Package ‘RRmorph’

May 14, 2025

Type Package

Title 3D Morphological Analyses with 'RRphylo'

Date 2025-05-07

Version 0.0.1

Maintainer Silvia Castiglione <`silvia.castiglione@unina.it`>

Description Combined with 'RRphylo', this package provides a powerful tool to analyse and visualise 3d models (surfaces and meshes) in a phylogenetically explicit context (Melchionna et al., 2024 <doi:10.1038/s42003-024-06710-8>).

License GPL-2

Encoding UTF-8

Depends R (>= 3.6.0)

Imports Morpho, rgl, Rvcg, RRphylo

Suggests inflection, ddpcr, ape, knitr, rmarkdown

RoxygenNote 7.3.2

VignetteBuilder knitr

NeedsCompilation no

Author Marina Melchionna [aut],
Silvia Castiglione [aut, cre],
Carmela Serio [aut],
Giorgia Girardi [aut],
Alessandro Mondanaro [aut],
Pasquale Raia [aut]

Repository CRAN

Date/Publication 2025-05-14 08:30:06 UTC

Contents

`col2mesh` *Color a mesh according to provided values*

Description

The function colors a `mesh` according to a vector of continuous `values` related to individual vertices.

Usage

```
col2mesh(mesh,values,pal,from=NULL,to=NULL,NAcol="gray90")
```

Arguments

`mesh`	a `mesh3d` object.
`values`	a vector of continuous values associated to individual vertices of the `mesh`.
`pal`	a vector of colors to be passed to `colorRampPalette`.
`from, to`	lower and upper `values` to be associated to the ends of `pal`.
`NAcol`	the color associated to NA `values`.

Value

A `mesh3d` object colored according to `values`.

Author(s)

Marina Melchionna, Silvia Castiglione

Examples

```
 da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
  download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
  load(paste0(tempdir(),"/RRmorphdata.rda"))

  require(rgl)
  require(Morpho)
  require(Rvcg)

  pca<-procSym(endo.set)
  ldm<-endo.set[,,"Homo_sapiens"]
  sur<-endo.sur[["Homo_sapiens"]]
```

```
rec<- vcgBallPivoting(pca$mshape, radius = 0)
rec$vb[1:3,]<-t(ldm)
val<-rnorm(ncol(rec$vb))

interp<-interpolMesh(sur = rec,refsur = sur,refmat = ldm,
                     values = val,element ="vertices",k = 4)

colmesh<-col2mesh(mesh = sur,values = interp,pal = heat.colors(5))
plotLegend(mesh = colmesh,values = interp, main = "Pan troglodytes")
open3d()
shade3d(colmesh,specular="black")
```

`conv.map` *Mapping morphological convergence on 3D surfaces*

Description

Given vectors of RW (or PC) scores for some converging species, the function selects the RW (PC) axes which best account for convergence and maps convergent areas on the corresponding 3D surfaces.

Usage

```
conv.map(x1,x2=NULL,scores, pcs, mshape,focal=NULL,mshape_sur=NULL,
  refmat = NULL,refsur = NULL, k = 4, exclude = NULL, out.rem = TRUE, plot =
  TRUE, col = "blue", NAcol = "gray", names = TRUE, nsim = 1000)
```

Arguments

`x1, x2`	vectors of convergent species. When convergence within a single clade was found, `x1` represents the vector of species belonging to the clade (`x2=NULL`). When convergence between groups/clades was found, `x1` and `x2` are the two convergent groups/clades.
`scores`	data frame (or matrix) with the RW (or PC) scores returned by RWA/PCA. Species not included in `x1` or `x2` are ignored.
`pcs`	RW (or PC) vectors (eigenvectors of the covariance matrix) returned by RWA/PCA.
`mshape`	the consensus configuration.
`focal`	vector of species included in `x1/x2` to be plotted. To be provided if `refsur=NULL` and `refmat=NULL`.
`mshape_sur`	a `mesh3d` object used as a reference for mesh reconstruction. The vertices of `mshape_sur` must be the consensus configuration. If `NULL`, it is automatically generated by applying `vcgBallPivoting` on `mshape`.
`refmat`	a named list of landmark sets corresponding to `refsur`.

`refsur`	a named list of `mesh3d` objects for species in `x1/x2` to be plotted. If `focal` is not `NULL` this is ignored.
`k`	the argument `k` passed to `interpolMesh`.
`exclude`	integer: the index numbers of the RWs (or PCs) to be excluded from the comparison.
`out.rem`	logical: if `TRUE` triangles with outlying area difference are removed.
`plot`	logical: if `TRUE`, the pairwise comparisons are plotted. For more than 5 pairwise comparisons, the plot is not shown.
`col`	character: the color for plotting.
`NAcol`	the argument `NAcol` passed to `col2mesh`.
`names`	logical: if `TRUE`, the names of the groups or species are displayed in the 3d plot.
`nsim`	the number of iterations to evaluate significance.

Details

After selecting the RW (PC) axes which best account for convergence, `conv.map` uses such axes (and related scores) within `restoreShapes` (**Morpho**) to reconstruct landmark matrices for each convergent species (in `x1/x2`). The reconstruction of species 3d surfaces is based on `mshape_sur`, either provided by the user or generated within the function. Finally, the area differences between corresponding triangles of reconstructed 3d meshes for each possible pair of convergent species are calculated. In the calculation of differences, the possibility to find and remove outliers is supplied (`out.rem=TRUE`, we suggest considering this possibility if the mesh may contain degenerate facets).

If the combination of `focal` species (or species within `refsur/refmat`) contains a number equal or lower then 5 items, `conv.map` returns a `rgl` plot mapping the convergence on the 3D models. If lists of `refsur/refmat` are not provided, the area differences are plotted onto reconstructed surfaces. If `refsur/refmat` are available, difference values are interpolated by means of `interpolMesh` to be plotted onto real surfaces. When species in either `x1` or `x2` are missing from `focal` or `refmat/refsur`, `conv.map` plots the reconstructed surface of the species having the smallest `$selected` angle with the focal (see `angle.compare` in the description of outputs).

`conv.map` further gives the opportunity to exclude some RW (or PC) axes from the analysis because, for example, in most cases the first axes are mainly related to high-order morphological differences driven by phylogeny and size variations.

Value

The function returns a list including:

- **$angle.compare**: a data frame including the real angles between species shape vectors `$real.angle`, the angles computed between vectors of the selected RWs (or PCs) `$selected`, the angles between vectors of the non-selected RWs (or PCs) `$others`, the differences `selected-others` and its p-values.
- **$selected.pcs** RWs (or PCs) axes selected for convergence.
- **$average.dist** symmetric matrix of pairwise distances between 3D surfaces.
- **$suface1** list of colored surfaces representing convergence between mesh A and B charted on mesh A.

- **$suface2** list of colored surfaces representing convergence between mesh A and B charted on mesh B.
- **$scale** the value used to set the color gradient, computed as the maximum of all differences between each surface and the mean shape.

Author(s)

Marina Melchionna, Antonio Profico, Silvia Castiglione, Carmela Serio, Gabriele Sansalone, Pasquale Raia

References

Schlager, S. (2017). *Morpho and Rvcg–Shape Analysis in R: R-Packages for geometric morphometrics, shape analysis and surface manipulations.* In: Statistical shape and deformation analysis. Academic Press.

Melchionna, M., Profico, A., Castiglione, S., Serio, C., Mondanaro, A., Modafferi, M., Tamagnini, D., Maiorano, L. , Raia, P., Witmer, L.M., Wroe, S., & Sansalone, G. (2021). A method for mapping morphological convergence on three-dimensional digital models: the case of the mammalian sabretooth. *Palaeontology*, 64, 573–584. doi:10.1111/pala.12542

See Also

`search.conv` vignette ; `relWarps` ; `procSym`

Examples

```
da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
 download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
 load(paste0(tempdir(),"/RRmorphdata.rda"))

 require(Morpho)

 pca<-procSym(endo.set)
 ldm_homo<-endo.set[,,"Homo_sapiens"]
 sur_homo<-endo.sur[["Homo_sapiens"]]
 ldm_macaca<-endo.set[,,"Macaca_fuscata"]
 sur_macaca<-endo.sur[["Macaca_fuscata"]]


 # Convergence within group plotted on reconstructed surfaces
 cm1<-conv.map(x1=c("Pan_troglodytes","Gorilla_gorilla","Pongo_abelii"),
               scores=pca$PCscores,pcs=pca$PCs,mshape=pca$mshape,
               focal=c("Pan_troglodytes","Gorilla_gorilla"))

 # Convergence between group plotted on reconstructed surfaces
 cm2<-conv.map(x1=c("Pongo_abelii"),x2=c("Alouatta_caraya"),
               scores=pca$PCscores,pcs=pca$PCs,mshape=pca$mshape,
               focal="Alouatta_caraya")

 # Convergence within group plotted on real surfaces
 cm3<-conv.map(x1=c("Homo_sapiens","Gorilla_gorilla","Pongo_abelii"),
```

```
              scores=pca$PCscores,pcs=pca$PCs,mshape=pca$mshape,
              refsur=list("Homo_sapiens"=sur_homo),
              refmat=list("Homo_sapiens"=ldm_homo))

# Convergence between group plotted on real surfaces
cm3<-conv.map(x1=c("Homo_sapiens","Pongo_abelii"),x2=c("Macaca_fuscata"),
              scores=pca$PCscores,pcs=pca$PCs,mshape=pca$mshape,
              refsur=list("Homo_sapiens"=sur_homo,"Macaca_fuscata"=sur_macaca),
              refmat=list("Homo_sapiens"=ldm_homo,"Macaca_fuscata"=ldm_macaca))
```

`interpolMesh` *Interpolate values on a 3d mesh*

Description

The function takes a reconstructed `mesh3d` object (`sur`) with some related `values` (to either triangles or vertices of the mesh) and transfers such values to the real mesh (`refsur`) from which `sur` was derived.

Usage

```
interpolMesh(sur,values,refsur,refmat,element=c("triangles","vertices"),k=4)
```

Arguments

`sur`	a reconstructed `mesh3d` object with vertices matching to `refmat`.
`values`	the vector of values related to `sur` to be interpolated. `values` can be related to either triangles or vertices (see `element`).
`refsur`	the reference mesh (`mesh3d` object) to interpolate the `values` on.
`refmat`	the landmark set related to `refsur`.
`element`	one of `"triangles"` or `"vertices"`, depending on which of them `values` is related to.
`k`	the number of nearest neighbor vertices used for interpolation (see details).

Details

The function starts by locating a set of points (NNps) on `refsur`, each being the single nearest neighbor for each vertex of `sur` (or barycenter if `element="triangles"`). Then, interpolation is performed by identifying the `k` points among NNps being the closest to each vertex of `refsur` and computing the mean of their `values` weighted by their distance.

Value

The vector of values related to each vertex of `refsur`.

Author(s)

Marina Melchionna, Silvia Castiglione

Examples

```
da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
 download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
 load(paste0(tempdir(),"/RRmorphdata.rda"))

 require(rgl)
 require(Morpho)
 require(Rvcg)

 pca<-procSym(endo.set)
 ldm<-endo.set[,,"Homo_sapiens"]
 sur<-endo.sur[["Homo_sapiens"]]

 rec<- vcgBallPivoting(pca$mshape, radius = 0)
 rec$vb[1:3,]<-t(ldm)
 val1<-rnorm(ncol(rec$vb))

 # Interpolate values associated to vertices
 val1<-rnorm(ncol(rec$vb))
 interp1<-interpolMesh(sur = rec,refsur = sur,refmat = ldm,
                       values = val1,element ="vertices",k = 4)

 colmesh1<-col2mesh(mesh = sur,values = interp1,pal = heat.colors(5))
 open3d()
 shade3d(colmesh1,specular="black")


 # Interpolate values associated to triangles
 val2<-rnorm(ncol(rec$it))
 interp2<-interpolMesh(sur = rec,refsur = sur,refmat = ldm,
                       values = val2,element ="triangles",k = 4)

 colmesh2<-col2mesh(mesh = sur,values = interp2,pal = heat.colors(5))
 open3d()
 shade3d(colmesh2,specular="black")
```

`plotland` *Plot landmarks importance on 3d mesh*

Description

The function relates PCA loadings of a single PC axis to individual landmarks and plots them on a 3d mesh by means of interpolation.

Usage

```
plotland(pca,sel=1,refsur=NULL,refmat=NULL,k=5,pal=NULL,
  defo=FALSE,radius=0.001)
```

Arguments

`pca`	the result of a relative warp analysis. Classes `relwarps` and `nosymproc` are supported.
`sel`	numeric indicating the focal RW/PC axis.
`refsur`	the `mesh3d` object to plot on. If `NULL`, the mesh is reconstructed by means of `vcgBallPivoting` from the consensus configuration derived from `pca`.
`refmat`	the landmark set related to `refsur`. If `NULL`, the consensus configuration derived from `pca` is used.
`k`	the argument `k` passed to `interpolMesh`.
`pal`	a vector of colors to be passed to `colorRampPalette`.
`defo`	when `refsur` and `refmat` are provided, `defo` = `TRUE` warps `refsur` on the consensus shape.
`radius`	argument `radius` passed to `spheres3d`

Value

A list including a `mesh3d` object colored according to landmarks importance and a matrix of landmarks importance on each RW/PC axis. Additionally, the function returns a 3d plot of the mesh.

Author(s)

Marina Melchionna, Silvia Castiglione, Carmela Serio, Giorgia Girardi

Examples

```
da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
 download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
 load(paste0(tempdir(),"/RRmorphdata.rda"))

 require(rgl)
 require(Morpho)

 pca<-procSym(endo.set)
 ldm<-endo.set[,,"Homo_sapiens"]
 sur<-endo.sur[["Homo_sapiens"]]

 plotland(pca=pca,sel=1,refsur = sur,refmat = ldm)
```

`plotLegend` *Plot legend for colored mesh.*

Description

Assuming a `mesh` is colored according to a vector of `values`, the function takes the color sequence from the `mesh` and plots it associated to `values`.

Usage

```
plotLegend(mesh,values,main)
```

Arguments

`mesh`	a `mesh3d` object
`values`	a vector of continuous values associated to individual vertices of the `mesh`.
`main`	plot title.

Value

A plot of the color sequence associated to `values` on the `mesh`.

Author(s)

Marina Melchionna, Silvia Castiglione

Examples

```
da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
 download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
 load(paste0(tempdir(),"/RRmorphdata.rda"))

 require(rgl)
 require(Morpho)
 require(Rvcg)

 pca<-procSym(endo.set)
 ldm<-endo.set[,,"Homo_sapiens"]
 sur<-endo.sur[["Homo_sapiens"]]

 rec<- vcgBallPivoting(pca$mshape, radius = 0)
 rec$vb[1:3,]<-t(ldm)
 val<-rnorm(ncol(rec$vb))

 interp<-interpolMesh(sur = rec,refsur = sur,refmat = ldm,
                      values = val,element ="vertices",k = 4)

 colmesh<-col2mesh(mesh = sur,values = interp,pal = heat.colors(5))
 plotLegend(mesh = colmesh,values = interp, main = "Pan troglodytes")
```

```
open3d()
shade3d(colmesh,specular="black")
```

---

rate.map *Mapping rate and direction of phenotypic change on 3D surfaces.*

Description

Given vectors of RW (or PC) scores, the function selects the RW (PC) axes linked to highest (and lowest) evolutionary rate values and reconstructs the morphology weighted on them. In this way, `rate.map` shows where and how the phenotype changed the most between any pair of taxa.

Usage

```
rate.map(x, RR, scores, pcs, mshape, mshape_sur=NULL,refsur=NULL,
  refmat=NULL, k=4,out.rem = TRUE, plot=TRUE, pal=NULL,
  NAcol="gray90",from=NULL, to=NULL,show.names=TRUE)
```

Arguments

`x`	the species/nodes to be compared; it can be a single species, or a vector containing two species or a species and any of its parental nodes.
`RR`	an object generated by using the `RRphylo` function.
`scores`	RW or PC scores.
`pcs`	RW (or PC) vectors (eigenvectors of the covariance matrix) returned by RWA/PCA.
`mshape`	the consensus configuration.
`mshape_sur`	a `mesh3d` object used as a reference for mesh reconstruction. The vertices of `mshape_sur` must be the consensus configuration. If `NULL`, it is automatically generated by applying `vcgBallPivoting` on `mshape`.
`refsur`	a list of `mesh3d` to be provided for all species in `x`.
`refmat`	a list of landmark sets to be provided for all species in `x`.
`k`	the argument `k` passed to `interpolMesh`.
`out.rem`	logical: if `TRUE` mesh triangles with outlying area difference are removed.
`plot`	logical indicating if the 3d plot must be shown.
`pal`	a vector of colors to be passed to `colorRampPalette`.
`NAcol`	the argument `NAcol` passed to `col2mesh`.
`from, to`	lower and upper limits to be associated to the ends of `pal`.
`show.names`	logical: if `TRUE`, the names of the species are displayed in the 3d plot.

Details

After selecting the RW (PC) axes, `rate.map` automatically builds a 3D mesh on the mean shape calculated from the Relative Warp Analysis (RWA) or Principal Component Analysis (PCA) (*Schlager 2017*) by applying the function `vcgBallPivoting` (**Rvcg**). The reconstruction of species 3d surfaces is based on `mshape_sur`, either provided by the user or generated within the function. Finally, for each species in `x`, the function computes the area differences between corresponding triangles of its reconstructed 3D mesh and the surface of the ancestor (most recent common ancestor in the case of two species in `x`). In the calculation of differences, the possibility to find and remove outliers is supplied (`out.rem=TRUE`, we suggest considering this possibility if the mesh may contain degenerate facets).

Finally, `rate.map` returns a 3D plot showing such comparisons displayed on shape of the ancestor/mrca used as the reference. The color gradient goes from blue to red, where blue areas represent expansion of the mesh, while the red areas represent contraction of the mesh triangles. If a list `refsur` (and `refmat`) is provided, convergence is plotted onto them (see `interpolMesh` for further details).

Value

The function returns a list including:

- **$selected** a list of RWs/PCs axes selected for higher evolutionary rates for each species.
- **$surfaces** a list of reconstructed colored surfaces of the given species/node and the most recent common ancestor.
- **differences** a list area differences between corresponding triangles of species reconstructed 3d mesh and the surface of the ancestor.
- **lmks** if `refmat` is not `NULL`, this is the landmark configuration rotated on the reconstructed surface .

Author(s)

Marina Melchionna, Antonio Profico, Silvia Castiglione, Gabriele Sansalone, Pasquale Raia

References

Schlager, S. (2017). *Morpho and Rvcg-Shape Analysis in R: R-Packages for geometric morphometrics, shape analysis and surface manipulations.* In: Statistical shape and deformation analysis. Academic Press.

Castiglione, S., Melchionna, M., Profico, A., Sansalone, G., Modafferi, M., Mondanaro, A., Wroe, S., Piras, P., & Raia, P. (2021). Human face-off: a new method for mapping evolutionary rates on three-dimensional digital models. *Palaeontology*, 65, 1. doi:10.1111/pala.12582

Melchionna, M., Castiglione, S., Girardi, G., Serio, C., Esposito, A., Mondanaro, A., Profico, A., Sansalone, G., & Raia, P. (2024). RRmorph—a new R packageto map phenotypic evolutionary rates and patterns on 3D meshes. *Communications Biology*, 7, 1009.

See Also

`RRphylo` vignette ; `relWarps` ; `procSym`

Examples

```
da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
 download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
 load(paste0(tempdir(),"/RRmorphdata.rda"))

 require(Morpho)
 require(Rvcg)

 pca<-procSym(endo.set)
 ldm_homo<-endo.set[,,"Homo_sapiens"]
 sur_homo<-endo.sur[["Homo_sapiens"]]
 ldm_macaca<-endo.set[,,"Macaca_fuscata"]
 sur_macaca<-endo.sur[["Macaca_fuscata"]]

 cc<- 2/parallel::detectCores()
 RR<-RRphylo::RRphylo(tree.prima,pca$PCscores,clus=cc)

 # plotting on reconstructed surfaces
 Rmap1<-rate.map(x=c("Homo_sapiens","Macaca_fuscata"),RR=RR, scores=pca$PCscores,
                 pcs=pca$PCs, mshape=pca$mshape)

 # plotting on real surfaces
 Rmap2<-rate.map(x=c("Homo_sapiens","Macaca_fuscata"),RR=RR, scores=pca$PCscores,
                 pcs=pca$PCs, mshape=pca$mshape,
                 refsur=list("Homo_sapiens"=sur_homo,"Macaca_fuscata"=sur_macaca),
                 refmat=list("Homo_sapiens"=ldm_homo,"Macaca_fuscata"=ldm_macaca))
```

`shapeDiff` *Shape difference between 3d meshes*

Description

The function reconstructs two specimens' meshes (`x`) by using their superimposed configurations (from within `pca`), calculates the shape difference between them, and plots such differences on provided meshes (`refsur`).

Usage

```
shapeDiff(x,pca,refsur,refmat,mshape_sur = NULL,
  pal=NULL,NAcol="gray90",show.names=TRUE)
```

Arguments

`x`	a vector of specimens pair.
`pca`	the result of a relative warp analysis. Classes `relwarps` and `nosymproc` are both accepted.
`refsur`	a list of two `mesh3d` objects to be provided in the same order as `x`.

`refmat`	a list of two landmark sets related to `refsur` to be provided in the same order as `x`.
`mshape_sur`	a `mesh3d` object used as a reference for mesh reconstruction. The vertices of `mshape_sur` must be the consensus configuration. If `NULL`, it is automatically generated by applying `vcgBallPivoting` on the consensus configuration derived from `pca`.
`pal`	a vector of colors to be passed to `colorRampPalette`.
`NAcol`	the color associated to `refsur` vertices falling outside the range of `refmat` (not involved in interpolation).
`show.names`	logical: if `TRUE`, the names of the specimens as in `x` are displayed in the 3d plot.

Value

Two `mesh3d` objects colored according to shape differences. Additionally, the function returns 3d plots of the meshes.

Author(s)

Marina Melchionna, Silvia Castiglione

Examples

```
da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
load(paste0(tempdir(),"/RRmorphdata.rda"))

require(Morpho)

pca<-procSym(endo.set)
ldm_homo<-endo.set[,,"Homo_sapiens"]
sur_homo<-endo.sur[["Homo_sapiens"]]
ldm_macaca<-endo.set[,,"Macaca_fuscata"]
sur_macaca<-endo.sur[["Macaca_fuscata"]]

diffs<-RRmorph::shapeDiff(x=c("Homo_sapiens","Macaca_fuscata"),
                 pca = pca,refsur = list(sur_homo,sur_macaca),
                 refmat = list(ldm_homo,ldm_macaca))
```

`tri2verts` *Triangles to vertices*

Description

The function transfers values associated to triangles of a `mesh3d` object to its vertices.

Usage

```
tri2verts(mesh,values)
```

Arguments

`mesh`	a `mesh3d` object.
`values`	a vector of continuous values associated to individual triangles of the `mesh`.

Value

A vector of continuous values associated to individual vertices of the `mesh`.

Author(s)

Marina Melchionna, Silvia Castiglione

Examples

```
da<-"https://github.com/pasraia/RRmorph_example_data/raw/refs/heads/main/RRmorphdata.rda"
 download.file(url=da,destfile = paste0(tempdir(),"/RRmorphdata.rda"))
 load(paste0(tempdir(),"/RRmorphdata.rda"))

 require(Morpho)
 require(Rvcg)

 pca<-procSym(endo.set)
 ldm<-endo.set[,,"Homo_sapiens"]
 sur<-endo.sur[["Homo_sapiens"]]

 rec<- vcgBallPivoting(pca$mshape, radius = 0)
 rec$vb[1:3,]<-t(ldm)
 val<-rnorm(ncol(rec$vb))

 vertval<-tri2verts(rec,val)
```

Index