

Package ‘vegan3d’

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Title Static and Dynamic 3D and Editable Interactive Plots for the
‘vegan’ Package

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Imports cluster, rgl, scatterplot3d (>= 0.3-40)

Description Static and dynamic 3D plots to be used with ordination
results and in diversity analysis, especially with the vegan package.

License GPL-2

BugReports <https://github.com/vegandevs/vegan3d/issues>

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Description

The **vegan3d** package provides 3D plotting for all **vegan** ordination methods or any other ordination method that **vegan scores** function can handle. It can also display **hclust** results in 3D over a 2D plane. Dynamic 3D plots are based on the **rgl** package and static plots are drawn with the **scatterplot3d** package. The package also provides 2D editable interactive plots for ordination. The points are fixed at their ordination scores, but labels can be moved to better position, and the result can be saved in various graphics formats or saved in **R** session and re-created with **R** plot commands.

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Drawing with rgl Functions

The **rgl** graphics are dynamic 3D plots that can be spinned and zoomed by mouse. The **vegan3d** package provides interface to ordination and clustering objects. The functions use **rgl** setting and conventions and do not change the user settings. For general configuration of the plots, users should check **rgl** documentation. For instance, general look and feel of drawn items can be configured with **material3d**.

The **rgl** package may not be available in all platforms, and therefore the package is not automatically attached. If you want to use **rgl** functions, you must either prefix commands with `rgl::` or call `library(rgl)` in your session.

Function `ordirgl` is similar as `ordiplot` in **vegan**, and any ordination result can be drawn with similar conventions. Functions with `orgl` prefix add items to existing plots, for instance, `orglellipse` is analogous to `ordiellipse`.

Function `ordirgltree` draws an **hclust** dendrogram over a plane. It was originally developed for 2D ordination planes, but any other plane can be used, for instance a projected map.

Functions `rgl.isomap` and `rgl.renyiaccum` provide alternative dynamic 3D plots for **vegan isomap** and **renyiaccum** functions.

Drawing with scatterplot3d Functions

The **scatterplot3d** package draws static 3D graphics, and **vegan3d** provides an interface for ordination and clustering objects. You must consult the [scatterplot3d](#) documentation for configuring your plots.

Function `ordipLOT3d` is similar to `ordirgl` or `ordipLOT` and draws a static 3D plot in the standard graphical device. It returns invisibly a plotting object which contains the projected points, and **vegan** ordi* prefix functions can use this object. For instance, `ordiellipse` will add ellipses on the projected points.

Function `orditree3d` will draw an `hclust` dendrogram over a plane similarly as `ordirgltree`.

Editable Graphics with Tcl/Tk based orditkplot

Function draws ordination scores in a new Tcl/Tk window with fixed points and their editable labels. The labels can be moved to better positions which helps with crowded plots. It is also possible to zoom into graph to display only a part of the complete graph. The edited result can be saved in various graphical formats or saved as an R object in the session for further manipulation or re-creating the graph with standard `**R**` plotting tools.

There are obvious ways of improving the function. Contributions are welcome.

ordipLOT3d

Three-Dimensional Ordination Graphics

Description

Function `ordipLOT3d` displays three-dimensional ordination graphics using [scatterplot3d](#). Function works with all ordination results from **vegan** and all ordination results known by `scores` function.

Usage

```
ordipLOT3d(object, display = "sites", choices = 1:3, col = "black",
           ax.col = "red", arr.len = 0.1, arr.col = "blue", envfit,
           xlab, ylab, zlab, ...)
```

Arguments

<code>object</code>	An ordination result or any object known by scores .
<code>display</code>	Display "sites" or "species" or other ordination object recognized by scores .
<code>choices</code>	Selected three axes.
<code>col</code>	Colours of points. Can be a vector, and factors are interpreted as their internal numerical codes.
<code>ax.col</code>	Axis colour (concerns only the crossed axes through the origin).
<code>arr.len</code>	'Length' (width) of arrow head passed to arrows function.
<code>arr.col</code>	Colour of biplot arrows and centroids of environmental variables.

<code>envfit</code>	Fitted environmental variables from <code>envfit</code> displayed in the graph.
<code>xlab, ylab, zlab</code>	Axis labels passed to <code>scatterplot3d</code> . If missing, labels are taken from the ordination result. Set to NA to suppress labels.
<code>...</code>	Other parameters passed to graphical functions.

Details

Function `ordiplot3d` plots static three-dimensional scatter diagrams using `scatterplot3d`. Function uses most default settings of underlying graphical functions, and you must consult their help pages to change graphics to suit your taste (see `scatterplot3d`).

Function returns invisibly an object of class `ordiplot3d` which inherits from `ordiplot`. The result object contains the projected coordinates of plotted items and functions to convert 3D data to 2D (see `scatterplot3d`). Function will display only one selected set of `scores`, typically either "sites" or "species". Examples show how to use the invisible return object to add another set of points to the projected plot.

In constrained ordination (`cca`, `rda`, `capscale`), biplot arrows and centroids are always displayed similarly as in two-dimensional plotting function `plot.cca`. Alternatively, it is possible to display fitted environmental vectors or class centroids from `envfit`. These are displayed similarly as the results of constrained ordination, and they can be shown only for non-constrained ordination. The user must remember to specify at least three axes in `envfit` if the results are used with these functions.

The function has a `scores` method to extract the projected coordinates from the invisible return object. Standard **vegan** functions can be used with the returned object. You can use any function from the `ordihull` and `ordiarrows` families (see Examples).

Value

Function `ordiplot3d` returns invisibly an object of class "ordiplot3d" inheriting from `ordiplot`. The return object will contain the coordinates projected onto two dimensions for points, and the projected coordinates of origin, and possibly the projected coordinates of the heads of arrows and centroids of environmental variables. The result will also contain the object returned by `scatterplot3d`, including function `xyz.convert` which projects three-dimensional coordinates onto the plane used in the current plot (see Examples). In addition, there is a function `envfit.convert` that projects a three-dimensional `envfit` object to the current plot.

Warning

Please note that `scatterplot3d` sets internally some graphical parameters (such as `mar` for margins) and does not honour default settings. It is advisable to study carefully the documentation and examples of `scatterplot3d`.

Author(s)

Jari Oksanen

See Also

`scatterplot3d`, `ordiplot`, `ordiarrows`, `ordihull`.

Examples

```

### Default 'ordiplot3d'
data(dune, dune.env)
ord <- cca(dune ~ A1 + Moisture, dune.env)
ordiplot3d(ord)
### A boxed 'pin' version
ordiplot3d(ord, type = "h")
### More user control
pl <- ordiplot3d(ord, scaling = "symmetric", angle=15, type="n")
points(pl, "points", pch=16, col="red", cex = 0.7)
### identify(pl, "arrows", col="blue") would put labels in better positions
text(pl, "arrows", col="blue", pos=3)
text(pl, "centroids", col="blue", pos=1, cex = 1)
### Add species using xyz.convert function returned by ordiplot3d
sp <- scores(ord, choices=1:3, display="species", scaling="symmetric")
text(pl$xyz.convert(sp), rownames(sp), cex=0.7, xpd=TRUE)
### Two ways of adding fitted variables to ordination plots
ord <- cca(dune)
ef <- envfit(ord ~ Moisture + A1, dune.env, choices = 1:3)
### 1. use argument 'envfit'
ordiplot3d(ord, envfit = ef)
### 2. use returned envfit.convert function for better user control
pl3 <- ordiplot3d(ord)
plot(pl3$envfit.convert(ef), at = pl3$origin)
### envfit.convert() also handles different 'choices' of axes
pl3 <- ordiplot3d(ord, choices = c(1,3,2))
plot(pl3$envfit.convert(ef), at = pl3$origin)
### vegan::ordiXXXX functions can add items to the plot
ord <- cca(dune)
pl4 <- with(dune.env, ordiplot3d(ord, col = Management, pch=16))
with(dune.env, ordiellipse(pl4, Management, draw = "poly", col = 1:4,
  alpha = 60))
with(dune.env, ordispider(pl4, Management, col = 1:4, label = TRUE))

```

ordirgl

Three-Dimensional Dynamic Ordination Graphics

Description

Function `ordirgl` displays three-dimensional dynamic ordination graphs which can be rotated and zoomed. This function works with all ordination results from `vegan` and all ordination results known by the `scores` function. The `orgl`-prefixed functions add elements to the `ordirgl` graph similarly as `ordi`-prefixed functions in **vegan**.

Usage

```

ordirgl(object, display = "sites", choices = 1:3, type = "p", col = "black",
  ax.col = "red", arr.col = "yellow", radius, text, envfit, ...)
orglpoints(object, display = "sites", choices = 1:3, radius, col = "black", ...)

```

```

orgltext(object, text, display = "sites", choices = 1:3, adj = 0.5,
  col = "black", ...)
orglsegments(object, groups, order.by, display = "sites", choices = 1:3,
  col = "black", ...)
orglspider(object, groups, display = "sites", w = weights(object, display),
  choices = 1:3, col = "black", ...)
orglellipse(object, groups, display = "sites", w = weights(object, display),
  kind = c("sd", "se", "ehull"), conf, choices = 1:3, alpha = 0.3,
  col = "red", ...)
orglspantree(object, spantree, display = "sites", choices = 1:3,
  col = "black", ...)
orglcluster(object, cluster, prune = 0, display = "sites", choices = 1:3,
  col = "black", ...)

```

Arguments

object	An ordination result or any object known by scores .
display	Display "sites" or "species" or other ordination object recognized by scores .
choices	Selected three axes.
type	The type of plots: "p" for points or "t" for text labels.
ax.col	Axis colour (concerns only the crossed axes through the origin).
arr.col	Colour of biplot arrows and centroids of environmental variables.
radius	Size of points in the units of ordination scores.
text	Text to override the default with type = "t".
envfit	Fitted environmental variables from envfit displayed in the graph. Use <code>envfit = NA</code> to suppress display of environmental variables in constrained ordination.
adj	Text justification passed to text3d .
groups	Factor giving the groups for which the graphical item is drawn.
order.by	Order points by this variable within groups.
w	Weights used to find the average within group. Weights are used automatically for cca and decorana results, unless undone by the user. <code>w=NULL</code> sets equal weights to all points.
kind	Draw ellipse for standard deviations of points ("sd") or standard deviations of their averages ("se") or an ellipsoid hull enclosing all points in the group ("ehull").
conf	Confidence limit for ellipses, e.g., 0.95. If not given, sd or se ellipses are drawn.
col	Colour of items. This can be a vector and factors are interpreted as their internal numerical values. If the function has a <code>groups</code> argument, vector <code>col</code> is used for each of these, and for other functions it is matched to points in ordirgl (see Details below).
alpha	Transparency of colour between 0.0 (fully transparent) and 1.0 (non-transparent).
spantree	A minimum spanning tree object from vegan spantree .
cluster	Result of hierarchic cluster analysis, such as hclust or agnes .

prune	Number of upper levels hierarchies removed from the tree. If prune > 0, tree will be cut into prune + 1 disconnected trees.
...	Other parameters passed to graphical functions.

Details

Function `ordirgl` plots dynamic graphics using OpenGL with the `rgl` package. It clears the graphics device and starts a new plot. The function was designed for ordination methods in the `vegan` package, but it can handle any method known to `vegan scores` function, or to any three column matrix. The `orgl`-prefixed functions add items to the opened `rgl` graphics device.

Function `ordirgl` uses most default settings of underlying graphical functions in `rgl`. It plots only one set of points, but functions `orglpoints` and `orgltext` can add new items to an existing plot. The points are plotted using `spheres3d` and the text using `texts3d` which both have their own configuration switches and their general look and feel can be modified with `material3d`. The point size is directly defined by `radius` argument in the units of ordination scores in `spheres3d`, but `ordirgl` uses a default size of 1% of the length of the longest axis, and this can be further modified by the `cex` multiplier.

In constrained ordination (`cca`, `rda`, `capscale`), biplot arrows and centroids are always displayed similarly as in two-dimensional plotting function `plot.cca`. Alternatively, it is possible to display fitted environmental vectors or class centroids from `envfit` in both graphs. These are displayed similarly as the results of constrained ordination, and they can be shown only for non-constrained ordination. The user must remember to specify at least three axes in `envfit` if the results are used with these functions.

Function `orglsegments` is similar to `vegan ordisegments` and connects points by line segments. This can be useful for regular transects. The colour of segments can be a vector which corresponds to the groups and will be recycled.

Function `orglspider` is similar as `vegan ordispider`: it connects points to their weighted centroid within "groups", and in constrained ordination it can connect "wa" or weighted averages scores to corresponding "lc" or linear combination scores if "groups" is missing. Function `orglellipse` is similar as `vegan ordiellipse` and draws ellipsoids of standard deviance, standard error or confidence regions for groups. At least four points are needed to define an ellipsoid in 3D, and even these will fail if all points are strictly on 2D. The `col` argument for both of these functions can be a vector corresponding to the groups.

Function `orglspantree` adds a minimum spanning tree from `vegan spantree`. This a 3D equivalent of `lines.spantree`. Function `orglcluster` adds a hierarchic cluster tree from `hclust` or related functions. This is a 3D equivalent of `ordicluster`. The `col` argument for both of these functions can be a vector corresponding to the connected points. In `orglspantree` the line colour is a mixture of colours of joined points, and in `orglcluster` it is a mixture of all points in the cluster.

Value

Function `ordirgl` returns nothing.

Warning

Function `ordirgl` uses OpenGL package `rgl` which may not be functional in all platforms.

Author(s)

Jari Oksanen

See Also

[rgl](#), [spheres3d](#), [text3d](#), [rgl.viewpoint](#), [envfit](#). These are 3D dynamic variants of **vegan** functions [ordiplot](#), [ordisegments](#), [ordispider](#) and [ordiellipse](#), [ordicluster](#) and [lines.spantree](#).

Examples

```
if (interactive() && require(rgl, quietly = TRUE)) {
  data(mite, mite.env)
  ord <- rda(decostand(mite, "hellinger"))
  ordirgl(ord, size=4, col = "yellow")
  orgltext(ord, display = "species")
  ## show groups of Shrub abundance
  ## ordirgl: col by points
  with(mite.env, ordirgl(ord, col = as.numeric(Shrub), scaling = "sites"))
  ## orglspider & orglellipse: col by groups
  with(mite.env, orglspider(ord, Shrub, col = 1:3, scaling = "sites"))
  with(mite.env, orglellipse(ord, Shrub, col = 1:3, kind = "se", conf = 0.95,
    scaling = "sites"))
}
```

orditkplot

*Ordination Plot with Movable Labels***Description**

Function `orditkplot` produces an editable ordination plot with points and labels. The labels can be moved with mouse, and the edited plot can be saved as an encapsulated postscript file or exported via R plot function to other graphical formats, or saved in the R session for further processing.

Usage

```
orditkplot(x, display = "species", choices = 1:2, width, xlim, ylim,
  tcex = 0.8, tcol, pch = 1, pcol, pbg, pcex = 0.7, labels, ...)
## S3 method for class 'orditkplot'
plot(x, ...)
## S3 method for class 'orditkplot'
points(x, pch = x$args$pch, cex = x$args$pcex,
  col = x$args$pcol, bg = x$args$pbg, ...)
## S3 method for class 'orditkplot'
text(x, cex = x$args$tcex, col = x$args$tcol,
  font = attr(x$labels, "font"), ...)
## S3 method for class 'orditkplot'
scores(x, display, ...)
```


Arguments

x	An ordination result or any other object that scores can handle, or for the plot function the object dumped from the interactive orditkplot session.
display	Type of scores displayed. For ordination scores this typically is either "species" or "sites", and for orditkplot result it is either "points" or "labels".
choices	Axes displayed.
width	Width of the plot in inches; defaults to the current width of the graphical device.
xlim, ylim	x and y limits for plots: points outside these limits will be completely removed.
tcex	Character expansion for text labels.
tcol	Colour of text labels.
pch, pcol, pbg	Point type and outline and fill colours. Defaults pcol="black" and pbg="transparent". Argument pbg has an effect only in filled plotting characters pch = 21 to 25.
pcex	Expansion factor for point size.
labels	Labels used instead of row names.
cex, col, bg, font	graphical parameters used in the points and text methods. See par .
...	Other arguments passed to the function. These can be graphical parameters (see par) used in the plot, or extra arguments to scores. These arguments are ignored in plot, but honoured in text and points.

Details

Function `orditkplot` uses **tcltk** package to draw Tcl/Tk based ordination graphics with points and labels. The function opens an editable canvas with fixed points, but the labels can be dragged with mouse to better positions or edited. In addition, it is possible to zoom to a part of the graph.

The function knows the following mouse operations:

- **Left mouse button** can be used to move labels to better positions. A line will connect a label to the corresponding point.
- **Double clicking left mouse button** opens a window where the label can be edited. After editing the label, hit the Return key.
- **Right mouse button** (or alternatively, Shift-Mouse button with one-button mouse) can be used for zooming to a part of the graph. Keeping the mouse button down and dragging will draw a box of the zoomed area, and after releasing the button, a new plot window will be created (this is still preliminary: all arguments are not passed to the new plot).

In addition there are buttons for the following tasks: **Copy to EPS** copies the current plot to an encapsulated postscript (eps) file using standard Tcl/Tk utilities. The faithfulness of this copy is system dependent. Button **Export plot** uses `plot.orditkplot` function to redraw the plot into graphical file formats. Depending on the system, the following graphical formats may be available: eps, pdf, svg, png, jpeg, tiff, bmp or xfig. Some of the output formats may be edited with external software: svg files with Illustrator or Inkscape, and xfig with the legacy program XFig. Button **Save to R** writes the edited coordinates of labels and points to the R session for further processing, and the `plot.orditkplot` function can be used to display the results. For faithful replication of the plot, the graph must have similar dimensions as the `orditkplot` canvas had originally. The plot

function cannot be configured, but it uses the same settings as the original Tcl/Tk plot. However, points and text functions are fully configurable, but use the stored defaults for consistency with `plot.orditkplot` if none are supplied. Finally, button **Close** closes the window.

The produced plot will have equal aspect ratio. The width of the horizontal axis is fixed, but vertical axes will be scaled to needed height, and you can use scrollbar to move vertically if the whole canvas does not fit the window. If you use dumped labels in ordinary R plots, your plot must have the same dimensions as the `orditkplot` canvas to have identical location of the labels.

The function only displays one set of scores. However, you can use `ordipointlabel` (**vegan**) to produce a result object that has different points and text types for several sets of scores and this can be further edited with `orditkplot`. For a good starting solution you need to scale the `ordipointlabel` result so that the points span over the whole horizontal axis. The function cannot show environmental variables or constraints, but it is limited to unconstrained ordination.

The plot is a Tcl/Tk canvas, but the function tries to replicate standard graphical device of the platform, and it honours several graphical parameters (see `par`). Many of the graphical parameters can be given on the command line, and they will be passed to the function without influencing other graphical devices in R. At the moment, the following graphical parameters are honoured: `pch`, `bg`, `cex`, `cex.axis`, `cex.lab`, `col` (for labels), `col.axis`, `col.lab`, `family` (for font faces), `fg`, `font`, `font.axis`, `font.lab`, `lheight`, `lwd` (for the box), `mar`, `mex`, `mgp`, `ps`, `tcl`. These can be set with `par`, and they also will influence other plots similarly.

The `tkcanvas` text cannot be rotated, and therefore vertical axis is not labelled, and `las` parameter will not be honoured in the Tcl/Tk plot, but it will be honoured in the exported R plots and in `plot.orditkplot`.

Value

Function returns nothing useful directly, but you can save the edited graph to a file or save the edited positions to an R session for further processing and plotting.

Note

You need `tcltk` package and R must have been configured with `capabilities` for `tcltk`. Depending on your OS, you may need to start X11 and set the display before loading `tcltk` and starting the function (for instance, with `Sys.setenv("DISPLAY"=":0")`). See `tcltk-package`.

Author(s)

Jari Oksanen

See Also

Function `ordipointlabel` is an automatic procedure with similar goals of avoiding overplotting, and its output can be edited with `orditkplot`. See `ordiplot`, `plot.cca`, and `orditorp` for alternative ordination plots.

Examples

```
if(interactive() && capabilities("tcltk")) {
  data(varespec)
  ord <- cca(varespec)
```

```

## Do something with the graph and end by clicking "Dismiss"
orditkplot(ord, mar = c(4,4,1,1)+.1, font=3)
## Use ordipointlabel to produce a plot that has both species and site
## scores in different colors and plotting symbols
pl <- ordipointlabel(ord)
orditkplot(pl)
}

```

orditree3d

Draw Cluster Tree over a Plane

Description

Function draws a 3D plot where ordination result is at the bottom plane and a `hclust` dendrogram is drawn above the plane.

Usage

```

orditree3d(ord, cluster, prune = 0, display = "sites", choices = c(1, 2),
  col = "blue", text, type = "p", ...)
ordirgltree(ord, cluster, prune = 0, display = "sites", choices = c(1, 2),
  col = "blue", text, type = "p", ...)

```

Arguments

<code>ord</code>	An ordination object or an <code>ordiplot</code> object or any other structure defining a 2D plane.
<code>cluster</code>	Result of hierarchic cluster analysis, such as <code>hclust</code> or <code>agnes</code> or any other clustering that can be coerced to a compliant format by <code>as.hclust</code> .
<code>prune</code>	Number of upper levels hierarchies removed from the tree. If <code>prune > 0</code> , tree will be cut into <code>prune + 1</code> disconnected trees.
<code>choices</code>	Choice of ordination axes.
<code>display</code>	Ordination scores displayed.
<code>col</code>	Colour of tree. The colour can be a vector and it is used for the points, text and terminal branches. The colour of internal branches is a mixture of connected leaves.
<code>text</code>	Text to replace the default of item labels when <code>type = "t"</code> .
<code>type</code>	Display of leaves: "p" for points, "t" for text, and "n" for no display.
<code>...</code>	Arguments passed to <code>scores</code> and graphical functions.

Details

`orditree3d` uses `scatterplot3d` package to draw a static 3D plot of the dendrogram over the ordination, and `ordirgltree` uses `rgl` to make a dynamic, spinnable plot. The functions were developed to plot a cluster dendrogram over a 2D ordination plane, but any other plane can be used, for instance, a map.

Value

Function `orditree3d` returns invisibly a `scatterplot3d` result object amended with items `points` and `internal` that give the projected coordinates of ordination scores and internal nodes, and `col.points` and `col.internal` that give their colours. All matrix-like objects can be accessed with `scores`.

Function `ordirgltree` returns nothing.

Author(s)

Jari Oksanen.

See Also

`orglcluster` and `ordicluster` (in **vegan**).

Examples

```
data(dune, dune.env)
d <- vegdist(dune)
m <- metaMDS(d)
cl <- hclust(d, "aver")
orditree3d(m, cl, pch=16, col=cutree(cl, 3))
## ordirgltree makes ordinary rgl graphics. It accepts
## material3d() settings, and you can add elements to the
## open graph (for instance, bbox3d()).
if (interactive() && require(rgl, quietly = TRUE)) {
  with(dune.env, ordirgltree(m, cl, col = as.numeric(Management), size = 6,
    lwd = 2, alpha = 0.6))
}
```

rgl.isomap

Dynamic 3D plot of isomap ordination.

Description

Function displays a dynamic 3D plot from `isomap` ordination.

Usage

```
rgl.isomap(x, web = "white", ...)
```

Arguments

<code>x</code>	Result from <code>isomap</code> .
<code>web</code>	Colour of the web. If this is a vector matching the number of points, the colour of links is a mixture of joined points. NA skips drawing the web.
<code>...</code>	Other parameters passed to <code>ordirgl</code> and <code>scores</code> .

Details

Function `rgl.isomap` displays dynamic 3D plots that can be rotated on the screen. The functions is based on `ordirgl`, but it adds the connecting lines. The function passes extra arguments to `scores` or `ordirgl` functions so that you can select axes, or define colours and sizes of points.

Value

Function returns nothing.

Note

This is a support function for `isomap` ordination in the **vegan** package.

Author(s)

Jari Oksanen.

See Also

`isomap`, `ordirgl`, `scores`.

Examples

```
if (interactive() && require(rgl, quietly = TRUE)) {
  data(BCI)
  dis <- vegdist(BCI)
  ## colour points and links by the dominant species
  dom <- factor(make.cepnames(names(BCI))[apply(BCI, 1, which.max)])
  ord <- isomap(dis, k=3)
  rgl.isomap(ord, col = as.numeric(dom), web = as.numeric(dom), lwd=2)
}
```

`rgl.renyiaccum`

Dynamic Perspective Plot of Renyi Diversity Accumulation

Description

Function `rgl.renyiaccum` displays a dynamic 3D plot of the result of `renyiaccum` function in the **vegan** package. Function `persp.renyiaccum` (in **vegan**) produces similar static plots.

Usage

```
rgl.renyiaccum(x, rgl.height = 0.2, ...)
```

Arguments

<code>x</code>	A <code>renyiaccum</code> result.
<code>rgl.height</code>	Vertical scaling of the plot.
<code>...</code>	Other arguments passed to the function (ignored).

Details

This is a graphical support function to [renyiaccum](#) in **vegan**. Similar static plots can be produced by [persp.renyiaccum](#).

Value

Function returns nothing.

Author(s)

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See Also

[renyiaccum](#), [persp.renyiaccum](#), [rgl](#).

Examples

```
if (interactive() && require(rgl, quietly = TRUE)){  
  data(BCI)  
  mod <- renyiaccum(BCI[1:12,])  
  persp(mod)  
  rgl.renyiaccum(mod)  
}
```

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