**defaultPalettePCA3D**  
*Default palette*

**Description**

Default set of colors for the pca3d package. This is a colorblind-friendly palette, following the R cookbook.

**Usage**

`defaultPalettePCA3D(n = NULL, transparent = NULL, d3 = FALSE)`

**Arguments**

- `n` Number of colors to return
- `transparent` character string which will be pasted to each color
- `d3` if true, no transparency information will be added to the colors

**Details**

The default palette contains 21 colors.

**Value**

A character vector with the color palette

---

**listShapes**  
*Show all permissible shapes for pca3d*

**Description**

Show all permissible shapes for pca3d

**Usage**

`listShapes()`

**Details**

Show all permissible shapes for the functions pca3d and pca2d. The shapes may be abbreviated using (matching is done with `pmatch`).

**Value**

A data frame with permissible 3d shapes for plotting and their pch counterparts is returned invisibly.
**Description**

Make a basic movie using movie3d()

**Usage**

```r
makeMoviePCA(...)```

**Arguments**

... Any parameters will be passed to movie3d()

**Details**

A wrapper around movie3d with some default settings. Used to create a movie on the fly.

**Value**

The value returned by movie3d()

**Examples**

```r
## Not run:
data( metabo )
pca <- prcomp( metabo[,1], scale.= TRUE )
pca3d(pca, group=metabo[,1])
makeMoviePCA()
## End(Not run)
```

---

**metabo**

*Metabolic profiles in tuberculosis.*

**Description**

Relative abundances of metabolites from serum samples of three groups of individuals

**Details**

A data frame with 136 observations on 425 metabolic variables.

Serum samples from three groups of individuals were compared: tuberculin skin test negative (NEG), positive (POS) and clinical tuberculosis (TB).
References


Examples

```r
data(metabo)
# maybe str(metabo) ; plot(metabo) ...
pca <- prcomp( metabo[,,-1] )
```

---

```r
pca2d
Show a three- or two-dimensional plot of a prcomp object
```

Description

Show a three- two-dimensional plot of a prcomp object or a matrix, using different symbols and colors for groups of data

Usage

```r
pca2d(
pca,
components = 1:2,
col = NULL,
title = NULL,
new = FALSE,
axes.color = "black",
bg = "white",
radius = 1,
group = NULL,
shape = NULL,
palette = NULL,
fancy = FALSE,
biplot = FALSE,
biplot.vars = 5,
legend = NULL,
show.scale = FALSE,
show.labels = FALSE,
labels.col = "black",
show.axes = TRUE,
show.axe.titles = TRUE,
axe.titles = NULL,
show.plane = TRUE,
show.shadows = FALSE,
show.centroids = FALSE,
show.group.labels = FALSE,
```

```r
```
Arguments

pca Either a prcomp object or a matrix with at least three columns
components Vector of length 3 (pca3d) or 2 (pca2d) containing the components to be shown
col Either a single value or a vector of length equal to number of rows, containing color definitions for the plot points to be shown
title Window title
new Use TRUE to open a new window
axes.color Axis color This option has no effect in pca2d.
bg Background color
radius Scaling item for the size of points to be shown. In pca2d, this corresponds to the cex parameter.
group either NULL or a factor of length equal to number of rows. Factor levels can be used to automatically generate symbols and colors for the points shown
shape Either a single value or a character vector describing the shapes to be used when drawing data points. Allowed shapes are: sphere, tetrahaedron and cube, and may be abbreviated. In pca2d, the parameter is passed directly on to the pch option of the points() function.
palette Specifies the color palette when colors are automatically assigned to the groups. See Details.
fancy set 'show.labels', 'show.shadows', 'show.centroids' and 'show.group.labels' to TRUE.
biplot Specify whether to show a biplot (see section 'biplots' below)
biplot.vars Specify which loading to show on the biplot (see section 'biplots' below)
legend If NULL, no legend will be drawn. Otherwise the value specifies the legend position in a form accepted by legend and legend3d.
show.scale TRUE for showing a numeric scale at the edges of the plot. This option has no effect in pca2d.
show.labels TRUE for showing labels (taken from the coordinate matrix or the prcomp object). Alternatively, a vector with labels to be shown next to the data points.
labels.col Single value or vector describing the colors of the labels.
show.axes TRUE to show the axes. This option has no effect in pca2d.
show.axe.titles If TRUE, show axe titles (PC 1, PC 2 etc.) This option has no effect in pca2d.
axe.titles A vector with two (pca2d) or three (pca3d) values containing the axe titles (corresponds to xlab and ylab in regular plot). If missing, but show.axe.titles is TRUE, axe titles will be generated automatically.
show.plane If TRUE, show a grey horizontal plane at y = 0. This option has no effect in pca2d.
show.shadows If TRUE, show a "lollipop" representation of the points on the y = 0 plane: a vertical line joining the data point with the plane and a shadow. In pca2d, for each sample at (x,y), a grey line is drawn from (x,y) to (x,0).
show.centroids If TRUE and the group variable is defined, show cluster centroids (using apropriate group symbols) and lines from each data point to the corresponding centroid.
show.group.labels Either TRUTH/FALSE or a vector equal to the number of unique values in the group parameter. If set, labels for each of the defined group will be shown at the group’s centroid. If the value of the parameter is TRUE, then the group names will be taken from the group parameter. Otherwise, the values from this parameter will be used.
show.ellipses A TRUTH/FALSE value indicating whether to show confidence interval ellipses or ellipsoids around each defined group.
elliptci

The confidence level of a pairwise confidence region for the CI. The default is 0.95, for a 95 the size of the ellipse being plotted.

... For pca2d, any further argument will be passed on to the points() function.

show.shapes

A TRUTH/FALSE value indicating whether the different symbols (shapes) for the shown data points should be plotted (default TRUE).

Details

The pca3d function shows a three dimensional representation of a PCA object or any other matrix. It uses the rgl package for rendering.
	pca2d is the 2D counterpart. It creates a regular, two-dimensional plot on the standard graphic device. However, it takes exactly the same options as pca3d, such that it is easy to create 2D variants of the 3D graph.

Often, PCA visualisation requires using different symbols and colors for different groups of data. pca3d() and pca2d() aim at creating reasonable defaults, such that a simple call with two parameters – the pca object and the vector with group assignments of the samples – is sufficient for a basic diagnosis.

Value

Both pca2d and pca3d return invisibly a data frame which can be used to generate a legend for the figure. The data frame has as many rows as there are groups, and column with the group name, assigned color and assigned shape.

Biplots

If option ‘biplot’ is TRUE, a biplot showing both the PCA results (samples) and variables is shown. This corresponds to the biplot function which works for the prcomp class objects. However, a biplot showing all variable loadings will be unreadable if the data is highly dimensional (for example, gene expression data). Therefore, the option ‘biplot.vars’ specifies which variables are shown on the biplot.

If ‘biplot.vars’ is a vector of length larger than one, it will be interpreted as a direct selection of the variables to be shown; for example, for a prcomp object pca, the variable selection will happen through pca$rotation[biplot.vars,].

If ‘biplot.vars’ is a single number, then for each of the components shown, a number of variables equal to ‘biplot.vars’ with the highest absolute loadings will be shown on the biplot.

Examples

data( metabo )
pca <- prcomp( metabo[,1], scale.= TRUE )

pca3d( pca, group= metabo[,1] )
pca2d( pca, group= metabo[,1] )

## a bit more fancy:
## black background, white axes,
## centroids
pca3d( pca, group = metabo[,1],
   fancy = TRUE, bg = "black",
   axes.color = "white", new = TRUE )

snapshotPCA3d

---

**Description**

Take a snapshot of the 3D PCA to a file.

**Usage**

`snapshotPCA3d(file)`

**Arguments**

- `file` Name of the file to save the snapshot to

```r
data( metabo )
pca <- prcomp( metabo[,-1], scale = TRUE )
pca3d(pca, group = metabo[,1])
snapshotPCA3d("testfile.png")
```

**Details**

This is just a wrapper around `rgl.snapshot`. 

---

`snapshotPCA3d` **Save a 3D PCA snapshot**
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