Package 'NetWeaver'

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Type Package

Title Graphic Presentation of Complex Genomic and Network Data
Analysis

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Description Implements various simple function utilities and flexible pipelines to generate circu-
lar images for visualizing complex genomic and network data analysis features.

Depends R (>= 3.3.0)

License GPL-3

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL https://github.com/mw201608/NetWeaver/

BugReports https://github.com/mw201608/NetWeaver/issues

NeedsCompilation no

Repository CRAN

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R topics documented:

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ensemble_rank   *Ensemble Rank*

Description

Compute composite rank score using evidence from multiple features.

Usage

```
ensemble_rank(x, method=c('ProductOfRank','MeanOfLog','MeanOfLogLog','Mean'),
small=1.0e-320, standardize=TRUE)
```

Arguments

x	a matrix of discriminant values (e.g., P values) measuring the strength of the association between objects (eg modules) (in rows) and variables/features (in columns).
method	a character string specifyign the ranking metric. See `Details`.
small	offset the small p values before taking log transformation.
standardize	whether to rescale the final ranking score by dividing the maximum value.

Details

Three ranking metrics are currently implemented:

ProductOfRank is the one used in Zhang et al. (Cell 2013, 153: 707-720) with a slight change to standardize the scores to be between 0 and 1;

MeanOfLog computes the mean of -log(p value) which penalizes insignificant p values;

MeanOfLogLog computes the mean of log(-log(p value)) which penalizes insignificant p values and shrinks the difference in the ranges of p values.

Means computes the row mean of absolute values of x.

Value

A vector of ranking scores. The larger the score, the higher the rank.

Author(s)

Minghui Wang <m.h.wang@live.com>

Examples

```
#Rank US cities by the significance test of excessive arrests compared to average
#compute the p value of one-tailed z-test
x=apply(USArrests,2,function(x) pnorm((x-mean(x))/sd(x),lower.tail=FALSE))
#compute ranking score using three different metrics
score1=ensemble_rank(x,method='ProductOfRank')
score2=ensemble_rank(x,method='MeanOfLog')
score3=ensemble_rank(x,method='MeanOfLogLog')
#plot the top 5 worst cities by each metric
par(mfrow=c(1,3))
barplot(sort(score1,decreasing=TRUE)[1:5],las=2)
barplot(sort(score2,decreasing=TRUE)[1:5],las=2)
barplot(sort(score3,decreasing=TRUE)[1:5],las=2)
```

---

getrankp   *getrankp*

Description

Compute probability (fraction) of values in a large population more extreme than input series.

Usage

```
getrankp(x, y, truncated.size=0)
```

Arguments

x	A vector of input series.
y	A vector of population values.
truncated.size	See `Details`. Only use when you know this.

Details

This function can be used to compute permutation-based false discovery rate (two-tailed). In such case, x contains test statistics from observed data while y contains test statistics from permutation. x could be a truncated set, with small values discarded to save memory.

Value

A vector of the same size as x.

Author(s)

Minghui Wang <m.h.wang@live.com>

Examples

```
x=abs(rnorm(100))
y=abs(rnorm(10000))
getrankp(x,y)[1:4]
```

---

is.overlap   *Region overlap test*

Description

Test if two regions are overlapping.

Usage

```
is.overlap(x,y)
```

Arguments

x	a vector of two numeric values specifying the start and end positions of the first region.
y	a vector of two numeric values specifying the start and end positions of the second region

Value

Logic test output.

Author(s)

Minghui Wang <m.h.wang@live.com>

Examples

```
is.overlap(c(10,100),c(90,120))
is.overlap(c(10,100),c(110,120))
```

Modules   *Example Module Dataset*

Description

This example dataset and sample code illustrate the use of `NetWeaver` to visualize the complex features of gene coexpression network modules.

Usage

```
data(Modules)
```

Details

This dataset contains a data.frame called `Modules`. Each row is a module, with the module id in the first column. The second column is ranking score. The next 4 columns are coefficients of module-trait correlations. The rest columns are P values of enrichment for various gene signatures. The sample R code shows a pipeline for visualizing the module feature data using a circos style plot.

Author(s)

Minghui Wang <m.h.wang@live.com>, Bin Zhang <bin.zhang@mssm.edu>

See Also

rc.initialize

Examples

```
## Not run:
#see a tutorial for how to plot this dataset
vignette("netweaver")

## End(Not run)
```

NetWeaver   *Graphic Presentation of Complex Genomic and Network Data Analysis*

Description

`NetWeaver` is motivated towards developing a simple and flexible pipeline for visualizing the complex features of enrichment and correlation of gene coexpression network modules. While circos style 2D track plot is one natural choice for such practice, existing packages are designed primarily for handling genome structure and intervals. They are either too complicated to use, requiring certain level of knowledge of scripting, or limited in applications to only genomic structure data. To address these issues, particularly extend beyond applications in genomic structure data, `NetWeaver` offers a lightweight implementation of circular track plot, providing simple and flexible R function utilities and pipelines to generate circular images for visualizing different types of structure/relationship data.

The original version of this package was developed for Figure 7 of Wang et al (2016) *Genome Medicine* 8:104, which illustrates more than 20 properties for 50 coexpression network modules with a circular track plot. Please try to cite the paper when you use results from this software in a publication:

Wang M, Roussos P, McKenzie A, Zhou X, Kajiwara Y, Brennand K, DeLuca GC, Crary JF, Casaccia P, Buxbaum J et al. 2016. Integrative Network Analysis of Nineteen Brain Regions Identifies Molecular Signatures and Networks Underlying Selective Regional Vulnerability to Alzheimer's Disease. *Genome Medicine* 8: 104.

Details

There are two sample pipelines available:

1. Analysis of a real dataset of gene coexpression network modules can be reached through `vignette("netweaver")`.

2. Analysis of a hypothetical data is shown in sample code of `rc.initialize`.

Author(s)

Minghui Wang <m.h.wang@live.com>, Bin Zhang <bin.zhang@mssm.edu>

References

Wang M, Roussos P, McKenzie A, Zhou X, Kajiwara Y, Brennand K, DeLuca GC, Crary JF, Casaccia P, Buxbaum J et al. 2016. Integrative Network Analysis of Nineteen Brain Regions Identifies Molecular Signatures and Networks Underlying Selective Regional Vulnerability to Alzheimer's Disease. *Genome Medicine* 8: 104.

See Also

`rc.initialize`, `Modules`

---

rc.get.coordinates	*Get Coordinates*

Description

Retrieve x and y coordinates in a track.

Usage

```
rc.get.trackCoordinates(track.id, Start, End, Chr=NULL, degree=NULL, trackThickness=NULL)
rc.get.coordinates(track.id, Pos, Chr=NULL, degree=NULL, innerSide=TRUE, bottomSide=TRUE)
```

Arguments

track.id	number of track from outermost.
Start, End	start/end position on a chromosome or since first chromosome. See `Details`.
Pos	a vector of positions on a chromosome or since first chromosome. See `Details`.
Chr	a chromosome id. See `Details`.
degree	the angle of the arc rotation, overwrites `Start`, `End`, `Pos` and `Chr`.
trackThickness	thickness (height) of a track.
innerSide	whether to compute coordinates on the inner side of a track. Outer side coordinates will be returned if FALSE. Used for `circular` layout.
bottomSide	whether to compute coordinates on the bottom side of a track. Upper side coordinates will be returned if FALSE. Used for `landscape` layout.

Details

If `Chr` is `NULL`, `Start`, `End` and `Pos` will be considered as cumulative positions since first chromosome.

Value

A list of x and y coordinates.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.initialize](#), [rc.reset.params](#)

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.get.params   *Get Parameters*

Description

Retrieve parameters of Circos plot after initialization.

Usage

```
rc.get.params()
```

Value

A list.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.initialize](), [rc.reset.params]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.initialize   *Initialize Circos Plot Parameters*

Description

Setup default parameter for Circos plot.

Usage

```
rc.initialize(cyto.info, num.tracks=NULL, chr.order=NULL,
stepUnit=10^7, Layout=c('circular','landscape'), params=list())
```

Arguments

cyto.info	data.frame, see `Details`.
num.tracks	integer, number of tracks.
chr.order	character vector of chromosome ids specifying the ordering of chromosomes.
stepUnit	integer, smoothing factor for faster plotting.
Layout	layout for plotting.
params	a list of named items. See `Details`.

Details

cyto.info is a data.frame of chromosomal position ordered cytobands, with columns: Chr, Start, End, Stain, and any additional information (like band color), where Chr is chromosome name, Start and End are the start and end positions on the chromosome, and Stain is the cyto stain. The stain is normally one of the "gneg", "acen", "stalk", "gvar", "gpos", "gpos100", "gpos75", "gpos66", "gpos50", "gpos33", and "gpos25", which will be plotted by color "white", "red", "steelblue", "light-grey", "black", "black", "gray40", "gray50", "gray60", "gray70" and "gray80", accordingly. Customized colors for the cyto bands can be specified in an additional column named "BandColor".

Additional plot parameters can be specified through argument params, including:

- color.line, color for lines and links, default "black".
- chr.padding, padding between chromsomes is a fraction of the total chromosome sizes, default 0.1.
- track.padding, paddings between tracks is a fraction of the track height, default 0.1
- track.height, track height, default 0.15.
- radius radius of the circos, default 1.
- sector.degree, a value between 0 and 2*Pi (the default) specifying the circular sector size of the circos plot.

After initialization, the parameter settings can be retrieved by rc.get.params.

Noted that while cyto.info requires input to be in a form of chromosome cytobands, the input is not limited to genomic features. As illustrated in example data Modules, complex features of gene coexpression network modules can also be plotted with the current circos visualization technique.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

rc.get.params, rc.reset.params, rc.plot.ideogram, rc.plot.histogram, rc.plot.mHistogram, rc.plot.barchart, rc.plot.link, rc.plot.ribbon, Modules

Examples

```
library(NetWeaver)
options(stringsAsFactors=FALSE)
## set fake Cyto data
Cyto=data.frame(Chr=paste0('C',1:20), Start=1, End=100, BandColor=colors()[2:21])

## initialize circos
#firstly set number of tracks, should be larger than the actual number of tracks
#used for plotting in order to leave sufficient sapce in the middle
num.tracks=9
rc.initialize(Cyto, num.tracks=num.tracks, params=list(chr.padding=0.1,sector.degree=2*pi))

##retrieve parameters
```

```
params=rc.get.params()
#make plot area
rc.plot.area(size=0.95)

##plot ideogram on track 1 and 2 (start from the outside to inside)
track.num=1:2
rc.plot.ideogram(track.num, plot.band=TRUE, plot.chromosome.id=TRUE)

##plot histogram/barchart that span multiple chromosomes
MultHistData=data.frame(Chr1=paste0('C',seq(1,18,3)), Start1=50,
Chr2=paste0('C',seq(3,20,3)), End2=20, Col=1:6)
track.num=3
rc.plot.mHistogram(MultHistData, track.id=track.num, data.col=5,
color.col=5, fixed.height=FALSE)

##plot histogram that occupies two tracks 4 and 5
HistData=data.frame(Chr=paste0('C',1:20), Start=1, End=50, Data=runif(20))
params$color.hist <- 'black'
rc.reset.params(params)
track.num=5
rc.plot.histogram(HistData, track.num, data.col=4, fixed.height=FALSE,
track.border=NA, custom.track.height=params$track.height*2)

##plot heatmap on track 6
HeatData=data.frame(Chr=paste0('C',1:20), Start=1,End=100, Data=1:20)
colfuncHeat=function(n) rev(heat.colors(n))
track.num=track.num+1
rc.plot.histogram(HeatData, track.num, data.col=4, color.gradient=colfuncHeat(50),
fixed.height=TRUE)

##plot stacked barchart on track 7
BarData=data.frame(Chr=paste0('C',1:20), Start=1,
End=seq(10,86,length.out=20), Data=matrix(runif(20*4),nrow=20))
track.num=track.num+1
rc.plot.barchart(BarData, track.num, data.col=4:7)

##plot links in the middle
LinkData=data.frame(Chr1=sample(Cyto$Chr,40,replace=TRUE), Pos1=20,
Chr2=sample(Cyto$Chr,40,replace=TRUE),Pos2=20, Data=runif(20))
LinkData=LinkData[LinkData$Chr1 != LinkData$Chr2,]
params$color.line='blue'
rc.reset.params(params)
track.num=track.num+1
rc.plot.link(LinkData, track.num, data.col=4, arrow.length=0.1)
ribbonData=data.frame(Chr1=c('C1','C3'), Start1=c(10,10), End1=c(40,40),
Chr2=c('C17','C10'), Start2=20, End2=60, Col=c('red','brown'))
rc.plot.ribbon(ribbonData, track.num, color.col='Col', twist=TRUE)
#label track id
rc.plot.track.id(2:7, col=2)
#add text label
rc.plot.text(data.frame(Chr='C3',Pos=50,Label='GeneX'),
track.id=3,srt=45,cex=0.8,col='blue')
#add line mark
```

```
rc.plot.line(data.frame(Chr='C19',Pos=seq(10,90,by=15),Col='red'),
track.id=3, color.col=3,arrow.length=0.2)
```

---

rc.plot.area	*Setup Plot Area*

Description

Create new graphics frame for circle plot .

Usage

```
rc.plot.area(size=1, oma=rep(0,4), mar=rep(0,4))
```

Arguments

size	a value between 0 to 1, specifying the effective size of the circle plot area in the current window. The smaller the size, the larger the blank area around the circle plot.
oma	A vector of the form c(bottom, left, top, right) giving the size of the outer margins in lines of text.
mar	A numerical vector of the form c(bottom, left, top, right) which gives the number of lines of margin to be specified on the four sides of the plot.

Details

After setting up, the extremes of the user coordinates of the plotting region can be found out by par('usr').

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.initialize](), [rc.reset.params]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

`rc.plot.barchart`   *Bar Plots*

Description

Add a track of barcharts.

Usage

```
rc.plot.barchart(Data, track.id, data.col, color.col=NULL, bar.color=NULL,
track.color=NA, track.border=NULL, polygon.border=NULL,
custom.track.height=NULL, ratio=FALSE)
```

Arguments

Data	data.frame, data to be plotted. See `Details`.
track.id	integer, in which track to plot.
data.col	integer, specifying the column(s) that contain the data for plotting. A stacked barchart is created if there are multiple columns of data.
color.col	integer, specifying the column that contains the color. Only used when there is only one data column.
bar.color	a vector of colors for the bars or bar components. By default, `grey` is used if there is one data column, and a gamma-corrected grey palette if there are multiple columns of data.
track.color	NA or color code for the track background.
track.border	the color to draw the track border. Use NA to omit borders.
polygon.border	the color to draw the polygon border. See explanation for `polygon`.
custom.track.height	NULL or numeric, specifying customized track height to overwrite the default. See `rc.get.params` for default value.
ratio	logical, specifying whether the data values in each row should be converted to ratios. Used only for stacked barchart.

Details

`Data` must have at least three columns. The first three columns must be named as `Chr`, `Start` and `End`, specifying the chromosomes and positions for the start and end points of the links. Additional columns can be used to specify data and color.

`rc.plot.histogram` can also be used for plotting barcharts except stacked barchart.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

rc.plot.link, rc.plot.mHistogram

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.grColLegend   *Plot Gradient Color Legend*

Description

Plot gradient color legend at given position.

Usage

```
rc.plot.grColLegend(x, y, cols, at=NULL, legend=at,
title='Color', width=0.1, height=0.3, gap=0,
direction=c('vertical', 'horizontal'), cex.text=1, cex.title=1)
```

Arguments

x, y	numeric values of coordinates where the legend is plotted. See details.
cols	a vector of colors.
at	integers; index legend text in the color vector cols. See details.
legend	character strings of legend text with the same length of vector at.
title	character string of the legend title.
width	numeric, width of the color legend bar.
height	numeric, height of the color legend bar.
gap	numeric, size of the gap between two color blocks.
direction	plot the color legend bar in either vertical or horizontal direction.
cex.text	numeric, magnitude of the legend text.
cex.title	numeric, magnitude of the legend title.

Details

x and y set the coordinates of bottom left starting point. The extremes of the user coordinates of the plotting region can be found out by par('usr').

By default NULL, parameter at will be set as a vector with values 1, ceiling(length(cols)/2), and length(cols).

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

rc.plot.link, rc.plot.histogram

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.heatmap   *Plot Heat-map*

Description

Add multiple tracks of heat-map on a circos plot.

Usage

```
rc.plot.heatmap(Data, track.id, color.gradient=NULL,
track.color=NA, track.border=NULL, polygon.border=NULL)
```

Arguments

Data   matrix, data to be plotted. See Details.

track.id   integer, starting track id.

color.gradient a vector of gradient colors. See details.

track.color   NA or color code for the track background.

track.border   the color to draw the track border. Use NA to omit borders.

polygon.border the color to draw the polygon border. See explanation for polygon.

Details

This function employs rc.plot.histogram to plot heat-map. Every row of Data will be plotted as heat-map in one track. The column names of Data must be the chromosome ids.

If color.gradient is not NULL, the data will be scaled to positive integers in the range of 1~length(color.gradient) to index the colors in vector color.gradient. If color.gradient isNULL, the input Data must be a matrix of colors or anything that can be converted to colors.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

rc.plot.histogram

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.histogram   *Plot Histogram, Barchart or Heat-map*

Description

Add a track of histogram, barchart, or heat-map on a circos plot.

Usage

```
rc.plot.histogram(Data, track.id, data.col=NULL, color.col=NULL,
 color.gradient=NULL, fixed.height=FALSE, track.color=NA, track.border=NULL,
 polygon.border=NULL, custom.track.height=NULL, max.value=NULL)
```

Arguments

Data	data.frame, data to be plotted. See Details.
track.id	integer, in which track to plot.
data.col	integer, specifying the column that contains the data for plotting.
color.col	integer, specifying the column that contains the color.
color.gradient	a vector of gradient colors. See details.
fixed.height	logical, whether to fix the histogram height which results in heat-map. TRUE if data.col is bar.color.
track.color	NA or color code for the track background.
track.border	the color to draw the track border. Use NA to omit borders.
polygon.border	the color to draw the polygon border. See explanation for [polygon](#).
custom.track.height	
	NULL or numeric, specifying customized track height to overwrite the default. See [rc.get.params](#) for default value.
max.value	NULL or numeric, specifying the maximum data value for normalization. Default NULL, get max from data column.

Details

Data must have at least three columns. The first three columns must be named as Chr, Start and End, specifying the chromosomes and positions for the start and end points of the links. Additional columns can be used to specify data and color.

If color.gradient is not NULL, color.col is ignored and the data will be scaled to positive integers in the range of 1~length(color.gradient) to index the colors in vector color.gradient.

For plotting stacked barcharts, use function [rc.plot.barchart](#) instead.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

rc.plot.link, rc.plot.mHistogram, rc.plot.barchart

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.ideogram   *Plot Ideogram*

Description

Add chromosome ideogram on circos plot.

Usage

```
rc.plot.ideogram(track.ids, plot.band=TRUE, plot.chromosome.id=TRUE,
chrom.alias=NULL, color.chromosome.id=NULL, cex.text=1, track.border=NULL,
polygon.border=NULL, las=0, custom.track.height=NULL)
```

Arguments

track.ids	vector, two integers specifying the two tacks for plotting chromosome name and cyto band respectively.
plot.band	logic, whether to plot ideogram cyto band.
plot.chromosome.id	
	logic, whether to plot chromosome id.
chrom.alias	NULL or a chromosome named vector of alias.
color.chromosome.id	
	NULL or a chromosome named vector of colors.
cex.text	numeric, scale of text.
track.border	the color to draw the track border. Use NA to omit borders.
polygon.border	the color to draw the polygon border. See explanation for polygon.
las	numeric in 0,1,2,3; the style of chromosome labels. 0, always parallel to the track [default]; 1, always horizontal; 2, always perpendicular to the track; 3, always vertical.
custom.track.height	
	NULL or numeric, specifying customized track height when plotting cyto band.

Author(s)

Minghui Wang <m.h.wang@live.com>

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.line *Plot Line*

Description

Plot lines at designated position.

Usage

```
rc.plot.line(Data, track.id, color.col=NULL, custom.length=NULL, arrow.length=0,
arrow.angle=30, arrow.code=2, ...)
```

Arguments

Data	a data.frame. See `Details`.
track.id	a vector of integers, specifying the tracks for plotting line.
color.col	integer, specifying the column that contains the color.
custom.length	NULL or numeric, specifying line length.
arrow.length	length of the edges of the arrow head (in inches). See [arrows](#)
arrow.angle	angle from the shaft of the arrow to the edge of the arrow head. See [arrows](#)
arrow.code	integer code, determining kind of arrows to be drawn. See [arrows](#)
...	further graphical parameters (from [par](#)), such as lty and lwd.

Details

`Data` is a data.frame, with at least two columns named 'Chr' and 'Pos', specifying the chromosomal positoins for each line in every row. An additional column can be used to specify the line color. Default line length is determined by track height.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.plot.histogram](#), [rc.plot.track](#)

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.link *Plot Link*

Description

Add a track of links on circos plot.

Usage

```
rc.plot.link(Data, track.id, data.col=NULL, color.col = NULL,
 max.lwd=1, sort.links=TRUE, arrow.length=0, arrow.angle=30, ...)
```

Arguments

Data	data.frame of at least four columns. See Details.
track.id	integer, the track number for plotting.
data.col	integer or character string, specifies the column of data.
color.col	integer or character string, specifies the column of colors.
max.lwd	integer, maximum line width.
sort.links	logical, whether to re-assign link start and end positions by sorting them. See details
arrow.length	length of the edges of the arrow head (in inches). See arrows
arrow.angle	angle from the shaft of the arrow to the edge of the arrow head. See arrows
...	further graphical parameters (from par), such as lty and lwd.

Details

Data must have at least four columns: Chr1, Pos1, Chr2 and Pos2, specifying the chromosomes and positions for the start and end points of the links. Additional columns may be used to specify the data, color and max line width.

If data.col is not NULL, the line width will be proportional to the values in column data.col with the maximum line width determined by max.lwd.

If sort.links is true, the links originate from the same chromosome will be sorted and equally spaced to minimize crossing.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

rc.plot.histogram, rc.plot.ribbon

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.mHistogram *Plot Histogram or Barplot Across Chromosomes*

Description

Plot histogram or barplot that overlaps with multiple chromosomes.

Usage

```
rc.plot.mHistogram(Data, track.id, data.col, color.col=NULL, color.gradient=NULL,
 fixed.height=FALSE, track.color=NA, track.border=NULL, polygon.border=NULL,
 custom.track.height=NULL, max.value=NULL)
```

Arguments

Data	data.frame of at least four columns. See Details.
track.id	integer, the track number for plotting.
data.col	integer or character string, specifies the column of data.
color.col	integer or character string, specifies the column of colors.
color.gradient	a vector of gradient colors.
fixed.height	logical, whether to fix the histogram height, resulting in heat-map if TRUE.
track.color	NA or color code for the track background.
track.border	the color to draw the track border. Use NA to omit borders.
polygon.border	the color to draw the polygon border. See explanation for polygon.
custom.track.height	
	NULL or numeric, specifying customized track height to overwrite the default. See rc.get.params for default value.
max.value	NULL or numeric, specifying the maximum data value for normalization. Default NULL, get max from data column data.col.

Details

Data must have at least four columns: Chr1, Start1, Chr2 and End2, specifying the chromosomes and positions for the start and end points. Additional columns may be used to specify the data, color, etc.

If color.gradient is not NULL, it will supersede color.col.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.plot.link](), [rc.plot.histogram]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

rc.plot.point   *Plot Point*

Description

Plot point(s) at designated position.

Usage

```
rc.plot.point(Data, track.id, color.col=NULL, custom.track.height=NULL, ...)
```

Arguments

Data	a data.frame. See `Details`.
track.id	a vector of integers, specifying the tracks for plotting point(s).
color.col	column id in `Data` specifying the colors.
custom.track.height	
	NULL or numeric, specifying customized track height.
...	further graphical parameters (from [par]()).

Details

`Data` is a data.frame with at least two columns named 'Chr', 'Pos', and 'Height', specifying the chrosomal positoin and the height within the track of the points. `"Height"` will be sacled to have a maximum of 1.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.plot.histogram](), [rc.plot.track]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

`rc.plot.ribbon` *Plot Ribbon*

Description

Add a track of ribbons on circos plot.

Usage

```
rc.plot.ribbon(Data, track.id, color.col = NULL, twist=FALSE)
```

Arguments

Data   data.frame of at least six columns. See `Details`.

track.id   integer, the track number for plotting.

color.col   integer or character string, specifies the column of colors.

twist   logic, whehter to twist the ribbon.

Details

`Data` must have at least six columns: `Chr1`, `Start1`, `End1`, `Chr2`, `Start2` and `End2`, specifying the chromosomes and positions for the start and end points of the ribbons. Additional columns may be used to specify the color.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.plot.histogram](), [rc.plot.link]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

rc.plot.text   *Plot Text*

Description

Plot text labels at designated position.

Usage

```
rc.plot.text(Data, track.id, col='black', custom.track.height=NULL, ...)
```

Arguments

Data   a data.frame. See `Details`.

track.id   a vector of integers, specifying the tracks for plotting text.

col   a vector of color for the text.

custom.track.height
                NULL or numeric, specifying customized track height.

...   further graphical parameters (from [par](par)), such as srt and family.

Details

`Data` is a data.frame with at least three columns named 'Chr', 'Pos', and 'Label', specifying the chrosomal positoin and text labels.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

rc.plot.histogram, rc.plot.track

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

```
rc.plot.track                    Plot Track
```

Description

Add a track to a circos plot.

Usage

```
rc.plot.track(track.id, border='black', col=NA, custom.track.height=NULL)
```

Arguments

track.id   integer, track id.

border   the color to draw the track border. Use NA to omit borders.

col   NA or color code for the track background.

custom.track.height
                  NULL or numeric, specifying customized track height. See `details`.

Details

`custom.track.height` sets customized track height, which will be useful for track(s) requiring bigger/smaller height than default.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.plot.histogram](), [rc.plot.mHistogram]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

rc.plot.track.id   *Plot Track Id*

Description

Plot labels in designated tracks.

Usage

```
rc.plot.track.id(track.id, labels=NULL, degree=0,
col='black', custom.track.height=NULL, ...)
```

Arguments

track.id   a vector of integers, specifying the tracks for plotting id.

labels   NULL or a vector of character string, specifying the text to be written.

degree   the angle of the arc rotation.

col   color for the text.
custom.track.height
                    NULL or numeric, specifying customized track height.

...   further graphical parameters (from par), such as srt and family.

Details

If labels is NULL, values of track.id will be used as text labels.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.plot.histogram](), [rc.plot.track]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

`rc.reset.params` *Reset Circos Plot Parameters*

Description

Reset parameters for Circos plot.

Usage

```
rc.reset.params(params)
```

Arguments

params   list.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.initialize](), [rc.get.params]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

`rc.track.pos` *Get Track Positions*

Description

Calculate inner and outer radius of a track.

Usage

```
rc.track.pos(track.id)
```

Arguments

track.id   integer, number of the track from the outermost.

Value

A vector with two radius values: out.pos and in.pos.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.initialize](), [rc.reset.params]()

Examples

```
#This is not to be run alone. Please see tutorial vignette("netweaver") for usage.
```

---

ucsc.hg19.cytoband   *Human chromosome cytoband*

Description

Human chromosome cytoband information from UCSC (http://genome.ucsc.edu/).

Usage

```
data(ucsc.hg19.cytoband)
data(ucsc.hg38.cytoband)
```

Details

Cytoband is useful for drawing the chromosome ideograms for the genome. Two human cytoband datasets are provided in this package, corresponding to two genome versions hg19 and hg38. Each cytoband dataset is a five-column tab-delimited data.frame. Each row of the data describes the position of a cytogenetic band.

Author(s)

Minghui Wang <m.h.wang@live.com>

See Also

[rc.initialize]()

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