

Package ‘monogeneaGM’

July 16, 2015

Version 1.0

Date 2015-07-16

Title Geometric Morphometric Analysis of Monogenean Anchors

Author Tsung Fei Khang

Maintainer Tsung Fei Khang <tfkhang@um.edu.my>

Depends R (>= 3.0.3)

Imports ape, cluster, circular, geomorph, gplots, phytools, rgl

ZipData no

Description Geometric morphometric and evolutionary biology analyses of anchor shape from four-anchored monogeneans.

License GPL (>= 2)

Repository CRAN

Date/Publication 2015-07-16 17:29:06

NeedsCompilation no

LazyData true

R topics documented:

anglecheck	2
anglePolygon	3
boxplotSort	4
colorBar	5
estimated_ancestral_va	7
heatmapAnnot	8
hsplot	9
liewi_gpa	11
ligophorus_shape	12
ligophorus_tpsdata	13
ligotree	14
matrix2list	15
matrix2list.2	16

pca2d	18
ploadhm	19
plotCircular	21
plotLM	22
polyVis	24
procrustesFit	25
procrustesFit.2	26
pwdist	28
pwed_pd	29
Qscore	29
shapeEvo	31
spcolmap	33
stdLM	33
tpColorPlot2d	35
tpColorPlot3d	36
tpsRead	38
va_mean	39
Index	40

anglecheck	<i>Angle swept by a ray</i>
------------	-----------------------------

Description

This function computes angle swept by a ray in anti-clockwise direction. The ray starts at the half-line pointing towards the positive x direction, and passes through the origin and a point defined by the user.

Usage

```
anglecheck(x, radians = TRUE)
```

Arguments

x	a vector of length 2 giving the xy-coordinates of the point defined by the user
radians	if FALSE, returns angle in degrees instead of radians

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogean anchor morphometry: systematic value, phylogenetic signal and evolution.

Examples

```
anglecheck(c(0,1),radians=FALSE)
```

anglePolygon	<i>Internal angles of a polygon</i>
--------------	-------------------------------------

Description

This function computes the internal angles of a polygon, given the coordinates of its vertices.

Usage

```
anglePolygon(point, degree = FALSE)
```

Arguments

point	a list containing coordinates of the polygon vertices in either clockwise or anti-clockwise direction
degree	if TRUE, returns the internal angles in degrees instead of radians

Details

The sum of all the internal angles of a polygon with n -vertices must be equal to the product of $n-2$ with 180 (degrees) or pi (radians). This function is useful for detecting tps data files that contain errors (e.g. wrong sequence of digitizing landmarks, missing landmarks) so that corrective steps can be taken.

Value

A list with two components:

angle	a matrix; the rows represents the vertices and the columns contain the latters' geometrical information: first column for x coordinate, second column for y coordinate, and third column for the associated internal angle (in radians)
orientation	a character indicating the direction of ordering the vertices: m for anti-clockwise and p for clockwise

Author(s)

Thian Liang Cheow <Tl2cheow@yahoo.com>

References

Khong TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogean anchor morphometry: systematic value, phylogenetic signal and evolution.

Examples

```
#internal angles of a right-angled triangle in degrees
anglePolygon(list(c(0,1),c(0,0),c(1,0)),degree=TRUE)

data(ligophorus_tpsdata)

#polygonal approximation of anchor shape
#the right ventral anchor
anchorpolygon <- anglePolygon(matrix2list(ligophorus_tpsdata$bantingensis[[1]][1:11,]), degree=TRUE)

#there are 11 landmarks, do the sum of internal angles should be (11-2)x180 = 1620
sum(anchorpolygon$angle[,3])

#does this make sense?
polyVis(1, havelist=TRUE, listdata=ligophorus_tpsdata$bantingensis)
```

 boxplotSort

Median-ordered box plot

Description

This is a modification of the standard box plot to produce box plots ordered on the basis of descending median, for more effective graphical representation of data.

Usage

```
boxplotSort(x, italic = FALSE, srt = 45, df = 0.5, varwidth = TRUE,
  col = NULL, ylab = "", main = "", clade = NULL)
```

Arguments

<code>x</code>	a list, with species as the names of the list
<code>italic</code>	if TRUE, the species names are italicized
<code>srt</code>	the angle of the x-axis labels relative to the x-axis
<code>df</code>	displacement factor for positioning x-axis labels
<code>varwidth</code>	if TRUE, the width of the box plot for a species is proportional to the square root of the species's sample size
<code>col</code>	a character vector specifying the box colors for two clades
<code>ylab</code>	y-axis title
<code>main</code>	title for the plot
<code>clade</code>	a character vector specifying the species names for the first clade; currently supports only two clades

Details

The box plots produced using this function are helpful for documenting sample quality score distributions of each species. They are also useful for checking the distribution of pairwise Euclidean distance between two landmarks.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal, and evolution.

See Also

[Qscore](#)

Examples

```
data(pwed_pd)
pwed_pd <- matrix2list.2(pwed_pd)

cladeI <- c("liewi", "fenestrum", "grandis", "johorensis", "kedahensis", "kederai")
#We just want to look at distance between LM1 and LM3 in for dorsal anchor
boxplotSort(lapply(pwed_pd, function(k) k[,which(colnames(k)=="D1_3")] ), italic=TRUE,
col=c("dodgerblue", "violetred"), clade=cladeI,
ylab=expression(paste("Length ", "(", italic(mu), "m", ")")))

#Separation of two lineage seems possible at 15 micrometers
abline(h=15)
```

colorBar

Add a color bar

Description

This function produces a color bar.

Usage

```
colorBar(colpalette = NULL, min, max = -min, nticks = 11,
ticks = seq(min, max, len = nticks), tit = "")
```

Arguments

colpalette	a color palette supplied by the user; defaults to the red-white-blue palette if left undefined
min	the smallest numeric value corresponding to the color on the extreme left of the color palette
max	the largest numeric value corresponding to the color on the extreme right of the color palette
nticks	number of tick lines on the color bar
ticks	spacing for the tick marks on the color bar
tit	title for the color bar

Details

This R code is based on John Colby's (2011) `color.bar` code. A user-defined color palette can be generated using the `colorRampPalette` function. See www.colorbrewer2.org for interesting color palette options.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

- Colby J. (2011). Color bar legends for neuroimaging in R. Available at <http://www.colbyimaging.com/wiki/statistics/color-bars>.
- Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[ploadhm](#), [colorRampPalette](#)

Examples

```
#define a color scale
tones <- c("#99000D", "#FB6A4A", "white", "#6BAED6", "#084594")
multihue <- colorRampPalette(tones, space = "Lab")(101)

#create a two-panel figure with width ratio of 4:1
nf <- layout(matrix(c(1,1,1,1,2),2,5,byrow=TRUE))
layout.show(nf)

#mapping a matrix of randomly chosen numbers between -1 and 1 to
#colors in the color scale
h <- matrix(runif(100, -1, 1),10,10)
image(h,col=multihue,xaxt="n", yaxt="n")

#add color bar
```

```
par(mar=c(5,5,5,2))  
colorBar(colpalette=multihue, min=-1,max=1)
```

estimated_ancestral_va

Estimated Generalized Procrustes Analysis (GPA) coordinates of ventral anchors of root ancestor

Description

Estimated GPA landmark configuration of the ventral anchors of the root ancestor of 13 *Ligophorus* species.

Usage

```
data(estimated_ancestral_va)
```

Format

A matrix of 11 rows (landmarks) and 2 columns (xy-coordinates) representing the estimated GPA landmark configuration of the ventral anchors of the root ancestor (left and right anchors averaged).

Details

The root ancestor's GPA landmark configuration is unknown, but can be estimated using similar data from extant species. The estimation is done using `fastAnc` function in the `phytools` package (Revell, 2012). Root ancestor mean GPA coordinates of anchor landmarks are required for shape evolution analysis.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

References

Revell LJ. (2012). `phytools`: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* 3:217-223.

See Also

[shapeEvo](#)

Examples

```

library(gplots)
library(circular)

data(va_mean)
data(estimated_ancestral_va)
data(spcolmap)

cladeII <- spcolmap$species[spcolmap$host %in% "L.subviridis"]
shapeEvo(va_mean, estimated_ancestral_va, col.lab="dodgerblue",
clade=cladeII, exfac=2, tit="Ventral anchors")

#Some journals want the title to be left-adjusted, so set tit="" and then:
#title("a)", adj=0)

```

heatmapAnnot

Annotated heat map

Description

This function produces a heat map with hierarchical clustering of samples using multivariate size or shape data.

Usage

```
heatmapAnnot(x, labcol, xlab = "", ylab = "", genus = "", rowlab = TRUE,
pt = 0.25)
```

Arguments

x	a matrix with rows representing species samples and columns representing morphometrical variables of interest
labcol	a character vector giving the color annotation for the species
xlab	title for x-axis
ylab	title for y-axis
genus	single character abbreviation for genus
rowlab	if FALSE, suppresses row labels on the heat map
pt	if the rows have been ranked, two lines are drawn - one at the ptx100th percentile (bottom), the other at the (1-pt)x100th percentile (top); set to 0 to disable

Details

This function customizes the heatmap.2 function in the gplots package (Version 2.17.0). Pairwise distances between samples are computed using unsquared Euclidean distance, therefore clustering is based on the generalized Ward criterion (Batagelj, 1988). Row standardization is switched on, and a color legend for species is given in the left panel.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Batagelj V. (1988). Generalized Ward and related clustering problems. In: Classification and Related Methods of Data Analysis. H.H.Bock (ed.). Amsterdam: North-Holland, pp. 67-74.

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogean anchor morphometry: systematic value, phylogenetic signal and evolution.

Warnes GR, Bolker B, Bonebakker L, Gentleman R, Huber W, Liaw A, Lumley T, Maechler M, Magnusson M, Moeller S, Schwartz M, Venables B. (2015). gplots: Various R programming tools for plotting data. R package version 2.17.0. Available at: <http://CRAN.R-project.org/package=gplots>.

Examples

```
library(gplots)

data(ligophorus_shape)
data(spcolmap)

dendrogram <- hclust(dist(ligophorus_shape))

#check dendrogram and note cut-off for the two main clades
plot(dendrogram)

clade_id <- cutree(dendrogram, h=0.55)

f_s <- numeric(ncol(ligophorus_shape))

for(i in 1:ncol(ligophorus_shape)){
  dat <- stack(ligophorus_shape[,i])
  #replace species label with clade label
  dat[,2] <- clade_id
  f_s[i] <- t.test(values~ind, data=dat)$statistic
}

rank_s <- order(f_s, decreasing=TRUE)

heatmapAnnot(ligophorus_shape[,rank_s], labcol=spcolmap$color,
  xlab="Specimens", genus="L. ")
```

hsplot

Scatter plot with marginal histograms

Description

This function creates a scatter plot that is augmented with marginal histograms (with smoothed splines) on the x and y-axes.

Usage

```
hsplot(dat, seqx, seqy, ybound, xbound, y.label = "", x.label = "", labcol,
       type = "ru", sep1, sep2, phylo = FALSE, phy, pointscale = 1.5,
       supp.hist.y = FALSE, supp.hist.x = FALSE, y.axis.label = TRUE,
       x.axis.label = TRUE, addline = NULL)
```

Arguments

<code>dat</code>	a matrix with rows representing species samples and two columns representing the variables of interest (typically a selected principal component of size and shape variables)
<code>seqx</code>	range of values on the x-axis, for histogram plotting
<code>seqy</code>	range of values on the y-axis, for histogram plotting
<code>ybound</code>	range of values on the y-axis
<code>xbound</code>	range of values on the x-axis
<code>y.label</code>	title for y-axis
<code>x.label</code>	title for x-axis
<code>labcol</code>	a character vector giving the color annotation for species names in alphabetical order
<code>type</code>	a character that controls where the marginal histograms are located: right-up ("ru"), left-up ("lu"), left-down ("ld"), right-down ("rd")
<code>sep1</code>	tick mark separation for x-axis
<code>sep2</code>	tick mark separation for y-axis
<code>phylo</code>	if TRUE, the centroids of species are joined into a tree-like object corresponding to their phylogeny given in <code>phy</code>
<code>phy</code>	a tree object of class <code>phylo</code>
<code>pointscale</code>	a constant specifying the symbol size of the centroids
<code>supp.hist.y</code>	if TRUE, suppresses the plotting of marginal histogram at the y-axis
<code>supp.hist.x</code>	if TRUE, suppresses the plotting of marginal histogram at the x-axis
<code>y.axis.label</code>	if FALSE, suppresses the y-axis title
<code>x.axis.label</code>	if FALSE, suppresses the x-axis title
<code>addline</code>	an optional numeric vector of length two specifying the intercept and slope of linear line

Details

This function is similar to `tpColorPlot2d`, and is mainly useful for its additional option for visualising the marginal distributions. The `ape` and `phytools` packages are required.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

- Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.
- Paradis E, Claude J & Strimmer K. (2004). APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* 20: 289-290.
- Revell LJ. (2012). phytools: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* 3:217-223.

Examples

```
library(phytools)

data(pwed_pd)
data(ligotree)
data(spcolmap)

#principal component analysis of size variables from ventral and dorsal anchors
pca2d_pwedv <- pca2d(pwed_pd[,1:55], sgn=-1, labcol=spcolmap$color,
  phylo=TRUE, phy=ligotree, genus="L. ", bound.y=c(-0.2, 0.2),
  bound.x1=c(-0.2,0.2), bound.x2 = c(-0.2,0.2))
pca2d_pwedd <- pca2d(pwed_pd[,56:110], sgn=-1, labcol=spcolmap$color,
  phylo=TRUE, phy=ligotree, genus="L. ", bound.y=c(-0.2, 0.2),
  bound.x1=c(-0.2,0.2), bound.x2 = c(-0.2,0.2))

#comparing size PC1 between ventral and dorsal anchors
hsplot(cbind(pca2d_pwedv$scores[,1], pca2d_pwedd$scores[,1]),
  seqx=seq(-0.2,0.15,0.01), seqy=seq(-0.2,0.15,0.01),
  xbound=c(-0.2,0.15), ybound=c(-0.2,0.15), y.label="Dorsal size PC1",
  x.label="Ventral size PC1", labcol=spcolmap$color, type="ru",
  sep1=0.1, sep2=0.1, phylo=FALSE, addline=c(0,1))
```

liewi_gpa	<i>Array data of Generalized Procrustes Analysis (GPA) coordinates of dorsal anchors of Ligophorus liewi samples</i>
-----------	--

Description

An array data of GPA coordinates of dorsal anchors (left-right averaged) from 31 *Ligophorus liewi* samples.

Usage

```
data(liewi_gpa)
```

Format

An array of 31 matrices, each having 11 rows (landmarks) and 2 columns (xy GPA coordinates)

Details

All samples in this array have quality score above 10.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[Qscore](#), [plotLM](#)

Examples

```
data(liewi_gpa)

nice_title <- expression(paste("Dorsal anchor ", italic(L.liewi)))
plotLM(liewi_gpa, tit=nice_title, pointscale=0.8, axispointscale=0.8,
meansize=1.2, polygon.outline=TRUE,c(-.6,.6),c(-.6,.6) )
```

ligophorus_shape *Shape variable data for 13 Ligophorus species*

Description

This data set contains shape variable data for samples from 13 *Ligophorus* species.

Usage

```
data(ligophorus_shape)
```

Format

A matrix containing 443 rows (samples) and 44 columns (shape variables). The shape variables are the GPA-coordinates of the 11 landmarks for both ventral and dorsal anchors. GPA was performed using the geomorph R package (Adams & Otárola-Castillo, 2013; Version 2.1.1 or higher).

Details

All specimens in this data set have quality score above 10.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

References

Adams DC, Otárola-Castillo E. (2013). geomorph: an R package for the collection and analysis of geometric morphometric shape data. *Methods in Ecology and Evolution* 4:393-399.

See Also

[Qscore](#)

Examples

```
library(gplots)

data(ligophorus_shape)
data(spcolmap)

#shape variables unsorted
heatmapAnnot(ligophorus_shape,labcol=spcolmap$color,xlab="Specimens",genus="L. ")
```

ligophorus_tpsdata *Raw landmark coordinate data for 13 Ligophorus species*

Description

This data set contains raw landmark coordinate data for samples from 13 *Ligophorus* species obtained using the TPSDIG2 program (Rohlf, 2013).

Usage

```
data(ligophorus_tpsdata)
```

Format

a list of 13 objects; each object is a list containing objects that are matrices with 44 rows (landmarks 1 to 11 of ventral right, ventral left, dorsal right and dorsal left anchors) and 2 columns (xy-coordinates)

Details

Quality control via Qscore has not yet been applied to this data set (n=537), so examples of good and poor quality specimens can be inspected using polyVis.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

References

Rohlf FJ. (2013). Morphometrics at SUNY Stony Brook. Available at <http://life.bio.sunysb.edu/morph/soft-dataacq.html>

See Also

[Qscore](#), [polyVis](#)

Examples

```
library(cluster)

data(ligophorus_tpsdata)

#A poor quality specimen (dissimilar dorsal anchors)
polyVis(5, havelist=TRUE, listdata=ligophorus_tpsdata$bantingensis)
#A good quality specimen
polyVis(18, havelist=TRUE, listdata=ligophorus_tpsdata$johorensis)
```

ligotree

Maximum likelihood tree for 13 Ligophorus species

Description

This data set contains the maximum likelihood (Felsenstein, 1981) phylogenetic tree of 13 *Ligophorus* species, inferred using concatenated 28S rRNA, 18S rRNA and ITS DNA sequences (500 bootstrap replicates). The best DNA substitution model was GTR+G. Multiple sequence alignment was done using online MAFFT server (Version 7; Katoh, 2013; Katoh & Standley, 2013) with default parameters.

Usage

```
data(ligotree)
```

Format

A phylo object, so the ape package (Paradis et al., 2004) needs to be installed

Details

The phylogenetic tree comes with bootstrap support for the internal nodes.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

References

Felsenstein J. (1981). Evolutionary trees from DNA sequences: A maximum likelihood approach. *Journal of Molecular Evolution* 17: 368-376.

Katoh K. (2013). MAFFT - a multiple sequence alignment program. Available at <http://mafft.cbrc.jp/alignment/server>.

Katoh K, Standley DM. (2013). MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. *Molecular Biology and Evolution* 30: 772-780.

Paradis E, Claude J & Strimmer K. (2004). APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* 20: 289-290.

See Also

[tpColorPlot2d](#)

Examples

```
library(ape)

data(ligotree)
plot.phylo(ligotree, show.node.label=TRUE)
```

matrix2list

Partitioning a matrix by row into objects of a list

Description

This function partitions each row of a matrix into objects of a list.

Usage

```
matrix2list(x)
```

Arguments

x a matrix

Details

This function converts the landmark coordinate data into a format suitable as input for `anglePolygon`.

Value

a list of objects; the number of objects is equal to the number of rows of x ; each object is a vector of length equal to the number of columns of x

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[anglePolygon](#)

Examples

```
data(ligophorus_tpsdata)

#Check right ventral anchor polygon of the first specimen
anglePolygon(matrix2list(ligophorus_tpsdata$bantingensis[[1]][1:11,]), degree=TRUE)

#Now check the rest
anglePolygon(matrix2list(ligophorus_tpsdata$bantingensis[[1]][12:22,]), degree=TRUE)
anglePolygon(matrix2list(ligophorus_tpsdata$bantingensis[[1]][23:33,]), degree=TRUE)
anglePolygon(matrix2list(ligophorus_tpsdata$bantingensis[[1]][34:44,]), degree=TRUE)

#A more efficient way of doing things
result <- mapply(function(k) {
  anglePolygon(matrix2list(ligophorus_tpsdata$bantingensis[[1]][(11*(k-1)+1):(11*k,)],
    degree=TRUE)}, k=1:4)

result_angle <- mapply(function(k) list(result[[2*k-1]]), k=1:4)
result_orientation <- mapply(function(k) list(result[[2*k]]), k=1:4)
names(result_angle) <- names(result_orientation) <- c("VR", "VL", "DR", "DL")
```

matrix2list.2

Partitioning a matrix by row labels into objects of a list

Description

This function partitions a matrix according to row labels and assigns the partitioned submatrices as objects of a list.

Usage

```
matrix2list.2(x)
```


Arguments

x a matrix with row labels, typically species names

Details

The output from this function is passed as input for `boxplotSort`.

Value

a list of objects; the number of objects is equal to the length of levels of the rownames of x. Each object is a matrix with the same row names.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[boxplotSort](#)

Examples

```
data(pwed_pd)
data(spcolmap)

pwed_pd <- matrix2list.2(pwed_pd)

cladeI <- spcolmap$species[spcolmap$host %in% "M.buchanani"]
#We just want to look at distance between LM1 and LM3 in for dorsal anchor
boxplotSort(lapply(pwed_pd, function(k) k[,which(colnames(k)=="D1_3")]),
  italic=TRUE, col=c("dodgerblue","violetred"), clade=cladeI,
  ylab=expression(paste("Length ", "(", italic(mu),"m", ")")))

#Separation of two lineage seems possible at 15 micrometers
abline(h=15)
```

pca2d

*Principal component analysis***Description**

This function performs principal component analysis (PCA) and produces color-annotated scatter plots of a reference principal component (typically the first one) against two other principal components (typically the second and third).

Usage

```
pca2d(x, a = 1:3, sgn = 1, labcol, bound.x1 = c(-0.15, 0.15),
      bound.x2 = c(-0.15, 0.15), bound.y = c(-0.15, 0.15), pointscale = 1,
      phylo = FALSE, phy, genus = "")
```

Arguments

x	a matrix with rows representing samples and columns representing morphometrical variables of interest
a	a vector of length 3 for the principal component ranks specified by the user; defaults to the first three principal components
sgn	a numeric constant, either -1 or 1, that controls the sign of the principal component scores; defaults to 1
labcol	a character vector giving the color-annotation of the species
bound.x1	a numeric vector specifying the range of values on the x-axis for the first plot
bound.x2	a numeric vector specifying the range of values on the x-axis for the second plot
bound.y	a numeric vector specifying the range of values on the y-axis for both plots
pointscale	a constant for the size of species centroids; defaults to 1
phylo	if TRUE, coordinates of ancestral nodes from a supplied phylogeny (phy) are estimated using <code>fastAnc</code> from the <code>phytools</code> package (Revell, 2012), and edges between nodes are joined according to the tree topology specified in phy
phy	an object of class <code>phylo</code>
genus	single character abbreviation for genus

Details

To be specific, this function implements an R-mode, covariance-based PCA. When variables differ in their units of measurement or show large magnitude differences, a correlation-based PCA is more reasonable. In this case, the data in the input matrix must first be normalized by subtracting mean and dividing by standard deviation. In R-mode PCA, the principal components can be interpreted contextually by checking the loadings of the variables of interest (graphically using `pcloadhm`). However, this requires that the number of rows exceeds the number of columns (variables). If specimen sample size is small, Q-mode PCA is possible. In this case, the input data matrix is transposed. Although species clusters can still be visualized, the principal components do not seem

to be interpretable. If a phylogeny of the species is available, it can be superimposed onto the principal component space to yield a phylomorphospace to provide a graphical complement to formal phylogenetic signal testing. For the latter, see `physignal` in the `geomorph` package (Adams & Otarola-Castillo, 2013).

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Adams DC, Otarola-Castillo E. (2013). `geomorph`: an R package for the collection and analysis of geometric morphometric shape data. *Methods in Ecology and Evolution* 4:393-399.

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

Revell LJ. (2012). `phytools`: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* 3:217-223.

See Also

[ploadhm](#)

Examples

```
library(phytools)

data(ligotree)
data(ligophorus_shape)
data(spcolmap)

#PCA plot for the shape variables of the ventral anchors
pca2d(ligophorus_shape[,1:22], labcol=spcolmap$color, phylo=TRUE,
      phy=ligotree, genus="L. ", bound.y=c(-0.08, 0.1), bound.x1=c(-0.2,0.2),
      bound.x2 = c(-0.2,0.2))
```

ploadhm

Heat map representation of principal component loadings of shape variables

Description

This function produces a graphical representation of selected principal component loadings of shape variables in the form of a heat map.

Usage

```
ploadhm(x, pc = 1, sgn = 1, nrow = 11, color.code = NULL,
        ylab = "Landmark", xlab = "Coordinate", yaxis = FALSE, tit = NULL)
```

Arguments

<code>x</code>	a matrix containing the loadings of shape variables (row) of each principal component (column)
<code>pc</code>	a constant specifying the principal component of interest
<code>sgn</code>	the sign of the loadings; this value should follow the one used in pca2d
<code>nrow</code>	a constant indicating the number of landmarks defined in the anchors; defaults to 11
<code>color.code</code>	a character vector of hex color codes that define the color palette; if left undefined, defaults to the red-white-blue palette
<code>ylab</code>	y-axis title for the plot
<code>xlab</code>	x-axis title for the plot
<code>yaxis</code>	if TRUE, the y-axis values are labelled
<code>tit</code>	title for the plot

Details

The sign and magnitude of loadings of shape variables for a particular principal component is important for the latter's biological interpretation. A heat map representation is an alternative to the usual manner of presenting them in tabular form, and may be more effective for presentation purpose. Reference to the circular plots ([plotCircular](#)) for each landmark and the PCA plots can be very useful in determining the biological interpretation of a particular principal component.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[plotCircular](#), [pca2d](#), [colorBar](#)

Examples

```
library(phytools)

data(ligophorus_shape)
data(ligotree)
data(spcolmap)

shapev <- pca2d(ligophorus_shape[,1:22], sgn=1, labcol=spcolmap$color,
  phylo=TRUE, phy=ligotree, genus="L. ",
  bound.y = c(-0.1, 0.1), bound.x1 =c(-0.15,0.2), bound.x2=c(-0.15,0.2))
```

```

fff <- c(0,1,1,2,2,3,3,0,4,4)
nf <- layout(matrix(c(rep(0,length(fff)),rep(fff,5),rep(0,length(fff))),
7,length(fff),byrow=TRUE))
layout.show(nf)
par(mar=c(5,4,4,1))
#the loadings for the first three PC of shape variables of the ventral anchors
ploadhm(shapev$variable,sgn=1,pc=1,yaxis=TRUE,tit="VPC1")
ploadhm(shapev$variable,sgn=1,pc=2,ylab="", tit="VPC2")
ploadhm(shapev$variable,sgn=1,pc=3,ylab="", tit="VPC3")

#add a colorbar for completeness
par(mar=c(5,2,4,3))
colorBar(min=-1, max=1)

```

plotCircular

Circular plot

Description

This function creates a circular plot (Batschelet, 1981) showing how mean directional change of GPA coordinates in species of interest is distributed relative the root ancestor. Magnitude of directional change is proportional to the length of ray projecting from a data point.

Usage

```

plotCircular(x, ancestor, col.lab, clade, LM, f = c(100, 0.1), sf = 1.5,
ptscale = 1, tit = NULL)

```

Arguments

x	a list containing objects that are matrices of average GPA coordinates for a set of species. The names of this x contains should contain the species names
ancestor	a matrix specifying the GPA coordinates of the root ancestor estimated using the fastAnc function in the phytools package
col.lab	a character vector specifying colors for species with matching indices in x
clade	a character vector specifying the species that form a clade of interest; currently supports only two clades
LM	the landmark of interest
f	scaling factors for the magnitude of directional change
sf	shrinking factor for shrink argument in plot.circular from the circular package
ptscale	scaling factor for size of data point on the circle perimeter
tit	title for the circular plot

Details

The arms in the circle are color-annotated according to clade of interest, with their direction and length indicating mean directional and magnitude change in the clades of interest, respectively. The circular plot is a useful complement to the wireframe-lollipop plot produced using `shapeEvo`, as it shows directional distribution details for all species at the individual landmark level. When used in conjunction with the principal component loadings heat map produced using `pcloadhm`, it can greatly aid biological interpretation of the principal components. This function depends on the `phytools` (Revell, 2012) and `circular` (Agostinelli & Lund, 2013) packages.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Agostinelli C, Lund U. (2013). R package 'circular': Circular Statistics (version 0.4-7). Available at: <https://r-forge.r-project.org/projects/circular>.

Batschelet E. (1981). *Circular Statistics in Biology*. London: Academic Press.

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogean anchor morphometry: systematic value, phylogenetic signal and evolution.

Revell LJ. (2012). `phytools`: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* 3:217-223.

See Also

[anglecheck](#), [shapeEvo](#), [pcloadhm](#)

Examples

```
library(circular)

data(va_mean)
data(estimated_ancestral_va)
data(spcolmap)

#the species in the defined clade infects the fish host Liza subviridis (dodger blue color)
plotCircular(va_mean, estimated_ancestral_va, col.lab=spcolmap$color,
            clade=spcolmap[spcolmap$host %in% "L.subviridis",]$species, LM=6, tit=6)
```

plotLM

Scatter plot of Generalized Procrustes Analysis (GPA) coordinates of anchor landmarks

Description

This function generates a scatter plot of GPA coordinates of anchor landmarks, with the option of making a wireframe plot by joining mean GPA coordinates of adjacent landmarks.

Usage

```
plotLM(x, tit = "", pointscale = 1, axispointscale = 1, meansize = 1,
       polygon.outline = FALSE, xbound = NULL, ybound = NULL,
       pch.suppress = FALSE)
```

Arguments

<code>x</code>	an array containing GPA coordinate data of anchor landmarks
<code>tit</code>	title of the plot
<code>pointscale</code>	a numeric constant for controlling the symbol size for observations
<code>axispointscale</code>	a numeric constant for controlling the font size of labels of values on the xy axes
<code>meansize</code>	a constant for controlling the symbol size of the mean coordinates
<code>polygon.outline</code>	if TRUE, a wireframe plot connecting all adjacent landmarks is made
<code>xbound</code>	a numeric vector specifying the range of x values for the plot
<code>ybound</code>	a numeric vector specifying the range of y values for the plot
<code>pch.suppress</code>	if TRUE, only the mean coordinates of the landmarks are plotted

Details

The resulting scatter plot is an important graphical sanity check for potential problems after performing GPA.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[procrustesFit](#), [stdLM](#)

Examples

```
data(liewi_gpa)

nice_title <- expression(paste("Dorsal anchor ", italic(L.liewi)))
plotLM(liewi_gpa, tit=nice_title, pointscale=0.8, axispointscale=0.8,
       meansize=1.2, polygon.outline=TRUE,c(-.6,.6),c(-.6,.6) )
```

 polyVis

Wireframe plot of monogenean anchor

Description

This function plots the ventral and dorsal anchors as polygons in their natural positions on the specimen slide.

Usage

```
polyVis(index, spacing = 250, havelist = FALSE, listdata = NULL,
        tit = "")
```

Arguments

index	the index of a (tps) text file or matrix containing the (eleven) landmark coordinates in the following order: right ventral, left ventral, right dorsal, left dorsal
spacing	a numeric constant specifying the spacing on the x and y coordinates relative to slide center
havelist	choose TRUE if the landmark coordinate data are contained in a list
listdata	a list containing objects that are matrices of 44 rows and 2 columns containing raw landmark coordinate data
tit	title for the plot

Details

This plot is useful for detecting slides with inconsistencies in magnification. It is also useful for detecting poor quality samples, as indicated by large shape variation between left and right forms.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

Examples

```
data(ligophorus_tpsdata)
#Simultaneously visualise the first four specimen slides
par(mfrow=c(2,2))
par(mar=c(3,3,2,1.5))
mapply(function(k) polyVis(k, spacing=300, havelist=TRUE,
listdata=ligophorus_tpsdata$grandis), k=1:4)
```

procrustesFit *Generalized Procrustes Analysis*

Description

This function aligns a set of landmark configurations using Generalized Procrustes Analysis (GPA).

Usage

```
procrustesFit(dat, anchor.index, x, PrinAxes = FALSE, showplot = FALSE)
```

Arguments

dat	a list containing landmark coordinate data of anchor from the specimens of interest
anchor.index	a numeric constant for the anchor of interest; 1 for ventral right; 2 for ventral left; 3 for dorsal right; 4 for dorsal left
x	a list providing the indices of specimens with anti-clockwise and clockwise orientation of landmarks for the anchor with index anchor.index
PrinAxes	logical; controls the argument with the same name in gpagen
showplot	logical; if TRUE, a scatter plot of the GPA coordinates of all specimens of interest is returned

Details

This function is essentially a wrapper for the gpagen function in the geomorph package (Version 2.1.6) to help convert raw landmark coordinates of monogenean anchors to GPA coordinates for downstream analysis.

Value

a list where the components are arrays of GPA coordinates for the specimens of interest

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

Adams DC, Otarola-Castillo E. (2013). geomorph: an R package for the collection and analysis of geometric morphometric shape data. *Methods in Ecology and Evolution* 4:393-399.

See Also

[matrix2list](#), [anglePolygon](#)

Examples

```

library(geomorph)

data(ligophorus_tpsdata)

#A data processing step to parse out the orientation of landmarks
#from samples of L.parvicopulatrix

O <- matrix(0, length(ligophorus_tpsdata$parvicopulatrix), 4)
for(w in 1:length(ligophorus_tpsdata$parvicopulatrix)){
  result <- mapply(function(k)
  anglePolygon(matrix2list(ligophorus_tpsdata$parvicopulatrix[[w]][(11*(k-1)+1):(11*k)],),
  degree=TRUE), k=1:4)

  result_angle <- mapply(function(k) list(result[[2*k-1]]), k=1:4)
  result_orientation <- mapply(function(k) list(result[[2*k]]), k=1:4)
  names(result_angle) <- names(result_orientation) <- c("VR", "VL", "DR", "DL")
  O[w,] <- unlist(result_orientation)
}

mdir <- apply(O, 2, function(k) which(k == "m") )
pdir <- apply(O, 2, function(k) which(k == "p") )

e <- 1 #Ventral right anchor
result <- procrustesFit(ligophorus_tpsdata$parvicopulatrix, e,
list(mdir[[e]], pdir[[e]]), PrinAxes=TRUE, showplot=TRUE)

#Standardize the x-coordinate of Landmark 7 by rotating the x-coordinate
#of its mean GPA xy-coordinate to x=0.
coordinates <- stdLM(result$coords, reflect=FALSE, swap=TRUE, sgn=c(1,-1))

plotLM(coordinates, "VR", pointscale=0.8,axispointscale=0.8,
meansize=1.2,polygon.outline=TRUE,c(-.6,.6),c(-.6,.6) )

```

procrustesFit.2

Mass Extraction of Generalized Procrustes Analysis Coordinates from Anchors

Description

Given a list of landmark coordinate data, this function performs Generalized Procrustes Analysis (GPA) and extracts the GPA-coordinates.

Usage

```

procrustesFit.2(x, e, makeplot = FALSE, reflect = FALSE, swap = TRUE,
axispointscale = 0.8, sgn = c(1, -1))

```

Arguments

x	a list containing landmark coordinate data of anchors from the specimens of interest
e	a constant specifying the anchor of interest: ventral right(1), ventral left(2), dorsal right(3), dorsal left(4)
makeplot	if TRUE, returns a scatter plot of the GPA-coordinates
reflect	logical; if TRUE, x-coordinates are reflected around the x=0 axis
swap	logical; if TRUE, the x and y-coordinates are swapped
axispointscale	a numeric constant for controlling the font size of numeric values on the xy axes
sgn	a numeric vector; two choices 1 and -1; defaults to c(1,-1)

Details

This function is essentially a wrapper for `procrustesFit` and `stdLM` to ease extraction of GPA-coordinates from list data. Both require the `geomorph` package (Version 2.1.6).

Value

an array containing GPA-coordinates of the specimens of interest

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

Adams DC, Otarola-Castillo E. (2013). `geomorph`: an R package for the collection and analysis of geometric morphometric shape data. *Methods in Ecology and Evolution* 4:393-399.

See Also

[procrustesFit](#), [stdLM](#)

Examples

```
library(geomorph)

data(ligophorus_tpsdata)
vright <- procrustesFit.2(ligophorus_tpsdata$johorensis, 1, makeplot=TRUE,
reflect=FALSE, swap=TRUE)

vleft <- procrustesFit.2(ligophorus_tpsdata$johorensis, 2, makeplot=TRUE,
reflect=TRUE, swap=TRUE)

va <- (vright+vleft)/2
```

```
plotLM(va, "VA", pointscale=0.8, meansize=1.2, polygon.outline=TRUE,
axispointscale=0.8, c(-.6,.6),c(-.6,.6))
```

pwwdist

Pairwise Euclidean distances between landmarks

Description

This function computes all possible $n(n-1)/2$ pairwise Euclidean distances between n landmarks.

Usage

```
pwwdist(x, average = TRUE)
```

Arguments

x	a two-column matrix for the xy landmark coordinates
average	if TRUE, the pairwise distances for both left and right anchors are averaged. For data quality checks, set to FALSE

Details

Comparison of the pairs of pairwise Euclidean distance from the left and right form of anchors is the basis of the quality control procedure implemented in Qscore. In addition, pairwise Euclidean distances provide length variables useful for the analysis of size variation (Lele & Richtsmeier, 2001).

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

Lele SR, Richtsmeier JT. 2001. An Invariant Approach to Statistical Analysis of Shape. Boca Raton: Chapman and Hall.

Examples

```
library(cluster)

data(ligophorus_tpsdata)

#There are 11 landmarks for the ventral and dorsal anchors,
#yielding 110 pairwise Euclidean distances
#The indices for the pairwise Euclidean distances map to the upper triangle
#of the pairwise distance matrix by row
pwwdist(ligophorus_tpsdata$bantingensis[[1]],average=FALSE)
```

pwed_pd	<i>Physical distance between landmarks in ventral and dorsal anchors of 13 Ligophorus species</i>
---------	---

Description

This data set contains all pairwise physical distance between landmarks in ventral and dorsal anchors of samples from 13 *Ligophorus species*.

Usage

```
data(pwed_pd)
```

Format

a matrix containing 443 rows (samples) and 110 columns (physical distance)

Details

The pairwise physical distances are estimated from a subset (n=97) of the 443 samples based on a regression equation, using physical distances between landmarks 1 to 3 and landmarks 1 to 5 and corresponding distances computed from `pwdist`, which have arbitrary units.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[pwdist](#)

Qscore	<i>Data quality control</i>
--------	-----------------------------

Description

This function checks data quality of anchor images by comparing the pairwise Euclidean distances of landmarks on the left and right anchors for both dorsal and ventral anchors.

Usage

```
Qscore(x, id.out = FALSE, tit = "", bound = 50)
```

Arguments

<code>x</code>	a numeric vector generated from <code>pwdist</code>
<code>id.out</code>	if TRUE, allows the user to query data indices in the TMD plot
<code>tit</code>	title for the plot
<code>bound</code>	magnitude of upper and lower bounds on the y-axis

Details

The quality control method implemented here is based on consideration of the difference (M) and average (A) of pairwise Euclidean distances between the left and right anchors. Let the residual be defined as the deviation of M from 0. Assuming that left and right anchors are more or less symmetric, good quality data should have squared residuals that are small on average and show more or less random deviation from 0 along A. The latter corresponds to slope that is near 0 in a linear regression of M against A. The result is visualized using the Tukey Mean-Difference (TMD) plot (also known as the Bland-Altman plot; see Bland & Altman (1986)), in which mean M and the 95 % limits of agreement (within 2 standard deviations from mean M) are indicated as dashed horizontal lines. Good quality data have small values of `sqasr` and `slope`, resulting in high Q scores, and vice versa.

Value

A matrix with three columns:

<code>sqasr</code>	the square root of average squared residuals
<code>slope</code>	slope of regressing M against A, multiplied by 100 to be on the same scale as average squared residuals
<code>Q</code>	quality score, which is given by $Q=100[10^{-(\sqrt{sqasr^2+slope^2})/10}]$

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Bland JM, Altman DG. (1986). Statistical methods for assessing agreement between two methods of clinical measurement. *Lancet* 327:307-310.

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[pwdist](#), [boxplotSort](#)

Examples

```

library(cluster)

data(ligophorus_tpsdata)
data(spcolmap)

#A low quality specimen
Qscore(pwdist(ligophorus_tpsdata$bantingensis[[5]],average=FALSE))
#A high quality specimen
Qscore(pwdist(ligophorus_tpsdata$bantingensis[[11]],average=FALSE))

#Useful diagnostic plots
Qmat <- vector("list",length(ligophorus_tpsdata))
for(i in 1:13){
Qmat[[i]] <- do.call(rbind,lapply(ligophorus_tpsdata[[i]],
function(k) Qscore(pwdist(k, average=FALSE))))
rownames(Qmat[[i]]) <- rep(names(ligophorus_tpsdata)[i],nrow(Qmat[[i]]))
}
names(Qmat) <- names(ligophorus_tpsdata)

#Box plot for quality score by species, sorted using descending median quality score
Q <- lapply(Qmat, function(k) k[,3])
boxplotSort(Q, italic=TRUE, ylab="Quality score", df=1)

```

shapeEvo

Statistical test of deviation from directional uniformity and estimation of average magnitude of directional change

Description

This function performs the Rayleigh test (Batschelet, 1981) for detecting deviation from uniformity of directional change at each landmark. Additionally, it estimates the mean magnitude of directional change, and then summarizes the result graphically using a wireframe-lollipop plot (Klingenberg, 2013).

Usage

```

shapeEvo(x, ancestor, col.lab = "black", col.tones = redgreen(101), clade,
exfac = 1, tit = NULL)

```

Arguments

x	a list of objects that are matrices containing average GPA coordinates of anchor landmarks. The species names should be the names of this list
ancestor	a matrix specifying the GPA coordinates of the root ancestor, estimated using fastAnc function in the phytools package
col.lab	color for arrows in the wireframe-lollipop plot
col.tones	color tones for p-values; defaults to red-black-green spectrum

clade	a character vector specifying the species that form a clade of interest
exfac	an expansion factor for the magnitude of direction change
tit	title for the wireframe-lollipop plot

Value

A wireframe-lollipop plot and a list containing:

magnitude	a matrix of the mean magnitude of directional change (column) of each landmark for each species (row)
pvalue	p-values for each landmark from the Rayleigh test

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

- Batschelet E. (1981). Circular Statistics in Biology. London: Academic Press.
- Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogean anchor morphometry: systematic value, phylogenetic signal and evolution.
- Klingenberg CP. (2013). Visualizations in geometric morphometrics: how to read and how to make graphs showing shape changes. *Hystrix* 24:15-24.

See Also

[plotCircular](#), [anglecheck](#)

Examples

```
library(gplots)
library(circular)

data(va_mean)
data(estimated_ancestral_va)
data(spcolmap)

nf <- layout(matrix(c(1,1,1,2),1, 4,byrow=TRUE))
layout.show(nf)

cladeII <- spcolmap$species[spcolmap$host %in% "L.subviridis"]
shapeEvo(va_mean, estimated_ancestral_va, col.lab="dodgerblue",
clade=cladeII, exfac=2, tit="Ventral anchors")
#Some journals want the title to be left-adjusted, so set tit="" and then:
#title("a)", adj=0)

#Add a nice color bar
par(mar=c(5,6,4,2))
colorBar(redgreen(101),min=0, max=1, tit="p-value")
```

spcolmap *Species-color map*

Description

Guide for species coloring in plots.

Usage

```
data(spcolmap)
```

Format

a matrix - the first column gives the species names; the second their corresponding color code; the third their host species

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

stdLM *Standardization of landmark configuration by a reference landmark*

Description

This function provides options for reflecting GPA coordinates around $x=0$, swapping of GPA xy -coordinates, and rotating all GPA coordinates in such a way that landmark 7 is standardized at $x=0$.

Usage

```
stdLM(x, reflect = FALSE, swap = FALSE, sgn = c(1, 1))
```

Arguments

x	an array containing landmark coordinate data of anchor from the specimens of interest
reflect	if TRUE, x-coordinates are reflected around the $x=0$ axis
swap	if TRUE, the x and y-coordinates are swapped
sgn	a numeric vector; two choices 1 and -1; defaults to c(1,1)

Details

The values in the `sgn` vector should be tuned to obtain the desired orientation of landmark configuration. This function processes the output from `procrustesFit`, which requires the `geomorph` package (Adams & Otarola-Castillo, 2013).

Value

an array of landmark coordinates

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Adams DC, Otarola-Castillo E. (2013). `geomorph`: an R package for the collection and analysis of geometric morphometric shape data. *Methods in Ecology and Evolution* 4:393-399.

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

See Also

[procrustesFit](#), [plotLM](#)

Examples

```
library(geomorph)

data(ligophorus_tpsdata)
#A data processing step to parse out the orientation of landmarks
#from samples of L.parvicopulatrix

O <- matrix(0, length(ligophorus_tpsdata$parvicopulatrix), 4)
for(w in 1:length(ligophorus_tpsdata$parvicopulatrix)){
  result <- mapply(function(k)
  anglePolygon(matrix2list(ligophorus_tpsdata$parvicopulatrix[[w]][(11*(k-1)+1):(11*k)],),
  degree=TRUE), k=1:4)

  result_angle <- mapply(function(k) list(result[[2*k-1]]), k=1:4)
  result_orientation <- mapply(function(k) list(result[[2*k]]), k=1:4)
  names(result_angle) <- names(result_orientation) <- c("VR", "VL", "DR", "DL")
  O[w,] <- unlist(result_orientation)
}

mdir <- apply(O, 2, function(k) which(k == "m") )
pdir <- apply(O, 2, function(k) which(k == "p") )

e <- 1 #Ventral right anchor
result <- procrustesFit(ligophorus_tpsdata$parvicopulatrix, e,
list(mdir[[e]], pdir[[e]]), PrinAxes=TRUE, showplot=TRUE)
#Standardize the x-coordinate of Landmark 7 by rotating the x-coordinate
```

```
#of its mean GPA xy-coordinate to x=0.
coordinates <- stdLM(result$coords, reflect=FALSE, swap=TRUE, sgn=c(1,-1))

plotLM(coordinates, "VR", pointscale=0.8,axispointscale=0.8,
meansize=1.2,polygon.outline=TRUE,c(-.6,.6),c(-.6,.6) )
```

tpColorPlot2d

Color-annotated scatter plot with transparency control

Description

This function enhances a typical two-dimensional scatter plot by enabling transparency control of color annotation. In addition, it provides option for phylogenetic tree superimposition.

Usage

```
tpColorPlot2d(x, labcol = "", xlab = "", ylab = "", tit = "",
  circlesize = rep(1.5, nrow(x)), tpfac = c(60, 255), xbound = NULL,
  ybound = NULL, centroid = FALSE, phylo = FALSE, phy, pointscale = 1)
```

Arguments

x	a two-column matrix with rownames (usually, the species names)
labcol	a character vector specifying species colors
xlab	title for the x-axis
ylab	title for the y-axis
tit	title for the plot
circlesize	a numeric vector that controls the centroid symbol size; defaults to 1 if centroid = FALSE
tpfac	a numeric vector specifying the transparency level (0 to 255) for individual data points and the label mean
xbound	range of values on the x-axis
ybound	range of values on the y-axis
centroid	if TRUE, plots the centroid for each species
phylo	if TRUE, coordinates of ancestral nodes from a supplied phylogeny (phy) are estimated using fastAnc from the phytools package, and edges between nodes are joined according to the topology specified in phy
phy	an object of class phylo from the ape package
pointscale	a constant for controlling the size of the plotted ancestral nodes

Details

Transparency control of color-annotated data points reduces visual saturation caused by the use of solid colours, thus allowing species centroids to be accentuated in the plot. In addition, if a user-supplied phylogeny is given, it is superimposed onto the plot. This function depends on the phytools (Revell, 2012) and ape (Paradis et al., 2004) packages.

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

- Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.
- Paradis E, Claude J & Strimmer K. (2004). APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* 20: 289-290.
- Revell LJ. (2012). phytools: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* 3:217-223.

Examples

```
data(pwed_pd)
data(spcolmap)

pwed_pd_list <- matrix2list.2(pwed_pd)
lm1 <- c("V1_3", "V1_5")

#scatter plot of LM1-LM3 length against LM1-LM5 length for the ventral anchors
tpColorPlot2d(pwed_pd[,colnames(pwed_pd) %in% lm1], labcol=spcolmap$color,
xlab=expression(paste("V1_3 ", "(", italic(mu), "m", ")")),
ylab=expression(paste("V1_5 ", "(", italic(mu), "m", ")")), centroid=TRUE)
```

tpColorPlot3d	<i>Color-annotated three-dimensional scatter plot with transparency control</i>
---------------	---

Description

This function enhances a three-dimensional scatter plot by enabling transparency control of color annotation. In addition, it provides option for phylogenetic tree superimposition.

Usage

```
tpColorPlot3d(x, r = 0.005, phylo = FALSE, phy, labcol, xyzlabel = NULL,
alpha.set = 0.2, mean.show = FALSE, asp = c(1, 1, 1))
```

Arguments

- | | |
|-------|--|
| x | a matrix with rows representing samples and columns representing three variables of interest, typically principal components |
| r | radius of plotting sphere |
| phylo | if TRUE, coordinates of ancestral nodes from a supplied phylogeny (phy) are estimated using fastAnc from the phytools package, and edges between nodes are joined according to the topology specified in phy |

phy	an object of class phylo from the ape package
labcol	a character vector specifying species colors
xyzlabel	a vector of characters specifying the titles for the xyz-axes
alpha.set	a constant for controlling degree of transparency (0 for complete transparency; 1 for solid color) of the data points
mean.show	if TRUE, the centroids of each species is plotted in solid color
asp	a vector specifying the aspect ratio of the xyz axes; the default gives a cube

Details

Transparency control of color-annotated data points reduces visual saturation caused by the use of solid colors for all data points. Guide for choosing optimal value of r : for data range between -0.1 and 0.1, a value of 0.005 should be adequate. If a phylogenetic tree is supplied, it may be superimposed onto the three-dimensional space to allow visualization of evolutionary trajectories.

References

- Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.
- Paradis E, Claude J & Strimmer K. (2004). APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* 20: 289-290.
- Revell LJ. (2012). phytools: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* 3:217-223.

See Also

[tpColorPlot2d](#)

Examples

```
library(phytools)
library(rgl)

data(ligophorus_shape)
data(ligotree)
data(spcolmap)

#Perform PCA of shape data for ventral anchors and make 2D plots
pcashape <- pca2d(ligophorus_shape[,1:22],labcol=spcolmap$color,phylo=TRUE,phy=ligotree,genus="L. ")

#Check for proportion of variation explained by each PC
summary(pcashape$pca)

#A closer look with 3D plot
tpColorPlot3d(pcashape$scores[,3:1], r=0.005, phylo=TRUE, phy=ligotree, labcol=spcolmap$color,
xyzlabel=c("PC3 (11%)", "PC2 (19%)", "PC1 (55%)"), mean.show=TRUE)
```

tpsRead

Reading tps files into R

Description

This function converts all tps files in a folder to a list of matrices. The tps files are created using the TPSDIG2 software (Rohlf, 2013, 2015).

Usage

```
tpsRead(x)
```

Arguments

x a constant that indexes the folder of interest

Value

a list of matrices containing the xy-coordinates of landmarks

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

References

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

Rohlf FJ. (2013). Morphometrics at SUNY Stony Brook. Available at <http://life.bio.sunysb.edu/morph/soft-dataacq.html>.

Rohlf FJ. (2015). The tps series of software. *Hystrix*. 26, doi: 10.4404/hystrix-26.1-11264.

Examples

```
##not run
##download the tps data folders from Khang et al. (2015) and unzip them into a folder called ligotps

#setwd("ligotps/")
#dir()
##read tps files from the /bantingensis folder and turn them into objects of a list
#xydata <- tpsRead(1)
```

va_mean	<i>Mean Generalized Procrustes Analysis (GPA) coordinates for ventral anchors of 13 Ligophorus species</i>
---------	--

Description

A data set containing mean GPA coordinates for the ventral anchors of 13 *Ligophorus* species.

Usage

```
data(va_mean)
```

Format

A list containing 13 objects, each object being a matrix of 11 rows (landmarks) and 2 columns (xy-coordinates) representing GPA-coordinates averaged from samples belonging to the same species

Details

For each specimen, GPA coordinates of all landmarks are averages of those from left and right anchors. Mean GPA coordinates of landmarks are required for shape evolution analysis as well as performing Adam's K test for presence of phylogenetic signal (Adams, 2014).

Author(s)

Tsung Fei Khang <tfkhang@um.edu.my>

Source

Khang TF, Soo OYM, Tan WB, Lim LHS. (2015). Monogenean anchor morphometry: systematic value, phylogenetic signal and evolution.

References

Adams DC. (2014). A generalized K statistic for estimating phylogenetic signal from shape and other high-dimensional multivariate data. *Systematic Biology* 63: 685-697.

See Also

[shapeEvo](#)

Index

*Topic **datasets**

estimated_ancestral_va, [7](#)
liewi_gpa, [11](#)
ligophorus_shape, [12](#)
ligophorus_tpsdata, [13](#)
ligotree, [14](#)
pwed_pd, [29](#)
spcolmap, [33](#)
va_mean, [39](#)

anglecheck, [2](#), [22](#), [32](#)
anglePolygon, [3](#), [16](#), [25](#)

boxplotSort, [4](#), [17](#), [30](#)

colorBar, [5](#), [20](#)
colorRampPalette, [6](#)

estimated_ancestral_va, [7](#)

heatmapAnnot, [8](#)
hsplot, [9](#)

liewi_gpa, [11](#)
ligophorus_shape, [12](#)
ligophorus_tpsdata, [13](#)
ligotree, [14](#)

matrix2list, [15](#), [25](#)
matrix2list.2, [16](#)

pca2d, [18](#), [20](#)
ploadhm, [6](#), [19](#), [19](#), [22](#)
plotCircular, [20](#), [21](#), [32](#)
plotLM, [12](#), [22](#), [34](#)
polyVis, [14](#), [24](#)
procrustesFit, [23](#), [25](#), [27](#), [34](#)
procrustesFit.2, [26](#)
pwdist, [28](#), [29](#), [30](#)
pwed_pd, [29](#)

Qscore, [5](#), [12–14](#), [29](#)

shapeEvo, [7](#), [22](#), [31](#), [39](#)
spcolmap, [33](#)
stdLM, [23](#), [27](#), [33](#)

tpColorPlot2d, [15](#), [35](#), [37](#)
tpColorPlot3d, [36](#)
tpsRead, [38](#)

va_mean, [39](#)