using another orthonormal basis (derived from Abouheif’s proximity)
myOrthoBasis <- orthobasis.phylo(tre, method="oriAbouheif") # Abouheif’s proximities
orthogram(resid, ortho=myOrthoBasis) # significant phylog. signal

## Abouheif’s test
W <- proxTips(tre, method="oriAbouheif") # proximity matrix
abouheif.moran(resid, W)
}
```

## End(Not run)
**palm**

*Phylogenetic and quantitative traits of amazonian palm trees*

---

**Description**

This data set describes the phylogeny of 66 amazonian palm trees. It also gives 7 traits corresponding to these 66 species.

**Usage**

```r
data(palm)
```

**Format**

palm is a list containing the 2 following objects:

- **tre** is a character string giving the phylogenetic tree in Newick format.
- **traits** is a data frame with 66 species (rows) and 7 traits (columns).

**Details**

Variables of palm$traits are the following ones:
- **rord**: specific richness with five ordered levels
- **h**: height in meter (squared transform)
- **dqual**: diameter at breast height in centimeter with five levels: subterranean, d1(0, 5 cm), d2(5, 15 cm), d3(15, 30 cm) and d4(30, 100 cm)
- **vfruit**: fruit volume in \(mm^3\) (logged transform)
- **vgrain**: seed volume in \(mm^3\) (logged transform)
- **aire**: spatial distribution area (\(km^2\))
- **alti**: maximum altitude in meter (logged transform)

**Note**

This dataset replaces the former version in ade4.

**Source**

This data set was obtained by Clémentine Gimaret-Carpentier
<gimaret@biomserv.univ-lyon1.fr>.

**Examples**

```r
## Not run:
if(require(ape) && require(phylobase)){

## load data, make a tree and a phylo4d object
data(palm)
```
ppca <- read.tree(text=palm$tre)
ord <- as.integer(palm$traits$ord)  # just use this for plotting purpose
traits <- data.frame(ord, palm$traits[,,-1])
x <- phylo4d(tre, traits)

## plot data
par(mar=rep(.1,4))
table.phylo4d(x, cex.lab=.6)

## test phylogenetic autocorrelation
if(require(ade4)){
  prox <- proxTips(x, method="sumDD")
  phylAutoTests <- gearymoran(prox, traits[,,-3], nrep=499)
  plot(phylAutoTests)
}
}

## End(Not run)

---

**ppca**

*Phylogenetic principal component analysis*

**Description**

These functions are designed to perform a phylogenetic principal component analysis (pPCA, Jombart et al. 2010) and to display the results.

**ppca** performs the phylogenetic component analysis. Other functions are:

- `print.p pca`: prints the p pca content
- `summary.p pca`: provides useful information about a p pca object, including the decomposition of eigenvalues of all axes
- `scatter.p pca`: plot principal components using `table.phylo4d`
- `screeplot.p pca`: graphical display of the decomposition of pPCA eigenvalues
- `plot.p pca`: several graphics describing a p pca object

**Usage**

```r
ppca(x, prox=NULL, method=c("patristic","nNodes","oriAbouheif","Abouheif","sumDD"), a=1,
  center=TRUE, scale=TRUE, scannf=TRUE, nfposi=1, nfnega=0)
```

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

## S3 method for class 'ppca'
summary(object, ..., printres=TRUE)

## S3 method for class 'ppca'
scatter(x, axes = 1:ncol(x$li), useLag = FALSE, ...)

## S3 method for class 'ppca'
screepplot(x, ..., main=NULL)

## S3 method for class 'ppca'
plot(x, axes = 1:ncol(x$li), useLag=FALSE, ...)

**Arguments**

- **x** a `phylo4d` object (for `ppca`) or a `ppca` object (for other methods).
- **prox** a matrix of phylogenetic proximities as returned by `proxTips`. If not provided, this matrix will be constructed using the arguments `method` and `a`.
- **method** a character string (full or abbreviated without ambiguity) specifying the method used to compute proximities; possible values are:
  - `patrismic`: (inversed sum of) branch lengths
  - `nNodes`: (inversed) number of nodes on the path between the nodes
  - `oriAbouheif`: original Abouheif’s proximity, with diagonal (see details in `proxTips`)
  - `Abouheif`: Abouheif’s proximity (see details in `proxTips`)
  - `sumDD`: (inversed) sum of direct descendants of all nodes on the path (see details in `proxTips`).
- **a** the exponent used to compute the proximity (see `?proxTips`).
- **center** a logical indicating whether traits should be centred to mean zero (TRUE, default) or not (FALSE).
- **scale** a logical indicating whether traits should be scaled to unit variance (TRUE, default) or not (FALSE).
- **scannf** a logical stating whether eigenvalues should be chosen interactively (TRUE, default) or not (FALSE).
- **nfposi** an integer giving the number of positive eigenvalues retained (`'global structures'`).
- **nfnega** an integer giving the number of negative eigenvalues retained (`'local structures'`).
- **...** further arguments passed to other methods. Can be used to provide arguments to `table.phylo4d` in `plot` method.
- **object** a `ppca` object.
- **printres** a logical stating whether results should be printed on the screen (TRUE, default) or not (FALSE).
- **axes** the index of the principal components to be represented.
useLag a logical stating whether the lagged components (xl$s) should be used instead of the components (xl$i).

main a title for the screeplot; if NULL, a default one is used.

Details

The phylogenetic Principal Component Analysis (pPCA, Jombart et al., 2010) is derived from the spatial Principal Component Analysis (spca, Jombart et al., 2008), implemented in the adegenet package (see spca).

pPCA is designed to investigate phylogenetic patterns a set of quantitative traits. The analysis returns principal components maximizing the product of variance of the scores and their phylogenetic autocorrelation (Moran’s I), therefore reflecting life histories that are phylogenetically structured. Large positive and large negative eigenvalues correspond to global and local structures.

Value

The class ppca are given to lists with the following components:

eig a numeric vector of eigenvalues.

nfposi an integer giving the number of global structures retained.
nfnega an integer giving the number of local structures retained.
c1 a data.frame of loadings of traits for each axis.
li a data.frame of coordinates of taxa onto the ppca axes (i.e., principal components).
ls a data.frame of lagged principal components; useful to represent of global scores.
as a data.frame giving the coordinates of the axes of an ‘ordinary’ PCA onto the ppca axes.
call the matched call.
tre a phylogenetic tre with class phylo4.
prox a matrix of phylogenetic proximities.

Other functions have different outputs:

- scatter.p pca returns the matched call.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>
ppca

References


See Also

The implementation of spca in the adegenet package (adegenet)

Examples

data(lizards)

if(require(ape) & require(phylobase)){

    ### ORIGINAL EXAMPLE FROM JOMBART ET AL 2010 ###

    # BUILD A TREE AND A PHYLO4D OBJECT
    liz.tre <- read.tree(text=lizards$tree)
    liz.4d <- phylo4d(liz.tre, lizards$traits)
    par(mar=rep(.1,4))
    table.phylo4d(liz.4d, var.lab=c(names(lizards$traits),
        "ACP \\
        "size effect""), show.node=FALSE, cex.lab=1.2)

    # REMOVE DUPLICATED POPULATIONS
    liz.4d <- prune(liz.4d, c(7,14))
    table.phylo4d(liz.4d)

    # CORRECT LABELS
        "Pb", "Pm", "Ae", "Tt", "Ts", "Lviv", "La", "Ls", "Lvir")
    tiplabels(liz.4d) <- lab

    # REMOVE SIZE EFFECT
    dat <- tdata(liz.4d, type="tip")
    dat <- log(dat)
    newdat <- data.frame(lapply(dat, function(v) residuals(lm(v~mean.L)))))
    rownames(newdat) <- rownames(dat)
    tdata(liz.4d, type="tip") <- newdat[-1] # replace data in the phylo4d object

    # pPCA
    liz.p pca <- ppca(liz.4d, scale=FALSE, scannf=FALSE, nfposi=1, nfnega=1, method="Abouheif")
    liz.p pca
    tempcol <- rep("grey",7)}
tempcol[c(1,7)] <- "black"
barplot(liz.ppca$eig,main='pPCA eigenvalues',cex.main=1.8,col=tempcol)

par(mar=rep(.1,4))
plot(liz.ppca,ratio.tree=.7)

## CONTRIBUTIONS TO PC (LOADINGS) (viewed as dotcharts)
dotchart(liz.ppca$c[,1],lab=rownames(liz.ppca$c1),main="Global principal component 1")
abline(v=0,lty=2)
dotchart(liz.ppca$c[,2],lab=rownames(liz.ppca$c1),main="Local principal component 1")
abline(v=0,lty=2)

## REPRODUCE FIGURES FROM THE PAPER
obj.ppca <- liz.4d
tdata(obj.ppca, type="tip") <- liz.ppca$li
mylab <- paste(" ",rownames(liz.ppca$li), sep="")

## FIGURE 1
par(mar=c(.1,4.2,1.1))
table.phylo4d(obj.ppca, ratio=.7, var.lab=c("1st global PC", "1st local PC"), tip.label=myLab, box=FALSE,cex.lab=1.4, cex.sym=1.2, show.node.label=TRUE)
add.scatter.eig(liz.ppca$eig,1,1,1, csub=.2, posi="topleft", ratio=.23)

## FIGURE 2
s.arrow(liz.ppca$c1,xlim=c(-1,1),clab=1.3, cgrid=1.3)

#### ANOTHER EXAMPLE - INCLUDING NA REPLACEMENT ####
## LOAD THE DATA
data(maples)
tre <- read.tree(text=maples$tre)
x <- phylo4d(tre, maples$tab)

## FUNCTION TO REPLACE NAS
f1 <- function(vec){
  if(any(is.na(vec))){
    m <- mean(vec, na.rm=TRUE)
    vec[is.na(vec)] <- m
  }
  return(vec)
}
# procella

Phylogeny and quantitative traits of birds

## Description

This data set describes the phylogeny of 19 birds as reported by Bried et al. (2002). It also gives 6 traits corresponding to these 19 species.

## Usage

data(procella)

## Format

procella is a list containing the 2 following objects:

- **tre** is a character string giving the phylogenetic tree in Newick format.
- **traits** is a data frame with 19 species and 6 traits
Details

Variables of procella$traits are the following ones:
- site.fid: a numeric vector that describes the percentage of site fidelity
- mate.fid: a numeric vector that describes the percentage of mate fidelity
- mass: an integer vector that describes the adult body weight (g)
- ALE: a numeric vector that describes the adult life expectancy (years)
- BF: a numeric vector that describes the breeding frequencies
- col.size: an integer vector that describes the colony size (no nests monitored)

Note

This dataset replaces the former version in ade4.

References


Examples

```r
## Not run:
if(require(ape) && require(phylorbase)){

## load data, make tree and phylo4d object
data(procella)
tre <- read.tree(text=procella$tre)
x <- phylo4d(tre, procella$traits)
par(mar=rep(.1,4))
table.phylo4d(x, cex.lab=.7)
}
## End(Not run)
```

**proxTips**

Compute some phylogenetic proximities between tips

Description

The function proxTips computes a given proximity between a set of tips of a phylogeny. A vector of tips is supplied: proximities between all possible pairs of these tips are computed. The proximities are computed from the shortest path between the tips.

Proximities are computed as the inverse (to the power a) of a phylogenetic distance (computed by distTips). Denoting $D = [d_{ij}]$ a matrix of phylogenetic distances, the proximity matrix $M = [m_{ij}]$ is computed as:

$$m_{ij} = \frac{1}{d_{ij}^a} \forall i \neq j$$
and 
\[ m_{ii} = 0 \]

Several distances can be used, defaulting to the sum of branch lengths (see argument method). Proximities are not true similarity measures, since the proximity of a tip with itself is always set to zero.

The obtained matrix of phylogenetic proximities \( M \) defines a bilinear symmetric form when \( M \) is symmetric (default):
\[ f(x, y) = x^T M y \]

In general, \( M \) is not a metric because it is not positive-definite. Such a matrix can be used to measure phylogenetic autocorrelation (using Moran’s index):
\[ I(x) = \frac{x^T M x}{\text{var}(x)} \]

or to compute lag vectors \( Mx \) used in autoregressive models, like:
\[ x = M x + \ldots + e \]

where ‘...' is the non-autoregressive part of the model, and ‘e’ are residuals.

Usage

\[
\text{proxTips}(x, \text{tips}, \text{method}=c("patristic","nNodes","oriAbouheif","Abouheif","sumDD"), a=1, \text{normalize}=c("row","col","none"), \text{symmetric}=\text{TRUE}, \text{useC}=\text{TRUE})
\]

Arguments

- \( x \) a tree of class \text{phylo}, \text{phylo4} or \text{phylo4d}.
- \( \text{tips} \) A vector of integers identifying tips by their numbers, or a vector of characters identifying tips by their names. Distances will be computed between all possible pairs of tips.
- \( \text{method} \) a character string (full or abbreviated without ambiguity) specifying the method used to compute proximities; possible values are:
  - \text{patristic}: (inversed sum of) branch length
  - \text{nNodes}: (inversed) number of nodes on the path between the nodes
  - \text{oriAbouheif}: original Abouheif’s proximity, with diagonal (see details)
  - \text{Abouheif}: Abouheif’s proximity without diagonal (see details)
  - \text{sumDD}: (inversed) sum of direct descendants of all nodes on the path (see details)
- \( a \) the exponent used to compute the proximity
- \( \text{normalize} \) a character string specifying whether the matrix must be normalized by row (row), column (col), or not (none). Normalization amounts to dividing each row (or column) so that the marginal sum is 1. Hence, default is matrix with each row summing to 1.
proxTips

symmetric

A logical stating whether M must be coerced to be symmetric (TRUE, default) or not. This is achieved by taking (denoting N the matrix of proximities before re-symmetrization):

\[ M = 0.5 \times (N + N^T) \]

Note that \( x^T N y = x^T M y \), but the latter has the advantage of using a bilinear symmetric form (more appropriate for optimization purposes).

useC

A logical indicating whether computations of distances (before transformation into proximities) should be performed using compiled C code (TRUE, default), or using a pure R version (FALSE). C version is several orders of magnitude faster, and R version is kept for backward compatibility.

Details

Abouheif proximity refers to the phylogenetic proximity underlying the test of Abouheif (see references). Let \( P \) be the set of all the nodes in the path going from node1 to node2. Let DDP be the number of direct descendants from each node in \( P \). Then, the so-called ‘Abouheif’ distance is the inverse of the product of all terms in DDP. oriAbouheif returns a matrix with non-null diagonal elements, as formulated in Pavoine et al. (2008). This matrix is bistochastic (all marginal sums equal 1), but this bilinear symmetric form does not give rise to a Moran’s index, since it requires a null diagonal. Abouheif contains Abouheif’s proximities but has a null diagonal, giving rise to a Moran’s index.

sumDD refers to a phylogenetic proximity quite similar to that of Abouheif. We consider the same sets \( P \) and DDP. But instead of taking the inverse of the product of all terms in DDP, this proximity computes the inverse of the sum of all terms in DDP. This matrix was denoted ’\( M \)’ in Pavoine et al. (2008), who reported that it is related to May’s index (May, 1990).

Value

A matrix of phylogenetic proximities.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

References

== About Moran’s index with various proximities ==

== About regression on phylogenetic lag vector ==

== Abouheif’s original paper ==

== May’s index ==

See Also

distTips which computes several phylogenetic distances between tips.

Examples

```r
if(require(ape) & require(phylobase)){
  ## make a tree
  x <- as(rtree(10),"phylo4")
  plot(x, show.node=TRUE)
  axisPhylo()
  ## compute different distances
  proxTips(x, 1:5)
  proxTips(x, 1:5, "nNodes")
  proxTips(x, 1:5, "Abouheif")
  proxTips(x, , "sumDD")

  ## see what one proximity looks like
  M <- proxTips(x)
  obj <- phylo4d(x,as.data.frame(M))
  table.phylo4d(obj,symbol="sq")
}
```

---

**sp.tips**

*Find the shortest path between tips of a tree*

---

**Description**

The function `sp.tips` finds the shortest path between tips of a tree, identified as `tip1` and `tip2`. This function applies to trees with the class `phylo`, `phylo4` or `phylo4d`. Several tips can be provided at a time.

**Usage**

`sp.tips(x, tip1, tip2, useTipNames=FALSE, quiet=FALSE, include.mrca=TRUE)`
Arguments

- **x**: A tree of class `phylo`, `phylo4` or `phylo4d`.
- **tip1**: A vector of integers identifying tips by their numbers, or a vector of characters identifying tips by their names. Recycled if needed.
- **tip2**: A vector of integers identifying tips by their numbers, or a vector of characters identifying tips by their names. Recycled if needed.
- **useTipNames**: a logical stating whether the output must be named using tip names in all cases (TRUE), or not (FALSE). If not, names of tip1 and tip2 will be used.
- **quiet**: a logical stating whether a warning must be issued when tip1==tip2, or not (see details).
- **include.mrca**: a logical stating whether the most recent common ancestor shall be included in the returned path (TRUE, default) or not (FALSE).

Details

The function checks if there are cases where tip1 and tip2 are the same. These cases are deleted when detected, issuing a warning (unless quiet is set to TRUE).

Value

A list whose components are vectors of named nodes forming the shortest path between a couple of tips.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

See Also

- `shortestPath` which does the same thing as `sp.tips`, for any node (internal or tip), but much more slowly.

Examples

```r
## Not run:
if(require(ape) & require(phylobase)){
  ## make a tree
  x <- as(rtree(20),"phylo4")
  plot(x,show.node=TRUE)
  ## get shortest path between tip 1 and all other tips.
  sp.tips(x, "t1", "t2")
  sp.tips(x, 1, 2:20, TRUE)
}

## End(Not run)
```
Graphical display of phylogeny and traits

definition
This function represents traits onto the tips of a phylogeny. Plotted objects must be valid phylo4d objects (implemented by the phylobase package). Current version allows plotting of a tree and one or more quantitative traits (possibly containing missing data, represented by an 'x').

The plot of phylogenies is performed by a call to plot.phylo from the ape package. Hence, many of the arguments of plot.phylo can be passed to table.phylo4d, through the ... argument, but their names must be complete.

For large trees, consider using bullseye.

usage

table.phylo4d(x, treetype=c("phylogram","cladogram"),
    symbol=c("circles","squares","colors"),
    repVar=1:ncol(tdata(x, type="tip")), center=TRUE,
    scale=TRUE, legend=TRUE, grid=TRUE, box=TRUE,
    show.tip.label=TRUE, show.node.label=TRUE,
    show.var.label=TRUE, ratio.tree=1/3, font=3,
    tip.label=tipLabels(x),
    var.label=colnames(tdata(x, type="tip")), cex.symbol=1,
    cex.label=1, cex.legend=1, pch=20, col=heat.colors(100),
    coord.legend=NULL, ...)

arguments

x
a phylo4d object

treetype
the type of tree to be plotted ("phylogram" or "cladogram")

symbol
the type of symbol used to represent data ("circles", "squares", or "colors")

repVar
the numerical index of variables to be plotted

center
a logical stating whether variables should be centred (TRUE, default) or not (FALSE)

scale
a logical stating whether variables should be scaled (TRUE, default) or not (FALSE)

legend
a logical stating whether a legend should be added to the plot (TRUE, default) or not (FALSE)

grid
a logical stating whether a grid should be added to the plot (TRUE, default) or not (FALSE)

box
a logical stating whether a box should be added around the plot (TRUE, default) or not (FALSE)
show.tip.label a logical stating whether tip labels should be printed (TRUE, default) or not (FALSE)
show.node.label a logical stating whether node labels should be printed (TRUE, default) or not (FALSE)
show.var.label a logical stating whether labels of variables should be printed (TRUE, default) or not (FALSE)
ratio.tree the proportion of width of the figure occupied by the tree
font an integer specifying the type of font for the labels: 1 (plain text), 2 (bold), 3 (italic, default), or 4 (bold italic).
tip.label a character vector giving the tip labels
var.label a character vector giving the labels of variables
cex.symbol a numeric giving the factor scaling the symbols
cex.label a numeric giving the factor scaling all labels
cex.legend a numeric giving the factor scaling the legend
pch is symbol is set to 'colors', a number indicating the type of point to be plotted (see ?points)
col is symbol is set to 'colors', a vector of colors to be used to represent the data
coord.legend an optional list with two components 'x' and 'y' indicating the lower-left position of the legend. Can be set to locator(1) to position the legend interactively.
... further arguments to be passed to plot methods from ape. See plot.phylo.

Details

The function table.phylo4d is based on former plot method for phylo4d objects from the phylobase package. It replaces the deprecated ade4 functions symbols.phylog and table.phylog.

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

See Also

The phylo4d class for storing phylogeny+data.

For large trees, consider using bullseye.
plot.phylo from the ape package.

An alternative (deprecated) representation is available from dotchart.phylog.
Examples

```r
if(require(ape) & require(phylobase) & require(ade4)){

## simulated data
tr <- rtree(20)
dat <- data.frame(a = rnorm(20), b = scale(1:20), c=runif(20,-2,2))
dat[3:6, 2] <- NA # introduce some NAs
obj <- phylo4d(tr, dat) # build a phylo4d object
table.phylo4d(obj) # default scatterplot
table.phylo4d(obj, cex.leg=.6, use.edge.length=FALSE) # customized

table.phylo4d(obj, treetype="clad", show.node=FALSE, cex.leg=.6,
use.edge.length=FALSE, edge.color="blue", edge.width=3) # more customized

## teleost fishes data
data(mjrochet)
temp <- read.tree(text=mjrochet$tre) # make a tree
mjr <- phylo4d(x=temp, tip.data=mjrochet$tab) # make a phylo4d object
table.phylo4d(mjr, cex.lab=.5, show.node=FALSE, symb="square")

## lizards data
data(lizards)
liz.tr <- read.tree(tex=lizards$hpra) # make a tree
liz <- phylo4d(liz.tr, lizards$traits) # make a phylo4d object
table.phylo4d(liz)

## plotting principal components
liz.pca1 <- dudi.pca(lizards$traits, scannf=FALSE, nf=2) # PCA of traits
myPC <- phylo4d(liz.tr, liz.pca1$l1) # store PC in a phylo4d object
varlab <- paste("Principal \ncomponent", 1:2) # make labels for PCs
table.phylo4d(myPC, ratio=.8, var.lab=varlab) # plot the PCs
add.scatter.eig(liz.pca1$eig, 2, 1, 2, pos="topleft", inset=c(0,.15))
title("Phylogeny and the principal components")
}
```

---

**tithonia**

*Phylogeny and quantitative traits of flowers*

**Description**

This data set describes the phylogeny of 11 flowers as reported by Morales (2000). It also gives morphologic and demographic traits corresponding to these 11 species.

**Usage**

data(tithonia)
**Format**

*tithonia* is a list containing the 2 following objects:

- **tre** is a character string giving the phylogenetic tree in Newick format.
- **tab** is a data frame with 11 species and 14 traits (6 morphologic traits and 8 demographic).

**Details**

Variables of *tithonia$tab* are the following ones:
- morho1: is a numeric vector that describes the seed size (mm)
- morho2: is a numeric vector that describes the flower size (mm)
- morho3: is a numeric vector that describes the female leaf size (cm)
- morho4: is a numeric vector that describes the head size (mm)
- morho5: is an integer vector that describes the number of flowers per head
- morho6: is an integer vector that describes the number of seeds per head
- demo7: is a numeric vector that describes the seedling height (cm)
- demo8: is a numeric vector that describes the growth rate (cm/day)
- demo9: is a numeric vector that describes the germination time
- demo10: is a numeric vector that describes the establishment (per cent)
- demo11: is a numeric vector that describes the viability (per cent)
- demo12: is a numeric vector that describes the germination (per cent)
- demo13: is an integer vector that describes the resource allocation
- demo14: is a numeric vector that describes the adult height (m)

**Note**

This dataset replaces the former version in ade4.

**Source**


**Examples**

```r
if(require(ape) && require(phylbase)){

data(tithonia)
tre <- read.tree(text=tithonia$tre)
traits <- log(tithonia$tab + 1)
rownames(traits) <- gsub("-", ".", rownames(traits))

## build a phylo4d object
x <- phylo4d(tre, traits)
par(mar=rep(.1,4))
table.phylo4d(x)
}
```
Define partitions of tips according from a tree

Description

The function treePart defines partitions of tips reflecting the topology of a tree. There are two possible outputs (handled by the argument result):
- basis mode: each node but the root is translated into a dummy vector having one value for each tip: this value is '1' if the tip descends from this node, and '0' otherwise.
- orthobasis: in this mode, an orthonormal basis is derived from the basis previously mentioned. This orthobasis was proposed in the orthogram (Ollier et al. 2006).

Usage

treePart(x, result=c("dummy", "orthobasis"))

Arguments

x a tree of class phylo, phylo4 or phylo4d.
result a character string specifying the type of result: either a basis of dummy vectors (dummy), or an orthobasis derived from these dummy vectors (orthobasis).

Details

Orthobasis produced by this function are identical to those stored in the \$Bscores component of deprecated phylog objects, from the ade4 package.

Value

A matrix of numeric vectors (in columns) having one value for each tip (rows).

Author(s)

Thibaut Jombart <tjombart@imperial.ac.uk>

References


See Also

- listDD which is called by treePart.
- orthogram, which uses by default the orthobasis produced by treePart.
ungulates

Description

This data set describes the phylogeny of 18 ungulates as reported by Pélabon et al. (1995). It also gives 4 traits corresponding to these 18 species.

Usage

data(ungulates)

Format

fission is a list containing the 2 following objects:

- **tre** is a character string giving the phylogenetic tree in Newick format.
- **tab** is a data frame with 18 species and 4 traits

Details

Variables of `ungulates$tab` are the following ones:

- `afbw`: is a numeric vector that describes the adult female body weight (g)
- `mnw`: is a numeric vector that describes the male neonatal weight (g)
- `fnw`: is a numeric vector that describes the female neonatal weight (g)
- `ls`: is a numeric vector that describes the litter size

Note

This dataset replaces the former version in ade4.
Source


Examples

```r
## Not run:
if(require(ape) && require(phylobase)){
  ## load data
data(ungulates)
tre <- read.tree(text=ungulates$tre)
plot(tre)

  ## look at two traits
afbw <- log(ungulates$tab[,1])
neonatw <- log((ungulates$tab[,2]+ungulates$tab[,3])/2)
names(afbw) <- tre$tip.label
names(neonatw) <- tre$tip.label
plot(afbw, neonatw) # relationship between traits
lm1 <- lm(neonatw~afbw)
abline(lm1)
x <- phylo4d(tre, cbind.data.frame(afbw, neonatw)) # traits on the phylogeny

  ## test phylogenetic inertia in residuals
orthogram(residuals(lm1), x)
}

## End(Not run)
```
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