

Package ‘LSD’

June 17, 2020

Version 4.1-0

Date 2020-06-16

Title Lots of Superior Depictions

Author Bjoern Schwalb [aut, cre],
Achim Tresch [aut],
Phillipp Torkler [ctb],
Sebastian Duemcke [ctb],
Carina Demel [ctb],
Brian Ripley [ctb],
Bill Venables [ctb]

Maintainer Bjoern Schwalb <schwalb.bjoern@gmail.com>

Description Create lots of colorful plots in a plethora of variations. Try the LSD demotour().

License GPL-2 | GPL-3

LazyData true

RoxygenNote 7.1.0

NeedsCompilation no

Repository CRAN

Date/Publication 2020-06-17 09:50:18 UTC

R topics documented:

| | |
|------------------------------|----|
| align | 2 |
| clusterplot | 4 |
| colorpalette | 6 |
| comparisonplot | 7 |
| complementarycolor | 9 |
| convertcolor | 10 |
| convertgrey | 10 |
| daltonize | 11 |
| demotour | 12 |
| densitylane | 13 |
| disco | 14 |

| | |
|-----------------------------|----|
| distinctcolors | 15 |
| ellipsescatter | 16 |
| emptyplot | 17 |
| fusionplot | 18 |
| heatbarplot | 20 |
| heatboxplot | 21 |
| heathist | 23 |
| heatpairs | 25 |
| heatscatter | 28 |
| heatscatterpoints | 30 |
| homer | 32 |
| intersphere | 33 |
| linesplot | 34 |
| LSD.pie | 36 |
| makemovie | 38 |
| msdplot | 39 |
| plotit | 40 |
| plotmatrix | 42 |
| seqs | 44 |
| singleclusterplot | 44 |
| singlefusionplot | 46 |
| singlemsdplot | 47 |
| webdesign | 48 |
| windowxy | 49 |

Index **51**

| | |
|-------|--|
| align | <i>Visualize two-dimensional data in a color encoded fashion</i> |
|-------|--|

Description

Depict any matrix or list in a color encoded rectangular fashion.

Usage

```
align(
  input,
  colpal = "heat",
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  alpha = NULL,
  label = FALSE,
  digits = 1,
  border = NULL,
  xlim = NULL,
  ylim = NULL,
```

```

    main = NULL,
    axes = TRUE,
    ...
)

```

Arguments

| | |
|-----------|--|
| input | matrix or list with any type of entries. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| label | logical: if TRUE (FALSE by default), labels are added according to the color scheme (i.e. binning). |
| digits | integer indicating the number of decimals to be used for binning of continuous data. |
| border | color for rectangle border(s). Use <code>border = NA</code> to omit borders. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| main | title of the plot, standard graphics parameter. |
| axes | logical: if TRUE (by default), a box and axes are added to the plot (if FALSE, custom specification of axes can be achieved via basic R graphics functions). |
| ... | additional parameters to be passed to <code>points</code> and <code>plot</code> . |

Author(s)

Phillipp Torkler, Bjoern Schwalb

See Also

[clusterplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```

data(seqs)
colpal = c("A" = "darkgreen", "C" = "darkblue", "G" = "yellow", "T" = "darkred")
align(seqs, colpal = colpal, label = TRUE, main = "DNA sequences")

data(homer)
colpal = c("white", "black", "yellow", "wheat3")
align(homer, colpal = colpal, main = "D'OH!", asp = 1, axes = FALSE)

```

clusterplot

Visualize two-dimensional data clusters

Description

Depict a numeric matrix or list utilizing the underlying distribution quantiles of one dimension in a color encoded fashion.

Usage

```
clusterplot(
  input,
  label = NULL,
  at = NULL,
  main = NULL,
  xlim = NULL,
  ylim = NULL,
  xlabel = NULL,
  fromto = c(0.05, 0.95),
  colpal = "standardheat",
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  nrcol = 25,
  outer.col = "lightgrey",
  quartiles.col = c("grey", "black", "grey"),
  add.quartiles = TRUE,
  separate = TRUE,
  rev = FALSE,
  size = TRUE,
  alpha = NULL,
  axes = TRUE,
  ...
)
```

Arguments

| | |
|-------|--|
| input | matrix or list with numerical entries. |
| label | a character vector assigning rows/elements of 'input' to clusters (if specified, multiple clusters can be depicted in different colors and/or subsequent plots). |
| at | a integer vector containing the x-positions corresponding to the columns of 'input'. |
| main | title(s) of the plot, standard graphics parameter. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |

| | |
|---------------|--|
| xlabels | a character vector containing labels for the x-axis. |
| fromto | a numeric vector containing the range of quantiles (between 0 and 1) to be plotted. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to 25, if not specified). |
| outer.col | R built-in color to be used for outlier lines (lines outside of 'fromto'). |
| quartiles.col | a character vector containing three R built-in colors for quartile lines (<code>c('0.25','0.5','0.75')</code>). |
| add.quartiles | logical: if TRUE (by default), lines are plotted corresponding to the quartiles. |
| separate | if TRUE (by default), different clusters are depicted in subsequent plots. |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| size | logical: if TRUE (by default), the size of each cluster is added to the title of the respective plot. |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| axes | logical: if TRUE (by default), a box and axes are added to the plot (if FALSE, custom specification of axes can be achieved via basic R graphics functions). |
| ... | additional parameters to be passed to <code>points</code> and <code>plot</code> . |

Author(s)

Achim Tresch, Bjoern Schwalb

See Also

[singleclusterplot](#), [align](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```

samples = 100
probes = 75
at = 1:probes
clus = matrix(rnorm(probes*samples, sd=1), ncol=probes)

clus = rbind(
  t(t(clus)+sin(1:probes/10))+1:nrow(clus)/samples,
  t(t(clus)+sin(pi/2+1:probes/10))+1:nrow(clus)/samples)

```

```

quartiles.col = c("transparent", "black", "transparent")
colpal = c("standardheat", "crazyblue", "crazyred", "crazygreen")

labs = paste("cluster", kmeans(clus, 4)$cluster)
clusterplot(clus, fromto=c(0, 1))

clusterplot(clus, labs, separate=FALSE, xaxt="n", fromto=c(0.4, 0.6), colpal=colpal,
outer.col="none", ylim=c(-2, 3), quartiles.col = quartiles.col)

clusterplot(clus, labs, colpal=colpal)

labs = paste("cluster", kmeans(clus, 2)$cluster)
colpal = c("greens", "purples")
clusterplot(clus, labs, separate=FALSE, xaxt="n", fromto=c(0.3, 0.7), colpal=colpal,
outer.col="none", ylim=c(-1, 2), alpha=50, quartiles.col = quartiles.col)

```

colorpalette

Provides colorpalettes containing R built-in colors

Description

Provides pre-designed colorpalettes (character vectors containing R built-in colors) of this and several other R packages (grDevices, RColorBrewer, colorRamps) as well as custom-made ones.

Usage

```

colorpalette(
  colpal,
  nrcol = NULL,
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  alpha = NULL,
  rev = FALSE
)

```

Arguments

| | |
|-----------|--|
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>). |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to length of colpal, if not specified). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is returned to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is returned to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |

alpha alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default).

rev logical: if TRUE (FALSE by default), a reversed colorpalette is returned.

Value

colorpalette returns a vector containing R built-in colors in hexadecimal representation.

Author(s)

Achim Tresch, Bjoern Schwalb

See Also

[disco](#), [demotour](#)

Examples

```
colorpalette("heat")
colorpalette(c("darkred", "grey", "darkblue"), 10)
```

comparisonplot

Comparisonplot: a fancy scatterplot

Description

A function to compare two vectors extensively.

Usage

```
comparisonplot(
  x,
  y,
  histbreaks = 30,
  adjust = 1,
  colpal = "heat",
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  alpha = NULL,
  rev = FALSE,
  main = "comparisonplot",
  cor = FALSE,
  xlab = NULL,
  ylab = NULL,
  xlim = NULL,
  ylim = NULL,
  ab = FALSE,
```

```

    add.density = FALSE,
    col.density = "darkred",
    pimp = FALSE,
    ...
)

```

Arguments

| | |
|-------------|--|
| x | a numeric vector. |
| y | a numeric vector. |
| histbreaks | a non-negative integer specifying the number of breaks of the histograms. |
| adjust | scale the used bandwidth of the density estimate, if <code>add.density = TRUE</code> . |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| main | title(s) of the plot, standard graphics parameter. |
| cor | if TRUE (FALSE by default), the correlation is added to the title. |
| xlab | x label, standard graphics parameter. |
| ylab | y label, standard graphics parameter. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| ab | if TRUE (FALSE by default), <code>abline(0, 1)</code> is added to the heatscatter. |
| add.density | if TRUE (FALSE by default), density lines are added to the barplots. |
| col.density | R built-in color to specify the color of the density line. |
| pimp | if TRUE (FALSE by default), the plot is pimped. |
| ... | additional parameters to be passed to <code>points</code> and <code>plot</code> . |

Author(s)

Bjoern Schwalb

See Also

[align](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```
points = 10^4
x = c(rnorm(points/2),rnorm(points/2)+4)
y = x + rnorm(points,sd=0.8)
x = sign(x)*abs(x)^1.3

comparisonplot(x,y,histbreaks=30,pch=20)
```

complementarycolor *Complement R colors*

Description

Convert R built-in colors to their color complement

Usage

```
complementarycolor(cols, alpha = NULL)
```

Arguments

`cols` a character vector containing R built-in colors.

`alpha` alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default).

Value

`complementarycolor` returns a vector containing R built-in colors in hexadecimal representation.

Author(s)

Bjoern Schwalb

See Also

[disco](#), [colorpalette](#), [demotour](#)

Examples

```
complementarycolor(c("red", "green", "blue"))
```

`convertcolor`*Map R colors to hexadecimal representation*

Description

Convert R built-in colors to hexadecimal representation.

Usage

```
convertcolor(cols, alpha = NULL)
```

Arguments

`cols` a character vector containing R built-in colors.
`alpha` alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default).

Value

`convertcolor` returns a vector containing R built-in colors in hexadecimal representation.

Author(s)

Bjoern Schwalb

See Also

[disco](#), [colorpalette](#), [demotour](#)

Examples

```
convertcolor(c("red", "green", "blue"))
```

`convertgrey`*Convert R colors to greyscale*

Description

Greyscale R built-in colors.

Usage

```
convertgrey(cols, alpha = NULL)
```

Arguments

| | |
|-------|---|
| cols | a character vector containing R built-in colors. |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |

Value

convertgrey returns a vector containing R built-in colors in hexadecimal representation.

Author(s)

Bjoern Schwalb

See Also

[disco](#), [colorpalette](#), [demotour](#)

Examples

```
convertgrey(c("red", "green", "blue"))
```

daltonize

Dichromat vision simulation for colorpalettes

Description

Dichromat vision simulation and enhancement according to <http://www.daltonize.org>.

Usage

```
daltonize(colpal, cvd = "p", show = TRUE)
```

Arguments

| | |
|--------|---|
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see disco() or disco). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| show | logical: if TRUE (by default), the resulting colorpalettes are depicted in an R plot. |

Value

daltonize returns a list, where each entry is a vector containing R built-in colors in hexadecimal representation:

| | |
|-----------|----------------------------|
| simulated | vector of simulated colors |
| enhanced | vector of enhanced colors |

Author(s)

Bjoern Schwalb

References

<http://www.daltonize.org>

See Also

[disco](#), [colorpalette](#), [demotour](#)

Examples

```
daltonize("heat",cvd = "d")
daltonize("colorblind",cvd = "p")
```

demotour

LSD teaser

Description

A compilation of selected plot examples.

Usage

```
demotour()
```

Author(s)

Bjoern Schwalb

See Also

[heatscatter](#), [clusterplot](#), [disco](#), [colorpalette](#), [daltonize](#)

Examples

```
demotour()
```

densitylane

Visualize a density in a rectangular fashion

Description

Add a color stripe to an existing plot based on a kernel density estimate.

Usage

```
densitylane(
  x,
  y,
  pos = 1,
  width = 0.4,
  colpal = "standard",
  rev = FALSE,
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  alpha = NULL,
  horizontal = horizontal,
  nrcol = 75
)
```

Arguments

| | |
|------------|--|
| x | density\$x values of a density object. |
| y | density\$y values of a density object. |
| pos | the x co-ordinate of the lane (mid point). |
| width | a numeric value giving the width of the lane. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| horizontal | logical: if TRUE (FALSE by default), rotation of 90 degrees is applied. |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to 100, if not specified). |

Author(s)

Bjoern Schwalb

See Also

[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)

disco

Disco (DISplays COLORpalettes)

Description

Displays pre-designed colorpalettes as well as custom-made ones (see [colorpalette](#)).

Usage

```
disco(colpal = NULL, nrcol = NULL, alpha = NULL)
```

Arguments

| | |
|--------|--|
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (displays all colorpalettes, if not specified). |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to length of colpal, if not specified). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |

Author(s)

Bjoern Schwalb

See Also

[colorpalette](#), [demotour](#)

Examples

```
disco()  
disco("rdbu",10)
```

distinctcolors *Find preferably distinct R built-in colors*

Description

Find a vector of distinct R built-in colors for a pre-defined length ('nrcol').

Usage

```
distinctcolors(  
  nrcol = 10,  
  method = "RGB",  
  bw = FALSE,  
  show = TRUE,  
  simulate = TRUE  
)
```

Arguments

| | |
|----------|--|
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to the length of 10, if not specified). |
| method | character string implying the method for color selection to be used ("RGB" uses a grid in the RGB space (default), "Lab" uses a grid in the Lab space, "golden-ratio" uses the golden ratio as spacing between colors in the HSV color space). |
| bw | logical: if TRUE (FALSE by default), the colors "black" and "white" are removed from the resulting colorpalette. |
| show | logical: if TRUE (by default), the resulting colorpalettes are depicted in an R plot. |
| simulate | logical: if TRUE (by default), a converted colorpalettes are additionally depicted to simulate dichromat vision according to http://www.daltonize.org (see daltonize). |

Value

distinctcolors returns a vector containing R built-in colors in hexadecimal representation.

Author(s)

Bjoern Schwalb

See Also

[disco](#), [colorpalette](#), [demotour](#)

Examples

```
distinctcolors()
```

| | |
|----------------|--|
| ellipsescatter | <i>Visualize subgroups of two-dimensional data assuming normal distributions</i> |
|----------------|--|

Description

A scatterplot with additional colored ellipses based on a gaussianity assumption.

Usage

```
ellipsescatter(
  x,
  y,
  groups,
  colors = NULL,
  pch = 20,
  bgcol = "darkgrey",
  main = "ellipsescatter",
  xlab = NULL,
  ylab = NULL,
  scaled = 1,
  level = 0.75,
  legend.cex = 1,
  location = "topright",
  ...
)
```

Arguments

| | |
|--------|--|
| x | a numeric vector. |
| y | a numeric vector. |
| groups | a list of indices or vector names to be plotted as groups (not necessarily all of x and y). |
| colors | a character vector of R build-in colors corresponding to the chosen groups. |
| pch | the plotting character (to be passed to plot). |
| bgcol | a R build-in color for non-grouped points. |
| main | title(s) of the plot, standard graphics parameter. |
| xlab | x label, standard graphics parameter. |
| ylab | y label, standard graphics parameter. |
| scaled | a numeric value giving the scaling factor for standard deviations in each dimension (defaults to 1). |
| level | a numeric value (between 0 and 1) giving the confidence level of a pairwise confidence region. |

legend.cex a numerical value giving the amount by which the added legend should be magnified relative to the default.

location the x and y co-ordinates to be used to position the legend (see 'xy.coords').

... additional parameters to be passed to points and plot.

Author(s)

Bjoern Schwalb

See Also

[demotour](#), [disco](#), [colorpalette](#)

Examples

```
x = c(rnorm(50),rnorm(100,2),rnorm(50,4))
y = (x + rnorm(200,0,0.8))*rep(c(1,4,1),c(50,100,50))
x = sign(x)*abs(x)^1.3

groups = list("Green" = 1:50,"Red" = 51:150,"Blue" = 151:200)
colors = c("darkgreen","darkred","darkblue")
ellipsescatter(x,y,groups,colors,location = "topleft")
```

emptyplot

Wrapper function for an empty graphics device

Description

Calls an empty graphics device with a coordinate system of choice.

Usage

```
emptyplot(xlim = c(-1, 1), ylim = c(-1, 1), ...)
```

Arguments

xlim x limits, standard graphics parameter.

ylim y limits, standard graphics parameter.

... additional parameters to be passed to points and plot.

Author(s)

Bjoern Schwalb

See Also

[demotour](#)

Examples

```
emptyplot()
```

fusionplot

Visualize two-dimensional data clusters

Description

Depict a numeric matrix or list utilizing the underlying distribution quantiles of one dimension in a color encoded fashion.

Usage

```
fusionplot(  
  x,  
  y,  
  label = NULL,  
  main = NULL,  
  xlim = NULL,  
  ylim = NULL,  
  fromto = c(0.05, 0.95),  
  colpal = "standardheat",  
  simulate = FALSE,  
  daltonize = FALSE,  
  cvd = "p",  
  nrcol = 25,  
  outer.col = "lightgrey",  
  quartiles.col = c("grey", "black", "grey"),  
  add.quartiles = TRUE,  
  separate = TRUE,  
  rev = FALSE,  
  size = TRUE,  
  alpha = NULL,  
  axes = TRUE,  
  ...  
)
```

Arguments

| | |
|-------|--|
| x | a numeric vector. |
| y | a numeric vector. |
| label | a character vector assigning rows/elements of 'input' to clusters (if specified, multiple clusters can be depicted in different colors and/or subsequent plots). |
| main | title(s) of the plot, standard graphics parameter. |
| xlim | x limits, standard graphics parameter. |

| | |
|----------------------------|--|
| <code>ylim</code> | y limits, standard graphics parameter. |
| <code>fromto</code> | a numeric vector containing the range of quantiles (between 0 and 1) to be plotted. |
| <code>colpal</code> | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>). |
| <code>simulate</code> | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| <code>daltonize</code> | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| <code>cvd</code> | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| <code>nrcol</code> | a non-negative integer specifying the number of colors to be used (defaults to 25, if not specified). |
| <code>outer.col</code> | R built-in color to be used for outlier lines (lines outside of 'fromto'). |
| <code>quartiles.col</code> | a character vector containing three R built-in colors for quartile lines (<code>c('0.25','0.5','0.75')</code>). |
| <code>add.quartiles</code> | logical: if TRUE (by default), lines are plotted corresponding to the quartiles. |
| <code>separate</code> | if TRUE (by default), different clusters are depicted in subsequent plots. |
| <code>rev</code> | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| <code>size</code> | logical: if TRUE (by default), the size of each cluster is added to the title of the respective plot. |
| <code>alpha</code> | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| <code>axes</code> | logical: if TRUE (by default), a box and axes are added to the plot (if FALSE, custom specification of axes can be achieved via basic R graphics functions). |
| <code>...</code> | additional parameters to be passed to <code>points</code> and <code>plot</code> . |

Author(s)

Achim Tresch, Bjoern Schwalb

See Also

[singlefusionplot](#), [align](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```
nr = 750
x = 1:nr/300
y = c(rnorm(nr)+sin(2*x)*3,rnorm(nr)+sin(2*x+pi/2)*3)
x = c(x,x)

labs = paste("cluster",c(rep(c(1,2),each = nr)))
colpals = c("oranges","pubu")
qcol = c("transparent","black","transparent")
fusionplot(x,y,labs,separate=FALSE,colpal=colpals,alpha=75,quartiles.col = qcol)
```

heatbarplot *Color a barplot.*

Description

Depict a histogram object as a barplot in a color encoded fashion based on a kernel density estimate.

Usage

```
heatbarplot(  
  x,  
  colpal = "heat",  
  simulate = FALSE,  
  daltonize = FALSE,  
  cvd = "p",  
  alpha = NULL,  
  rev = FALSE,  
  horizontal = FALSE,  
  nrcol = 100,  
  ...  
)
```

Arguments

| | |
|------------|--|
| x | a histogram object. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| horizontal | logical: if TRUE (FALSE by default), rotation of 90 degrees is applied. |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to 100, if not specified). |
| ... | additional parameters to be passed to <code>points</code> and <code>plot</code> . |

Author(s)

Bjoern Schwalb

See Also

[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```
points = 10^4
x = c(rnorm(points/2),rnorm(points/2)+4)
x = sign(x)*abs(x)^1.3
xhist = hist(x,plot = FALSE)

heatbarplot(xhist)
```

heatboxplot

Heatboxplot: a colored boxplot

Description

A boxplot with an additional color stripe based on a kernel density estimate.

Usage

```
heatboxplot(
  x,
  horizontal = FALSE,
  add = FALSE,
  colpal = "standard",
  rev = FALSE,
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  alpha = NULL,
  colpals = NULL,
  nrcol = 75,
  lwd = 1.75,
  axes = TRUE,
  labels = NULL,
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = "",
  main = "heatboxplot",
  nolab = FALSE,
  outline = TRUE,
  boxonly = FALSE,
  adjust = 1,
  quant.from = 0.25,
  quant.to = 0.75,
```

```

    range = 1.5,
    border = "black",
    plot.boxplot = TRUE,
    add.quartiles = TRUE,
    add.box = FALSE,
    n.density = 1024,
    cexbox = 0.6,
    ...
)

```

Arguments

| | |
|------------|--|
| x | data as vector, matrix, list or data.frame. |
| horizontal | logical: if TRUE (FALSE by default), rotation of 90 degrees is applied. |
| add | logical: if TRUE (FALSE by default), the boxplot is added to an existing plot. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| colpals | a character vector containing names of LSD colorpalettes (see <code>disco()</code> or <code>disco</code>). |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to 100, if not specified). |
| lwd | linewidth of the box and whiskers. |
| axes | logical: if TRUE (by default), the axes are plotted. |
| labels | a character vector of labels. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| xlab | x label, standard graphics parameter. |
| ylab | y label, standard graphics parameter. |
| main | title(s) of the plot, standard graphics parameter. |
| nolab | logical: if TRUE (FALSE by default), the title and ylab are suppressed. |
| outline | logical: if TRUE (by default), outliers are plotted. |
| boxonly | logical: if TRUE (FALSE by default), the density is only be plotted in the box. |
| adjust | a numeric value giving the scaling factor for the used bandwidth (defaults to 1). |

| | |
|----------------------------|---|
| <code>quant.from</code> | a numeric value (between 0 and 1) giving the quantile from which the density lane should be plotted. |
| <code>quant.to</code> | a numeric value (between 0 and 1) giving the quantile to which the density lane should be plotted. |
| <code>range</code> | a numeric value to determine how far the plot whiskers extend out from the box. |
| <code>border</code> | an R build-in color for the box and whiskers. |
| <code>plot.boxplot</code> | logical: if TRUE (by default), the boxplot is added to the density. |
| <code>add.quantiles</code> | if TRUE (FALSE by default), only the box of the boxplot is added (if <code>plot.boxplot = FALSE</code>). |
| <code>add.box</code> | logical: if TRUE (by default), the box is added to the plot. |
| <code>n.density</code> | an integer specifying the number of equally spaced points at which the density is to be estimated. |
| <code>cexbox</code> | a numerical value giving the amount by which the boxes should be magnified relative to the default. |
| <code>...</code> | additional parameters to be passed to <code>points</code> and <code>plot</code> . |

Author(s)

Bjoern Schwalb

See Also[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)**Examples**

```
f = c(rnorm(200), rnorm(200)+4)
h = rf(500, 15, 15)*10
g = rnorm(300)+1

heatboxplot(h)

heatboxplot(list(f=f, g=g), colpals=c("rdpu", "greens"), labels=c("bimodal", "unimodal"))
```

`heathist`*Color a histogram*

Description

A histogram with an additional color stripe based on a kernel density estimate.

Usage

```

heathist(
  x,
  breaks = 20,
  xlab = NULL,
  ylab = NULL,
  main = "heathist",
  colpal = "greys",
  rev = FALSE,
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  alpha = NULL,
  nobox = FALSE,
  add.density = FALSE,
  col.density = "darkred",
  add.rug = TRUE,
  col.rug = "black",
  nrcol = 100,
  ...
)

```

Arguments

| | |
|-------------|--|
| x | a numeric vector. |
| breaks | a numeric value giving the breaks of the histogram. |
| xlab | x label, standard graphics parameter. |
| ylab | y label, standard graphics parameter. |
| main | title(s) of the plot, standard graphics parameter. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| nobox | logical: if TRUE (FALSE by default), the box of the plot is omitted. |
| add.density | if TRUE (FALSE by default), a density line is added to the histogram. |
| col.density | a R build-in color for the density line (if <code>add.density = TRUE</code>). |

| | |
|----------------------|--|
| <code>add.rug</code> | if TRUE (FALSE by default), a rug (1-d plot of the data) is added below the histogram-bars. |
| <code>col.rug</code> | a R build-in color for the rug (if <code>add.rug = TRUE</code>). |
| <code>nr.col</code> | a non-negative integer specifying the number of colors to be used (defaults to 100, if not specified). |
| <code>...</code> | additional parameters to be passed to <code>points</code> and <code>plot</code> . |

Author(s)

Bjoern Schwalb

See Also[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)**Examples**

```
x = rnorm(1000,mean = sample(c(0,3),size = 1000,prob = c(0.4,0.6),replace = TRUE))
heathist(x,xlab="x",add.density=TRUE,col.rug="darkred")
```

```
heathist(x,xlab="x",colpal = "matlablike")
```

| | |
|-----------|--|
| heatpairs | <i>Pairwise colored scatterplot based on a two-dimensional Kernel Density Estimation</i> |
|-----------|--|

Description

Pairwise visualization of two dimensional data in a three dimensional fashion facilitating a color encoded Kernel Density Estimation.

Usage

```
heatpairs(
  mat,
  main = "heatpairs",
  xlim = NULL,
  ylim = NULL,
  labels = NULL,
  add.points = FALSE,
  group = NULL,
  color.group = "magenta",
  method = "spearman",
  colpal = "heat",
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
```

```

alpha = NULL,
rev = FALSE,
pch = 19,
cexplot = 0.5,
cor.cex = 2.5,
nrcol = 30,
grid = 100,
only = "none",
add.contour = FALSE,
nlevels = 10,
color.contour = "black",
greyscale = FALSE,
log = "",
...
)

```

Arguments

| | |
|--------------------------|--|
| <code>mat</code> | a matrix with numerical entries. |
| <code>main</code> | title(s) of the plot, standard graphics parameter. |
| <code>xlim</code> | x limits, standard graphics parameter. |
| <code>ylim</code> | y limits, standard graphics parameter. |
| <code>labels</code> | a character vector giving the labels to be shown on the diagonal. |
| <code>add.points</code> | logical: if TRUE (FALSE by default), a certain 'group' of points can be colored in all pairwise plots. |
| <code>group</code> | indices or rownames of 'mat' to be highlighted in all pairwise plots (not necessarily all). |
| <code>color.group</code> | R build-in color in which the 'group' of points should be highlighted. |
| <code>method</code> | a character specifying the correlation method to use ('spearman' (default), 'pearson' or 'kendall'). |
| <code>colpal</code> | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |
| <code>simulate</code> | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| <code>daltonize</code> | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| <code>cvd</code> | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| <code>alpha</code> | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| <code>rev</code> | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| <code>pch</code> | plotting 'character'. This can either be a single character or an integer code for one of a set of graphics symbols. (see '?pch', to be passed to plot). |

| | |
|----------------------------|---|
| <code>cexplot</code> | a numerical value giving the amount by which the points should be magnified relative to the default. |
| <code>cor.cex</code> | a numerical value giving the amount by which the correlation characters should be magnified relative to the default. |
| <code>nrcol</code> | a non-negative integer specifying the number of colors to be used (defaults to 100, if not specified). |
| <code>grid</code> | an integer specifying the size of the grid used for the KDE. |
| <code>only</code> | a character string which contains 'x' if the density should only be computed for the x axis, 'y' for the y axis (defaults to 'none' for the two-dimensional case). |
| <code>add.contour</code> | logical: if TRUE (FALSE by default), the contour lines are added to the plot. |
| <code>nlevels</code> | an integer giving the number of levels of the contour lines. |
| <code>color.contour</code> | R build-in color for the contour lines. |
| <code>greyscale</code> | logical: if TRUE (FALSE by default), the used colorpalette is converted to greyscales. |
| <code>log</code> | a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic. |
| <code>...</code> | additional parameters to be passed to points and plot |

Author(s)

Bjoern Schwalb

See Also

[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```

points = 10^4
x = rnorm(points/2)
x = c(x,x+2.5)
y = x + rnorm(points,sd=0.75)
x = sign(x)*abs(x)^1.3
mat = cbind(x,y,x + rnorm(points,sd=0.5))
colnames(mat) = c("x","y","z")
rownames(mat) = 1:nrow(mat)

heatpairs(mat,labels=c(expression(Xi),expression(Lambda),expression(Delta)))

```

| | |
|-------------|---|
| heatscatter | <i>A colored scatterplot based on a two-dimensional Kernel Density Estimation</i> |
|-------------|---|

Description

Visualize two dimensional data in a three dimensional fashion facilitating a color encoded Kernel Density Estimation.

Usage

```
heatscatter(  
  x,  
  y,  
  pch = 19,  
  cexplot = 0.5,  
  nrcol = 30,  
  grid = 100,  
  colpal = "heat",  
  simulate = FALSE,  
  daltonize = FALSE,  
  cvd = "p",  
  alpha = NULL,  
  rev = FALSE,  
  xlim = NULL,  
  ylim = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  main = "heatscatter",  
  cor = FALSE,  
  method = "spearman",  
  only = "none",  
  add.contour = FALSE,  
  nlevels = 10,  
  color.contour = "black",  
  greyscale = FALSE,  
  log = "",  
  ...  
)
```

Arguments

| | |
|-----|--|
| x | a numeric vector. |
| y | a numeric vector. |
| pch | plotting 'character'. This can either be a single character or an integer code for one of a set of graphics symbols. (see '?pch', to be passed to plot). |

| | |
|---------------|--|
| cexplot | a numerical value giving the amount by which the points should be magnified relative to the default. |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to 100, if not specified). |
| grid | an integer specifying the size of the grid used for the KDE. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| xlab | x labels, standard graphics parameter. |
| ylab | y labels, standard graphics parameter. |
| main | title(s) of the plot, standard graphics parameter. |
| cor | logical: if TRUE (FALSE by default), the correlation is added to the title. |
| method | a character specifying the correlation method to use ('spearman' (default), 'pearson' or 'kendall'). |
| only | a character string which contains 'x' if the density should only be computed for the x axis, 'y' for the y axis (defaults to 'none' for the two-dimensional case). |
| add.contour | logical: if TRUE (FALSE by default), the contour lines are added to the plot. |
| nlevels | an integer giving the number of levels of the contour lines. |
| color.contour | R build-in color for the contour lines. |
| greyscale | logical: if TRUE (FALSE by default), the used colorpalette is converted to greyscales. |
| log | a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic. |
| ... | additional parameters to be passed to points and plot. |

Note

Two-Dimensional Kernel Density Estimation adapted and modified from Venables and Ripley's MASS package (see reference).

Author(s)

Achim Tresch, Bjoern Schwalb

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```
points = 10^4
x = c(rnorm(points/2), rnorm(points/2)+4)
y = x + rnorm(points, sd=0.8)
x = sign(x)*abs(x)^1.3

heatscatter(x,y)

heatscatter(x,y, colpal="bl2gr2rd", main="bl2gr2rd", cor=FALSE)

heatscatter(x,y, cor=FALSE, add.contour=TRUE, color.contour="red", greyscale=TRUE)

heatscatter(x,y, colpal="spectral", cor=FALSE, add.contour=TRUE)
```

| | |
|-------------------|---|
| heatscatterpoints | <i>A colored scatterplot based on a two-dimensional Kernel Density Estimation (add to an existing plot)</i> |
|-------------------|---|

Description

Visualize two dimensional data in a three dimensional fashion facilitating a color encoded Kernel Density Estimation (add to an existing plot).

Usage

```
heatscatterpoints(
  x,
  y,
  pch = 19,
  cexplot = 0.5,
  nrcol = 30,
  grid = 100,
  colpal = "heat",
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  alpha = NULL,
  rev = FALSE,
  xlim = NULL,
  ylim = NULL,
```

```

    only = "none",
    add.contour = FALSE,
    nlevels = 10,
    color.contour = "black",
    greyscale = FALSE,
    log = "",
    ...
)

```

Arguments

| | |
|---------------|--|
| x | a numeric vector. |
| y | a numeric vector. |
| pch | plotting 'character'. This can either be a single character or an integer code for one of a set of graphics symbols. (see '?pch', to be passed to plot). |
| cexplot | a numerical value giving the amount by which the points should be magnified relative to the default. |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to 100, if not specified). |
| grid | an integer specifying the size of the grid used for the KDE. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| only | a character string which contains 'x' if the density should only be computed for the x axis, 'y' for the y axis (defaults to 'none' for the two-dimensional case). |
| add.contour | logical: if TRUE (FALSE by default), the contour lines are added to the plot. |
| nlevels | an integer giving the number of levels of the contour lines. |
| color.contour | R build-in color for the contour lines. |
| greyscale | logical: if TRUE (FALSE by default), the used colorpalette is converted to greyscales. |
| log | a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic. |
| ... | additional parameters to be passed to points and plot. |

Note

Two-Dimensional Kernel Density Estimation adapted and modified from Venables and Ripley's MASS package (see reference).

Author(s)

Bjoern Schwalb

References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

See Also

[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```
points = 10^4
x = c(rnorm(points/2),rnorm(points/2)+4)
y = x + rnorm(points,sd=0.8)
x = sign(x)*abs(x)^1.3

plot.new()
plot.window(xlim = c(-5,15),ylim = c(-4,8))
heatscatterpoints(x,y,add.contour=TRUE,color.contour="green",greyscale=TRUE)
axis(1)
axis(2)
box()
```

homer

homer

Description

Homer Simpson as a list!

Usage

```
homer
```

Format

This list contains 31 character vectors of length 22 encoding Homer Simpson.

`intersphere`*Intersphere: a fancy Venn diagram*

Description

Create circles for visualizing overlaps between up to 4 datasets.

Usage

```
intersphere(  
  data,  
  colors = NULL,  
  alpha = 25,  
  cex = 1,  
  expand.circles = 1,  
  expand.lims = 1.5,  
  main = "intersphere: overlap diagram",  
  onlySets = seq(length(data), 2, by = -1)  
)
```

Arguments

| | |
|-----------------------------|---|
| <code>data</code> | a list with <code>n</code> entries having elements that can be represented as sets (have union and intersect methods). |
| <code>colors</code> | a character vector of R build-in colors for circles representing different sets. |
| <code>alpha</code> | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| <code>cex</code> | a numeric value giving the character expansion factor for intersect size text inside each circle. |
| <code>expand.circles</code> | a numeric value giving the expansion factor of circles (multiplicative). |
| <code>expand.lims</code> | a numeric value giving the expansion of x and y limits (additive). |
| <code>main</code> | title(s) of the plot, standard graphics parameter. |
| <code>onlySets</code> | vectors, which <code>n</code> -overlaps should be shown, default to all $1 < n < \text{length}(\text{data})$. |

Author(s)

Sebastian Duemcke, Bjoern Schwalb

See Also

[demotour](#), [disco](#), [colorpalette](#)

Examples

```
data = list(
  "A" = sample(1:200,100),
  "B" = sample(1:200,150),
  "C" = sample(1:200,50))

intersphere(data,colors = c("orange","skyblue","green"))

data = list(
  "A" = sample(1:200,100),
  "B" = sample(1:200,150),
  "C" = sample(1:200,50),
  "D" = sample(1:200,75))

colors = c("orange","skyblue","green","purple")
intersphere(data,colors,expand.circles = 0.5,expand.lims = 0.5)
```

linesplot

One-dimensional scatterplot

Description

Visualize one-dimensional data in its every detail.

Usage

```
linesplot(
  x,
  labels = NULL,
  col = "black",
  cols = NULL,
  alpha = 25,
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = "",
  las = 1,
  outline = TRUE,
  cexbox = 0.6,
  addboxes = FALSE,
  border = "black",
  range = 1.5,
  lwd = 1.5,
  main = "LSD.linesplot",
  ...
)
```

Arguments

| | |
|----------|---|
| x | numeric data as vector, matrix, list or data.frame. |
| labels | a character vector of labels. |
| col | a R build-in color. |
| cols | a character vector of R build-in colors. |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| xlab | x label, standard graphics parameter. |
| ylab | y label, standard graphics parameter. |
| las | las=1: horizontal text, las=2: vertical text (x-axis labels). |
| outline | logical: if TRUE (by default), outliers are plotted. |
| cexbox | a numerical value giving the amount by which the boxes should be magnified relative to the default. |
| addboxes | logical: if TRUE (FALSE by default), boxplots be added to the plot. |
| border | a R build-in color for the box and the whiskers (if addboxes = TRUE). |
| range | this determines how far the plot whiskers extend out from the box. |
| lwd | linewidth of the box and whiskers. |
| main | title(s) of the plot, standard graphics parameter. |
| ... | additional parameters to be passed to points and plot. |

Author(s)

Bjoern Schwalb

See Also

[demotour](#), [disco](#), [colorpalette](#)

Examples

```
l = list()
for (i in 1:10){l[[i]] = rnorm(100,sqrt(i^2.5),1+i/2)}

linesplot(l,alpha=25,border="darkred",addboxes = TRUE,outline=FALSE)
```

`LSD.pie`*Custom-built piechart version*

Description

Piecharts at arbitrary position and radii.

Usage

```
LSD.pie(  
  props,  
  x = 0,  
  y = 0,  
  radius = 1,  
  colpal = "prgn",  
  simulate = FALSE,  
  daltonize = FALSE,  
  cvd = "p",  
  edges = 1000,  
  add = FALSE,  
  xlim = c(-1, 1),  
  ylim = c(-1, 1),  
  main = "LSD.pie: piecharts",  
  alpha = NULL,  
  addPercent = FALSE,  
  textcol = "black",  
  clockwise = FALSE,  
  init.angle = 0,  
  labels = c(),  
  cex = 1,  
  cex.percentage = cex,  
  border = NA,  
  ...  
)
```

Arguments

| | |
|---------------------|--|
| <code>props</code> | a numeric vector giving the relations of the pie pieces (need not to be normalized). |
| <code>x</code> | x-position of the piechart. |
| <code>y</code> | y-position of the piechart. |
| <code>radius</code> | a numeric value giving the radius of the piechart. |
| <code>colpal</code> | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>) (defaults to "heat", if not specified). |

| | |
|----------------|---|
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see daltonize). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see daltonize). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| edges | an integer giving the number of edges the "circle" will have. |
| add | logical: if TRUE (FALSE by default), the pie is added to an existing plot. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| main | title(s) of the plot, standard graphics parameter. |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| addPercent | logical: if TRUE (FALSE by default), the percentage of each slice is written inside of the pie. |
| textcol | a R build-in color for the percentages of addPercent. |
| clockwise | if TRUE (FALSE by default), slices drawn clockwise (counter clockwise, if FALSE). |
| init.angle | a numerical value representing an angle as a starting angle for the drawn slices. |
| labels | a character vector giving the names for the pie slices. |
| cex | scaling a numeric value giving the expansion factor for the slice names (if labels are given). |
| cex.percentage | a numeric value giving the expansion factor for the percentage values (if addPercent = TRUE). |
| border | a R build-in color giving the border color (NA by default). |
| ... | additional parameters to be passed to points and plot. |

Author(s)

Bjoern Schwalb, Carina Demel

See Also

[demotour](#), [disco](#), [colorpalette](#)

Examples

```
emptyplot(xlim=c(1,9),ylim=c(1,9))
mtext(paste("LSD.pie: piecharts"),3,2,cex=1.25)
polygon(c(4,2,4,7,8),c(4,8,4,2,8))
LSD.pie(sample(1:50,5),4,4,add=TRUE,radius=2,colpal="prgn",alpha=75)
LSD.pie(sample(1:50,5),2,8,add=TRUE,colpal="prgn",alpha=75)
LSD.pie(sample(1:50,5),8,8,add=TRUE,colpal="prgn",alpha=75)
LSD.pie(sample(1:50,5),7,2,add=TRUE,colpal="prgn",alpha=75)
```

`makemovie`*Interpolate rows of a matrix to extend the number of cols*

Description

Interpolate rows of a matrix to yield a smooth transitions.

Usage

```
makemovie(input, timepoints = NULL, timestep = 1, motionline = NULL)
```

Arguments

| | |
|-------------------------|--|
| <code>input</code> | a matrix with numerical entries. |
| <code>timepoints</code> | a integer vector containing the timepoints corresponding to the columns of 'input'. |
| <code>timestep</code> | a non-negative integer specifying the number of timesteps between the existing timepoints (defaults to 1, if not specified). |
| <code>motionline</code> | a integer vector giving the timepoints of the resulting matrix (derived from timepoints and timesteps by default). |

Author(s)

Achim Tresch, Bjoern Schwalb

See Also

[clusterplot](#), [align](#), [demotour](#)

Examples

```
len = 10
x = sin(seq(0,2*pi,length=len*2))
fun = function(){n=sample(1:len,1);return(x[n:(n+len-1)])}
input = t(replicate(7,fun(),simplify=TRUE))
input = input + rnorm(length(input))/2
par(mfrow=c(1,2))
plotmatrix(input,main="original",cols=1:7,type="o")
mov = makemovie(input,timestep=0.2)
plotmatrix(mov,main="interpolated",cols=1:7,type="o")
```

`msdplot`*Visualize two-dimensional data clusters*

Description

Depict a numeric matrix or list utilizing the underlying mean and standard deviation estimates of one dimension in a color encoded fashion.

Usage

```
msdplot(  
  input,  
  label = NULL,  
  at = NULL,  
  xlim = NULL,  
  ylim = NULL,  
  xlab = "",  
  ylab = "",  
  main = "msdplot",  
  xaxt = "s",  
  xlabels = NULL,  
  las = 1,  
  separate = TRUE,  
  size = TRUE,  
  col = "darkgreen",  
  bars = TRUE,  
  alpha = 50,  
  ...  
)
```

Arguments

| | |
|----------------------|--|
| <code>input</code> | matrix or list with numerical entries, quantiles of cols will define lines. |
| <code>label</code> | a character vector assigning rows/elements of 'input' to clusters (if specified, multiple clusters can be depicted in different colors and/or subsequent plots). |
| <code>at</code> | a integer vector containing the x-positions corresponding to the columns of 'input'. |
| <code>xlim</code> | x limits, standard graphics parameter. |
| <code>ylim</code> | y limits, standard graphics parameter. |
| <code>xlab</code> | x labels, standard graphics parameter. |
| <code>ylab</code> | y labels, standard graphics parameter. |
| <code>main</code> | title(s) of the plot, standard graphics parameter. |
| <code>xaxt</code> | a character which specifies the x axis type ("n" suppresses plotting of the axis). |
| <code>xlabels</code> | a character vector containing labels for the x-axis. |

| | |
|----------|---|
| las | las=1: horizontal text, las=2: vertical text (x-axis labels). |
| separate | if TRUE (by default), different clusters are depicted in subsequent plots. |
| size | logical: if TRUE (by default), the size of each cluster is added to the title of the respective plot. |
| col | a character vector giving R build-in colors for different clusters. |
| bars | logical: if TRUE (by default), error bars are added at each position. |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| ... | additional parameters to be passed to points and plot. |

Author(s)

Bjoern Schwalb

See Also

[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```
at = c(2,4,8,16,32)
clus = matrix(rnorm(500,sd=0.5),ncol=5)
batch = sample(c(-8,-6,-4,-2),100,replace=TRUE)
clus = clus + cbind(0,0.25*batch,0.5*batch,0.75*batch,batch)
clus = clus - clus[,1]
clus = t(t(clus)*c(0,0.1,0.25,0.5,1))
labs = paste("cluster",kmeans(clus,4)$cluster)

colpal = c("darkgreen","darkblue","darkred","black")
msdplot(clus,labs,at,separate=FALSE,col=colpal,alpha=25,xlabels=at)

msdplot(clus,labs,at,col=colpal,alpha=50,xlabels=at)
```

| | |
|--------|--|
| plotit | <i>Plotting wrapper function to plot plots in printable quality and all kinds of formats</i> |
|--------|--|

Description

Plotting wrapper function to save plots in R as "pdf", "ps", "jpeg", "png", "bmp" or "tiff".

Usage

```

plotit(
  filename,
  sw = 1,
  sh = 1,
  sres = 1,
  plotsfkt,
  ww = 7,
  wh = 7,
  pointsize = 12,
  dev.pointsize = 8,
  paper = "special",
  quality = 100,
  units = "px",
  bg = "white",
  fileformat = "jpeg",
  saveit = FALSE,
  notinR = FALSE,
  addformat = NULL
)

```

Arguments

| | |
|---------------|---|
| filename | name of the plot to be saved with the format type suffix. |
| sw | scaling factor of weight. |
| sh | scaling factor of height. |
| sres | scaling factor of the resolution. |
| plotsfkt | list of plots to be plotted. |
| ww | width of window. |
| wh | height of window. |
| pointsize | the default pointsize of plotted text, interpreted as big points (1/72 inch) for plots to be saved. |
| dev.pointsize | pointsize of plotted text, interpreted as big points (1/72 inch) for display in R. |
| paper | needed only if filformat = "pdf" or "ps". |
| quality | needed only if filformat = "jpeg". |
| units | needed only if filformat = "jpeg", "png", "bmp" or "tiff". |
| bg | backgroundcolor. |
| fileformat | save the plot as "pdf", "ps", "jpeg", "png", "bmp" or "tiff". |
| saveit | should plot be saved. |
| notinR | should plot be not plotted in R. |
| addformat | should plot be saved additionally in another format ("pdf", "ps", "jpeg", "png", "bmp" or "tiff"). |

Author(s)

Bjoern Schwalb

See Also

[demotour](#), [disco](#), [colorpalette](#)

Examples

```
data(homer)

plotsfkt = function(){
  colpal = c("white","black","yellow","wheat3")
  align(homer,colpal = colpal,main = "D'OH!",asp = 1,axes = FALSE)
}

# choose 'saveit = TRUE' for saving the plot in the specified fileformat #

# choose 'notinR = TRUE' to suppress plotting in R #

plotit("homer",sw = 2,sh = 2,sres = 2,plotsfkt,saveit = FALSE,notinR = FALSE,fileformat = "jpeg")
plotit("homer",sw = 2,sh = 2,sres = 2,plotsfkt,saveit = FALSE,notinR = FALSE,fileformat = "png")
plotit("homer",sw = 2,sh = 2,sres = 2,plotsfkt,saveit = FALSE,notinR = FALSE,fileformat = "bmp")
plotit("homer",sw = 2,sh = 2,sres = 2,plotsfkt,saveit = FALSE,notinR = FALSE,fileformat = "tiff")
plotit("homer",sw = 2,sh = 2,sres = 2,plotsfkt,saveit = FALSE,notinR = FALSE,fileformat = "ps")
plotit("homer",sw = 2,sh = 2,sres = 2,plotsfkt,saveit = FALSE,notinR = FALSE,fileformat = "pdf")
```

plotmatrix

Visualize two-dimensional data

Description

Plot the rows of a matrix as lines along the cols.

Usage

```
plotmatrix(
  input,
  xlim = NULL,
  ylim = NULL,
  xlab = "",
  ylab = "",
  main = "plotmatrix",
  type = "l",
```

```

    lwd = 2,
    at = NULL,
    xlabels = NULL,
    ltys = NULL,
    add = FALSE,
    cols = NULL,
    ...
)

```

Arguments

| | |
|---------|--|
| input | a matrix with numerical entries. |
| xlim | x limits, standard graphics parameter. |
| ylim | y limits, standard graphics parameter. |
| xlab | x lab, standard graphics parameter. |
| ylab | y lab, standard graphics parameter. |
| main | title of the plot, standard graphics parameter. |
| type | what 'type' of plot should be drawn (to be passed to points). |
| lwd | a positive number giving the line width. |
| at | a integer vector containing the x-positions corresponding to the columns of 'input'. |
| xlabels | a character vector containing labels for the x-axis. |
| ltys | a numeric vector giving the line types for each row of 'input'. |
| add | logical: if TRUE (FALSE by default), lines are added to existing plot. |
| cols | a character vector of R build-in colors. |
| ... | additional parameters to be passed to points and plot. |

Author(s)

Achim Tresch, Bjoern Schwalb

See Also

[clusterplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```

len = 20
x = sin(seq(0,2*pi,length=len*2))
fun = function(){n=sample(1:len,1); return(x[n:(n+len-1)])}
input = t(replicate(7,fun(),simplify=TRUE))
input = input + rnorm(length(input))/2

plotmatrix(input,cols=1:7)

```

`seqs``seqs`

Description

TATAbox containing DNA-sequences!

Usage`seqs`**Format**

This list contains 20 character vectors of TATAbox containing DNA-sequences of length 30.

`singleclusterplot`*Visualize two-dimensional data clusters (add to an existing plot)*

Description

Depict a numeric matrix or list utilizing the underlying distribution quantiles of one dimension in a color encoded fashion (add to an existing plot).

Usage

```
singleclusterplot(  
  input,  
  at = NULL,  
  fromto = c(0.05, 0.95),  
  colpal = "standardheat",  
  simulate = FALSE,  
  daltonize = FALSE,  
  cvd = "p",  
  nrcol = 25,  
  outer.col = "lightgrey",  
  rev = FALSE,  
  alpha = NULL,  
  quartiles.col = c("grey", "black", "grey"),  
  add.quartiles = TRUE  
)
```

Arguments

| | |
|---------------|--|
| input | matrix or list with numerical entries. |
| at | a integer vector containing the x-positions corresponding to the columns of 'input'. |
| fromto | a numeric vector containing the range of quantiles (between 0 and 1) to be plotted. |
| colpal | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>). |
| simulate | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| daltonize | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| cvd | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| nrcol | a non-negative integer specifying the number of colors to be used (defaults to 25, if not specified). |
| outer.col | R built-in color to be used for outlier lines (lines outside of 'fromto'). |
| rev | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| quartiles.col | a character vector containing three R built-in colors for quartile lines (<code>c('0.25','0.5','0.75')</code>). |
| add.quartiles | logical: if TRUE (by default), lines are plotted corresponding to the quartiles. |

Author(s)

Achim Tresch, Bjoern Schwalb

See Also

[clusterplot](#), [align](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```

samples = 100
probes = 200
clus = matrix(rnorm(probes*samples, sd=1), ncol=probes)

clus = rbind(
  t(t(clus)+sin(1:probes/10))+1:nrow(clus)/samples,
  t(t(clus)+sin(pi/2+1:probes/10))+1:nrow(clus)/samples)

emptyplot(xlim = c(1,ncol(clus)),ylim = range(clus))
singleclusterplot(clus)
axis(1)
axis(2)
box()

```

| | |
|------------------|--|
| singlefusionplot | <i>Visualize two-dimensional data clusters (add to an existing plot)</i> |
|------------------|--|

Description

Depict a numeric matrix or list utilizing the underlying distribution quantiles of one dimension in a color encoded fashion (add to an existing plot).

Usage

```
singlefusionplot(
  x,
  y,
  fromto = c(0.05, 0.95),
  colpal = "standardheat",
  simulate = FALSE,
  daltonize = FALSE,
  cvd = "p",
  nrcol = 25,
  outer.col = "grey",
  rev = FALSE,
  alpha = NULL,
  quartiles.col = c("grey", "black", "grey"),
  add.quartiles = TRUE
)
```

Arguments

| | |
|------------------------|--|
| <code>x</code> | a numeric vector. |
| <code>y</code> | a numeric vector. |
| <code>fromto</code> | a numeric vector containing the range of quantiles (between 0 and 1) to be plotted. |
| <code>colpal</code> | a character vector containing R built-in color names or a name of a LSD colorpalette as a character string (see <code>disco()</code> or <code>disco</code>). |
| <code>simulate</code> | logical: if TRUE (FALSE by default), a converted colorpalette is used to simulate dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| <code>daltonize</code> | logical: if TRUE (FALSE by default), a converted colorpalette is used to enhance dichromat vision according to http://www.daltonize.org (see <code>daltonize</code>). |
| <code>cvd</code> | character string implying the type of color vision deficiency ("p" for protanope, "d" for deuteranope or "t" for tritanope). |
| <code>nrcol</code> | a non-negative integer specifying the number of colors to be used (defaults to 25, if not specified). |
| <code>outer.col</code> | R built-in color to be used for outlier lines (lines outside of 'fromto'). |
| <code>rev</code> | logical: if TRUE (FALSE by default), a reversed colorpalette is used. |

`alpha` alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default).

`quartiles.col` a character vector containing three R built-in colors for quartile lines (`c("0.25","0.5","0.75")`).

`add.quartiles` logical: if TRUE (by default), lines are plotted corresponding to the quartiles.

Author(s)

Achim Tresch, Bjoern Schwalb

See Also

[fusionplot](#), [align](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```
x = 1:1000/300
y = rnorm(1000)+sin(2*x)*3

emptyplot(xlim = range(x),ylim = range(y))
singlefusionplot(x,y,colpal = "ylgnbu")
axis(1)
axis(2)
box()
```

singlemsdplot

Visualize two-dimensional data clusters (add to an existing plot)

Description

Depict a numeric matrix or list utilizing the underlying mean and standard deviation estimates of one dimension in a color encoded fashion (add to an existing plot).

Usage

```
singlemsdplot(
  input,
  col = "darkgreen",
  alpha = 50,
  bars = TRUE,
  length = 0.25,
  at = NULL
)
```

Arguments

| | |
|--------|---|
| input | data as matrix or list. |
| col | a character vector of R build-in colors. |
| alpha | alpha value: a two-digit integer between 01 and 99 for color opacity, i.e. appearance of partial or full transparency (usage omitted by default). |
| bars | logical: if TRUE (by default), error bars are added at each position. |
| length | a numeric value scaling the width of the bars. |
| at | a integer vector containing the x-positions corresponding to the columns of 'input'. |

Author(s)

Bjoern Schwalb

See Also

[comparisonplot](#), [demotour](#), [disco](#), [colorpalette](#)

Examples

```

samples = 100
probes = 200
clus = matrix(rnorm(probes*samples, sd=1), ncol=probes)

clus = rbind(
  t(t(clus)+sin(1:probes/10))+1:nrow(clus)/samples,
  t(t(clus)+sin(pi/2+1:probes/10))+1:nrow(clus)/samples)

emptyplot(xlim = c(1, ncol(clus)), ylim = range(clus))
singlemsdplot(clus)
axis(1)
axis(2)
box()

```

webdesign

Colored rectangular grid

Description

Adds a colored rectangular grid to an existing plot.

Usage

```
webdesign(xlim, ylim, colpal = "rdbu", xlabel = NULL, ylabel = NULL, ...)
```

Arguments

| | |
|----------------------|--|
| <code>xlim</code> | x limits, standard graphics parameter. |
| <code>ylim</code> | y limits, standard graphics parameter. |
| <code>colpal</code> | a character vector containing R built-in color names or a name of a LSD color-palette as a character string (see <code>disco()</code> or <code>disco</code>). |
| <code>xlabels</code> | a character vector containing labels depicted parallel to the x-axis. |
| <code>ylabels</code> | a character vector containing labels depicted parallel to the y-axis. |
| <code>...</code> | additional parameters to be passed to <code>abline()</code> . |

Author(s)

Bjoern Schwalb

See Also

[demotour](#), [disco](#), [colorpalette](#)

Examples

```
emptyplot(c(-5,5),c(-5,5))
labels = c("2 fold","4 fold","8 fold")
webdesign(c(-5,5),c(-5,5),lty = 2,xlabels = labels,ylabels = labels)
```

windowxy

Factorization of the number of windows for plots with device partitions

Description

Create a factorization of the number of windows for plots with device partitions to be used in `par(mfrow = ...)`.

Usage

```
windowxy(nrwin = 1)
```

Arguments

`nrwin` a non-negative integer specifying the number of windows.

Author(s)

Bjoern Schwalb

See Also

[demotour](#)

Examples`windowxy(20)`

Index

- *Topic **Venn**
 - intersphere, 33
- *Topic **alignment**
 - align, 2
- *Topic **alpha**
 - colorpalette, 6
 - disco, 14
- *Topic **barplot**
 - comparisonplot, 7
 - heatbarplot, 20
- *Topic **bmp**
 - plotit, 40
- *Topic **boxplotlike**
 - linesplot, 34
- *Topic **boxplot**
 - heatboxplot, 21
- *Topic **clusterplot**
 - demotour, 12
- *Topic **cluster**
 - clusterplot, 4
 - fusionplot, 18
 - singleclusterplot, 44
 - singlefusionplot, 46
- *Topic **colorblind**
 - daltonize, 11
- *Topic **colorpalette**
 - demotour, 12
- *Topic **color**
 - colorpalette, 6
 - complementarycolor, 9
 - convertcolor, 10
 - convertgrey, 10
 - disco, 14
 - distinctcolors, 15
- *Topic **daltonize**
 - daltonize, 11
 - demotour, 12
- *Topic **dataset**
 - homer, 32
 - seqs, 44
- *Topic **density**
 - densitylane, 13
- *Topic **disco**
 - demotour, 12
- *Topic **empty**
 - emptyplot, 17
- *Topic **factorization**
 - windowxy, 49
- *Topic **greyscale**
 - convertgrey, 10
- *Topic **grid**
 - webdesign, 48
- *Topic **heatcolors**
 - heatpairs, 25
 - heatscatter, 28
 - heatscatterpoints, 30
- *Topic **heatscatter**
 - demotour, 12
- *Topic **histogram**
 - heathist, 23
- *Topic **intersphere**
 - intersphere, 33
- *Topic **jpeg**
 - plotit, 40
- *Topic **matrix**
 - makemovie, 38
 - plotmatrix, 42
- *Topic **mean**
 - msdplot, 39
 - singlemsdplot, 47
- *Topic **pdf**
 - plotit, 40
- *Topic **pie**
 - LSD.pie, 36
- *Topic **plotting**
 - emptyplot, 17
- *Topic **plot**
 - plotit, 40

- *Topic **png**
 - plotit, 40
- *Topic **ps**
 - plotit, 40
- *Topic **region**
 - emptyplot, 17
- *Topic **scatterplot**
 - comparisonplot, 7
 - ellipsescatter, 16
 - heatpairs, 25
 - heatscatter, 28
 - heatscatterpoints, 30
- *Topic **sd**
 - msdplot, 39
 - singlmsdplot, 47
- *Topic **sequence**
 - align, 2
- *Topic **tiff**
 - plotit, 40
- *Topic **web**
 - webdesign, 48
- align, 2, 5, 8, 19, 38, 45, 47
- clusterplot, 3, 4, 12, 38, 43, 45
- colorpalette, 3, 5, 6, 8–12, 14, 15, 17, 19, 21, 23, 25, 27, 30, 32, 33, 35, 37, 40, 42, 43, 45, 47–49
- comparisonplot, 7, 14, 21, 23, 25, 27, 30, 32, 40, 48
- complementarycolor, 9
- convertcolor, 10
- convertgrey, 10
- cplot (comparisonplot), 7
- daltonize, 3, 5, 6, 8, 11, 12, 13, 15, 19, 20, 22, 24, 26, 29, 31, 37, 45, 46
- demotour, 3, 5, 7–12, 12, 14, 15, 17, 19, 21, 23, 25, 27, 30, 32, 33, 35, 37, 38, 40, 42, 43, 45, 47–49
- densitylane, 13
- disco, 3, 5–14, 14, 15, 17, 19–27, 29–33, 35–37, 40, 42, 43, 45–49
- display.colorpalette (disco), 14
- distinctcolors, 15
- ellipsescatter, 16
- emptyplot, 17
- fusionplot, 18, 47
- heatbarplot, 20
- heatboxplot, 21
- heathist, 23
- heatpairs, 25
- heatscatter, 12, 28
- heatscatterpoints, 30
- homer, 32
- intersphere, 33
- linesplot, 34
- LSD.align (align), 2
- LSD.clusterplot (clusterplot), 4
- LSD.colorpalette (colorpalette), 6
- LSD.complementarycolor (complementarycolor), 9
- LSD.convertcolor (convertcolor), 10
- LSD.convertgrey (convertgrey), 10
- LSD.daltonize (daltonize), 11
- LSD.demotour (demotour), 12
- LSD.densitylane (densitylane), 13
- LSD.disco (disco), 14
- LSD.display.colorpalette (disco), 14
- LSD.distinctcolors (distinctcolors), 15
- LSD.ellipsescatter (ellipsescatter), 16
- LSD.emptyplot (emptyplot), 17
- LSD.fusionplot (fusionplot), 18
- LSD.heatbarplot (heatbarplot), 20
- LSD.heatboxplot (heatboxplot), 21
- LSD.heathist (heathist), 23
- LSD.heatpairs (heatpairs), 25
- LSD.heatscatter (heatscatter), 28
- LSD.heatscatterpoints (heatscatterpoints), 30
- LSD.intersphere (intersphere), 33
- LSD.linesplot (linesplot), 34
- LSD.makemovie (makemovie), 38
- LSD.msdplot (msdplot), 39
- LSD.pie, 36
- LSD.plotit (plotit), 40
- LSD.plotmatrix (plotmatrix), 42
- LSD.singleclusterplot (singleclusterplot), 44
- LSD.singlefusionplot (singlefusionplot), 46
- LSD.singlmsdplot (singlmsdplot), 47
- LSD.webdesign (webdesign), 48
- LSD.windowxy (windowxy), 49

`makemovie`, 38

`msdplot`, 39

`plotit`, 40

`plotmatrix`, 42

`seqs`, 44

`singleclusterplot`, 5, 44

`singlefusionplot`, 19, 46

`singlemsdplot`, 47

`webdesign`, 48

`windowxy`, 49