

Package ‘circlize’

April 3, 2019

Type Package

Title Circular Visualization

Version 0.4.6

Date 2019-04-03

Author Zuguang Gu

Maintainer Zuguang Gu <z.gu@dkfz.de>

Depends R (>= 3.0.0), graphics

Imports GlobalOptions (>= 0.1.0), shape, grDevices, utils, stats, colorspace, methods, grid

Suggests knitr, dendextend (>= 1.0.1), ComplexHeatmap (>= 1.13.2), gridBase, png

VignetteBuilder knitr

Description Circular layout is an efficient way for the visualization of huge amounts of information. Here this package provides an implementation of circular layout generation in R as well as an enhancement of available software. The flexibility of the package is based on the usage of low-level graphics functions such that self-defined high-level graphics can be easily implemented by users for specific purposes. Together with the seamless connection between the powerful computational and visual environment in R, it gives users more convenience and freedom to design figures for better understanding complex patterns behind multiple dimensional data.

URL <https://github.com/jokergoo/circlize>,
http://jokergoo.github.io/circlize_book/book/

License MIT + file LICENSE

NeedsCompilation no

Repository CRAN

Date/Publication 2019-04-03 18:00:09 UTC

R topics documented:

circulize-package	4
add_transparency	6
adjacencyList2Matrix	6
calc_gap	7
CELL_META	8
chordDiagram	8
chordDiagramFromDataFrame	11
chordDiagramFromMatrix	14
circulize	17
circos.arrow	18
circos.axis	19
circos.clear	22
circos.dendrogram	23
circos.genomicAxis	24
circos.genomicDensity	25
circos.genomicHeatmap	26
circos.genomicIdeogram	27
circos.genomicInitialize	28
circos.genomicLabels	30
circos.genomicLines	31
circos.genomicLink	33
circos.genomicPoints	34
circos.genomicPosTransformLines	36
circos.genomicRainfall	38
circos.genomicRect	40
circos.genomicText	42
circos.genomicTrack	44
circos.genomicTrackPlotRegion	45
circos.info	47
circos.initialize	48
circos.initializeWithIdeogram	49
circos.lines	51
circos.link	53
circos.nested	55
circos.par	57
circos.points	59
circos.polygon	60
circos.raster	61
circos.rect	63
circos.segments	64
circos.text	64
circos.track	66
circos.trackHist	67
circos.trackLines	68
circos.trackPlotRegion	69
circos.trackPoints	71

circos.trackText	72
circos.update	73
circos.updatePlotRegion	74
circos.xaxis	75
circos.yaxis	75
col2value	77
colorRamp2	78
convert_height	79
convert_length	79
convert_x	80
convert_y	81
cytoband.col	82
degree	83
draw.sector	84
fontsize	85
generateRandomBed	86
genomicDensity	87
get.all.sector.index	88
get.all.track.index	88
get.cell.meta.data	89
get.current.chromosome	90
get.current.sector.index	91
get.current.track.index	92
getI	92
highlight.chromosome	93
highlight.sector	94
names.CELL_META	95
posTransform.default	96
posTransform.text	97
print.CELL_META	101
rainfallTransform	101
rand_color	102
read.chromInfo	103
read.cytoband	104
reverse.circlize	105
set.current.cell	106
show.index	107
smartAlign	108
uh	108
ux	109
uy	110
\$.CELL_META	110

Description

Circular visualization in R

Details

This package aims to implement circular layout in R.

Since most of the figures are composed of points, lines and polygons, we just need to implement low-level functions for drawing points, lines and polygons.

Current there are following low-level graphic functions:

- `circos.points`
- `circos.lines`
- `circos.rect`
- `circos.polygon`
- `circos.segments`
- `circos.text`
- `circos.axis`, `circos.xaxis`, `circos.yaxis`
- `circos.link`

For drawing points, lines and text through the whole track (among several sectors), the following functions are available:

- `circos.trackPoints`
- `circos.trackLines`
- `circos.trackText`

Functions to arrange circular layout:

- `circos.initialize`
- `circos.track`
- `circos.update`
- `circos.par`
- `circos.info`
- `circos.clear`

Theoretically, you are able to draw most kinds of circular plots by the above functions.

For specific use in genomics, we also implement functions which add graphics in genome scale.

Functions to initialize circos plot with genomic coordinates:

- `circos.initializeWithIdeogram`
- `circos.genomicInitialize`

Functions to arrange genomic circular layout:

- `circos.genomicTrack`

Functions to add basic graphics in genomic scale:

- `circos.genomicPoints`
- `circos.genomicLines`
- `circos.genomicText`
- `circos.genomicRect`
- `circos.genomicLink`

Functions with specific purpose:

- `circos.genomicDensity`
- `circos.genomicRainfall`
- `circos.genomicIdeogram`
- `circos.genomicHeatmap`
- `circos.genomicLabels`

Finally, function that draws Chord diagram:

- `chordDiagram`

Please refer to the vignettes (http://jokergoo.github.io/circlize_book/book/) to find out how to draw basic and advanced circular plots by this package.

Examples

```
# There is no example  
NULL
```

add_transparency *Add transparency to colors*

Description

Add transparency to colors

Usage

```
add_transparency(col, transparency = 0)
```

Arguments

col a vector of colors
transparency transparency, numeric value between 0 and 1

Value

A vector of colors

Examples

```
add_transparency("red", 0.5)  
add_transparency(1, 0.5)  
add_transparency("#FF00080", 0.2)
```

adjacencyList2Matrix *Convert adjacency list to adjacency matrix*

Description

Convert adjacency list to adjacency matrix

Usage

```
adjacencyList2Matrix(lt, square = FALSE)
```

Arguments

lt a data frame which contains adjacency list.
square is the returned matrix a square matrix?

Details

Convert adjacency list to adjacency matrix.

Examples

```
lt = data.frame(letters[1:5], letters[6:10])
adjacencyList2Matrix(lt)

lt = data.frame(letters[1:5], letters[6:10], 1:5)
adjacencyList2Matrix(lt)

set.seed(123)
lt = data.frame(sample(letters, 4), sample(letters, 4), 1:4)
adjacencyList2Matrix(lt)
adjacencyList2Matrix(lt, square = TRUE)
```

`calc_gap`*Calculate gap to make two Chord diagram with same scale*

Description

Calculate gap to make two Chord diagram with same scale

Usage

```
calc_gap(x1, x2, big.gap = 10, small.gap = 1)
```

Arguments

<code>x1</code>	The matrix or the data frame for the first Chord diagram.
<code>x2</code>	The matrix or the data frame for the second Chord diagram.
<code>big.gap</code>	<code>big.gap</code> for the first Chord diagram.
<code>small.gap</code>	<code>small.gap</code> for both Chord diagrams.

Details

There should be no overlap between the two sets of sectors.

Value

A numeric value which can be directly set to `big.gap` in the second Chord diagram.

Examples

```
# There is no example
NULL
```

`CELL_META`*Easy way to get meta data in the current cell*

Description

Easy way to get meta data in the current cell

Usage

```
CELL_META
```

Details

The variable `CELL_META` can only be used to get meta data of the "current" cell. Basically you can simply replace e.g. `get.cell.meta.data("sector.index")` to `CELL_META$sector.index`.

See Also

[get.cell.meta.data](#)

Examples

```
pdf(NULL)
circos.initialize("a", xlim = c(0, 1))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  print(CELL_META$sector.index)
  print(CELL_META$xlim)
})
dev.off()
```

`chordDiagram`*Plot Chord Diagram*

Description

Plot Chord Diagram

Usage

```
chordDiagram(x, grid.col = NULL, grid.border = NA, transparency = 0.5,
  col = NULL, row.col = NULL, column.col = NULL,
  order = NULL, directional = 0, xmax = NULL,
  symmetric = FALSE, keep.diagonal = FALSE,
  direction.type = "diffHeight", diffHeight = convert_height(2, "mm"),
  reduce = 1e-5, self.link = 2,
  preAllocateTracks = NULL,
```



```

annotationTrack = c("name", "grid", "axis"),
annotationTrackHeight = convert_height(c(3, 2), "mm"),
link.border = NA, link.lwd = par("lwd"), link.lty = par("lty"),
link.sort = FALSE, link.decreasing = TRUE,
link.arr.length = ifelse(link.arr.type == "big.arrow", 0.02, 0.4),
link.arr.width = link.arr.length/2,
link.arr.type = "triangle", link.arr.lty = par("lty"),
link.arr.lwd = par("lwd"), link.arr.col = par("col"),
link.largest.ontop = FALSE, link.visible = TRUE,
link.rank = NULL, scale = FALSE, big.gap = 10, small.gap = 1, ...)

```

Arguments

x	a matrix or a data frame. The function will pass all argument to chordDiagramFromMatrix or chordDiagramFromDataFrame depending on the type of x, also format of other arguments depends of the type of x. If it is in the form of a matrix, it should be an adjacency matrix. If it is in the form of a data frame, it should be an adjacency list.
grid.col	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
grid.border	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
transparency	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
col	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
row.col	pass to chordDiagramFromMatrix
column.col	pass to chordDiagramFromMatrix
order	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
directional	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
xmax	maximum value on x-axes, the value should be a named vector.
symmetric	pass to chordDiagramFromMatrix
keep.diagonal	pass to chordDiagramFromMatrix
direction.type	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
diffHeight	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
reduce	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
self.link	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
preAllocateTracks	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
annotationTrack	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
annotationTrackHeight	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.border	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.lwd	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.lty	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame

link.sort	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.decreasing	
link.arr.length	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.arr.width	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.arr.type	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.arr.lty	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.arr.lwd	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.arr.col	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.largest.ontop	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.visible	pass to <code>chordDiagramFromMatrix</code> or <code>chordDiagramFromDataFrame</code>
link.rank	order to add links to the circle, a large value means to add it later.
scale	scale each sector to same width
big.gap	Gap between the two sets of sectors. If the input is a matrix, the two sets are row sectors and column sectors. If the input is a data frame, the two sets correspond to the first column and the second column. It only works when there is no intersection between the two sets.
small.gap	Small gap between sectors.
...	pass to <code>circos.link</code> .

Details

Chord diagram is a way to visualize numeric tables (http://circos.ca/intro/tabular_visualization/), especially useful when the table represents information of directional relations. This function visualize tables in a circular way.

This function is flexible and contains some settings that may be a little difficult to understand. Please refer to vignette for better explanation.

Value

A data frame which contains positions of links, columns are:

rn	sector name corresponding to rows in the adjacency matrix or the first column in the adjacency list
cn	sector name corresponding to columns in the adjacency matrix or the second column in the adjacency list
value	value for the interaction or relation
o1	order of the link on the "from" sector
o2	order of the link on the "to" sector
x1	and position of the link on the "from" sector, the interval for the link on the "from" sector is $c(x1 - \text{abs}(\text{value}), x1)$
x2	and position of the link on the "to" sector, the interval for the link on the "from" sector is $c(x2 - \text{abs}(\text{value}), x2)$

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

See Also

http://jokergoo.github.io/circlize_book/book/the-chorddiagram-function.html

Examples

```
set.seed(999)
mat = matrix(sample(18, 18), 3, 6)
rownames(mat) = paste0("S", 1:3)
colnames(mat) = paste0("E", 1:6)

df = data.frame(from = rep(rownames(mat), times = ncol(mat)),
  to = rep(colnames(mat), each = nrow(mat)),
  value = as.vector(mat),
  stringsAsFactors = FALSE)

chordDiagram(mat)
chordDiagram(df)
circos.clear()
```

chordDiagramFromDataFrame

Plot Chord Diagram from a data frame

Description

Plot Chord Diagram from a data frame

Usage

```
chordDiagramFromDataFrame(df, grid.col = NULL, grid.border = NA, transparency = 0.5,
  col = NULL, order = NULL, directional = 0, xmax = NULL,
  direction.type = "diffHeight", diffHeight = convert_height(2, "mm"),
  reduce = 1e-5, self.link = 2, preAllocateTracks = NULL,
  annotationTrack = c("name", "grid", "axis"),
  annotationTrackHeight = convert_height(c(3, 2), "mm"),
  link.border = NA, link.lwd = par("lwd"), link.lty = par("lty"),
  link.sort = FALSE, link.decreasing = TRUE,
  link.arr.length = ifelse(link.arr.type == "big.arrow", 0.02, 0.4),
  link.arr.width = link.arr.length/2,
  link.arr.type = "triangle", link.arr.lty = par("lty"),
  link.arr.lwd = par("lwd"), link.arr.col = par("col"),
  link.largest.ontop = FALSE, link.visible = TRUE,
  link.rank = seq_len(nrow(df)),
```

```

scale = FALSE,
big.gap = 10, small.gap = 1,
...)
```

Arguments

<code>df</code>	A data frame with at least two columns. The first two columns specify the connections and the third column (optional) contains numeric values which are mapped to the width of links as well as the colors if <code>col</code> is specified as a color mapping function. The sectors in the plot will be <code>union(df[[1]], df[[2]])</code> .
<code>grid.col</code>	Grid colors which correspond to sectors. The length of the vector should be either 1 or the number of sectors. It's preferred that <code>grid.col</code> is a named vector of which names correspond to sectors. If it is not a named vector, the order of <code>grid.col</code> corresponds to order of sectors.
<code>grid.border</code>	border for grids. If it is NULL, the border color is same as grid color
<code>transparency</code>	Transparency of link colors, 0 means no transparency and 1 means full transparency. If transparency is already set in <code>col</code> or <code>row.col</code> or <code>column.col</code> , this argument will be ignored. NA also ignores this argument.
<code>col</code>	Colors for links. It can be a vector which corresponds to connections in <code>df</code> , or a function which generate colors according to values (the third column) in <code>df</code> , or a single value which means colors for all links are the same. You may use colorRamp2 to generate a function which maps values to colors.
<code>order</code>	Order of sectors. Default order is <code>union(df[[1]], df[[2]])</code> .
<code>directional</code>	Whether links have directions. 1 means the direction is from the first column in <code>df</code> to the second column, -1 is the reverse, 0 is no direction, and 2 for two directional. The value can be a vector which has same length as number of rows in <code>df</code> .
<code>xmax</code>	maximum value on x-axes, the value should be a named vector.
<code>direction.type</code>	type for representing directions. Can be one or two values in "diffHeight" and "arrows". If the value contains "diffHeight", different heights of the links are used to represent the directions for which starting root has long height to give people feeling that something is coming out. If the value contains "arrows", users can customize arrows with following arguments. The value can be a vector which has same length as number of rows in <code>df</code> . Note if you want to set both <code>diffHeight</code> and <code>arrows</code> for certain links, you need to embed these two options into one string such as "diffHeight+arrows".
<code>diffHeight</code>	The difference of height between two 'roots' if <code>directional</code> is set to TRUE. If the value is set to a positive value, start root is shorter than end root and if it is set to a negative value, start root is longer than the end root. The value can be a vector which has same length as number of rows in <code>df</code> .
<code>reduce</code>	if the ratio of the width of certain grid compared to the whole circle is less than this value, the grid is removed on the plot. Set it to value less than zero if you want to keep all tiny grid.
<code>self.link</code>	if there is a self link in one sector, 1 means the link will be degenerated as a 'mountain' and the width corresponds to the value for this connection. 2 means

the width of the starting root and the ending root all have the same width that corresponds to the value for the connection.

preAllocateTracks	Pre-allocate empty tracks before drawing Chord diagram. It can be a single number indicating how many empty tracks needed to be created or a list containing settings for empty tracks. Please refer to vignette for details.
annotationTrack	Which annotation track should be plotted? By default, a track containing sector names and a track containing grid will be created.
annotationTrackHeight	Track height corresponding to values in annotationTrack.
link.border	border for links, single scalar or a vector which has the same length as nrows of df or a data frame
link.lwd	width for link borders, single scalar or a vector which has the same length as nrows of df or a data frame
link.lty	style for link borders, single scalar or a vector which has the same length as nrows of df or a data frame
link.sort	whether sort links on every sector based on the width of the links on it. If it is set to "overall", all links are sorted regardless whether they are from the first column or the second column.
link.decreasing	for link.sort
link.arr.length	pass to circos.link . The format of this argument is same as link.lwd.
link.arr.width	pass to Arrowhead . The format of this argument is same as link.lwd.
link.arr.type	pass to circos.link , same settings as link.lwd. Default value is triangle.
link.arr.col	color or the single line link which is put in the center of the belt. The format of this argument is same as link.lwd.
link.arr.lwd	line width of the single line link which is put in the center of the belt. The format of this argument is same as link.lwd.
link.arr.lty	line type of the single line link which is put in the center of the belt. The format of this argument is same as link.lwd.
link.largest.ontop	controls the order of adding links, whether based on the absolute value?
link.visible	whether plot the link. The value is logical, if it is set to FALSE, the corresponding link will not plotted, but the space is still occupied. The format of this argument is same as link.lwd
link.rank	order to add links to the circle, a large value means to add it later.
scale	scale each sector to same width
big.gap	Gaps between the sectors in the first column of df and sectors in the second column in df.
small.gap	Small gap between sectors.
...	pass to circos.link

Details

The data frame can have a column named "rank" which is used to control the order of adding links to the diagram.

Value

A data frame which contains positions of links, see explanation in [chordDiagram](#).

Examples

```
# There is no example
NULL
```

```
chordDiagramFromMatrix
```

Plot Chord Diagram from an adjacency matrix

Description

Plot Chord Diagram from an adjacency matrix

Usage

```
chordDiagramFromMatrix(mat, grid.col = NULL, grid.border = NA, transparency = 0.5,
  col = NULL, row.col = NULL, column.col = NULL, order = NULL, directional = 0,
  direction.type = "diffHeight", diffHeight = convert_height(2, "mm"),
  reduce = 1e-5, xmax = NULL, self.link = 2,
  symmetric = FALSE, keep.diagonal = FALSE, preAllocateTracks = NULL,
  annotationTrack = c("name", "grid", "axis"),
  annotationTrackHeight = convert_height(c(3, 2), "mm"),
  link.border = NA, link.lwd = par("lwd"), link.lty = par("lty"),
  link.sort = FALSE, link.decreasing = TRUE,
  link.arr.length = ifelse(link.arr.type == "big.arrow", 0.02, 0.4),
  link.arr.width = link.arr.length/2,
  link.arr.type = "triangle", link.arr.lty = par("lty"),
  link.arr.lwd = par("lwd"), link.arr.col = par("col"),
  link.largest.ontop = FALSE, link.visible = TRUE,
  link.rank = NULL, scale = FALSE, big.gap = 10, small.gap = 1, ...)
```

Arguments

<code>mat</code>	A table which represents as a numeric matrix.
<code>grid.col</code>	Grid colors which correspond to matrix rows/columns (or sectors). The length of the vector should be either 1 or <code>length(union(rownames(mat), colnames(mat)))</code> . It's preferred that <code>grid.col</code> is a named vector of which names correspond to sectors. If it is not a named vector, the order of <code>grid.col</code> corresponds to order of sectors.

<code>grid.border</code>	border for grids. If it is NULL, the border color is same as grid color
<code>transparency</code>	Transparency of link colors, 0 means no transparency and 1 means full transparency. If transparency is already set in <code>col</code> or <code>row.col</code> or <code>column.col</code> , this argument will be ignored. NA also ignores this argument.
<code>col</code>	Colors for links. It can be a matrix which corresponds to <code>mat</code> , or a function which generate colors according to values in <code>mat</code> , or a single value which means colors for all links are the same, or a three-column data frame in which the first two columns correspond to row names and columns and the third column is colors. You may use <code>colorRamp2</code> to generate a function which maps values to colors.
<code>row.col</code>	Colors for links. Links from the same row in <code>mat</code> will have the same color. Length should be same as number of rows in <code>mat</code> . This argument only works when <code>col</code> is set to NULL.
<code>column.col</code>	Colors for links. Links from the same column in <code>mat</code> will have the same color. Length should be same as number of columns in <code>mat</code> . This argument only works when <code>col</code> and <code>row.col</code> is set to NULL.
<code>order</code>	Order of sectors. Default order is <code>union(df[[1]], df[[2]])</code> .
<code>directional</code>	Whether links have directions. 1 means the direction is from the first column in <code>df</code> to the second column, -1 is the reverse, 0 is no direction, and 2 for two directional. Same setting as <code>link.border</code> .
<code>xmax</code>	maximum value on x-axes, the value should be a named vector.
<code>direction.type</code>	type for representing directions. Can be one or two values in "diffHeight" and "arrows". If the value contains "diffHeight", different heights of the links are used to represent the directions for which starting root has long height to give people feeling that something is coming out. If the value contains "arrows", users can customize arrows with following arguments. Same setting as <code>link.border</code> . Note if you want to set both <code>diffHeight</code> and <code>arrows</code> for certain links, you need to embed these two options into one string such as "diffHeight+arrows".
<code>diffHeight</code>	The difference of height between two 'roots' if <code>directional</code> is set to TRUE. If the value is set to a positive value, start root is shorter than end root and if it is set to a negative value, start root is longer than the end root.
<code>reduce</code>	if the ratio of the width of certain grid compared to the whole circle is less than this value, the grid is removed on the plot. Set it to value less than zero if you want to keep all tiny grid.
<code>self.link</code>	if there is a self link in one sector, 1 means the link will be degenerated as a 'mountain' and the width corresponds to the value for this connection. 2 means the width of the starting root and the ending root all have the width that corresponds to the value for the connection.
<code>symmetric</code>	Whether the matrix is symmetric. If the value is set to TRUE, only lower triangular matrix without the diagonal will be used.
<code>keep.diagonal</code>	If the matrix is specified as symmetric, whether keep diagonal for visualization.
<code>preAllocateTracks</code>	Pre-allocate empty tracks before drawing Chord diagram. It can be a single number indicating how many empty tracks needed to be created or a list containing settings for empty tracks. Please refer to vignette for details.

annotationTrack	Which annotation track should be plotted? By default, a track containing sector names and a track containing grid will be created.
annotationTrackHeight	Track height corresponding to values in annotationTrack.
link.border	border for links, single scalar or a matrix with names or a data frame with three columns
link.lwd	width for link borders, single scalar or a matrix with names or a data frame with three columns
link.lty	style for link borders, single scalar or a matrix with names or a data frame with three columns
link.sort	whether sort links on every sector based on the width of the links on it. If it is set to "overall", all links are sorted regardless whether they are from rows or columns.
link.decreasing	for link.sort
link.arr.length	pass to circos.link . The format of this argument is same as link.lwd.
link.arr.width	pass to Arrowhead . The format of this argument is same as link.lwd.
link.arr.type	pass to circos.link , same format as link.lwd. Default value is triangle.
link.arr.col	color or the single line link which is put in the center of the belt. The format of this argument is same as link.lwd.
link.arr.lwd	line width of the single line link which is put in the center of the belt. The format of this argument is same as link.lwd.
link.arr.lty	line type of the single line link which is put in the center of the belt. The format of this argument is same as link.lwd.
link.largest.ontop	controls the order of adding links, whether based on the absolute value?
link.visible	whether plot the link. The value is logical, if it is set to FALSE, the corresponding link will not be plotted, but the space is still occupied. The format of this argument is same as link.lwd
link.rank	order to add links to the circle, a large value means to add it later.
scale	scale each sector to same width
big.gap	Gap between row sectors and column sectors.
small.gap	Small gap between sectors.
...	pass to circos.link

Details

Internally, the matrix is transformed to a data frame and sent to [chordDiagramFromDataFrame](#).

Value

A data frame which contains positions of links, see explanation in [chordDiagram](#).

Examples

```
# There is no example
NULL
```

circlize	<i>Convert to polar coordinate system</i>
----------	---

Description

Convert to polar coordinate system

Usage

```
circlize(x, y, sector.index = get.current.sector.index(),
        track.index = get.current.track.index())
```

Arguments

x	Data points on x-axis. The value can also be a two-column matrix/data frame if you put x and y data points into one variable.
y	Data points on y-axis.
sector.index	Index for the sector to convert the coordinates
track.index	Index for the track to convert the coordinates

Details

This is the core function in the package. It transform data points from data coordinate system (in a specific cell) to the polar coordinate system.

Value

A matrix with two columns (theta and rou). rou is measured in degree.

Examples

```
pdf(NULL)
factors = c("a", "b")
circos.initialize(factors, xlim = c(0, 1))
circos.track(ylim = c(0, 1))
# x = 0.5, y = 0.5 in sector a and track 1
circlize(0.5, 0.5, sector.index = "a", track.index = 1)
circos.clear()
dev.off()
```

circos.arrow *Draw arrow which is paralle to the circle*

Description

Draw arrow which is paralle to the circle

Usage

```
circos.arrow(x1, x2, y = get.cell.meta.data("ycenter", sector.index, track.index),
            width = get.cell.meta.data("yrange", sector.index, track.index)/2,
            sector.index = get.current.sector.index(), track.index = get.current.track.index(),
            arrow.head.length = convert_x(5, "mm", sector.index, track.index),
            arrow.head.width = width*2, arrow.position = c("end", "start"),
            tail = c("normal", "point"), border = "black", col = "white", lty = par("lty"), ...)
```

Arguments

x1	start position of the arrow on the x-axis.
x2	end position of the arrow on the x-axis.
y	position of the arrow on the y-axis. Note this is the center of the arrow on y-axis.
width	width of the arrow body.
sector.index	index of the sector.
track.index	index of the track.
arrow.head.length	length of the arrow head. Note the value should be smaller than the length of the arrow itself (which is $x2 - x1$).
arrow.head.width	width of the arrow head.
arrow.position	where is the arrow head on the arrow.
tail	the shape of the arrow tail (the opposite side of arrow head).
border	border color of the arrow.
col	filled color of the arrow.
lty	line style of the arrow.
...	pass to polygon .

Details

Note all position values are measured in the data coordinate (the coordinate in each cell).

If you see points overflow warnings, you can set `circos.par(points.overflow.warning = FALSE)` to turn it off.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```

circos.initialize(letters[1:4], xlim = c(0, 1))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  circos.arrow(0, 1, y = 0.5, width = 0.4, arrow.head.length = ux(1, "cm"),
  col = "red", tail = ifelse(CELL_META$sector.index %in% c("a", "c"),
  "point", "normal"))
}, bg.border = NA, track.height = 0.4)

##### cell cycle #####
cell_cycle = data.frame(phase = factor(c("G1", "S", "G2", "M"),
  levels = c("G1", "S", "G2", "M")),
  hour = c(11, 8, 4, 1))
color = c("#66C2A5", "#FC8D62", "#8DA0CB", "#E78AC3")
circos.par(start.degree = 90)
circos.initialize(cell_cycle$phase, xlim = cbind(rep(0, 4), cell_cycle$hour))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  circos.arrow(CELL_META$xlim[1], CELL_META$xlim[2],
  arrow.head.width = CELL_META$yrange*0.8, arrow.head.length = ux(1, "cm"),
  col = color[CELL_META$sector.numeric.index])
  circos.text(CELL_META$xcenter, CELL_META$ycenter, CELL_META$sector.index,
  facing = "downward")
}, bg.border = NA, track.height = 0.3)
circos.clear()

```

circos.axis

Draw x-axis

Description

Draw x-axis

Usage

```

circos.axis(h = "top", major.at = NULL, labels = TRUE, major.tick = TRUE,
  sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"),
  labels.font = par("font"), labels.cex = par("cex"),
  labels.facing = "inside", labels.direction = NULL, labels.niceFacing = TRUE,
  direction = c("outside", "inside"), minor.ticks = 4,
  major.tick.percentage = 0.1, labels.away.percentage = major.tick.percentage/2,
  major.tick.length = convert_y(1, "mm", sector.index, track.index),
  lwd = par("lwd"), col = par("col"), labels.col = par("col"), labels.pos.adjust = TRUE)

```

Arguments

<code>h</code>	Position of the x-axis, can be "top", "bottom" or a numeric value
<code>major.at</code>	If it is numeric vector, it identifies the positions of the major ticks. It can exceed <code>xlim</code> value and the exceeding part would be trimmed automatically. If it is NULL, about every 10 degrees there is a major tick.
<code>labels</code>	labels of the major ticks. Also, the exceeding part would be trimmed automatically. The value can also be logical (either an atomic value or a vector) which represents which labels to show.
<code>major.tick</code>	Whether to draw major tick. If it is set to FALSE, there would be no minor ticks.
<code>sector.index</code>	Index for the sector
<code>track.index</code>	Index for the track
<code>labels.font</code>	font style for the axis labels
<code>labels.cex</code>	font size for the axis labels
<code>labels.direction</code>	deprecated, use <code>facing</code> instead.
<code>labels.facing</code>	facing of labels on axis, passing to circos.text
<code>labels.niceFacing</code>	Should facing of axis labels be human-easy
<code>direction</code>	whether the axis ticks point to the outside or inside of the circle.
<code>minor.ticks</code>	Number of minor ticks between two close major ticks.
<code>major.tick.percentage</code>	not used. Length of the major ticks. It is the percentage to the height of the cell.
<code>labels.away.percentage</code>	not used. The distance for the axis labels to the major ticks. It is the percentage to the height of the cell.
<code>major.tick.length</code>	length of the major ticks, measured in "current" data coordinate. convert_y can be used to convert an absolute unit to the data coordinate.
<code>lwd</code>	line width for ticks
<code>col</code>	color for the axes
<code>labels.col</code>	color for the labels
<code>labels.pos.adjust</code>	whether to adjust the positions of the first label and the last label. The value can be a vector of length two which correspond to the first label and the last label.

Details

It can only draw axes on x-direction.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

See Also

`circos.yaxis` draws axes on y-direction.

Examples

```
factors = letters[1:8]
circos.par(points.overflow.warning = FALSE)
circos.initialize(factors = factors, xlim = c(0, 10))
circos.trackPlotRegion(factors = factors, ylim = c(0, 10), track.height = 0.1,
  bg.border = NA, panel.fun = function(x, y) {
    circos.text(5, 10, get.cell.meta.data("sector.index"))
  })

circos.trackPlotRegion(factors = factors, ylim = c(0, 10))
circos.axis(sector.index = "a")
circos.axis(sector.index = "b", direction = "inside", labels.facing = "outside")
circos.axis(sector.index = "c", h = "bottom")
circos.axis(sector.index = "d", h = "bottom", direction = "inside",
  labels.facing = "reverse.clockwise")
circos.axis(sector.index = "e", h = 5, major.at = c(1, 3, 5, 7, 9))
circos.axis(sector.index = "f", h = 5, major.at = c(1, 3, 5, 7, 9),
  labels = c("a", "c", "e", "g", "f"), minor.ticks = 0)
circos.axis(sector.index = "g", h = 5, major.at = c(1, 3, 5, 7, 9),
  labels = c("a1", "c1", "e1", "g1", "f1"), major.tick = FALSE,
  labels.facing = "reverse.clockwise")
circos.axis(sector.index = "h", h = 2, major.at = c(1, 3, 5, 7, 9),
  labels = c("a1", "c1", "e1", "g1", "f1"), major.tick.percentage = 0.3,
  labels.away.percentage = 0.2, minor.ticks = 2, labels.facing = "clockwise")
circos.clear()

## Not run:

##### real-time clock #####
factors = letters[1]

circos.par("gap.degree" = 0, "cell.padding" = c(0, 0, 0, 0), "start.degree" = 90)
circos.initialize(factors = factors, xlim = c(0, 12))
circos.trackPlotRegion(factors = factors, ylim = c(0, 1), bg.border = NA)
circos.axis(sector.index = "a", major.at = 0:12, labels = "",
  direction = "inside", major.tick.percentage = 0.3)
circos.text(1:12, rep(0.5, 12), 1:12, facing = "downward")

while(1) {
  current.time = as.POSIXlt(Sys.time())
  sec = ceiling(current.time$sec)
  min = current.time$min
  hour = current.time$hour

  # erase the clock hands
  draw.sector(rou1 = 0.8, border = "white", col = "white")

  sec.degree = 90 - sec/60 * 360
```

```
arrows(0, 0, cos(sec.degree/180*pi)*0.8, sin(sec.degree/180*pi)*0.8)

min.degree = 90 - min/60 * 360
arrows(0, 0, cos(min.degree/180*pi)*0.7, sin(min.degree/180*pi)*0.7, lwd = 2)

hour.degree = 90 - hour/12 * 360 - min/60 * 360/12
arrows(0, 0, cos(hour.degree/180*pi)*0.4, sin(hour.degree/180*pi)*0.4, lwd = 2)

  Sys.sleep(1)
}
circos.clear()

## End(Not run)
```

circos.clear

Reset the circular layout parameters

Description

Reset the circular layout parameters

Usage

```
circos.clear()
```

Details

Because there are several parameters for the circular plot which can only be set before [circos.initialize](#). So before you draw the next circular plot, you need to reset all these parameters.

If you meet some errors when re-drawing the circular plot, try running this function and it will solve most of the problems.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
# There is no example
NULL
```

circos.dendrogram *Add circular dendrograms*

Description

Add circular dendrograms

Usage

```
circos.dendrogram(dend, facing = c("outside", "inside"), max_height = NULL)
```

Arguments

dend	A dendrogram object.
facing	Is the dendrograms facing inside to the circle or outside.
max_height	Maximum height of the dendrogram. This is important if more than one dendrograms are drawn in one track and making them comparable.

Details

Assuming there are n nodes in the dendrogram, the positions for leaves on x-axis is $0.5, 1.5, \dots, n - 0.5$. So you must be careful with `xlim` when you initialize the circular layout.

You can use the `dendextend` package to render the dendrograms.

Examples

```
load(system.file(package = "circlize", "extdata", "bird.orders.RData"))

labels = hc$labels # name of birds
ct = cutree(hc, 6) # cut tree into 6 pieces
n = length(labels) # number of bird species
dend = as.dendrogram(hc)

circos.par(cell.padding = c(0, 0, 0, 0))
circos.initialize(factors = "a", xlim = c(0, n)) # only one sector
max_height = attr(dend, "height") # maximum height of the trees
circos.trackPlotRegion(ylim = c(0, 1), bg.border = NA, track.height = 0.3,
  panel.fun = function(x, y) {
    for(i in seq_len(n)) {
      circos.text(i-0.5, 0, labels[i], adj = c(0, 0.5),
        facing = "clockwise", niceFacing = TRUE,
        col = ct[labels[i]], cex = 0.7)
    }
  })

suppressPackageStartupMessages(require(dendextend))
dend = color_branches(dend, k = 6, col = 1:6)
```

```

circos.trackPlotRegion(ylim = c(0, max_height), bg.border = NA,
  track.height = 0.4, panel.fun = function(x, y) {
    circos.dendrogram(dend, max_height = max_height)
  })
circos.clear()

```

circos.genomicAxis *Add genomic axes*

Description

Add genomic axes

Usage

```

circos.genomicAxis(h = "top", major.by = NULL, tickLabelsStartFromZero = TRUE,
  labels.cex = 0.4*par("cex"), sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), ...)

```

Arguments

h	Position of the axes. "top" or "bottom".
major.by	Increment of major ticks. It is calculated automatically if the value is not set (about every 10 degrees there is a major tick).
tickLabelsStartFromZero	Whether axis tick labels start from 0? This will only affect the axis labels while not affect x-values in cells.
labels.cex	the font size for the axis tick labels.
sector.index	Index for the sector
track.index	Index for the track
...	Other arguments pass to circos.axis .

Details

It assigns proper tick labels under genomic coordinate.

Examples

```

circos.initializeWithIdeogram(plotType = NULL)
circos.track(ylim = c(0, 1), panel.fun = function(x, y) circos.genomicAxis())
circos.clear()

```

circos.genomicDensity *Calculate and add genomic density track*

Description

Calculate and add genomic density track

Usage

```
circos.genomicDensity(data, ylim.force = FALSE, window.size = NULL, overlap = TRUE,  
  col = ifelse(area, "grey", "black"), lwd = par("lwd"), lty = par("lty"), type = "l",  
  area = TRUE, area.baseline = NULL, baseline = 0, border = NA, ...)
```

Arguments

data	A bed-file-like data frame or a list of data frames
ylim.force	Whether to force upper bound of ylim to be 1.
window.size	Pass to genomicDensity
overlap	Pass to genomicDensity
col	Colors. It should be length of one. If data is a list of data frames, the length of col can also be the length of the list.
lwd	Width of lines
lty	Style of lines
type	Type of lines, see circos.lines
area	See circos.lines
area.baseline	Deprecated, use baseline instead.
baseline	See circos.lines
border	See circos.lines
...	Pass to circos.trackPlotRegion

Details

This function is a high-level graphical function, and it will create a new track.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:

load(system.file(package = "circlize", "extdata", "DMR.RData"))

# rainfall
circos.initializeWithIdeogram(plotType = c("axis", "labels"))

bed_list = list(DMR_hyper, DMR_hypo)
circos.genomicRainfall(bed_list, pch = 16, cex = 0.4, col = c("#FF000080", "#0000FF80"))

circos.genomicDensity(bed_list[[1]], col = c("#FF000080"), track.height = 0.1)
circos.genomicDensity(bed_list[[2]], col = c("#0000FF80"), track.height = 0.1)

circos.clear()

## End(Not run)
```

`circos.genomicHeatmap` *Add heatmaps for selected regions*

Description

Add heatmaps for selected regions

Usage

```
circos.genomicHeatmap(bed, col, numeric.column = NULL,
  border = NA, border_lwd = par("lwd"),
  border_lty = par("lty"), connection_height = convert_height(5, "mm"),
  line_col = par("col"), line_lwd = par("lwd"), line_lty = par("lty"),
  heatmap_height = 0.15, side = c("inside", "outside"),
  track.margin = circos.par("track.margin"))
```

Arguments

<code>bed</code>	a data frame in bed format, the matrix is stored from the fourth column.
<code>col</code>	colors for the heatmaps. The value can be a matrix or a color mapping function generated by colorRamp2 .
<code>numeric.column</code>	column index for the numeric columns. The values can be integer index or character index
<code>border</code>	border of the heatmap grids.
<code>border_lwd</code>	line width for borders of heatmap grids
<code>border_lty</code>	line style for borders of heatmap grids

connection_height	height of the connection lines
line_col	col of the connection line. The value can be a vector.
line_lwd	line width of the connection lines.
line_lty	line style of the connection lines.
heatmap_height	height of the heatmap track
side	side of the heatmaps. Is the heatmap facing inside or outside?
track.margin	bottom and top margins

Details

The function visualizes heatmaps which correspond to a subset of regions in the genome. The correspondance between heatmaps and regions are identified by connection lines.

The function actually creates two tracks, one track for the connection lines and one track for the heatmaps. The heatmaps always fill the whole track.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
## Not run:
circos.initializeWithIdeogram(plotType = c("labels", "axis"))
bed = generateRandomBed(nr = 100, nc = 4)
col_fun = colorRamp2(c(-1, 0, 1), c("green", "black", "red"))
circos.genomicHeatmap(bed, col_fun, side = "inside", border = "white")
circos.genomicHeatmap(bed, col_fun, side = "outside",
  line_col = as.numeric(factor(bed[[1]])))

## End(Not run)
```

```
circos.genomicIdeogram
```

Add an ideogram track

Description

Add an ideogram track

Usage

```
circos.genomicIdeogram(cytoband = system.file(package = "circlize",
  "extdata", "cytoBand.txt"), species = NULL, track.height = convert_height(2, "mm"),
  track.margin = circos.par("track.margin"))
```

Arguments

cytoband	a data frame or a file path, pass to read.cytoband
species	Abbreviations of species, pass to read.cytoband
track.height	height of the ideogram track
track.margin	margins for the track

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# There is no example
NULL
```

```
circos.genomicInitialize
```

Initialize circular plot with any genomic data

Description

Initialize circular plot with any genomic data

Usage

```
circos.genomicInitialize(data, sector.names = NULL, major.by = NULL,
  plotType = c("axis", "labels"), tickLabelsStartFromZero = TRUE,
  axis.labels.cex = 0.4*par("cex"), labels.cex = 0.8*par("cex"),
  track.height = NULL, ...)
```

Arguments

data	A data frame containing genomic data.
sector.names	Labels for each sectors which will be drawn along each sector. It will not modify values of sector index.
major.by	Increment of major ticks. It is calculated automatically if the value is not set (about every 10 degrees there is a major tick).
plotType	If it is not NULL, there will create a new track containing axis and names for sectors. This argument controls which part should be drawn, axis for genomic axis and labels for chromosome names
tickLabelsStartFromZero	Whether axis tick labels start from 0? This will only affect the axis labels while not affect x-values in cells.
axis.labels.cex	the font size for the axis tick labels.

```

labels.cex      the font size for the labels.
track.height    If PlotType is not NULL, height of the annotation track.
...            Pass to circos.initialize

```

Details

The function will initialize circular plot from genomic data. If `plotType` is set with value in `axis` or `labels`, there will create a new track.

The order of sectors related to data structure of `data`. If the first column in `data` is a factor, the order of sectors is `levels(data[[1]])`; If the first column is just a simple vector, the order of sectors is `unique(data[[1]])`.

For more details on initializing genomic plot, please refer to the vignettes.

References

Gu, Z. (2014) `circlize` implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```

## Not run:

df = read.cytoband()$df
circos.genomicInitialize(df)

df = data.frame(name = c("TP53", "TP63", "TP73"),
                start = c(7565097, 189349205, 3569084),
                end = c(7590856, 189615068, 3652765),
                stringsAsFactors = FALSE)
circos.genomicInitialize(df)
circos.clear()

circos.genomicInitialize(df, major.by = 10000)
circos.clear()

circos.genomicInitialize(df, plotType = "labels")
circos.clear()

circos.genomicInitialize(df, sector.names = c("tp53", "tp63", "tp73"))
circos.clear()

circos.genomicInitialize(df, sector.names = c("tp53x", "tp63x", "tp73"))
circos.clear()

df[[1]] = factor(df[[1]], levels = c("TP73", "TP63", "TP53"))
circos.genomicInitialize(df)
circos.clear()

## End(Not run)

```

circos.genomicLabels *Add labels to specified genomic regions*

Description

Add labels to specified genomic regions

Usage

```
circos.genomicLabels.bed, labels = NULL, labels.column = NULL,
  facing = "clockwise", niceFacing = TRUE,
  col = par("col"), cex = 0.8, font = par("font"), padding = 0.4,
  connection_height = convert_height(5, "mm"),
  line_col = par("col"), line_lwd = par("lwd"), line_lty = par("lty"),
  labels_height = min(c(convert_height(1.5, "cm"),
    max(strwidth(labels, cex = cex, font = font)))),
  side = c("inside", "outside"), track.margin = circos.par("track.margin"))
```

Arguments

bed	a data frame in bed format
labels	a vector of labels corresponding to rows in bed
labels.column	if the label column is already in bed, the index for this column in bed
facing	facing of the labels. The value can only be 'clockwise' or 'reverse.clockwise'.
niceFacing	whether automatically adjust the facing of the labels.
col	color for the labels
cex	size of the labels
font	font of the labels
padding	padding of the labels, the value is the ratio to the height of the label
connection_height	height of the connection track
line_col	color for the connection lines
line_lwd	line width for the connection lines
line_lty	line type for the connectioin lines
labels_height	height of the labels track
side	side of the labels track, is it in the inside of the track where the regions are marked?
track.margin	bottom and top margins

Details

The function adds labels for the specified regions. The positions of labels are arranged so that they are not overlapping to each other.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
## Not run:
circos.initializeWithIdeogram(plotType = c("labels", "axis"))
bed = generateRandomBed(nr = 100, fun = function(k) sample(letters, k, replace = TRUE))
bed[1, 4] = "aaaaaaa"
circos.genomicLabels(bed, labels.column = 4, side = "inside",
  col = as.numeric(factor(bed[[1]])))
circos.genomicLabels(bed, labels.column = 4, side = "outside",
  line_col = as.numeric(factor(bed[[1]])))

## End(Not run)
```

circos.genomicLines *Add lines to a plotting region, specifically for genomic graphics*

Description

Add lines to a plotting region, specifically for genomic graphics

Usage

```
circos.genomicLines(region, value, numeric.column = NULL,
  sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), posTransform = NULL,
  col = ifelse(area, "grey", "black"), lwd = par("lwd"),
  lty = par("lty"), type = "l",
  area = FALSE, area.baseline = NULL, border = "black", baseline = "bottom",
  pt.col = par("col"), cex = par("cex"), pch = par("pch"), ...)
```

Arguments

region	A data frame contains 2 column which correspond to start position and end position
value	A data frame contains values and other information
numeric.column	Which column in value data frame should be taken as y-value. If it is not defined, the whole numeric columns in value will be taken.
sector.index	Pass to circos.lines
track.index	Pass to circos.lines
posTransform	Self-defined function to transform genomic positions, see posTransform.default for explanation

col	col of lines/areas. If there are more than one numeric column, the length of col can be either one or number of numeric columns. If there is only one numeric column and type is either segment or h, the length of col can be either one or number of rows of region. pass to circos.lines
lwd	Settings are similar as col. Pass to circos.lines
lty	Settings are similar as col. Pass to circos.lines
type	There is an additional option segment which plot segment lines from start position to end position. Settings are similar as col. Pass to circos.lines .
area	Settings are similar as col. Pass to circos.lines
area.baseline	Deprecated, use baseline instead.
baseline	Settings are similar as col. Pass to circos.lines
border	Settings are similar as col. Pass to circos.lines
pt.col	Settings are similar as col. Pass to circos.lines
cex	Settings are similar as col. Pass to circos.lines
pch	Settings are similar as col. Pass to circos.lines
...	mysterious parameters

Details

The function is a low-level graphical function and usually is put in panel.fun when using [circos.genomicTrackPlotRegion](#)

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:

### test bed
circos.par("track.height" = 0.1)
circos.initializeWithIdeogram(plotType = NULL)

bed = generateRandomBed(nr = 100)
circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
  circos.genomicLines(region, value, type = "l", ...)
})

bed1 = generateRandomBed(nr = 100)
bed2 = generateRandomBed(nr = 100)
bed_list = list(bed1, bed2)

circos.genomicTrackPlotRegion(bed_list, panel.fun = function(region, value, ...) {
  i = getI(...)
  circos.genomicLines(region, value, col = i, ...)
})
```



```

circos.genomicTrackPlotRegion.bed_list, stack = TRUE,
  panel.fun = function(region, value, ...) {
    i = getI(...)
    circos.genomicLines(region, value, col = i, ...)
  })

bed = generateRandomBed(nr = 100, nc = 4)
circos.genomicTrackPlotRegion.bed, panel.fun = function(region, value, ...) {
  circos.genomicLines(region, value, col = 1:4, ...)
})

circos.genomicTrackPlotRegion.bed, stack = TRUE, panel.fun = function(region, value, ...) {
  i = getI(...)
  circos.genomicLines(region, value, col = i, ...)
})

bed = generateRandomBed(nr = 100)
circos.genomicTrackPlotRegion.bed, panel.fun = function(region, value, ...) {
  circos.genomicLines(region, value, type = "segment", lwd = 2, ...)
})

circos.clear()

## End(Not run)

```

circos.genomicLink *Add links from two sets of genomic positions*

Description

Add links from two sets of genomic positions

Usage

```

circos.genomicLink(region1, region2,
  rou = get_most_inside_radius(), rou1 = rou, rou2 = rou,
  col = "black", lwd = par("lwd"), lty = par("lty"), border = col, ...)

```

Arguments

region1	A genomic data frame
region2	A genomic data frame
rou	Pass to circos.link
rou1	Pass to circos.link
rou2	Pass to circos.link
col	Pass to circos.link , length can be either one or nrow of region1

lwd	Pass to <code>circos.link</code> , length can be either one or nrow of region1
lty	Pass to <code>circos.link</code> , length can be either one or nrow of region1
border	Pass to <code>circos.link</code> , length can be either one or nrow of region1
...	Pass to <code>circos.link</code>

Details

Of course, number of rows should be same in region1 and region2.

If you want to have more controls on links, please use `circos.link` directly.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:
set.seed(123)

bed1 = generateRandomBed(nr = 100)
bed1 = bed1[sample(nrow(bed1), 20), ]
bed2 = generateRandomBed(nr = 100)
bed2 = bed2[sample(nrow(bed2), 20), ]
circos.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram()

circos.genomicLink(bed1, bed2, col = sample(1:5, 20, replace = TRUE), border = NA)
circos.clear()

## End(Not run)
```

`circos.genomicPoints` *Add points to a plotting region, specifically for genomic graphics*

Description

Add points to a plotting region, specifically for genomic graphics

Usage

```
circos.genomicPoints(region, value, numeric.column = NULL,
  sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), posTransform = NULL,
  pch = par("pch"), col = par("col"), cex = par("cex"), bg = par("bg"), ...)
```

Arguments

region	A data frame contains 2 columns which correspond to start positions and end positions
value	A data frame contains values and other information
numeric.column	Which column in value data frame should be taken as y-value. If it is not defined, the whole numeric columns in value will be taken.
sector.index	Pass to circos.points
track.index	Pass to circos.points
posTransform	Self-defined function to transform genomic positions, see posTransform.default for explanation
col	color of points. If there is only one numeric column, the length of col can be either one or number of rows of region. If there are more than one numeric column, the length of col can be either one or number of numeric columns. Pass to circos.points
pch	Type of points. Settings are similar as col. Pass to circos.points
cex	Size of points. Settings are similar as col. Pass to circos.points
bg	background colors for points.
...	Mysterious parameters

Details

The function is a low-level graphical function and usually is put in `panel.fun` when using [circos.genomicTrackPlotRegion](#)

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:

circos.par("track.height" = 0.1)
circos.initializeWithIdeogram(plotType = NULL)

bed = generateRandomBed(nr = 100)
circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
  circos.genomicPoints(region, value, pch = 16, cex = 0.5, ...)
})

circos.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicPoints(region, value, pch = 16, cex = 0.5, ...)
  i = getI(...)
  cell.xlim = get.cell.meta.data("cell.xlim")
  circos.lines(cell.xlim, c(i, i), lty = 2, col = "#0000040")
})

bed1 = generateRandomBed(nr = 100)
```

```

bed2 = generateRandomBed(nr = 100)
bed_list = list(bed1, bed2)

# data frame list
circos.genomicTrackPlotRegion(bed_list, panel.fun = function(region, value, ...) {
  cex = (value[[1]] - min(value[[1]]))/(max(value[[1]]) - min(value[[1]]))
  i = getI(...)
  circos.genomicPoints(region, value, cex = cex, pch = 16, col = i, ...)
})

circos.genomicTrackPlotRegion(bed_list, stack = TRUE,
  panel.fun = function(region, value, ...) {
    cex = (value[[1]] - min(value[[1]]))/(max(value[[1]]) - min(value[[1]]))
    i = getI(...)
    circos.genomicPoints(region, value, cex = cex, pch = 16, col = i, ...)
    cell.xlim = get.cell.meta.data("cell.xlim")
    circos.lines(cell.xlim, c(i, i), lty = 2, col = "#00000040")
  })

bed = generateRandomBed(nr = 100, nc = 4)
circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
  cex = (value[[1]] - min(value[[1]]))/(max(value[[1]]) - min(value[[1]]))
  circos.genomicPoints(region, value, cex = 0.5, pch = 16, col = 1:4, ...)
})

circos.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  cex = (value[[1]] - min(value[[1]]))/(max(value[[1]]) - min(value[[1]]))
  i = getI(...)
  circos.genomicPoints(region, value, cex = cex, pch = 16, col = i, ...)
  cell.xlim = get.cell.meta.data("cell.xlim")
  circos.lines(cell.xlim, c(i, i), lty = 2, col = "#00000040")
})

circos.clear()

## End(Not run)

```

```
circos.genomicPosTransformLines
```

Add genomic position transformation lines between tracks

Description

Add genomic position transformation lines between tracks

Usage

```
circos.genomicPosTransformLines(data, track.height = 0.1, posTransform = NULL,
  horizontalLine = c("none", "top", "bottom", "both"), track.margin = c(0, 0),
  direction = c("inside", "outside"), col = "black", lwd = par("lwd"),
  lty = par("lty"), ...)
```

Arguments

<code>data</code>	A data frame containing genomic data
<code>track.height</code>	Height of the track
<code>posTransform</code>	Genomic position transformation function, see posTransform.default for an example.
<code>horizontalLine</code>	Whether to draw horizontal lines which indicate region width
<code>track.margin</code>	Margin of tracks
<code>direction</code>	Type of the transformation. <code>inside</code> means position transformed track are located inside and <code>outside</code> means position transformed track are located outside.
<code>col</code>	Color of lines, can be length of one or nrow of data
<code>lwd</code>	Width of lines
<code>lty</code>	Style of lines
<code>...</code>	pass to circos.trackPlotRegion

Details

There is one representative situation when such position transformation needs to be applied. For example, there are two sets of regions in a chromosome in which regions in one set are quite densely to each other and regions in other set are far from others. Heatmap or text is going to be drawn on the next track. If there is no position transformation, heatmap or text for those dense regions would be overlapped and hard to identify, also ugly to visualize. Thus, a way to transform original positions to new positions would help for the visualization.

References

Gu, Z. (2014) *circize* implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:

par(mfrow = c(2, 1))
### rect matrix
circos.par(cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram()

bed = generateRandomBed(nr = 100, nc = 4)

circos.genomicPosTransformLines(bed, posTransform = posTransform.default,
  horizontalLine = "top", track.height = 0.1)
```

```

f = colorRamp2(breaks = c(-1, 0, 1), colors = c("green", "black", "red"))
circos.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = f(value[[1]]),
    border = f(value[[1]]), posTransform = posTransform.default, ...)
}, bg.border = NA)

circos.clear()

circos.par(cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(plotType = NULL)

bed = generateRandomBed(nr = 20, nc = 4)

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1), panel.fun = function(region, value, ...) {
  circos.genomicText(region, value, y = 0, adj = c(1, 0.5),
    labels = "gene", facing = "reverse.clockwise",
    posTransform = posTransform.default)
}, bg.border = NA)

circos.genomicPosTransformLines(bed, posTransform = posTransform.default,
  horizontalLine = "bottom", direction = "outside", track.height = 0.1)

cytoband = read.cytoband()$df
circos.genomicTrackPlotRegion(cytoband, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = cytoband.col(value$V5), border = NA, ...)
}, track.height = 0.05)

circos.clear()

## End(Not run)

```

```
circos.genomicRainfall
```

Genomic rainfall plot

Description

Genomic rainfall plot

Usage

```

circos.genomicRainfall(data, mode = "min", ylim = NULL, col = "black",
  pch = par("pch"), cex = par("cex"), normalize_to_width = FALSE, ...)

```

Arguments

data	A bed-file-like data frame or a list of data frames
mode	how to calculate the distance of two neighbouring regions, pass to rainfallTransform
ylim	ylim for rainfall plot track. If <code>normalize_to_width</code> is FALSE, the value should correspond to $\log_{10}(\text{dist}+1)$, and if <code>normalize_to_width</code> is TRUE, the value should correspond to $\log_2(\text{rel_dist})$.
col	Color of points. It should be length of one. If data is a list, the length of col can also be the length of the list.
pch	Style of points
cex	Size of points
normalize_to_width	If it is TRUE, the value is the relative distance divided by the width of the region.
...	Pass to circos.trackPlotRegion

Details

This is high-level graphical function, which mean, it will create a new track.

Rainfall plot can be used to visualize distribution of regions. On the plot, y-axis corresponds to the distance to neighbour regions (log-based). So if there is a drop-down on the plot, it means there is a cluster of regions at that area.

On the plot, y-axis are log10-transformed.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:
load(system.file(package = "circlize", "extdata", "DMR.RData"))

# rainfall
circos.initializeWithIdeogram(plotType = c("axis", "labels"))

bed_list = list(DMR_hyper, DMR_hypo)
circos.genomicRainfall(bed_list, pch = 16, cex = 0.4, col = c("#FF000080", "#0000FF80"))

circos.genomicDensity(bed_list[[1]], col = c("#FF000080"), track.height = 0.1)
circos.genomicDensity(bed_list[[2]], col = c("#0000FF80"), track.height = 0.1)

circos.clear()

## End(Not run)
```

circos.genomicRect *Draw rectangle-like grid, specifically for genomic graphics*

Description

Draw rectangle-like grid, specifically for genomic graphics

Usage

```
circos.genomicRect(region, value = NULL,
  ytop = NULL, ybottom = NULL, ytop.column = NULL, ybottom.column = NULL,
  sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), posTransform = NULL,
  col = NA, border = "black", lty = par("lty"), ...)
```

Arguments

region	A data frame contains 2 column which correspond to start position and end position
value	A data frame contains values and other information
ytop	A vector or a single value indicating top position of rectangles
ybottom	A vector or a single value indicating bottom position of rectangles
ytop.column	If ytop is in value, the index of the column
ybottom.column	If ybottom is in value, the index of the column
sector.index	Pass to circos.rect
track.index	Pass to circos.rect
posTransform	Self-defined function to transform genomic positions, see posTransform.default for explanation
col	The length of col can be either one or number of rows of region. Pass to circos.rect
border	Settings are similar as col. Pass to circos.rect
lty	Settings are similar as col. Pass to circos.rect
...	Mysterious parameters

Details

The function is a low-level graphical function and usually is put in `panel.fun` when using [circos.genomicTrackPlotRegion](#)

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```

## Not run:

#####
### rect matrix
circos.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(plotType = NULL)

bed = generateRandomBed(nr = 100, nc = 4)
circos.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = sample(1:10, nrow(region), replace = TRUE),
    border = NA, ...)
  i = getI(...)
  cell.xlim = get.cell.meta.data("cell.xlim")
  #circos.lines(cell.xlim, c(i, i), lty = 2, col = "#00000040")
}, bg.border = NA)

circos.genomicPosTransformLines(bed, posTransform = posTransform.default,
  horizontalLine = "top")

circos.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = sample(1:10, nrow(region), replace = TRUE),
    border = NA, posTransform = posTransform.default, ...)
  i = getI(...)
  cell.xlim = get.cell.meta.data("cell.xlim")
  #circos.lines(cell.xlim, c(i, i), lty = 2, col = "#00000040")
}, bg.border = NA)

circos.genomicPosTransformLines(bed, posTransform = posTransform.default,
  direction = "outside", horizontalLine = "bottom")

circos.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = sample(1:10, nrow(region), replace = TRUE),
    border = NA, ...)
  i = getI(...)
  cell.xlim = get.cell.meta.data("cell.xlim")
  #circos.lines(cell.xlim, c(i, i), lty = 2, col = "#00000040")
}, bg.border = NA)

circos.clear()

#####
### rect from bed list
circos.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(plotType = NULL)

bed1 = generateRandomBed(nr = 100)
bed2 = generateRandomBed(nr = 100)
bed_list = list(bed1, bed2)
f = colorRamp2(breaks = c(-1, 0, 1), colors = c("green", "black", "red"))
circos.genomicTrackPlotRegion(bed_list, stack = TRUE,
  panel.fun = function(region, value, ...) {

```

```

    circos.genomicRect(region, value, col = f(value[[1]]),
                      border = NA, ...)
    i = getI(...)
    cell.xlim = get.cell.meta.data("cell.xlim")
    circos.lines(cell.xlim, c(i, i), lty = 2, col = "#000000")
  })

circos.genomicTrackPlotRegion(bed_list, ylim = c(0, 3),
  panel.fun = function(region, value, ...) {
    i = getI(...)
    circos.genomicRect(region, value, ytop = i+0.4, ybottom = i-0.4, col = f(value[[1]]),
                      border = NA, ...)

    cell.xlim = get.cell.meta.data("cell.xlim")
    circos.lines(cell.xlim, c(i, i), lty = 2, col = "#000000")
  })

circos.genomicTrackPlotRegion(bed1, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = "red", border = NA, ...)
})

circos.genomicTrackPlotRegion(bed_list, panel.fun = function(region, value, ...) {
  i = getI(...)
  circos.genomicRect(region, value, col = i, border = NA, ...)
})

circos.clear()

## End(Not run)

```

circos.genomicText *Draw text in a cell, specifically for genomic graphics*

Description

Draw text in a cell, specifically for genomic graphics

Usage

```

circos.genomicText(region, value = NULL, y = NULL, labels = NULL, labels.column = NULL,
  numeric.column = NULL, sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), posTransform = NULL,
  direction = NULL, facing = "inside", niceFacing = FALSE,
  adj = par("adj"), cex = 1, col = "black", font = par("font"), padding = 0,
  extend = 0, align_to = "region", ...)

```

Arguments

region	A data frame contains 2 column which correspond to start position and end position
value	A data frame contains values and other information
y	A vector or a single value indicating position of text.
labels	Labels of text corresponding to each genomic positions
labels.column	If labels are in value, index of column in value
numeric.column	Which column in value data frame should be taken as y-value. If it is not defined, only the first numeric columns in value will be taken.
sector.index	Pass to circos.rect
track.index	Pass to circos.rect
posTransform	Self-defined function to transform genomic positions, see posTransform.default for explanation
facing	Passing to circos.text . Settings are similar as col
niceFacing	Should the facing of text be adjusted to fit human eyes?
direction	Deprecated, use facing instead.
adj	Pass to circos.text . Settings are similar as col
cex	Pass to circos.text . Settings are similar as col
col	Pass to circos.text . The length of col can be either one or number of rows of region.
font	Pass to circos.text . Settings are similar as col
padding	pass to posTransform if it is set as posTransform.text
extend	pass to posTransform if it is set as posTransform.text
align_to	pass to posTransform if it is set as posTransform.text
...	Mysterious parameters

Details

The function is a low-level graphical function and usually is put in `panel.fun` when using [circos.genomicTrackPlotRegion](#)

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:
circos.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(plotType = NULL)

bed = generateRandomBed(nr = 20)

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1), panel.fun = function(region, value, ...) {
```

```
    circos.genomicText(region, value, y = 0.5, labels = "text", ...)
  })

  bed = cbind(bed, sample(letters, nrow(bed), replace = TRUE))
  circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
    circos.genomicText(region, value, labels.column = 2, ...)
  })

  circos.clear()

  ## End(Not run)
```

circos.genomicTrack *Create a track for genomic graphics*

Description

Create a track for genomic graphics

Usage

```
circos.genomicTrack(...)
```

Arguments

... pass to [circos.genomicTrackPlotRegion](#)

Details

shortcut function of [circos.genomicTrackPlotRegion](#).

Examples

```
# There is no example
NULL
```

```
circos.genomicTrackPlotRegion
```

Create a track for genomic graphics

Description

Create a track for genomic graphics

Usage

```
circos.genomicTrackPlotRegion(data = NULL, ylim = NULL, stack = FALSE,
  numeric.column = NULL, jitter = 0,
  panel.fun = function(region, value, ...) {NULL}, ...)
```

Arguments

<code>data</code>	A bed-file-like data frame or a list of data frames
<code>ylim</code>	If it is NULL, the value will be calculated from data. If <code>stack</code> is set to TRUE, this value is ignored.
<code>stack</code>	whether to plot in a "stack" mode.
<code>numeric.column</code>	Columns of numeric values in data that will be used for plotting. If data is a data frame list, <code>numeric.column</code> should be either length of one or length of data. If value of <code>numeric.column</code> is not set, its value will depend on the structure of data. If data is a data frame, the default value for <code>numeric.column</code> is all the numeric column starting from the fourth column. If data is a list of data frame, the default value for <code>numeric.column</code> is a vector which have the same length as data and the value in default <code>numeric.column</code> is the index of the first numeric column in corresponding data frame.
<code>jitter</code>	Numeric. Only works for adding points in <code>circos.genomicTrackPlotRegion</code> under stack mode
<code>panel.fun</code>	Self-defined function which will be applied on each sector. Please not it is different from that in <code>circos.trackPlotRegion</code> . In this function, there are two arguments (<code>region</code> and <code>value</code>) plus <code>...</code> . In them, <code>region</code> is a two-column data frame with start positions and end positions in current genomic category (e.g. chromosome). <code>value</code> is a data frame which is derived from data but excluding the first three columns. Rows in <code>value</code> correspond to rows in <code>region</code> . <code>...</code> is mandatory and is used to pass internal parameters to other functions. The definition of <code>value</code> will be different according to different input data (data frame or list of data frame) and different settings (stacked or not), please refer to 'details' section and vignettes to detailed explanation.
<code>...</code>	Pass to <code>circos.trackPlotRegion</code> .

Details

Similar as `circos.trackPlotRegion`, users can add customized graphics by `panel.fun`, but the behaviour of `panel.fun` will change depending on users' input data and `stack` setting.

When data is a single data frame, `region` in `panel.fun` is a data frame containing the second and third column in data in 'current' genomic category (e.g. current chromosome). `value` is also a data frame containing columns in data excluding the first three columns.

When data is a list containing data frames, `panel.fun` will be applied iteratively on each data frame, thus, `region` is extracted from the data frame which is in the current iteration. For example, if data contains two data frames, `panel.fun` will be applied with the first data frame in current chromosome and then applied with the second data frame in the same chromosome.

If `stack` is set to `TRUE`, `ylim` will be re-defined. in `stack` mode, the y-axis will be splitted into several part with equal height and graphics will be drawn on each 'horizontal' lines ($y = 1, 2, \dots$). In this case:

When data is a single data frame containing one or more numeric columns, each numeric column defined in `numeric.column` will be treated as a single unit. `ylim` is re-defined to `c(0.5, n+0.5)` in which `n` is number of numeric columns. `panel.fun` will be applied iteratively on each numeric column. In each iteration, in `panel.fun`, `region` is still the genomic regions in current genomic category, but `value` contains current numeric column plus all non-numeric columns. Under `stack` mode, in `panel.fun`, all low-level genomic graphical functions will draw on the 'horizontal line' $y = i$ in which `i` is the index of current numeric column and the value of `i` can be obtained by `getI`.

When data is a list containing data frames, each data frame will be treated as a single unit. The situation is quite similar as described in previous paragraph. `ylim` is re-defined to `c(0.5, n+0.5)` in which `n` is number of data frames. `panel.fun` will be applied iteratively on each data frame. In each iteration, in `panel.fun`, `region` is still the genomic regions in current genomic category, and `value` contains columns in current data frame excluding the first three columns. Under `stack` mode, in `panel.fun`, all low-level genomic graphical functions will draw on the 'horizontal line' $y = i$ in which `i` is the index of current data frame.

Being different from `panel.fun` in `circos.trackPlotRegion`, there should be an additional argument `...` in `panel.fun`. This additional argument is used to pass hidden values to low-level graphical functions. So if you are using functions like `circos.genomicPoints`, you should also add `...` as an additional argument into `circos.genomicPoints`.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
# There is no example
NULL
```

`circos.info`*Get information of the circular plot*

Description

Get information of the circular plot

Usage

```
circos.info(sector.index = NULL, track.index = NULL, plot = FALSE)
```

Arguments

<code>sector.index</code>	Which sectors you want to look at? It can be a vector.
<code>track.index</code>	Which tracks you want to look at? It can be a vector.
<code>plot</code>	Whether to add information on the plot

Details

It tells you the basic parameters for sectors/tracks/cells. If both `sector.index` and `track.index` are set to `NULL`, the function would print index for all sectors and all tracks. If `sector.index` and/or `track.index` are set, the function would print `xlim`, `ylim`, `cell.xlim`, `cell.ylim`, `xplot`, `yplot`, `track.margin` and `cell.padding` for every cell in specified sectors and tracks. Also, the function will print index of your current sector and current track.

If `plot` is set to `TRUE`, the function will plot the index of the sector and the track for each cell on the figure.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
factors = letters[1:4]
circos.initialize(factors, xlim = c(0, 1))
circos.trackPlotRegion(ylim = c(0, 1))
circos.trackPlotRegion(ylim = c(0, 1))
circos.info(sector.index = "a", track.index = 1)
circos.info(sector.index = "a", track.index = 1:2)
circos.info(sector.index = c("a", "b"), track.index = 1)
circos.info(sector.index = "a")
circos.info(track.index = 1)
circos.info()
circos.info(plot = TRUE)
circos.clear()
```

circos.initialize *Initialize the circular layout*

Description

Initialize the circular layout

Usage

```
circos.initialize(factors, x = NULL, xlim = NULL, sector.width = NULL)
```

Arguments

factors	A factor variable or a character vector which represent data categories
x	Data on x-axes, a vector
xlim	Ranges for values on x-axes, see "details" section for explanation of the format
sector.width	Width for each sector. The length of the vector should be either 1 which means all sectors have same width or as same as the number of sectors. Values for the vector are relative, and they will be scaled by dividing their summation. By default, it is NULL which means the width of sectors correspond to the data range in sectors.

Details

The function allocates the sectors according to the values on x-axis. The number of sectors are determined by the `factors` and the order of sectors are determined by the levels of factors. In this function, the start and end position for each sector on the circle (measured by degree) are calculated according to the values on x-axis or by `xlim`.

If `x` is set, the length of `x` must be equal to the length of `factors`. Then the data range for each sector are calculated from `x` by splitting `factors`.

If `xlim` is set, it should be a vector containing two numbers or a matrix with 2 columns. If `xlim` is a 2-element vector, it means all sector share the same `xlim`. If `xlim` is a 2-column matrix, the number of rows should be equal to the number of categories identified by `factors`, then each row of `xlim` corresponds to the data range for each sector and the order of rows is corresponding to the order of levels of `factors`. If `xlim` is a matrix for which row names cover all sector names, `xlim` is automatically adjusted.

Normally, width of sectors will be calculated internally according to the data range in sectors. But you can still set the width manually. However, it is not always a good idea to change the default sector width since the width can reflect the range of data in sectors. However, in some cases, it is useful to manually set the width such as you want to zoom some part of the sectors.

The function finally calls `plot` with enforcing aspect ratio to be 1 and be ready for adding graphics.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

See Also

http://jokergoo.github.io/circlize_book/book/circular-layout.html

Examples

```
circos.initialize(factors = sample(letters[1:4], 20, replace = TRUE), xlim = c(0, 1))
circos.info()
circos.clear()
```

```
circos.initialize(factors = sample(letters[1:4], 20, replace = TRUE), xlim = cbind(1:4, 1:4*2))
circos.info()
circos.clear()
```

```
circos.initialize(factors = sample(letters[1:4], 20, replace = TRUE), x = rnorm(20))
circos.info()
circos.clear()
```

`circos.initializeWithIdeogram`

Initialize the circular layout with an ideogram

Description

Initialize the circular layout with an ideogram

Usage

```
circos.initializeWithIdeogram(cytoband = system.file(package = "circlize",
  "extdata", "cytoBand.txt"), species = NULL, sort.chr = TRUE,
  chromosome.index = NULL, major.by = NULL,
  plotType = c("ideogram", "axis", "labels"),
  track.height = NULL, ideogram.height = convert_height(2, "mm"),
  ...)
```

Arguments

- `cytoband` A path of the cytoband file or a data frame that already contains cytoband data. By default it is cytoband for hg19. Pass to [read.cytoband](#).
- `species` Abbreviations of species. e.g. hg19 for human, mm10 for mouse. If this value is specified, the function will download cytoBand.txt.gz from UCSC website automatically. If there is no cytoband for user's species, it will keep on trying to download chromInfo file. Pass to [read.cytoband](#) or [read.chromInfo](#).
- `chromosome.index` subset of chromosomes, also used to reorder chromosomes.
- `sort.chr` Whether chromosome names should be sorted (first sort by numbers then by letters). If `chromosome.index` is set, this argumetn is enforced to FALSE

<code>major.by</code>	Increment of major ticks. Pass to <code>circos.genomicInitialize</code> .
<code>plotType</code>	Which tracks should be drawn. <code>ideogram</code> for ideogram rectangle, <code>axis</code> for genomic axis and labels for chromosome names. If there is no ideogram for specified species, <code>ideogram</code> will be enforced to be excluded. If it is set to <code>NULL</code> , the function just initialize the plot but draw nothing.
<code>track.height</code>	Height of the track which contains "axis" and "labels".
<code>ideogram.height</code>	Height of the ideogram track
<code>...</code>	Pass to <code>circos.genomicInitialize</code> .

Details

The function will initialize the circular plot in which each sector corresponds to a chromosome. You can control the order of chromosomes by `chromosome.index` or by `sort.chr`, or by setting a special format of `cytoband` (please refer to [read.cytoband](#) to find out how to control a proper `cytoband`).

The function finally pass data to `circos.genomicInitialize` to initialize the circular plot.

The style of ideogram is almost fixed, but you can customize it with your self-sefined code. Refer to vignette for demonstration.

References

Gu, Z. (2014) `circlize` implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:
circos.initializeWithIdeogram()

cytoband.file = system.file(package = "circlize"),
  "extdata", "cytoBand.txt")
circos.initializeWithIdeogram(cytoband.file)

cytoband.df = read.table(cytoband.file, colClasses = c("character", "numeric",
  "numeric", "character", "character"), sep = "\t")
circos.initializeWithIdeogram(cytoband.df)

circos.initializeWithIdeogram(species = "hg18")

circos.initializeWithIdeogram(species = "mm10")

circos.initializeWithIdeogram(chromosome.index = c("chr1", "chr2"))

cytoband = read.table(cytoband.file, colClasses = c("character", "numeric",
  "numeric", "character", "character"), sep = "\t")
circos.initializeWithIdeogram(cytoband, sort.chr = FALSE)

cytoband[[1]] = factor(cytoband[[1]], levels = paste0("chr", c(22:1, "X", "Y")))
circos.initializeWithIdeogram(cytoband, sort.chr = FALSE)
```

```

cytoband = read.table(cytoband.file, colClasses = c("character", "numeric",
  "numeric", "character", "character"), sep = "\t")
circos.initializeWithIdeogram(cytoband, sort.chr = TRUE)

circos.initializeWithIdeogram(plotType = c("axis", "labels"))

circos.initializeWithIdeogram(plotType = NULL)

circos.par("start.degree" = 90)
circos.initializeWithIdeogram()
circos.clear()

circos.par("gap.degree" = rep(c(2, 4), 12))
circos.initializeWithIdeogram()
circos.clear()

## End(Not run)

```

circos.lines	<i>Add lines to the plotting region</i>
--------------	---

Description

Add lines to the plotting region

Usage

```

circos.lines(x, y, sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"),
  col = ifelse(area, "grey", par("col")), lwd = par("lwd"), lty = par("lty"),
  type = "l", straight = FALSE, area = FALSE, area.baseline = NULL,
  border = "black", baseline = "bottom", pt.col = par("col"), cex = par("cex"),
  pch = par("pch"))

```

Arguments

x	Data points on x-axis, measured in "current" data coordinate
y	Data points on y-axis, measured in "current" data coordinate
sector.index	Index for the sector
track.index	Index for the track
col	Line color
lwd	line width
lty	line style
type	line type, similar as type argument in lines , but only in c("l", "o", "h", "s")

straight	whether draw straight lines between points.
area	whether to fill the area below the lines. If it is set to TRUE, col controls the filled color in the area and border controls color of the line.
area.baseline	deprecated, use baseline instead.
baseline	the base line to draw areas. By default it is the minimal of y-range (bottom). It can be a string or a number. If a string, it should be one of bottom and top. This argument also works if type is set to h.
border	color for border of the area
pt.col	if type is "o", point color
cex	if type is "o", point size
pch	if type is "o", point type

Details

Normally, straight lines in the Cartesian coordinate have to be transformed into curves in the circular layout. But if you do not want to do such transformation you can use this function just drawing straight lines between points by setting straight to TRUE.

Drawing areas below lines can help to identify the direction of y-axis in cells (since it is a circle). This can be done by specifying area to TURE.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. Bioinformatics.

Examples

```
factors = letters[1:9]
circos.par(points.overflow.warning = FALSE)
circos.initialize(factors = factors, xlim = c(0, 10))
circos.trackPlotRegion(factors = factors, ylim = c(0, 10), track.height = 0.5)

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "a")
circos.text(5, 9, "type = 'l'", sector.index = "a", facing = "outside")

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "b", type = "o")
circos.text(5, 9, "type = 'o'", sector.index = "b", facing = "outside")

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "c", type = "h")
circos.text(5, 9, "type = 'h'", sector.index = "c", facing = "outside")

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "d", type = "h", baseline = 5)
circos.text(5, 9, "type = 'h', baseline = 5", sector.index = "d", facing = "outside")

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "e", type = "s")
circos.text(5, 9, "type = 's'", sector.index = "e", facing = "outside")

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "f", area = TRUE)
circos.text(5, 9, "type = 'l', area = TRUE", sector.index = "f")
```

```

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "g", type = "o", area = TRUE)
circos.text(5, 9, "type = 'o', area = TRUE", sector.index = "g")

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "h", type = "s", area = TRUE)
circos.text(5, 9, "type = 's', area = TRUE", sector.index = "h")

circos.lines(sort(runif(10)*10), runif(10)*8, sector.index = "i", area = TRUE, baseline = "top")
circos.text(5, 9, "type = 'l', area = TRUE\nbaseline = 'top'", sector.index = "i")

circos.clear()

```

circos.link

Draw links between points or/and intervals

Description

Draw links between points or/and intervals

Usage

```

circos.link(sector.index1, point1, sector.index2, point2,
  rou = get_most_inside_radius(),
  rou1 = rou, rou2 = rou, h = NULL, h.ratio = 0.5, w = 1, h2 = h, w2 = w,
  col = "black", lwd = par("lwd"), lty = par("lty"), border = col,
  directional = 0, arr.length = ifelse(arr.type == "big.arrow", 0.02, 0.4),
  arr.width = arr.length/2, arr.type = "triangle", arr.lty = lty,
  arr.lwd = lwd, arr.col = col)

```

Arguments

sector.index1	Index for the first sector where one link end locates
point1	A single value or a numeric vector of length 2. If it is a 2-elements vector, then the link would be a belt/ribbon.
sector.index2	Index for the other sector where the other link end locates
point2	A single value or a numeric vector of length 2. If it is a 2-elements vector, then the link would be a belt/ribbon.
rou	The position of the the link ends (if rou1 and rou2 are not set). It is the percentage of the radius of the unit circle. By default its value is the position of bottom margin of the most inner track.
rou1	The position of end 1 of the link.
rou2	The position of end 2 of the link.
h	Height of the link, measured as percent to the radius to the unit circle. By default it is automatically inferred.
h.ratio	systematically change the link height. The value is between 0 and 1.

w	Since the link is a Bezier curve, it controls the shape of Bezier curve.
h2	Height of the bottom edge of the link if it is a ribbon.
w2	Shape of the bottom edge of the link if it is a ribbon.
col	Color of the link. If the link is a ribbon, then it is the filled color for the ribbon.
lwd	Line (or border) width
lty	Line (or border) style
border	If the link is a ribbon, then it is the color for the ribbon border.
directional	0 for no direction, 1 for direction from point1 to point2, -1 for direction from point2 to point1. 2 for two directional. The direction is important when arrow heads are added.
arr.width	Width of the arrows, pass to Arrowhead .
arr.type	Type of the arrows, pass to Arrowhead . Default value is triangle. There is an additional option <code>big.arrow</code> .
arr.length	Length of the arrows, measured in 'cm', pass to Arrowhead . If <code>arr.type</code> is set to <code>big.arrow</code> , the value is percent to the radius of the unit circle.
arr.col	Color of the arrows, pass to Arrowhead .
arr.lwd	Line width of arrows, pass to Arrowhead .
arr.lty	Line type of arrows, pass to Arrowhead .

Details

Links are implemented as quadratic Bezier curves (https://en.wikipedia.org/wiki/Bezier_curve#Rational_Bezier_curves).

Drawing links does not create any track. So you can think it is independent of the tracks.

By default you only need to set `sector.index1`, `point1`, `sector.index2` and `point2`. The links would look nice.

Please refer to the vignette for detailed explanation.

References

Gu, Z. (2014) *circize* implements and enhances circular visualization in R. Bioinformatics.

See Also

http://jokergoo.github.io/circize_book/book/graphics.html#links

Examples

```
factors = letters[1:8]
circos.par(points.overflow.warning = FALSE)
circos.initialize(factors = factors, xlim = c(0, 10))
circos.track(factors = factors, ylim = c(0, 1), bg.col = "grey",
             bg.border = NA, track.height = 0.05)
circos.link("a", 5, "c", 5, border = 1)
circos.link("b", 5, "d", c(4, 6), border = 1)
```

```

circos.link("a", c(2, 3), "f", c(4, 6), border = 1)
circos.link("e", c(2, 3), "g", 5, border = 1)
circos.clear()

circos.par(points.overflow.warning = FALSE)
circos.initialize(factors = factors, xlim = c(0, 10))
circos.track(factors = factors, ylim = c(0, 1), bg.col = "grey",
  bg.border = NA, track.height = 0.05)
circos.link("a", 5, "b", 5, directional = 1, arr.length = 0.2)
circos.link("c", c(3, 7), "d", c(3, 7), directional = 1,
  arr.col = "white", arr.length = 0.2)
circos.link("e", c(4, 6), "f", c(4, 6), directional = 1,
  arr.type = "big.arrow", arr.length = 0.04)
circos.clear()

```

circos.nested *Nested zooming with two circular plots*

Description

Nested zooming with two circular plots

Usage

```

circos.nested(f1, f2, correspondance, connection_height = convert_height(5, "mm"),
  connection_col = NA, connection_border = "black",
  connection_lty = par("lty"), connection_lwd = par("lwd"),
  adjust_start_degree = TRUE)

```

Arguments

f1	a self-defined function for making the first circular plot. The function should have no argument.
f2	a self-defined function for making the second circular plot. The function should have no argument.
correspondance	a six-column data frame which contains correspondance between the coordinates in two circular plots
connection_height	the height of the connection track, measured as the percent to the radius of the unit circle. The value can be specified by uh or convert_height with absolute units.
connection_col	filled color of the connection track. The value can be a vector with same length as number of rows of correspondance
connection_border	border color of the connection track.
connection_lty	line style of the connection track borders

connection_lwd line width of the connection track borders
 adjust_start_degree

If `circos.par(start.degree = ...)` is not set in `f2()`, the start degree for the second circular plot will be adjusted to make the distance of sectors between the two plots to the minimal.

Details

The function visualizes zoomings by combining two circular plots into one page where one is the normal circular plot and the other one only contains regions that need to be zoomed. This function automatically arranges the two plots to make it easy to correspond between the original and the zoomed sectors.

Since the function needs to know the information of the two circular plots, please do not call `circos.clear` in either `f1()` or `f2()`. It will be called internally in `circos.nested`.

If `adjust_start_degree` is set to `TRUE`, `start.degree` should not be set in `f2()`. Also `canvas.xlim` and `canvas.ylim` are reset in `f2()`, they should not be set in `f2()` either.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

http://jokergoo.github.io/circlize_book/book/nested-zooming.html

Examples

```
## Not run:
#### simulate data ####
set.seed(123)
df = data.frame(cate = sample(letters[1:8], 400, replace = TRUE),
               x = runif(400),
               y = runif(400),
               stringsAsFactors = FALSE)
df = df[order(df[[1]], df[[2]]), ]
rownames(df) = NULL
df$interval_x = as.character(cut(df$x, c(0, 0.2, 0.4, 0.6, 0.8, 1.0)))
df$name = paste(df$cate, df$interval_x, sep = ":")
df$start = as.numeric(gsub("^\\((\\d(\\.\\d)?)\\.?(\\d(\\.\\d)?)$)", "\\1", df$interval_x))
df$end = as.numeric(gsub("^\\((\\d(\\.\\d)?)\\.?(\\d(\\.\\d)?)$)", "\\3", df$interval_x))
nm = sample(unique(df$name), 20)
df2 = df[df$name %in% nm, ]

correspondance = unique(df2[, c("cate", "start", "end", "name", "start", "end")])
zoom_sector = unique(df2[, c("name", "start", "end", "cate")])
zoom_data = df2[, c("name", "x", "y")]

data = df[, 1:3]
sector = data.frame(cate = letters[1:8], start = 0, end = 1, stringsAsFactors = FALSE)

sector_col = structure(rand_color(8, transparency = 0.5), names = letters[1:8])
```



```

#### define two circular plots ####
f1 = function() {
  circos.par(gap.degree = 10)
  circos.initialize(sector[, 1], xlim = sector[, 2:3])
  circos.track(data[[1]], x = data[[2]], y = data[[3]], ylim = c(0, 1),
    panel.fun = function(x, y) {
      l = correspondance[[1]] == CELL_META$sector.index
      if(sum(l)) {
        for(i in which(l)) {
          circos.rect(correspondance[i, 2], CELL_META$cell.ylim[1],
            correspondance[i, 3], CELL_META$cell.ylim[2],
            col = sector_col[CELL_META$sector.index],
            border = sector_col[CELL_META$sector.index])
        }
      }
      circos.points(x, y, pch = 16, cex = 0.5)
      circos.text(CELL_META$xcenter, CELL_META$ylim[2] + uy(2, "mm"),
        CELL_META$sector.index, niceFacing = TRUE, adj = c(0.5, 0))
    })
}

f2 = function() {
  circos.par(gap.degree = 2, cell.padding = c(0, 0, 0, 0))
  circos.initialize(zoom_sector[[1]], xlim = as.matrix(zoom_sector[, 2:3]))
  circos.track(zoom_data[[1]], x = zoom_data[[2]], y = zoom_data[[3]],
    panel.fun = function(x, y) {
      circos.points(x, y, pch = 16, cex = 0.5)
    }, bg.col = sector_col[zoom_sector$cate],
    track.margin = c(0, 0))
}
circos.nested(f1, f2, correspondance, connection_col = sector_col[correspondance[[1]])

## End(Not run)

```

circos.par

Parameters for the circular layout

Description

Parameters for the circular layout

Usage

```
circos.par(..., RESET = FALSE, READ_ONLY = NULL, LOCAL = FALSE, ADD = FALSE)
```

Arguments

...	Arguments for the parameters, see "details" section
RESET	reset to default values
READ.ONLY	please ignore
LOCAL	please ignore
ADD	please ignore

Details

Global parameters for the circular layout. Currently supported parameters are:

`start.degree` The starting degree from which the circle begins to draw. Note this degree is measured in the standard polar coordinate which means it is always reverse-clockwise.

`gap.degree` Gap between two neighbour sectors. It can be a single value or a vector. If it is a vector, the first value corresponds to the gap after the first sector.

`gap.after` identical to `gap.degree` option, but a more understandable name. Modifying this option will also affect `gap.degree`.

`track.margin` Like margin in Cascading Style Sheets (CSS), it is the blank area out of the plotting region, also outside of the borders. Since left and right margin are controlled by `gap.degree`, only bottom and top margin need to be set. And all cells in a same track share the same margins, and that's why this parameter is called `track.margin`. The value for the `track.margin` is the percentage according to the radius of the unit circle. `convert_height` can be used to set to an absolute unit (e.g cm/inche).

`unit.circle.segments` Since curves are simulated by a series of straight lines, this parameter controls the amount of segments to represent a curve. The minimal length of the line segmentation is the length of the unit circle (2π) divided by `unit.circoe.segments`. More segments means better approximation for the curves while larger size if you generate figures as PDF format.

`cell.padding` Padding of the cell. Like padding in Cascading Style Sheets (CSS), it is the blank area around the plotting regions, but within the borders. The parameter has four values, which controls the bottom, left, top and right paddings respectively. The first and the third padding values are the percentages according to the radius of the unit circle and the second and fourth values are degrees. Similar as `track.margin` option, the first and the third value can be set by `convert_height` to an absolute unit.

`track.height` The default height of tracks. It is the percentage according to the radius of the unit circle. The height includes the top and bottom cell paddings but not the margins. `convert_height` can be used to set the height to an absolute unit.

`points.overflow.warning` Since each cell is in fact not a real plotting region but only an ordinary rectangle, it does not eliminate points that are plotted out of the region. So if some points are out of the plotting region, `circlize` would continue drawing the points and printing warnings. In some cases, draw something out of the plotting region is useful, such as draw some legend or text. Set this value to FALSE to turn off the warnings.

`canvas.xlim` The coordinate for the canvas. Because `circlize` draws everything (or almost everything) inside the unit circle, the default `canvas.xlim` and `canvas.ylim` for the canvas would be all $c(-1, 1)$. However, you can set it to a more broad interval if you want to draw

other things out of the circle. By choosing proper `canvas.xlim` and `canvas.ylim`, you can draw part of the circle. E.g. setting `canvas.xlim` to `c(0, 1)` and `canvas.ylim` to `c(0, 1)` would only draw circle in the region of $(0, \pi/2)$.

`canvas.ylim` The coordinate for the canvas. By default it is `c(-1, 1)`

`clock.wise` The direction for adding sectors. Default is `TRUE`.

Similar as `par`, you can get the parameter values by specifying the names of parameters and you can set the parameter values by specifying a named list which contains the new values.

`gap.degree`, `start.degree`, `canvas.xlim`, `canvas.ylim` and `clock.wise` only be set before the initialization of the circular layout (i.e. before calling `circos.initialize`) because these values will not be changed after adding sectors on the circle. The left and right padding for `cell.padding` will also be ignored after the initialization because all cells in a sector would share the same left and right paddings.

References

Gu, Z. (2014) `circize` implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
# There is no example
NULL
```

<code>circos.points</code>	<i>Add points to a plotting region</i>
----------------------------	--

Description

Add points to a plotting region

Usage

```
circos.points(x, y, sector.index = get.cell.meta.data("sector.index"),
             track.index = get.cell.meta.data("track.index"),
             pch = par("pch"), col = par("col"), cex = par("cex"), bg = par("bg"))
```

Arguments

<code>x</code>	Data points on x-axis, measured in "current" data coordinate
<code>y</code>	Data points on y-axis, measured in "current" data coordinate
<code>sector.index</code>	Index for the sector
<code>track.index</code>	Index for the track
<code>pch</code>	Point type
<code>col</code>	Point color
<code>cex</code>	Point size
<code>bg</code>	background of points

Details

This function can only add points in one specified cell. Pretending a low-level plotting function, it can only be applied in plotting region which has been created.

You can think the function similar as the normal `points` function, just adding points in the circular plotting region. The position of cell is identified by `sector.index` and `track.index`, if they are not specified, they are in 'current' sector and 'current' track.

Data points out of the plotting region will also be added, but with warning messages.

Other graphics parameters which are available in the function are `pch`, `col` and `cex` which have same meaning as those in the `par`.

It is recommended to use `circos.points` inside `panel.fun` in `circos.trackPlotRegion` so that it draws points directly on "curent" cell.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
circos.initialize(letters[1:8], xlim = c(0, 1))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  circos.points(runif(10), runif(10))
})
circos.points(runif(10), runif(10), sector.index = "c", pch = 16, col = "red")
circos.clear()
```

circos.polygon

Draw polygon

Description

Draw polygon

Usage

```
circos.polygon(x, y, sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), ...)
```

Arguments

<code>x</code>	Data points on x-axis
<code>y</code>	Data points on y-axis
<code>sector.index</code>	Index for the sector
<code>track.index</code>	Index for the track
<code>...</code>	pass to <code>polygon</code>

Details

similar as [polygon](#).

Note: start point should overlap with the end point,

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
set.seed(123)
factors = letters[1:4]
circos.initialize(factors, xlim = c(0, 1))
circos.trackPlotRegion(ylim = c(-3, 3), track.height = 0.4, panel.fun = function(x, y) {
  x1 = runif(20)
  y1 = x1 + rnorm(20)
  or = order(x1)
  x1 = x1[or]
  y1 = y1[or]
  loess.fit = loess(y1 ~ x1)
  loess.predict = predict(loess.fit, x1, se = TRUE)
  d1 = c(x1, rev(x1))
  d2 = c(loess.predict$fit + loess.predict$se.fit,
        rev(loess.predict$fit - loess.predict$se.fit))
  circos.polygon(d1, d2, col = "#CCCCCC", border = NA)
  circos.points(x1, y1, cex = 0.5)
  circos.lines(x1, loess.predict$fit)
})
circos.clear()
```

circos.raster

Add raster images

Description

Add raster images

Usage

```
circos.raster(image, x, y, width, height,
  facing = c("inside", "outside", "reverse.clockwise", "clockwise",
  "downward", "bending.inside", "bending.outside"),
  niceFacing = FALSE, sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"),
  scaling = 1)
```

Arguments

image	a raster object, or an object that can be converted by as.raster
x	position of the center of the raster image, measured in the data coordinate in the cell
y	position of the center of the raster image, measured in the data coordinate in the cell
width	width of the raster image. When facing is one of "inside", "outside", "clockwise" and "reverse.clockwise", the image should have absolute size where the value of width should be specified like 20mm, 1cm or 0.5inche. When facing is one of bending.inside and bending.outside, the value of width is measured in the data coordinate in the cell.
height	height of the raster image. Same format as width. If the value of height is omit, default height is calculated by taking the aspect ratio of the original image. But when facing is one of bending.inside and bending.outside, height is mandatory to set.
facing	facing of the raster image
niceFacing	facing of text. Please refer to vignette for different settings
sector.index	index for the sector
track.index	index for the track
scaling	scaling factor to resize the raster image.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(png)
image = system.file("extdata", "Rlogo.png", package = "circlize")
image = as.raster(readPNG(image))
circos.initialize(letters[1:8], xlim = c(0, 1))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  circos.raster(image, CELL_META$xcenter, CELL_META$ycenter, width = "2cm",
    facing = "inside", niceFacing = TRUE)
})
circos.clear()

## Not run:
# NOTE: following takes quite a long time to run
load(system.file("extdata", "doodle.RData", package = "circlize"))
circos.par("cell.padding" = c(0, 0, 0, 0))
circos.initialize(letters[1:16], xlim = c(0, 1))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  img = img_list[[CELL_META$sector.numeric.index]]
  circos.raster(img, CELL_META$xcenter, CELL_META$ycenter, width = 1,
    height = 1, facing = "bending.inside")
}, track.height = 0.25, bg.border = NA)
```

```

circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  img = img_list[[CELL_META$sector.numeric.index + 16]]
  circos.raster(img, CELL_META$xcenter, CELL_META$ycenter, width = 1,
    height = 1, facing = "bending.inside")
}, track.height = 0.25, bg.border = NA)
circos.clear()

## End(Not run)

```

circos.rect

Draw rectangle-like grid

Description

Draw rectangle-like grid

Usage

```

circos.rect(xleft, ybottom, xright, ytop,
  sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), ...)

```

Arguments

xleft	x for the left bottom points
ybottom	y for the left bottom points
xright	x for the right top points
ytop	y for the right top points
sector.index	Index for the sector
track.index	Index for the track
...	pass to polygon

Details

The name for this function is [circos.rect](#) because if you imagine the plotting region as Cartesian coordinate, then it is rectangle. in the polar coordinate, the up and bottom edge become two arcs.

This function can be vectorized.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```

# There is no example
NULL

```

circos.segments *Draw segments through pairwise of points*

Description

Draw segments through pairwise of points

Usage

```
circos.segments(x0, y0, x1, y1, sector.index = get.cell.meta.data("sector.index"),
               track.index = get.cell.meta.data("track.index"), straight = FALSE,
               col = par("col"), lwd = par("lwd"), lty = par("lty"), ...)
```

Arguments

x0	x coordinates for starting points
y0	y coordinates for ending points
x1	x coordinates for starting points
y1	y coordinates for ending points
sector.index	Index for the sector
track.index	Index for the track
straight	whether the segment is a straight line
col	color of the segments
lwd	line width of the segments
lty	line type of the segments
...	pass to lines

Examples

```
# There is no example
NULL
```

circos.text *Draw text in a cell*

Description

Draw text in a cell

Usage

```
circos.text(x, y, labels, sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), direction = NULL,
  facing = c("inside", "outside", "reverse.clockwise", "clockwise",
    "downward", "bending", "bending.inside", "bending.outside"), niceFacing = FALSE,
  adj = par("adj"), cex = 1, col = par("col"), font = par("font"), ...)
```

Arguments

x	Data points on x-axis
y	Data points on y-axis
labels	Labels for each points
sector.index	Index for the sector
track.index	Index for the track
direction	deprecated, use facing instead.
facing	Facing of text. Please refer to vignette for different settings
niceFacing	Should the facing of text be adjusted to fit human eyes?
adj	offset for text. By default the text position adjustment is either horizontal or vertical in the canvas coordinate system. The "circular horizontal" offset can be set as a value in degree unit and the value should be wrapped by degree .
...	Pass to text
cex	Font size
col	Font color
font	Font style

Details

The function is similar to [text](#). All you need to note is the facing settings.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

See Also

http://jokergoo.github.io/circlize_book/book/graphics.html#text

Examples

```
factors = letters[1:4]
circos.par(points.overflow.warning = FALSE)
circos.initialize(factors = factors, xlim = c(0, 10))
circos.trackPlotRegion(factors = factors, ylim = c(0, 10),
  track.height = 0.5, panel.fun = function(x, y) {
    circos.text(3, 1, "inside", facing = "inside", cex = 0.8)
    circos.text(7, 1, "outside", facing = "outside", cex = 0.8)
```

```
circos.text(0, 5, "reverse.clockwise", facing = "reverse.clockwise",
  adj = c(0.5, 0), cex = 0.8)
circos.text(10, 5, "clockwise", facing = "clockwise", adj = c(0.5, 0),
  cex = 0.8)
circos.text(5, 5, "downward", facing = "downward", cex = 0.8)
circos.text(3, 9, "====bending.inside====", facing = "bending.inside",
  cex = 0.8)
circos.text(7, 9, "====bending.outside====", facing = "bending.outside",
  cex = 0.8)
})
circos.clear()
```

circos.track

Create plotting regions for a whole track

Description

Create plotting regions for a whole track

Usage

```
circos.track(...)
```

Arguments

... pass to [circos.trackPlotRegion](#)

Details

Shortcut function of [circos.trackPlotRegion](#).

Examples

```
# There is no example
NULL
```

circos.trackHist *Draw histogram in cells among a whole track*

Description

Draw histogram in cells among a whole track

Usage

```
circos.trackHist(factors, x, track.height = circos.par("track.height"),
  track.index = NULL, force.ylim = TRUE, col = ifelse(draw.density, "black", NA),
  border = "black", lty = par("lty"), lwd = par("lwd"),
  bg.col = NA, bg.border = "black", bg.lty = par("lty"), bg.lwd = par("lwd"),
  breaks = "Sturges", include.lowest = TRUE, right = TRUE, draw.density = FALSE,
  bin.size = NULL, area = FALSE)
```

Arguments

factors	Factors which represent the categories of data
x	Data on the x-axis
track.index	Index for the track which is going to be updated. Setting it to NULL means creating the plotting regions in the next newest track.
track.height	Height of the track. It is the percentage to the radius of the unit circle. If to update a track, this argument is disabled.
force.ylim	Whether to force all cells in the track to share the same ylim. Btw, ylim is calculated automatically.
col	Filled color for histogram
border	Border color for histogram
lty	Line style for histogram
lwd	Line width for histogram
bg.col	Background color for the plotting regions
bg.border	Color for the border of the plotting regions
bg.lty	Line style for the border of the plotting regions
bg.lwd	Line width for the border of the plotting regions
breaks	see hist
include.lowest	see hist
right	see hist
draw.density	whether draw density lines instead of histogram bars.
area	whether to fill the area below the density lines. If it is set to TRUE, col controls the filled color in the area and border controls color of the line.
bin.size	size of the bins of the histogram

Details

It draw histogram in cells among a whole track. It is also an example to show how to add self-defined high-level graphics by this package.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:
x = rnorm(1600)
factors = sample(letters[1:16], 1600, replace = TRUE)
circos.initialize(factors = factors, x = x)
circos.trackHist(factors = factors, x = x, col = "#999999",
  border = "#999999")
circos.trackHist(factors = factors, x = x, bin.size = 0.1,
  col = "#999999", border = "#999999")
circos.trackHist(factors = factors, x = x, draw.density = TRUE,
  col = "#999999", border = "#999999")
circos.clear()

## End(Not run)
```

circos.trackLines *Add lines to the plotting regions in a same track*

Description

Add lines to the plotting regions in a same track

Usage

```
circos.trackLines(factors, x, y, track.index = get.cell.meta.data("track.index"),
  col = par("col"), lwd = par("lwd"), lty = par("lty"), type = "l", straight = FALSE,
  area = FALSE, area.baseline = NULL, border = "black", baseline = "bottom",
  pt.col = par("col"), cex = par("cex"), pch = par("pch"))
```

Arguments

factors	A factor or a character vector which represents the categories of data
x	Data points on x-axis
y	Data points on y-axis
track.index	Index for the track
col	Line color
lwd	line width

lty	line style
type	line type, similar as type argument in lines , but only in c("l", "o", "h", "s")
straight	whether draw straight lines between points
area	whether to fill the area below the lines. If it is set to TRUE, col controls the filled color in the area and border controls the color of the line.
area.baseline	deprecated, use baseline instead.
baseline	the base line to draw area, pass to circos.lines .
border	color for border of the area
pt.col	if type is "o", points color
cex	if type is "o", points size
pch	if type is "o", points type

Details

The function adds lines in multiple cells by first splitting data into several parts in which each part corresponds to one factor (sector index) and then add lines in cells by calling [circos.lines](#).

This function can be replaced by a for loop containing [circos.lines](#).

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
# There is no example
NULL
```

```
circos.trackPlotRegion
      Create plotting regions for a whole track
```

Description

Create plotting regions for a whole track

Usage

```
circos.trackPlotRegion(factors = NULL, x = NULL, y = NULL, ylim = NULL,
  force.ylim = TRUE, track.index = NULL,
  track.height = circos.par("track.height"),
  track.margin = circos.par("track.margin"),
  cell.padding = circos.par("cell.padding"),
  bg.col = NA, bg.border = "black", bg.lty = par("lty"), bg.lwd = par("lwd"),
  panel.fun = function(x, y) {NULL})
```

Arguments

factors	A factor or a character vector which represents categories of data, if it is NULL, then it uses all sector index.
x	Data on x-axis. It is only used if <code>panel.fun</code> is set.
y	Data on y-axis
ylim	Range of data on y-axis
force.ylim	Whether to force all cells in the track to share the same <code>ylim</code> . Normally, all cells on a same track should have same <code>ylim</code> .
track.index	Index for the track which is going to be created/updated. If the specified track has already been created, this function just updated corresponding track with new plot. If the specified track is NULL or has not been created, this function just creates it. Note the value for this argument should not exceed maximum track index plus 1.
track.height	Height of the track. It is the percentage to the radius of the unit circles. The value can be set by uh to an absolute unit. If updating a track (with proper <code>track.index</code> value), this argument is ignored.
track.margin	only affect current track
cell.padding	only affect current track
bg.col	Background color for the plotting regions. It can be vector which has the same length of sectors.
bg.border	Color for the border of the plotting regions. It can be vector which has the same length of sectors.
bg.lty	Line style for the border of the plotting regions. It can be vector which has the same length of sectors.
bg.lwd	Line width for the border of the plotting regions. It can be vector which has the same length of sectors.
panel.fun	Panel function to add graphics in each cell, see "details" section and vignette for explanation.

Details

This function tends to be a high-level plotting function, which means, you must first call this function to create plotting regions, then those low-level graphic function such as [circos.points](#), [circos.lines](#) can be applied.

Currently, all the cells that are created in a same track sharing same height, which means, there is no cell has larger height than others.

Since ranges for values on x-axis has already been defined by [circos.initialize](#), only ranges for values on y-axis should be specified in this function. There are two ways to identify the ranges for values on y-axis either by `y` or `ylim`. If `y` is set, it must has the same length as `factors` and the `ylim` for each cell is calculated from `y` values. Also, the `ylim` can be specified from `ylim` which can be a two-element vector or a matrix which has two columns and the number of rows is the same as the length of the levels of the factors.

If there is no enough space for the new track or the new track overlaps with other tracks, there will be an error.

If factors does not cover all sectors, the cells in remaining unselected sectors would also be created but without drawing anything. The ylim for these cells are the same as that in the last created cell.

The function can also update a already-created track if the index for the track is specified. If updating an existed track, those parameters related to the position (such as track height and track margin) of the plotting region can not be changed.

Panel

panel.fun provides a convenient way to add graphics in each cell when initializing the tracks. The self-defined function needs two arguments: x and y which correspond to the data points in the current cell. When factors, x, and y are set in circos.trackPlotRegion, a subset of x and y are split by factors and are sent to panel.fun in the "current" cell. circos.trackPlotRegion creates plotting regions one by one on the track and panel.fun adds graphics in the 'current' cell after the plotting region for a certain cell has been created.

See vignette for examples of how to use this feature.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. Bioinformatics.

See Also

http://jokergoo.github.io/circlize_book/book/circular-layout.html

Examples

```
circos.initialize(letters[1:8], xlim = c(0, 1))
set.seed(123)
df = data.frame(fa = sample(letters[1:8], 100, replace = TRUE),
               x = runif(100), y = rnorm(100))
circos.track(ylim = c(0, 1), bg.col = rand_color(8))
circos.track(df$fa, x = df$x, y = df$y, panel.fun = function(x, y) {
  circos.points(x, y)
}, track.height = 0.2, bg.border = rand_color(8))
circos.clear()
```

circos.trackPoints *Add points to the plotting regions in a same track*

Description

Add points to the plotting regions in a same track

Usage

```
circos.trackPoints(factors = NULL, x, y, track.index = get.cell.meta.data("track.index"),
                  pch = par("pch"), col = par("col"), cex = par("cex"), bg = par("bg"))
```

Arguments

factors	A factor or a character vector which represents the categories of data
x	Data points on x-axis
y	Data points on y-axis
track.index	Index for the track
pch	Point type
col	Point color
cex	Point size
bg	background color

Details

The function adds points in multiple cells by first splitting data into several parts in which each part corresponds to one factor (sector index) and then adding points in each cell by calling [circos.points](#).

Length of pch, col and cex can be one, length of levels of the factors or length of factors.

This function can be replaced by a for loop containing [circos.points](#).

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
circos.initialize(letters[1:8], xlim = c(0, 1))
df = data.frame(fa = sample(letters[1:8], 100, replace = TRUE),
               x = runif(100), y = runif(100))
circos.track(ylim = c(0, 1))
circos.trackPoints(df$fa, x = df$x, y = df$y, pch = 16, col = as.numeric(factor(df$fa)))
circos.clear()
```

circos.trackText	<i>Draw text in cells among the whole track</i>
------------------	---

Description

Draw text in cells among the whole track

Usage

```
circos.trackText(factors, x, y, labels, track.index = get.cell.meta.data("track.index"),
                direction = NULL, facing = c("inside", "outside", "reverse.clockwise", "clockwise",
                "downward", "bending", "bending.inside", "bending.outside"), niceFacing = FALSE,
                adj = par("adj"), cex = 1, col = par("col"), font = par("font"))
```


Arguments

factors	A factor or a character vector which represents the categories of data
x	Data points on x-axis
y	Data points on y-axis
labels	Labels
track.index	Index for the track
direction	deprecated, use facing instead.
facing	Facing of text
niceFacing	Should the facing of text be adjusted to fit human eyes?
adj	Adjustment for text
cex	Font size
col	Font color
font	Font style

Details

The function adds texts in multiple cells by first splitting data into several parts in which each part corresponds to one factor (sector index) and then add texts in cells by calling [circos.text](#).

This function can be replaced by a for loop containing [circos.text](#).

References

Gu, Z. (2014) circize implements and enhances circular visualization in R. Bioinformatics.

Examples

```
# There is no example
NULL
```

circos.update	<i>Create plotting regions for a whole track</i>
---------------	--

Description

Create plotting regions for a whole track

Usage

```
circos.update(...)
```

Arguments

... pass to [circos.updatePlotRegion](#)

Details

shortcut function of [circos.updatePlotRegion](#).

Examples

```
# There is no example  
NULL
```

```
circos.updatePlotRegion
```

Update the plotting region in an existed cell

Description

Update the plotting region in an existed cell

Usage

```
circos.updatePlotRegion(sector.index = get.cell.meta.data("sector.index"),  
  track.index = get.cell.meta.data("track.index"),  
  bg.col = NA, bg.border = "black", bg.lty = par("lty"), bg.lwd = par("lwd"))
```

Arguments

<code>sector.index</code>	Index for the sector
<code>track.index</code>	Index for the track
<code>bg.col</code>	Background color for the plotting region
<code>bg.border</code>	Color for the border of the plotting region
<code>bg.lty</code>	Line style for the border of the plotting region
<code>bg.lwd</code>	Line width for the border of the plotting region

Details

You can update an existed cell by this function by erasing all the graphics. But the `xlim` and `ylim` inside the cell still remain unchanged.

Note if you use [circos.track](#) to update an already created track, you can re-define `ylim` in these cells.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```

circos.initialize(letters[1:8], xlim = c(0, 1))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  circos.text(CELL_META$xcenter, CELL_META$ycenter, CELL_META$sector.index)
})
circos.update(sector.index = "b", track.index = 1)
circos.rect(CELL_META$cell.xlim[1], CELL_META$cell.ylim[1],
           CELL_META$cell.xlim[2], CELL_META$cell.ylim[2],
           col = "#FF000080")
circos.clear()

```

circos.xaxis *Draw x-axis*

Description

Draw x-axis

Usage

```
circos.xaxis(...)
```

Arguments

... all pass to [circos.axis](#)

Examples

```

# There is no example
NULL

```

circos.yaxis *Draw y-axis*

Description

Draw y-axis

Usage

```

circos.yaxis(side = c("left", "right"), at = NULL, labels = TRUE, tick = TRUE,
            sector.index = get.cell.meta.data("sector.index"),
            track.index = get.cell.meta.data("track.index"),
            labels.font = par("font"), labels.cex = par("cex"),
            labels.niceFacing = TRUE,
            tick.length = convert_x(1, "mm", sector.index, track.index),
            lwd = par("lwd"), col = par("col"), labels.col = par("col"))

```

Arguments

<code>side</code>	add the y-axis on the left or right of the cell
<code>at</code>	If it is numeric vector, it identifies the positions of the ticks. It can exceed <code>ylim</code> value and the exceeding part would be trimmed automatically.
<code>labels</code>	labels of the ticks. The exceeding part would be trimmed automatically. The value can also be logical (either an atomic value or a vector) which represents which labels to show.
<code>tick</code>	Whether to draw ticks.
<code>sector.index</code>	Index for the sector
<code>track.index</code>	Index for the track
<code>labels.font</code>	font style for the axis labels
<code>labels.cex</code>	font size for the axis labels
<code>labels.niceFacing</code>	Should facing of axis labels be human-easy
<code>tick.length</code>	length of the tick
<code>lwd</code>	line width for ticks
<code>col</code>	color for the axes
<code>labels.col</code>	color for the labels

Details

Note, you need to set the gap between sectors manually by `circos.par` to make sure there is enough space for y-axis.

Examples

```
op = par(no.readonly = TRUE)

factors = letters[1:8]
circos.par(points.overflow.warning = FALSE)
circos.par(gap.degree = 8)
circos.initialize(factors = factors, xlim = c(0, 10))
circos.trackPlotRegion(factors = factors, ylim = c(0, 10), track.height = 0.5)
par(cex = 0.8)
for(a in letters[2:4]) {
  circos.yaxis(side = "left", sector.index = a)
}
for(a in letters[5:7]) {
  circos.yaxis(side = "right", sector.index = a)
}
circos.clear()

par(op)
```

`col2value`*Transform back from colors to values*

Description

Transform back from colors to values

Usage

```
col2value(r, g, b, col_fun)
```

Arguments

<code>r</code>	red channel in sRGB color space, value should be between 0 and 1. The <code>r</code> , <code>g</code> and <code>b</code> arguments can be wrapped into one variable which is either a three-column matrix or a vector of colors.
<code>g</code>	green channel in sRGB color space, value should be between 0 and 1.
<code>b</code>	blue channel in sRGB color space, value should be between 0 and 1.
<code>col_fun</code>	the color mapping function generated by colorRamp2 .

Details

[colorRamp2](#) transforms values to colors and this function does the reversed job. Note for some color spaces, it cannot transform back to the original value perfectly.

Value

A vector of original numeric values.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
x = seq(0, 1, length = 11)
col_fun = colorRamp2(c(0, 0.5, 1), c("blue", "white", "red"))
col = col_fun(x)
col2value(col, col_fun = col_fun)
col2value("red", col_fun = col_fun)

col_fun = colorRamp2(c(0, 0.5, 1), c("blue", "white", "red"), space = "sRGB")
col = col_fun(x)
col2value(col, col_fun = col_fun)
```

`colorRamp2`*Color interpolation*

Description

Color interpolation

Usage

```
colorRamp2(breaks, colors, transparency = 0, space = "LAB")
```

Arguments

<code>breaks</code>	A vector indicating numeric breaks
<code>colors</code>	A vector of colors which correspond to values in breaks
<code>transparency</code>	A single value in $[\emptyset, 1]$. 0 refers to no transparency and 1 refers to full transparency
<code>space</code>	color space in which colors are interpolated. Value should be one of "RGB", "HSV", "HLS", "LAB", "XYZ", "sRGB", "LUV", see color-class for detail.

Details

Colors are linearly interpolated according to break values and corresponding colors through CIE Lab color space ([LAB](#)) by default. Values exceeding breaks will be assigned with corresponding maximum or minimum colors.

Value

It returns a function which accepts a vector of numeric values and returns interpolated colors.

References

Gu, Z. (2014) [circlize](#) implements and enhances circular visualization in R. *Bioinformatics*.

See Also

[col2value](#) converts back to the original values by providing the color mapping function generated by [colorRamp2](#).

Examples

```
col_fun = colorRamp2(c(-1, 0, 1), c("green", "white", "red"))
col_fun(c(-2, -1, -0.5, 0, 0.5, 1, 2))
```

convert_height	<i>Convert units</i>
----------------	----------------------

Description

Convert units

Usage

```
convert_height(...)
```

Arguments

... pass to [convert_length](#)

Details

This function is same as [convert_length](#). The reason for naming this function is [convert_length](#) is mostly used for defining the height of tracks and track margins.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see example in `convert_length` page  
NULL
```

convert_length	<i>Convert units</i>
----------------	----------------------

Description

Convert units

Usage

```
convert_length(x, unit = c("mm", "cm", "inches"))
```

Arguments

x a numeric vector
unit supported units, only "mm", "cm", "inches".

Details

This function converts mm/cm/inches units to units measured in the canvas coordinate, e.g. how much is it in the canvas coordinate for 1 mm/cm/inches.

Since in the circular plot, the aspect ratio is always 1, it does not matter this conversion is applied on x direction or y direction.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

[convert_x](#) and [convert_y](#) convert absolute units into a data coordinate in a specified cell.

Examples

```
fa = letters[1:10]
circos.par(cell.padding = c(0, 0, 0, 0), track.margin = c(0, 0))
circos.initialize(fa, xlim = cbind(rep(0, 10), runif(10, 0.5, 1.5)))
circos.track(ylim = c(0, 1), track.height = convert_length(5, "mm"))
circos.par(track.margin = c(0, convert_length(2, "mm")))
circos.track(ylim = c(0, 1), track.height = convert_length(1, "cm"))
circos.par(track.margin = c(0, convert_length(5, "mm")))
circos.track(ylim = c(0, 1), track.height = convert_length(1, "inches"))
circos.clear()
```

convert_x

Convert unit on x direction in data coordinate

Description

Convert unit on x direction in data coordinate

Usage

```
convert_x(x, unit = c("mm", "cm", "inches"),
          sector.index = get.cell.meta.data("sector.index"),
          track.index = get.cell.meta.data("track.index"),
          h = get.cell.meta.data("ycenter", sector.index = sector.index,
                                track.index = track.index))
```

Arguments

x	a numeric vector
unit	supported units, only "mm", "cm", "inches"
sector.index	index for the sector where the conversion is applied
track.index	index for the track where the conversion is applied

h since the width of the cell is not identical from the top to the bottom in the cell, the position on y direction needs to be specified. By default it is at the middle point on y-axis

Value

A vector of numeric values which are measured in the specified data coordinate

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

[convert_y](#) converts on y direction.

Examples

```
fa = letters[1:10]
circos.par(cell.padding = c(0, 0, 0, 0), track.margin = c(0, 0))
circos.initialize(fa, xlim = cbind(rep(0, 10), runif(10, 0.5, 1.5)))
circos.track(ylim = c(0, 1), track.height = convert_height(5, "mm"),
  panel.fun = function(x, y) {
    circos.lines(c(0, 0 + convert_x(5, "mm")), c(0.5, 0.5), col = "blue")
  })
circos.par(track.margin = c(0, convert_height(2, "mm")))
circos.track(ylim = c(0, 1), track.height = convert_height(1, "cm"),
  panel.fun = function(x, y) {
    xcenter = get.cell.meta.data("xcenter")
    circos.lines(c(xcenter, xcenter), c(0, convert_y(1, "cm")), col = "red")
  })
circos.par(track.margin = c(0, convert_height(5, "mm")))
circos.track(ylim = c(0, 1), track.height = convert_height(1, "inches"),
  panel.fun = function(x, y) {
    line_length_on_x = convert_x(1*sqrt(2)/2, "cm")
    line_length_on_y = convert_y(1*sqrt(2)/2, "cm")
    circos.lines(c(0, line_length_on_x), c(0, line_length_on_y), col = "orange")
  })
circos.clear()
```

convert_y

Convert unit on y direction in data coordinate

Description

Convert unit on y direction in data coordinate

Usage

```
convert_y(x, unit = c("mm", "cm", "inches"),
          sector.index = get.current.sector.index(),
          track.index = get.current.track.index())
```

Arguments

x	a numeric vector
unit	supported units, only "mm", "cm", "inches"
sector.index	index for the sector where the conversion is applied
track.index	index for the track where the conversion is applied

Value

A vector of numeric values which are measured in the specified data coordinate

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

[convert_x](#) converts on x direction.

Examples

```
# see example on `convert_x` page
NULL
```

cytoband.col	<i>Assign colors to cytogenetic band (hg19) according to the Giemsa stain results</i>
--------------	---

Description

Assign colors to cytogenetic band (hg19) according to the Giemsa stain results

Usage

```
cytoband.col(x)
```

Arguments

x	A vector containing the Giemsa stain results
---	--

Details

The color theme is from <http://circos.ca/tutorials/course/slides/session-2.pdf>, page 42.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. Bioinformatics.

Examples

```
## Not run:  
cytoband = read.cytoband()  
cytoband.col(cytoband$df[[5]])  
  
## End(Not run)
```

degree

Mark the value as a degree value

Description

Mark the value as a degree value

Usage

```
degree(x)
```

Arguments

x degree value

Value

a degree object

Examples

```
# There is no example  
NULL
```

draw.sector	<i>Draw sectors or rings in a circle</i>
-------------	--

Description

Draw sectors or rings in a circle

Usage

```
draw.sector(start.degree = 0, end.degree = 360, rou1 = 1, rou2 = NULL,
            center = c(0, 0), clock.wise = TRUE, col = NA, border = "black", lwd = par("lwd"),
            lty = par("lty"))
```

Arguments

start.degree	start degree for the sector
end.degree	end degree for the sector
rou1	Radius for one of the arc in the sector
rou2	Radius for the other arc in the sector
center	Center of the circle
clock.wise	The direction from start.degree to end.degree
col	Filled color
border	Border color
lwd	Line width
lty	Line style

Details

If the interval between start and end (larger or equal to 360 or smaller or equal to -360) it would draw a full circle or ring. If rou2 is set, it would draw part of a ring.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
plot(c(-1, 1), c(-1, 1), type = "n", axes = FALSE, ann = FALSE, asp = 1)
draw.sector(20, 0)
draw.sector(30, 60, rou1 = 0.8, rou2 = 0.5, clock.wise = FALSE, col = "#FF000080")
draw.sector(350, 1000, col = "#00FF0080", border = NA)
draw.sector(0, 180, rou1 = 0.25, center = c(-0.5, 0.5), border = 2, lwd = 2, lty = 2)
draw.sector(0, 360, rou1 = 0.7, rou2 = 0.6, col = "#0000FF80")

factors = letters[1:8]
```

```
circos.initialize(factors, xlim = c(0, 1))
for(i in 1:3) {
  circos.trackPlotRegion(ylim = c(0, 1))
}
circos.info(plot = TRUE)

draw.sector(get.cell.meta.data("cell.start.degree", sector.index = "a"),
            get.cell.meta.data("cell.end.degree", sector.index = "a"),
            rou1 = 1, col = "#FF000040")

draw.sector(0, 360,
            rou1 = get.cell.meta.data("cell.top.radius", track.index = 1),
            rou2 = get.cell.meta.data("cell.bottom.radius", track.index = 1),
            col = "#00FF0040")

draw.sector(get.cell.meta.data("cell.start.degree", sector.index = "e"),
            get.cell.meta.data("cell.end.degree", sector.index = "f"),
            get.cell.meta.data("cell.top.radius", track.index = 2),
            get.cell.meta.data("cell.bottom.radius", track.index = 3),
            col = "#0000FF40")

pos = circlize(c(0.2, 0.8), c(0.2, 0.8), sector.index = "h", track.index = 2)
draw.sector(pos[1, "theta"], pos[2, "theta"], pos[1, "rou"], pos[2, "rou"],
            clock.wise = TRUE, col = "#00FFFF40")
circos.clear()
```

fontsize

Convert fontsize to cex

Description

Convert fontsize to cex

Usage

```
fontsize(x)
```

Arguments

x value for fontsize

Details

It just mark the value as a fontsize setting for [circos.text](#)

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# There is no example  
NULL
```

generateRandomBed	<i>Generate random genomic data</i>
-------------------	-------------------------------------

Description

Generate random genomic data

Usage

```
generateRandomBed(nr = 10000, nc = 1, fun = function(k) rnorm(k, 0, 0.5),  
species = NULL)
```

Arguments

nr	Number of rows
nc	Number of numeric columns / value columns
fun	Function for generating random values
species	species, pass to read.cytoband

Details

The function will uniformly sample positions from the genome. Chromosome names start with "chr" and positions are sorted. The final number of rows may not be exactly as same as nr.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
bed = generateRandomBed()  
bed = generateRandomBed(nr = 200, nc = 4)  
bed = generateRandomBed(fun = function(k) runif(k))
```

genomicDensity	<i>Calculate genomic region density</i>
----------------	---

Description

Calculate genomic region density

Usage

```
genomicDensity(region, window.size = 1e7, n.window = NULL, overlap = TRUE, chr.len = NULL)
```

Arguments

region	Genomic positions. It can be a data frame with two columns which are start positions and end positions on a single chromosome. It can also be a bed-format data frame which contains the chromosome column.
window.size	Window size to calculate genomic density
n.window	number of windows, if it is specified, window.size is ignored
overlap	Whether two neighbouring windows have half overlap
chr.len	the chromosome length. The value should be named vector

Details

It calculate the percent of each genomic windows that is covered by the input regions.

Value

If the input is a two-column data frame, the function returns a data frame with three columns: start position, end position and percent of overlapping. And if the input is a bed-format data frame, there will be an additionally chromosome name column.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
bed = generateRandomBed()
bed = subset(bed, chr == "chr1")
head(genomicDensity(bed))
```

get.all.sector.index *Get index for all sectors*

Description

Get index for all sectors

Usage

```
get.all.sector.index()
```

Details

It simply returns a vector of all sector index.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. Bioinformatics.

Examples

```
## Not run:  
library(circlize)  
factors = letters[1:4]  
circos.initialize(factors, xlim = c(0, 1))  
circos.trackPlotRegion(ylim = c(0, 1))  
get.all.sector.index()  
circos.clear()  
  
## End(Not run)
```

get.all.track.index *Get index for all tracks*

Description

Get index for all tracks

Usage

```
get.all.track.index()
```

Details

It simply returns a vector of all track index.

Examples

```
## Not run:
library(circlize)
factors = letters[1:4]
circos.initialize(factors, xlim = c(0, 1))
circos.trackPlotRegion(ylim = c(0, 1))
circos.trackPlotRegion(ylim = c(0, 1))
circos.trackPlotRegion(ylim = c(0, 1))
get.all.track.index()
circos.clear()

## End(Not run)
```

get.cell.meta.data *Get the meta data of a cell*

Description

Get the meta data of a cell

Usage

```
get.cell.meta.data(name, sector.index = get.current.sector.index(),
  track.index = get.current.track.index())
```

Arguments

name	Only support one name at a time, see "details" section
sector.index	Index of the sector
track.index	Index of the track

Details

The following meta information for a cell can be obtained:

sector.index The name (index) for the sector
sector.numeric.index Numeric index for the sector
track.index Numeric index for the track
xlim Minimal and maximal values on the x-axis
ylim Minimal and maximal values on the y-axis
xrange Range of xlim. It equals to xlim[2] - xlim[1]
yrange Range of ylim
xcenter Center of x-axis. It equals to (xlim[2] + xlim[1])/2
ycenter Center of y-axis

`cell.xlim` Minimal and maximal values on the x-axis extended by cell paddings
`cell.ylim` Minimal and maximal values on the y-axis extended by cell paddings
`xplot` Degrees for right and left borders of the cell.
`yplot` Radius for top and bottom borders of the cell.
`cell.start.degree` Same as `xplot[1]`
`cell.end.degree` Same as `xplot[2]`
`cell.bottom.radius` Same as `yplot[1]`
`cell.top.radius` Same as `yplot[2]`
`track.margin` Margin for the cell
`cell.padding` Padding for the cell

The function is useful when using `panel.fun` in `circos.track` to get detailed information of the current cell.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

See Also

`CELL_META` is a short version of `get.cell.meta.data`.

Examples

```

factors = letters[1:4]
circos.initialize(factors, xlim = c(0, 1))
circos.trackPlotRegion(ylim = c(0, 1), panel.fun = function(x, y) {
  print(get.cell.meta.data("xlim"))
})
print(get.cell.meta.data("xlim", sector.index = "a", track.index = 1))
circos.clear()
  
```

`get.current.chromosome`

Get current chromosome name

Description

Get current chromosome name

Usage

```
get.current.chromosome()
```

Details

The function is same as [get.current.sector.index](#) and should only be put inside `panel.fun` when using `circos.genomicTrackPlotRegion`.

References

Gu, Z. (2014) *circlize* implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:
library(circlize)
circos.initializeWithIdeogram()
circos.genomicTrackPlotRegion(ylim = c(0, 1), panel.fun = function(region, value, ...) {
  print(get.current.chromosome())
})
circos.clear()

## End(Not run)
```

`get.current.sector.index`*Get current sector index*

Description

Get current sector index

Usage

```
get.current.sector.index()
```

Value

Simply returns the name of current sector

Examples

```
# There is no example
NULL
```

```
get.current.track.index
```

Get current track index

Description

Get current track index

Usage

```
get.current.track.index()
```

Value

Simply returns the numeric index for the current track.

Examples

```
# There is no example
NULL
```

```
getI
```

Which data that panel.fun is using

Description

Which data that panel.fun is using

Usage

```
getI(...)
```

Arguments

... Invisible arguments that users do not need to care

Details

The function should only be put inside panel.fun when using [circos.genomicTrackPlotRegion](#). If stack is set to TRUE in [circos.genomicTrackPlotRegion](#), the returned value indicates which stack the function will be applied to.

If data is a list of data frames, the value indicates which data frame is being used. Please see the vignette to get a more clear explanation.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
# There is no example
NULL
```

highlight.chromosome *Highlight chromosomes*

Description

Highlight chromosomes

Usage

```
highlight.chromosome(...)
```

Arguments

```
...          pass to highlight.sector
```

Details

This is only a shortcut function of [highlight.sector](#).

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:

par(mar = c(1.5, 1.5, 1.5, 1.5))
# highlight
circos.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(plotType = c("axis", "labels"))

bed = generateRandomBed(nr = 100)
circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
  circos.genomicPoints(region, value, pch = 16, cex = 0.5, ...)
})

bed = generateRandomBed(nr = 100)
circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
  circos.genomicPoints(region, value, pch = 16, cex = 0.5, ...)
})
```

```

}))

bed = generateRandomBed(nr = 100)
circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
  circos.genomicPoints(region, value, pch = 16, cex = 0.5, ...)
})

bed = generateRandomBed(nr = 100)
circos.genomicTrackPlotRegion(bed, panel.fun = function(region, value, ...) {
  circos.genomicPoints(region, value, pch = 16, cex = 0.5, ...)
})

highlight.chromosome("chr1", col = "#FF000040", padding = c(0.05, 0.05, 0.15, 0.05))
highlight.chromosome("chr3", col = NA, border = "red", lwd = 2,
  padding = c(0.05, 0.05, 0.15, 0.05))
highlight.chromosome("chr5", col = "#0000FF40", track.index = c(2, 4, 5))
highlight.chromosome("chr7", col = NA, border = "green", lwd = 2,
  track.index = c(2, 4, 5))
circos.clear()

## End(Not run)

```

highlight.sector *Highlight sectors and tracks*

Description

Highlight sectors and tracks

Usage

```

highlight.sector(sector.index, track.index = get.all.track.index(),
  col = "#FF000040", border = NA, lwd = par("lwd"), lty = par("lty"),
  padding = c(0, 0, 0, 0), text = NULL, text.col = par("col"),
  text.vjust = 0.5, ...)

```

Arguments

sector.index	A vector of sector index
track.index	A vector of track index that you want to highlight
col	Color for highlighting. Note the color should be semi-transparent.
border	Border of the highlighted region
lwd	Width of borders
lty	Style of borders

padding	Padding for the highlighted region. It should contain four values representing ratios of the width or height of the highlighted region
text	text added in the highlight region, only support plotting one string at a time
text.vjust	adjustment on 'vertical' (radical) direction. Besides to set it as numeric values, the value can also be a string contain absoute unit, e.g. "2.1mm", "-1 inche", but only "mm", "cm", "inches"/"inche" are allowed.
text.col	color for the text
...	pass to circos.text

Details

You can use [circos.info](#) to find out index for all sectors and all tracks.

The function calls [draw.sector](#).

Examples

```
factors = letters[1:8]
circos.initialize(factors, xlim = c(0, 1))
for(i in 1:4) {
  circos.trackPlotRegion(ylim = c(0, 1))
}
circos.info(plot = TRUE)

highlight.sector(c("a", "h"), track.index = 1)
highlight.sector("c", col = "#00FF0040")
highlight.sector("d", col = NA, border = "red", lwd = 2)
highlight.sector("e", col = "#0000FF40", track.index = c(2, 3))
highlight.sector(c("f", "g"), col = NA, border = "green",
  lwd = 2, track.index = c(2, 3))
highlight.sector(factors, col = "#FFFF0040", track.index = 4)
circos.clear()
```

names.CELL_META	<i>Names of all meta data in the current cell</i>
-----------------	---

Description

Names of all meta data in the current cell

Usage

```
## S3 method for class 'CELL_META'
names(x)
```

Arguments

x use [CELL_META](#).

Details

The variable `CELL_META` can only be used to get meta data of the "current" cell. Basically you can simply replace e.g. `get.cell.meta.data("sector.index")` to `CELL_META$sector.index`.

See Also

[get.cell.meta.data](#)

Examples

```
names(CELL_META)
```

`posTransform.default` *Genomic position transformation function*

Description

Genomic position transformation function

Usage

```
posTransform.default(region, ...)
```

Arguments

<code>region</code>	Genomic positions at a single chromosome. It is a data frame with two columns which are start position and end position.
<code>...</code>	other arguments

Details

The default position transformation functions transforms position to be equally distributed along the chromosome. If users want to define their own transformation function, the requirement is that the returned value should be a data frame with two columns: transformed start position and transformed end position. The returned value should have same number of rows as the input one.

For details why need to use position transformation, please refer to [circos.genomicPosTransformLines](#).

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
## Not run:

par(mfrow = c(2, 1))
### rect matrix
circos.par(cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram()

bed = generateRandomBed(nr = 100, nc = 4)

circos.genomicPosTransformLines(bed, posTransform = posTransform.default,
  horizontalLine = "top", track.height = 0.1)

f = colorRamp2(breaks = c(-1, 0, 1), colors = c("green", "black", "red"))
circos.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = f(value[[1]]),
    border = f(value[[1]]), posTransform = posTransform.default, ...)
}, bg.border = NA)

circos.clear()

circos.par(cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(plotType = NULL)

bed = generateRandomBed(nr = 20, nc = 4)

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1), panel.fun = function(region, value, ...) {
  circos.genomicText(region, value, y = 0, adj = c(1, 0.5), labels = "gene",
    facing = "reverse.clockwise", posTransform = posTransform.default)
}, bg.border = NA)

circos.genomicPosTransformLines(bed, posTransform = posTransform.default,
  horizontalLine = "bottom", direction = "outside", track.height = 0.1)

cytoband = read.cytoband()$df
circos.genomicTrackPlotRegion(cytoband, stack = TRUE, panel.fun = function(region, value, ...) {
  circos.genomicRect(region, value, col = cytoband.col(value$V5), border = NA, ...)
}, track.height = 0.05)

circos.clear()

## End(Not run)
```

Description

Genomic position transformation function specifically for text

Usage

```
posTransform.text(region, y, labels, cex = 1, font = par("font"),
  sector.index = get.cell.meta.data("sector.index"),
  track.index = get.cell.meta.data("track.index"), padding = 0,
  extend = 0, ...)
```

Arguments

region	Genomic positions at a single chromosome. It is a data frame with two columns which are start position and end position.
y	positions of texts
labels	text labels
cex	text size
font	text font style
sector.index	sector index
track.index	track index
padding	padding of text
extend	extend to allow labels to be put in a region which is wider than the current chromosome. The value should be a proportion value and the length is either one or two.
...	other arguments

Details

This position transformation function is designed specifically for text. Under the transformation, texts will be as close as possible to the original positions.

Examples

```
## Not run:

op = par(no.readonly = TRUE)

set.seed(123458)

par(mfrow = c(2, 2))

bed = generateRandomBed(nr = 400, fun = function(k) rep("text", k))
bed = bed[-(9:13), ]
#####
circos.par("start.degree" = 90, canvas.xlim = c(0, 1), canvas.ylim = c(0, 1),
  gap.degree = 270, cell.padding = c(0, 0, 0, 0), track.margin = c(0.005, 0.005))
circos.initializeWithIdeogram(plotType = c("axis"), chromosome.index = "chr1")
```

```

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),
  panel.fun = function(region, value, ...) {
    circos.genomicText(region, value, y = 0, labels.column = 1,
      facing = "clockwise", adj = c(0, 0.5),
      posTransform = posTransform.text, cex = 0.8, niceFacing = F)
  }, track.height = 0.1, bg.border = NA)
i_track = get.cell.meta.data("track.index")

circos.genomicPosTransformLines(bed,
  posTransform = function(region, value)
    posTransform.text(region, y = 0, labels = value[[1]],
      cex = 0.8, track.index = i_track),
  direction = "outside"
)

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),
  panel.fun = function(region, value, ...) {
    circos.points( (region[[1]] + region[[2]])/2, rep(0.5, nrow(region)), pch = 16)
  }, track.height = 0.02, bg.border = NA)

circos.clear()

text(0, 0.05, "posTransform.text\ndirection = 'outside'", adj = c(0, 0))

#####
circos.par("start.degree" = 90, canvas.xlim = c(0, 1), canvas.ylim = c(0, 1),
  gap.degree = 270, cell.padding = c(0, 0, 0, 0), track.margin = c(0.005, 0.005))
circos.initializeWithIdeogram(plotType = c("axis"), chromosome.index = "chr1")
circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),
  panel.fun = function(region, value, ...) {
    circos.genomicText(region, value, y = 0, labels.column = 1,
      facing = "clockwise", adj = c(0, 0.5),
      posTransform = posTransform.default, cex = 0.8, niceFacing = F)
  }, track.height = 0.1, bg.border = NA)
i_track = get.cell.meta.data("track.index")

circos.genomicPosTransformLines(bed, posTransform = posTransform.default,
  direction = "outside")

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),
  panel.fun = function(region, value, ...) {
    circos.points( (region[[1]] + region[[2]])/2, rep(0.5, nrow(region)), pch = 16)
  }, track.height = 0.02, bg.border = NA)

circos.clear()
text(0, 0.05, "posTransform.default\ndirection = 'outside'", adj = c(0, 0))

#####
circos.par("start.degree" = 90, canvas.xlim = c(0, 1), canvas.ylim = c(0, 1),
  gap.degree = 270, cell.padding = c(0, 0, 0, 0), track.margin = c(0.005, 0.005))
circos.initializeWithIdeogram(plotType = c("axis"), chromosome.index = "chr1")
circos.par(cell.padding = c(0, 0, 0, 0))
circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),

```

```

    panel.fun = function(region, value, ...) {
      circos.points( (region[[1]] + region[[2]])/2, rep(0.5, nrow(region)), pch = 16)
    }, track.height = 0.02, bg.border = NA)

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1), track.height = 0.1, bg.border = NA)
i_track = get.cell.meta.data("track.index")

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),
  panel.fun = function(region, value, ...) {
    circos.genomicText(region, value, y = 1, labels.column = 1,
      facing = "clockwise", adj = c(1, 0.5),
      posTransform = posTransform.text, cex = 0.8, niceFacing = F)
  }, track.height = 0.1, bg.border = NA)

circos.genomicPosTransformLines(bed,
  posTransform = function(region, value)
    posTransform.text(region, y = 1, labels = value[[1]],
      cex = 0.8, track.index = i_track+1),
  direction = "inside", track.index = i_track
)
circos.clear()
text(0, 0.05, "posTransform.text\ndirection = 'inside'", adj = c(0, 0))

#####
circos.par("start.degree" = 90, canvas.xlim = c(0, 1), canvas.ylim = c(0, 1),
  gap.degree = 270, cell.padding = c(0, 0, 0, 0), track.margin = c(0.005, 0.005))
circos.initializeWithIdeogram(plotType = c("axis"), chromosome.index = "chr1")
circos.par(cell.padding = c(0, 0, 0, 0))
circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),
  panel.fun = function(region, value, ...) {
    circos.points( (region[[1]] + region[[2]])/2, rep(0.5, nrow(region)), pch = 16)
  }, track.height = 0.02, bg.border = NA)

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1), track.height = 0.1, bg.border = NA)
i_track = get.cell.meta.data("track.index")

circos.genomicTrackPlotRegion(bed, ylim = c(0, 1),
  panel.fun = function(region, value, ...) {
    circos.genomicText(region, value, y = 1, labels.column = 1, facing = "clockwise",
      adj = c(1, 0.5), posTransform = posTransform.text, cex = 0.8,
      niceFacing = F, padding = 0.2)
  }, track.height = 0.1, bg.border = NA)

circos.genomicPosTransformLines(bed,
  posTransform = function(region, value)
    posTransform.text(region, y = 1, labels = value[[1]],
      cex = 0.8, track.index = i_track+1, padding = 0.2),
  direction = "inside", track.index = i_track
)
circos.clear()
text(0, 0.05, "posTransform.text\ndirection = 'inside'\npadding = 0.2", adj = c(0, 0))

```

```
par(op)  
  
## End(Not run)
```

<code>print.CELL_META</code>	<i>Print CELL_META</i>
------------------------------	------------------------

Description

Print CELL_META

Usage

```
## S3 method for class 'CELL_META'  
print(x, ...)
```

Arguments

<code>x</code>	input
<code>...</code>	additional parameters

Examples

```
# There is no example  
NULL
```

<code>rainfallTransform</code>	<i>Calculate inter-distance of genomic regions</i>
--------------------------------	--

Description

Calculate inter-distance of genomic regions

Usage

```
rainfallTransform(region, mode = c("min", "max", "mean", "left", "right"),  
normalize_to_width = FALSE)
```

Arguments

region	Genomic positions. It can be a data frame with two columns which are start positions and end positions on a single chromosome. It can also be a bed-format data frame which contains the chromosome column.
mode	How to calculate inter-distance. For a region, there is a distance to the previous region and also there is a distance to the next region. mode controls how to merge these two distances into one value.
normalize_to_width	If it is TRUE, the value is the relative distance divided by the width of the region.

Value

If the input is a two-column data frame, the function returns a data frame with three columns: start position, end position and distance. And if the input is a bed-format data frame, there will be the chromosome column added.

The row order of the returned data frame is as same as the input one.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. Bioinformatics.

Examples

```
bed = generateRandomBed()
bed = subset(bed, chr == "chr1")
head(rainfallTransform(bed))
```

rand_color	<i>Generate random colors</i>
------------	-------------------------------

Description

Generate random colors

Usage

```
rand_color(n, hue = NULL, luminosity = "random", transparency = 0)
```

Arguments

n	number of colors
hue	the hue of the generated color. You can use following default color name: red, orange, yellow, green, blue, purple, pink and monochrome. If the value is a hexadecimal color string such as #00FFFF, the function will extract its hue value and use that to generate colors.

luminosity controls the luminosity of the generated color. The value should be a string containing bright, light, dark and random.

transparency transparency, numeric value between 0 and 1.

Details

The code is adapted from randomColor.js (<https://github.com/davidmerfield/randomColor>).

Value

a vector of colors

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
plot(NULL, xlim = c(1, 10), ylim = c(1, 8), axes = FALSE, ann = FALSE)
points(1:10, rep(1, 10), pch = 16, cex = 5,
       col = rand_color(10, luminosity = "random"))
points(1:10, rep(2, 10), pch = 16, cex = 5,
       col = rand_color(10, luminosity = "bright"))
points(1:10, rep(3, 10), pch = 16, cex = 5,
       col = rand_color(10, luminosity = "light"))
points(1:10, rep(4, 10), pch = 16, cex = 5,
       col = rand_color(10, luminosity = "dark"))
points(1:10, rep(5, 10), pch = 16, cex = 5,
       col = rand_color(10, hue = "red", luminosity = "bright"))
points(1:10, rep(6, 10), pch = 16, cex = 5,
       col = rand_color(10, hue = "green", luminosity = "bright"))
points(1:10, rep(7, 10), pch = 16, cex = 5,
       col = rand_color(10, hue = "blue", luminosity = "bright"))
points(1:10, rep(8, 10), pch = 16, cex = 5,
       col = rand_color(10, hue = "monochrome", luminosity = "bright"))
```

read.chromInfo

Read/parse chromInfo data from a data frame/file/UCSC database

Description

Read/parse chromInfo data from a data frame/file/UCSC database

Usage

```
read.chromInfo(chromInfo = system.file(package = "circlize",
                                       "extdata", "chromInfo.txt"), species = NULL, chromosome.index = NULL, sort.chr = TRUE)
```

Arguments

chromInfo	Path of the chromInfo file or a data frame that already contains chromInfo data
species	Abbreviations of species. e.g. hg19 for human, mm10 for mouse. If this value is specified, the function will download chromInfo.txt.gz from UCSC website automatically.
chromosome.index	subset of chromosomes, also used to reorder chromosomes.
sort.chr	Whether chromosome names should be sorted (first sort by numbers then by letters). If chromosome.index is set, this argument is enforced to FALSE

Details

The function read the chromInfo data, sort the chromosome names and calculate the length of each chromosome. By default, it is human hg19 chromInfo data.

You can find the data structure for the chromInfo data from <http://hgdownload.cse.ucsc.edu/goldenpath/hg19/database/chromInfo.txt.gz>

Value

df Data frame for chromInfo data (rows are sorted if sort.chr is set to TRUE)

chromosome Sorted chromosome names

chr.len Length of chromosomes. Order are same as chromosome

Examples

```
data = read.chromInfo(species = "hg19")
data = read.chromInfo(chromInfo = system.file(package = "circlize", "extdata", "chromInfo.txt"))
chromInfo = read.table(system.file(package = "circlize", "extdata", "chromInfo.txt"),
  colClasses = c("character", "numeric"), sep = "\t")
data = read.chromInfo(chromInfo = chromInfo)
```

read.cytoband	<i>Read/parse cytoband data from a data frame/file/UCSC database</i>
---------------	--

Description

Read/parse cytoband data from a data frame/file/UCSC database

Usage

```
read.cytoband(cytoband = system.file(package = "circlize",
  "extdata", "cytoBand.txt"), species = NULL, chromosome.index = NULL, sort.chr = TRUE)
```


Arguments

cytoband	Path of the cytoband file or a data frame that already contains cytoband data
species	Abbreviations of species. e.g. hg19 for human, mm10 for mouse. If this value is specified, the function will download cytoBand.txt.gz from UCSC website automatically.
chromosome.index	subset of chromosomes, also used to reorder chromosomes.
sort.chr	Whether chromosome names should be sorted (first sort by numbers then by letters). If chromosome.index is set, this argument is enforced to FALSE

Details

The function read the cytoband data, sort the chromosome names and calculate the length of each chromosome. By default, it is human hg19 cytoband data.

You can find the data structure of the cytoband data from <http://hgdownload.cse.ucsc.edu/goldenpath/hg19/database/cytoBand.txt.gz>

Value

df Data frame for cytoband data (rows are sorted if sort.chr is set to TRUE)
 chromosome Sorted chromosome names
 chr.len Length of chromosomes. Orders are same as chromosome

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
data = read.cytoband(species = "hg19")
data = read.cytoband(cytoband = system.file(package = "circlize", "extdata", "cytoBand.txt"))
cytoband = read.table(system.file(package = "circlize", "extdata", "cytoBand.txt"),
  colClasses = c("character", "numeric", "numeric", "character", "character"), sep = "\t")
data = read.cytoband(cytoband = cytoband)
```

reverse.circlize *Convert to data coordinate system*

Description

Convert to data coordinate system

Usage

```
reverse.circlize(x, y, sector.index = get.current.sector.index(),
  track.index = get.current.track.index())
```

Arguments

x	degree values. The value can also be a two-column matrix/data frame if you put x and y data points into one variable.
y	distance to the circle center (the radius)
sector.index	Index for the sector where the data coordinate is used
track.index	Index for the track where the data coordinate is used

Details

This is the reverse function of `circlize`. It transform data points from polar coordinate system to a specified data coordinate system.

Value

A matrix with two columns (x and y)

Examples

```
pdf(NULL)
factors = letters[1:4]
circos.initialize(factors, xlim = c(0, 1))
circos.trackPlotRegion(ylim = c(0, 1))
reverse.circlize(c(30, 60), c(0.9, 0.8))
reverse.circlize(c(30, 60), c(0.9, 0.8), sector.index = "d", track.index = 1)
reverse.circlize(c(30, 60), c(0.9, 0.8), sector.index = "a", track.index = 1)
circos.clear()
dev.off()
```

set.current.cell	<i>Set flag to current cell</i>
------------------	---------------------------------

Description

Set flag to current cell

Usage

```
set.current.cell(sector.index, track.index)
```

Arguments

sector.index	sector index
track.index	track index

Details

After setting the current cell, all functions which need `sector.index` and `track.index` arguments and are applied to the current cell do not need to specify the two arguments explicitly.

Examples

```
pdf(NULL)
circos.initialize(letters[1:8], xlim = c(0, 1))
circos.track(ylim = c(0, 1))
circos.info()
set.current.cell("b", 1)
circos.info()
circos.clear()
dev.off()
```

show.index

Label the sector index and the track index on each cell

Description

Label the sector index and the track index on each cell

Usage

```
show.index()
```

Details

This function is deprecated, please use [circos.info](#) instead.

References

Gu, Z. (2014) circlize implements and enhances circular visualization in R. *Bioinformatics*.

Examples

```
# There is no example
NULL
```

smartAlign	<i>Adjust positions of text</i>
------------	---------------------------------

Description

Adjust positions of text

Usage

```
smartAlign(x1, x2, xlim)
```

Arguments

x1	position which corresponds to the top of the text
x2	position which corresponds to the bottom of the text
xlim	ranges on x-axis

Details

used internally

Examples

```
# There is no example  
NULL
```

uh	<i>Convert units</i>
----	----------------------

Description

Convert units

Usage

```
uh(...)
```

Arguments

...	pass to convert_length
-----	--

Details

This function is same as [convert_length](#).

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see example in `convert_length` page  
NULL
```

ux

Convert unit on x direction in data coordinate

Description

Convert unit on x direction in data coordinate

Usage

```
ux(...)
```

Arguments

... pass to [convert_x](#)

Details

This function is same as [convert_x](#).

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see example in `convert_x` page  
NULL
```

uy	<i>Convert unit on y direction in data coordinate</i>
----	---

Description

Convert unit on y direction in data coordinate

Usage

```
uy(...)
```

Arguments

... pass to [convert_y](#)

Details

This function is same as [convert_y](#).

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see example in `convert_y` page
NULL
```

\$.CELL_META	<i>Easy to way to get meta data in the current cell</i>
--------------	---

Description

Easy to way to get meta data in the current cell

Usage

```
## S3 method for class 'CELL_META'
x$name
```

Arguments

x	name of the variable should be "CELL_META"
name	name of the cell meta name

Details

The variable `CELL_META` can only be used to get meta data of the "current" cell. Basically you can simply replace e.g. `get.cell.meta.data("sector.index")` to `CELL_META$sector.index`.

See Also

[get.cell.meta.data](#)

Examples

```
# There is no example  
NULL
```

Index

`$.CELL_META`, 110

`add_transparency`, 6

`adjacencyList2Matrix`, 6

`Arrowhead`, 13, 16, 54

`as.raster`, 62

`calc_gap`, 7

`CELL_META`, 8, 8, 90, 95, 96, 111

`chordDiagram`, 5, 8, 14, 16

`chordDiagramFromDataFrame`, 9, 10, 11, 16

`chordDiagramFromMatrix`, 9, 10, 14

`circlize`, 17, 106

`circlize-package`, 4

`circos.arrow`, 18

`circos.axis`, 4, 19, 24, 75

`circos.clear`, 4, 22, 56

`circos.dendrogram`, 23

`circos.genomicAxis`, 24

`circos.genomicDensity`, 5, 25

`circos.genomicHeatmap`, 5, 26

`circos.genomicIdeogram`, 5, 27

`circos.genomicInitialize`, 5, 28, 50

`circos.genomicLabels`, 5, 30

`circos.genomicLines`, 5, 31

`circos.genomicLink`, 5, 33

`circos.genomicPoints`, 5, 34

`circos.genomicPosTransformLines`, 36, 96

`circos.genomicRainfall`, 5, 38

`circos.genomicRect`, 5, 40

`circos.genomicText`, 5, 42

`circos.genomicTrack`, 5, 44

`circos.genomicTrackPlotRegion`, 32, 35, 40, 43, 44, 45, 91, 92

`circos.info`, 4, 47, 95, 107

`circos.initialize`, 4, 22, 29, 48, 59, 70

`circos.initializeWithIdeogram`, 5, 49

`circos.lines`, 4, 25, 31, 32, 51, 69, 70

`circos.link`, 4, 10, 13, 16, 33, 34, 53

`circos.nested`, 55, 56

`circos.par`, 4, 57, 76

`circos.points`, 4, 35, 59, 60, 70, 72

`circos.polygon`, 4, 60

`circos.raster`, 61

`circos.rect`, 4, 40, 43, 63, 63

`circos.segments`, 4, 64

`circos.text`, 4, 20, 43, 64, 73, 85, 95

`circos.track`, 4, 66, 74, 90

`circos.trackHist`, 67

`circos.trackLines`, 4, 68

`circos.trackPlotRegion`, 25, 37, 39, 45, 46, 60, 66, 69, 71

`circos.trackPoints`, 4, 71

`circos.trackText`, 4, 72

`circos.update`, 4, 73

`circos.updatePlotRegion`, 73, 74, 74

`circos.xaxis`, 4, 75

`circos.yaxis`, 4, 21, 75

`col2value`, 77, 78

`colorRamp2`, 12, 15, 26, 77, 78, 78

`convert_height`, 55, 58, 79

`convert_length`, 79, 79, 108

`convert_x`, 80, 80, 82, 109

`convert_y`, 20, 80, 81, 81, 110

`cytoband.col`, 82

`degree`, 65, 83

`dendrogram`, 23

`draw.sector`, 84, 95

`factor`, 48, 68, 70, 72, 73

`fontsize`, 85

`generateRandomBed`, 86

`genomicDensity`, 25, 87

`get.all.sector.index`, 88

`get.all.track.index`, 88

`get.cell.meta.data`, 8, 89, 90, 96, 111

`get.current.chromosome`, 90

`get.current.sector.index`, 91, 91

get.current.track.index, 92
getI, 46, 92

highlight.chromosome, 93
highlight.sector, 93, 94
hist, 67

LAB, 78
lines, 51, 64, 69

names.CELL_META, 95

par, 59, 60
plot, 48
points, 60
polygon, 18, 60, 61, 63
posTransform.default, 31, 35, 37, 40, 43, 96
posTransform.text, 43, 97
print.CELL_META, 101

rainfallTransform, 39, 101
rand_color, 102
read.chromInfo, 49, 103
read.cytoband, 28, 49, 50, 86, 104
reverse.circlize, 105

set.current.cell, 106
show.index, 107
smartAlign, 108
sRGB, 77
Subset.CELL_META (\$.CELL_META), 110

text, 65

uh, 55, 70, 108
ux, 109
uy, 110