Package ‘barplot3d’

Type Package
Title Create 3D Barplots
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Description Creates 3D barplots. Includes a function for sequence context plots used in DNA sequencing analysis.
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bar3d

*Adds a single 3D bar to the current scene*

**Description**

Adds a single 3D bar to the current scene

**Usage**

```r
bar3d(x = c(0, 1), y = c(0, 1), z, alpha = 1, topcol = "#078E53",
       sidecol = "#aaaaaa", linecol = "#000000")
```

**Arguments**

- `x`: The x dimensions of the bar, a vector of length 2 e.g. c(0,1).
- `y`: The y dimensions of the bar, a vector of length 2 e.g. c(0,1).
- `z`: The height of the bar, a single number, e.g 3.
- `alpha`: The alpha channel (transparency) of the sides of the bar. Range 0-1.
- `topcol`: The color of the top of the bar. Text description or hexadecimal RGB color, like that returned by rgb() e.g. "red" or "#078E53"
- `sidecol`: The color of the sides of the bar. Text description or a hexadecimal RGB color, like that returned by rgb() e.g. "gray" or "#aaaaaa"
- `linecol`: The color of the edges of the bar. Text description or a hexadecimal RGB color, like that returned by rgb() e.g. "black" or "#000000"

**Value**

Nothing is returned (invisibly returns NULL).

**Examples**

```r
bar3d(c(0,1),c(0,1),3,alpha=0.6,topcol="#078E53",sidecol="#aaaaaa",linecol="#000000")
```

barplot3d

*Adds a 3D bar plot to the current RGL scene*

**Description**

Adds a 3D bar plot to the current RGL scene
barplot3d

Usage

barplot3d(rows, cols, x, y, z, alpha = 1, scalexy = 1, gap = 0.2,
         topcolors = c("#000000"), sidecolors = c("#aaaaaa"),
         linecolors = c("#000000"), theta = 50, phi = 40,
         gridlines = TRUE, xlabels = FALSE, ylabels = FALSE,
         zlabels = TRUE, xsub = FALSE, ysub = FALSE, zsub = FALSE)

Arguments

rows  How many rows the plotting area should have, an integer, e.g. 5.
cols  How many columns the plotting area should have, an integer, e.g. 5.
x     The x dimensions of each 3D bar, a vector of length 2 e.g. c(0,1).
y     The y dimensions of each 3D bar, a vector of length 2 e.g. c(0,1).
z     The height of each 3D bar, a numeric vector, e.g c(2,3,5,2,9).
alpha The alpha channel (transparency) of the sides of 3D bars. Range 0-1.
scalexy Scaling factor for x and y coordinates; this constant can be used to make the plot
"skinnier" or "fatter".
gap   Gap between 3D bars (recommended values are 0 or 0.2).
topcolors The color of the top of each 3D bar. Numeric vector of hexadecimal RGB colors,
like those returned by rgb() e.g. "#078E53".
sidecolors The color of the top of the bar. Should be a hexadecimal RGB color, like that
returned by rgb() e.g. "#aaaaaa".
linecolors The color of the edges of the bar. Should be a hexadecimal RGB color, like that
returned by rgb() e.g. "#aaaaaa".
theta  Polar coordinate for viewing the 3D barplot; range 0 to 360 (rotates the plot).
phi    Polar coordinate for viewing the 3D barplot; range -90 to 90 (-90 is directly
        below, 90 directly above).
gridlines Draw gridlines on the plot (TRUE or FALSE).
xlabels Labels for the x axis (must be a vector of names the same length as "cols" pa-
        rameter).
ylabels Labels for the y axis (must be a vector of names the same length as "rows" pa-
        rameter).
zlabels Labels for the z axis; add numeric scale to the vertical dimension of the plot
        (TRUE or FALSE).
xsub   Descriptive label for the x axis.
ysub   Descriptive label for the y axis.
zsub   Descriptive label for the z axis.

Value

Nothing is returned (invisibly returns NULL).
Examples

```r
barplot3d(rows=3,cols=5,z=1:12,topcolors=rainbow(12),alpha=0.7,scalexy=10,
xlabels=c("One","Two","Three","Four","Five"),ylabels=LETTERS[1:3])
```

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**legoplot3d**  

* A wrapper function to create a sequence context "legoplot"

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**Description**

A wrapper function to create a sequence context "legoplot"

**Usage**

```r
legoplot3d(contextdata, alpha = 1, scalexy = 1, gap = 0.2,
sixcolors = "broad", theta = 50, phi = 40, gridlines = TRUE,
labels = FALSE, zlabels = TRUE, zsub = FALSE)
```

**Arguments**

- `contextdata`: A numeric vector of counts or frequencies of the 96 possible somatic mutations and trinucleotide contexts. These MUST be in the same order as in the example (see example and/or vignette).
- `alpha`: The alpha channel (transparency) of the sides of 3D bars. Range 0-1.
- `scalexy`: Scaling factor for x and y coordinates; this constant can be used to make the plot "skinnier" or "fatter".
- `gap`: Gap between 3D bars.
- `sixcolors`: The color scheme. "broad" for Broad Institute colors, "sanger" for Sanger Institute colors or a vector of six hexadecimal RGB colors.
- `theta`: Polar coordinate for viewing the 3D barplot; range 0 to 360 (rotates the plot).
- `phi`: Polar coordinate for viewing the 3D barplot; range -90 to 90 (-90 is directly below, 90 directly above).
- `gridlines`: Draw gridlines on the plot (TRUE or FALSE).
- `labels`: Include the default axis labels (TRUE or FALSE).
- `zlabels`: Labels for the z axis; add numeric scale to the vertical dimension of the plot (TRUE or FALSE).
- `zsub`: Descriptive label for the z axis.

**Value**

Nothing is returned (invisibly returns NULL).
Examples

# Read in COSMIC signature probabilities
x = system.file("extdata", "signature_probabilities.txt", package = "barplot3d")
sigdata = read.table(x, header = TRUE, stringsAsFactors = FALSE)
# Plot signature 2 with Sanger colors and some transparency so we can see all bars
legoplot3d(contextdata = sigdata$Signature_2, labels = TRUE, scalexy = 0.05, sixcolors = "sanger", alpha = 0.4, zsub = "Probability")
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