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 circular images for visualizing complex genomic and network data analysis features.

Depends R (>= 3.3.0)

License GPL-3

Suggests knitr, rmarkdown

VignetteBuilder knitr

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

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**ensemble_rank**

Compute composite rank score using evidence from multiple features.

**Usage**

```r
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 (e.g., modules) (in rows) and variables/features (in columns).
- **method**: a character string specifying 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

```r
# 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

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]

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))
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)
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:


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


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

cytoNinfo 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 chromosomes 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 2π (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 space 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.histogram(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)
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
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>
**rc.plot.grColLegend**

**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**

```r
toolbox.rc.plot.grColLegend(x, y, cols, at=as.numeric(NULL), legend=as.numeric(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  
i 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 is NULL, 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=, color.col=, color.gradient=, 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>
rc.plot.ideogram

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.

---

**Description**

Add chromosome ideogram on circos plot.

**Usage**

```r
crc.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

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 positions 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

```r
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

```r
#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**

```r
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 chromosomal position and the height within the track of the points. "Height" will be scaled 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, whether 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`), 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.
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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