Package ‘analogueExtra’

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Type Package

Title Additional Functions for Use with the Analogue Package

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Depends vegan3d (>= 0.65-0), analogue (>= 0.16-0)

Imports rgl

Suggests testthat

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BugReports `https://github.com/gavinsimpson/analogueExtra/issues`

NeedsCompilation yes

Description Provides additional functionality for the analogue package
that is not required by all users of the main package.

License GPL-2

ByteCompile true

URL `https://github.com/gavinsimpson/analogueExtra`

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Repository CRAN

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`plot3d.prcurve` *Interactive 3D plot of a principal curve in principal coordinate space*

Description

Draws a 3D plot of the principal curve in principal coordinate space using the **rgl** package and functions from **vegan3d**.

Usage

```
## S3 method for class 'prcurve'
plot3d(x, choices = 1:3, display = "sites", scaling = 0,
        lcol = "darkorange", lwd = 2, decorate = TRUE, xlab = NULL,
        ylab = NULL, zlab = NULL, main = NULL, ...)
```

Arguments

`x`	an object of class `"prcurve"` resulting from a call to `prcurve`.
`choices`	numeric vector of length 3; the ordination axes to plot.
`display`	character; which scores to display. See `scores.rda`.
`scaling`	numeric; the scaling to use for the scores. Default is no scaling.
`lcol, lwd`	The colour and width, respectively, for the principal curve.
`decorate`	logical; should the plot be decorated with bounding box, axes and labels?
`xlab, ylab, zlab, main`	Labels for the plot.
`...`	Arguments passed to other functions. In particular, argments are passed to `ordirgl`, `lines3d`, and `decorate3d`.

Value

A plot is drawn on the active RGL device. If there is no active RGL device, one is opened upon plotting.

Author(s)

Gavin L. Simpson

See Also

`ordirgl`, `prcurve`.

Examples

```
## Only works if the analogue package is available
if (require("analogue")) {
    ## Load the Abernethy Forest late glacial pollen sequence
    data(abernethy)

    ## Remove the Depth and Age variables
    abernethy2 <- abernethy[, -(37:38)]

    ## Fit the principal curve using the median complexity over
    ## all species
    aber.pc <- prcurve(abernethy2, method = "ca", trace = TRUE,
                       vary = FALSE, penalty = 1.4)

    ## 3D plot of data with curve superimposed
    ## plot3d.prcurve(aber.pc) # now deprecated, instead use
    plot3d(aber.pc)
}
```

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