Package ‘circlize’

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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.

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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
- circospolygon
- 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.initializeWithIdeoagram`
• `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**

```r
# 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("#FF000080", 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

```r
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)
lr = data.frame(sample(letters, 4), sample(letters, 4), 1:4)
adjacencyList2Matrix(lr)
adjacencyList2Matrix(lr, square = TRUE)
```

Description

Calculate gap to make two Chord diagram with same scale

Usage

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

Arguments

- **x1**: The matrix or the data frame for the first Chord diagram.
- **x2**: The matrix or the data frame for the second Chord diagram.
- **big.gap**: big.gap for the first Chord diagram.
- **small.gap**: small.gap 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

```r
# There is no example
NULL
```
**CELL_META**

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

---

**Description**

Easy to way to get meta data in the current cell

**Usage**

```r
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**

```r
df(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**

```r
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)
```
chordDiagram

```
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.on.top = 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` or `chordDiagramFromDataFrame`
- **column.col**: pass to `chordDiagramFromMatrix` or `chordDiagramFromDataFrame`
- **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`
chordDiagram

link.sort pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.decreasing pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.arr.length pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.arr.width pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.arr.type pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.arr.lty pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.arr.lwd pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.largest.ontop pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.visible pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
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 circos.link.

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-abs(value), x1)
x2 and position of the link on the "to" sector, the interval for the link on the "from" sector is c(x2-abs(value), x2)
chordDiagramFromDataFrame

References

See Also

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()

cordDiagramFromDataFrame

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.on.top = FALSE, link.visible = TRUE,
link.rank = seq_len(nrow(df)),)
chordDiagramFromDataFrame

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

Arguments

df          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 col is specified as a color
            mapping function. The sectors in the plot will be union(df[[1]], df[[2]]).

grid.col    Grid colors which correspond to sectors. The length of the vector should be
            either 1 or the number of sectors. It’s preferred that grid.col is a named vector
            of which names correspond to sectors. If it is not a named vector, the order of
            grid.col corresponds to order of sectors.

grid.border border for grids. If it is NULL, the border color is same as grid color

transparency Transparency of link colors, 0 means no transparency and 1 means full trans-
           parency. If transparency is already set in col or row.col or column.col, this
            argument will be ignored. NA also ignores this argument.

col         Colors for links. It can be a vector which corresponds to connections in df, or
            a function which generate colors according to values (the third column) in df,
            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.

order       Order of sectors. Default order is union(df[[1]], df[[2]]).

directional Whether links have directions. 1 means the direction is from the first column
            in df 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 df.

xmax        maximum value on x-axes, the value should be a named vector.

direction.type 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 comming 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 df. Note if you want to set both
            diffHeight and arrows for certain links, you need to embed these two options
            into one string such as "diffHeight+arrows".

diffHeight  The difference of height between two 'roots' if directional 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 df.

reduce      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.

self.link   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.on.top**
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
mat A table which represents as a numeric matrix.
grid.col Grid colors which correspond to matrix rows/columns (or sectors). The length of the vector should be either 1 or length(union(rownames(mat), colnames(mat))). It's preferred that grid.col is a named vector of which names correspond to sectors. If it is not a named vector, the order of grid.col corresponds to order of sectors.
grid.border  border for grids. If it is NULL, the border color is same as grid color.
transparency  Transparency of link colors, 0 means no transparency and 1 means full transparency. If transparency is already set in col or row.col or column.col, this argument will be ignored. Nalso ignores this argument.
col  Colors for links. It can be a matrix which corresponds to mat, or a function which generate colors according to values in mat, 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 colorRamp2 to generate a function which maps values to colors.
row.col  Colors for links. Links from the same row in mat will have the same color. Length should be same as number of rows in mat. This argument only works when col is set to NULL.
column.col  Colors for links. Links from the same column in mat will have the same color. Length should be same as number of columns in mat. This argument only works when col and row.col is set to NULL.
order  Order of sectors. Default order is union(df[[1]], df[[2]]).
directional  Whether links have directions. 1 means the direction is from the first column in df to the second column, -1 is the reverse, 0 is no direction, and 2 for two directional. Same setting as link.border.
xmax  maximum value on x-axes, the value should be a named vector.
direction.type  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 link.border. Note if you want to set both diffHeight and arrows for certain links, you need to embed these two options into one string such as "diffHeight+arrows".
diffHeight  The difference of height between two 'roots' if directional 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.
reduce  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.
self.link  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.
symmetric  Whether the matrix is symmetric. If the value is set to TRUE, only lower triangular matrix without the diagonal will be used.
keep.diagonal  If the matrix is specified as symmetric, whether keep diagonal for visualization.
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 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 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.
circlize

Examples

# There is no example
NULL

---

circlize  
*Convert to polar coordinate system*

---

Description

Convert to polar coordinate system

Usage

```r
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

```r
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

**Description**

Draw arrow which is parallel to the circle

**Usage**

```r
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.currentsector.index(), track.index = get.currenttrack.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, 0.5, width = 0.1, y = 0.5, 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(1, 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 = 0.8)
circos.clear()
**Arguments**

- **h**  
  Position of the x-axis, can be "top", "bottom" or a numeric value

- **major.at**  
  If it is numeric vector, it identifies the positions of the major ticks. It can exceed xlim value and the exceeding part would be trimmed automatically. If it is NULL, about every 10 degrees there is a major tick.

- **labels**  
  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.

- **major.tick**  
  Whether to draw major tick. If it is set to FALSE, there would be no minor ticks.

- **sector.index**  
  Index for the sector

- **track.index**  
  Index for the track

- **labels.font**  
  font style for the axis labels

- **labels.cex**  
  font size for the axis labels

- **labels.direction**  
  deprecated, use facing instead.

- **labels.facing**  
  facing of labels on axis, passing to circos.text

- **labels.niceFacing**  
  Should facing of axis labels be human-easy

- **direction**  
  whether the axis ticks point to the outside or inside of the circle.

- **minor.ticks**  
  Number of minor ticks between two close major ticks.

- **major.tick.percentage**  
  not used. Length of the major ticks. It is the percentage to the height of the cell.

- **labels.away.percentage**  
  not used. The distance for the axis labels to the major ticks. It is the percentage to the height of the cell.

- **major.tick.length**  
  length of the major ticks, measured in "current" data coordinate. convert_y can be used to convert an absolute unit to the data coordinate.

- **lwd**  
  line width for ticks

- **col**  
  color for the axes

- **labels.col**  
  color for the labels

- **labels.pos.adjust**  
  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**

See Also

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

Examples

```r
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()
```

```r
## 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")
```

```r
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
```
circos.clear

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

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 dendograms 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 $0.5$, $1.5$, ..., $n - 0.5$. 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.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**

```r
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**

Examples

```r
## 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

```r
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

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

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

---

`circos.genomicInitialize`

Initialize circular plot with any genomic data

**Description**

Initialize circular plot with any genomic data

**Usage**

```r
ccircos.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


Examples

```r
## 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)
```
ciccos.genomicLabels  

Add labels to specified genomic regions

Description

Add labels to specified genomic regions

Usage

ciccos.genomicLabels(bed, labels = NULL, labels.column = NULL,
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 = ciccos.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
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 connection 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

```r
## Not run:
circos.initializeWithIdeogram(plotType = c("labels", "axis"))
bed = generateRandomBed(nr = 100, fun = function(k) sample(letters, k, replace = TRUE))
bed[1, 4] = "aaaaaaaa"
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`
circos.genomicLines

**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**


**Examples**

```r
## Not run:

### test bed

circos.par("track.height" = 0.4)
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)
```
Add links from two sets of genomic positions

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 circos.link, length can be either one or nrow of region1
lty Pass to circos.link, length can be either one or nrow of region1
border Pass to circos.link, length can be either one or nrow of region1
... Pass to circos.link
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


Examples

```R
## 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

```R
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.
circle.genomicPoints

sector.index  Pass to circle.points
track.index  Pass to circle.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 circle.points
pch  Type of points. Settings are similar as col. Pass to circle.points
cex  Size of points. Settings are similar as col. Pass to circle.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 circle.genomicTrackPlotRegion.

References


Examples

```r
## Not run:
circo.par("track.height" = 0.1)
circo.initializeWithIedrogram(plotType = NULL)

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

circo.genomicTrackPlotRegion(bed, stack = TRUE, panel.fun = function(region, value, ...) {
  circo.genomicPoints(region, value, pch = 16, cex = 0.5, ...)
  i = getI(...)
  cell.xlim = get.cell.meta.data("cell.xlim")
  circo.lines(cell.xlim, c(i, i), lty = 2, col = "#00000040")
})

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

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

circos.genomicPosTransformLines

Add genomic position transformation lines between tracks

## Description

Add genomic position transformation lines between tracks

## Usage

```r
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

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


Examples

```r
## 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)
```
```r
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 normalize_to_width is FALSE, the value should correspond to log10(dist+1), and if normalize_to_width is TRUE, the value should correspond to log2(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.
**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**


**Examples**

```r
# 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("#FF0000", "#0000FF"))
circos.genomicDensity(bed_list[[1]], col = c("#FF0000"), track.height = 0.1)
circos.genomicDensity(bed_list[[2]], col = c("#0000FF"), 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


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),
```
```r
border = NA, ...) 
i = getI(...)  
cell.xlim = get.cell.meta.data("cell.xlim")  
#circos.lines(cell.xlim, c(i, i), lty = 2, col = "#00000000")  
}, bg.border = NA)
circos.genomicPostTransformLines(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 = "#00000000")  
}, bg.border = NA)
circos.genomicPostTransformLines(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 = "#00000000")  
}, 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]])),
```
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, ...)
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

...: Mysterious parameters

Details

The function is a low-level graphical function and usually is put in panel.fun when using circos.genomicTrackPlotRegion.

References


Examples

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

bed = generateRandomBed(nr = 20)

circo.genomicTrackPlotRegion(bed, ylim = c(0, 1), panel.fun = function(region, value, ...) {
  circo.genomicText(region, value, y = 0.5, labels = "text", ...)
})

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

circo.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}, ...)

---

circosNgenomictrack

Create a track for genomic graphics

Description

Create a track for genomic graphics

Usage

circosNgenomictrackHNNNI

Arguments

NNN pass to circos.genomictrackplotregion

Details

shortcut function of circos.genomictrackplotregion.
Arguments

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

... Pass to circos.trackPlotRegion.

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, ...). 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


Examples

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

---

circos.info  

*Get information of the circular plot*

Description

Get information of the circular plot

Usage

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

Arguments

- `sector.index`: Which sectors you want to look at? It can be a vector.
- `track.index`: Which tracks you want to look at? It can be a vector.
- `plot`: 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**


**Examples**

```r
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()
```

---

**Description**

Initialize the circular layout

**Usage**

```r
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


See Also


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

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

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-defined code. Refer to vignette for demonstration.

**References**


**Examples**

```r
## 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)
```
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 = "1", 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("1", "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 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 TRUE.
References


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 percent-
                age 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 big.arrow.
arr.length    Length of the arrows, measured in 'cm', pass to Arrowhead. If arr.type is set
               to big.arrow, 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/B%C3%A9zier_curve#Rational_B%C3%A9zier_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


See Also


Examples

```r
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

Examples

```r
## 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.]+", "\1", df.interval_x))
df$end = as.numeric(gsub("[^\d.]+", "\1", df.interval_x))
mm = sample(unique(df$name), 20)
df2 = df[df$name %in% mm, ]
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.par

\begin{verbatim}
  circos.points(x, y, pch = 16, cex = 0.5)
  }, bg.col = sector_col[zoom_sector$cat],
  track.margin = c(0, 0))
}
circos.nested(f1, f2, correspondance, connection_col = sector_col[correspondance[[1]]])

## End(Not run)
\end{verbatim}

---

**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 (2pi) divided by unit.circle.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.

canvasxlim  The coordinate for the canvas. Because circlize draws everything (or almost everything) inside the unit circle, the default canvasxlim and canvarylim 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 canvasxlim and canvarylim, you can draw part of the circle. E.g. setting canvasxlim to c(0, 1) and canvasyylim to c(0, 1) would only draw circle in the region of (0, pi/2).

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

clockwise  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, canvasxlim, canvarylim and clockwise 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


Examples

# There is no example
NULL
circos.points

Add points to a plotting region

Description

Add points to a plotting region

Usage

```r
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

- `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
- `pch` : Point type
- `col` : Point color
- `cex` : Point size
- `bg` : 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 "current" cell.

References

Examples

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

circons.polygon

*Draw polygon*

Description

Draw polygon

Usage

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

Arguments

- **x**: Data points on x-axis
- **y**: Data points on y-axis
- **sector.index**: Index for the sector
- **track.index**: Index for the track
- ... pass to `polygon`

Details

similar as `polygon`.

Note: start point should overlap with the end point,

References


Examples

```
set.seed(123)
factors = letters[1:4]
circons.initialize(factors, xlim = c(0, 1))
circons.trackPlotRegion(ylim = c(-3, 3), track.height = 0.4, panel.fun = function(x, y) {
x1 = runif(20)
y1 = x1 + rnorm(20)
   or = order(x1)
```
\begin{verbatim}
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 = "#CCCCC", border = NA)
circos points(x1, y1, cex = 0.5)
circos lines(x1, loess.predict$fit)
}
circos.clear()
\end{verbatim}

### Description

Add raster images

### Usage

```r
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"))
circo$par("cell.padding" = c(0, 0, 0, 0))
circos.initialize(letters[1:16], xlim = c(0, 1))
circos.track(ylim = c(0, 1), xlim = c(0, 1), panel.fun = function(x, y) {
  img = img_list[[CELL_META$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
cordinate, then it is rectangle. in the polar coordinate, the up and bottom edge become two arcs.
This function can be vectorized.

References


Examples

   # There is no example
   NULL

Draw segments through pairwise of points

circos.segments

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

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

Description

Draw text in a cell

Usage

```r
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


See Also


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.trackHist

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


Examples

```r
## 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

```r
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


Examples

# There is no example
NULL

---

### `circos.trackPlotRegion`

Create plotting regions for a whole track

Description

Create plotting regions for a whole track

Usage

```r
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 `panel.fun` 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 `ylim`. Normally, all cells on a same track should have same `ylim`.
- **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.
trackNheight Height of the track. It is the percentage to the radius of the unit circles. The value can be set by \texttt{uh} to an absolute unit. If updating a track (with proper trackNindex value), this argument is ignored.

trackNmargin only affect current track
cellNpadding only affect current track

bgNcol Background color for the plotting regions. It can be vector which has the same length of sectors.
bgNborder Color for the border of the plotting regions. It can be vector which has the same length of sectors.
bgNlty Line style for the border of the plotting regions. It can be vector which has the same length of sectors.
bgNlwd Line width for the border of the plotting regions. It can be vector which has the same length of sectors.

panelNfun 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 \texttt{circos.points}, \texttt{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 \texttt{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-axes either by \texttt{y} or \texttt{ylim}. If \texttt{y} is set, it must has the same length as factors and the \texttt{ylim} for each cell is calculated from \texttt{y} values. Also, the \texttt{ylim} can be specified from \texttt{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 \texttt{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

\texttt{panelNfun} provides a convenient way to add graphics in each cell when initializing the tracks. The self-defined function needs two arguments: \texttt{x} and \texttt{y} which correspond to the data points in the current cell. When factors, \texttt{x}, and \texttt{y} are set in \texttt{circos.trackPlotRegion}, a subset of \texttt{x} and \texttt{y} are split by factors and are sent to \texttt{panelNfun} in the "current" cell. \texttt{circos.trackPlotRegion} creates plotting regions one by one on the track and \texttt{panelNfun} 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


See Also


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()
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


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(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?
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**


**Examples**

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

---

circos.update  
Create plotting regions for a whole track

**Description**

Create plotting regions for a whole track

**Usage**

circos.update(...)

**Arguments**

...  
pass to `circos.updatePlotRegion`

**Details**

shortcut function of `circos.updatePlotRegion`.

**Examples**

```r
# 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**

```r
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**

- `sector.index`: Index for the sector.
- `track.index`: Index for the track.
- `bg.col`: Background color for the plotting region.
- `bg.border`: Color for the border of the plotting region.
- `bg.lty`: Line style for the border of the plotting region.
- `bg.lwd`: 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**


**Examples**

```r
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 = "#FF000000")
circos.clear()
```
**circos.xaxis**  
*Draw x-axis*

**Description**
- Draw x-axis

**Usage**
```r
circos.xaxis(...)
```

**Arguments**
- `...` - all pass to `circos.axis`

**Examples**
```r
# There is no example
NULL
```

---

**circos.yaxis**  
*Draw y-axis*

**Description**
- Draw y-axis

**Usage**
```r
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**
- `side` - add the y-axis on the left or right of the cell
- `at` - If it is numeric vector, it identifies the positions of the ticks. It can exceed ylim value and the exceeding part would be trimmed automatically.
- `labels` - 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.
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

```r
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

r
  red channel in \textit{sRGB} color space, value should be between 0 and 1. The r, g and b arguments can be wrapped into one variable which is either a three-column matrix or a vector of colors.

g
  green channel in \textit{sRGB} color space, value should be between 0 and 1.

b
  blue channel in \textit{sRGB} color space, value should be between 0 and 1.

col_fun
  the color mapping function generated by \texttt{colorRamp2}.

Details

\texttt{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

\begin{verbatim}
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)
\end{verbatim}

---

\texttt{colorRamp2} \hspace{1cm} \textit{Color interpolation}

Description

Color interpolation

Usage

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

- **breaks**: A vector indicating numeric breaks
- **colors**: A vector of colors which correspond to values in `breaks`
- **transparency**: A single value in \([0, 1]\). 0 refers to no transparency and 1 refers to full transparency
- **space**: 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


See Also

- `col2value` converts back to the original values by providing the color mapping function generated by `colorRamp2`.

Examples

```r
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**

Convert units

### Description

Convert units

### Usage

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

### Arguments

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

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
## cytoband.col

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

### Description

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

### Usage

```r
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](http://circos.ca/tutorials/course/slides/session-2.pdf), page 42.

### References


### Examples

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

## See Also

`convert_x` converts on x direction.

## Examples

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

# not run
```
**degree**

*Mark the value as a degree value*

**Description**

Mark the value as a degree value

**Usage**

```r
degree(x)
```

**Arguments**

- `x`: degree value

**Value**

a degree object

**Examples**

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

---

**draw.sector**

*Draw sectors or rings in a circle*

**Description**

Draw sectors or rings in a circle

**Usage**

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

**Arguments**

- `start`: start degree for the sector
- `end`: 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


Examples

```r
plot(c(-1, 1), c(-1, 1), type = "n", axes = FALSE, ann = FALSE, asp = 1)
draw.sector(30, 0)
draw.sector(30, 60, rou1 = 0.8, rou2 = 0.5, clock.wise = FALSE, col = "#FF000000")
draw.sector(350, 1000, col = "#FF000000", 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 = "#0000FF00")

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 = "#0000FF40")
circos.clear()
```
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 \texttt{circos.text}

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
# There is no example
NULL

generateRandomBed Generate random genomic data

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 \texttt{read.cytoband}
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 \textit{nr}.


\textbf{Examples}

\begin{verbatim}
bed = generateRandomBed()
bed = generateRandomBed(nr = 200, nc = 4)
bed = generateRandomBed(fun = function(k) runif(k))
\end{verbatim}

\textbf{genomicDensity} \hspace{1cm} \textit{Calculate genomic region density}

\textbf{Description}

Calculate genomic region density

\textbf{Usage}

\begin{verbatim}
genomicDensity(region, window.size = 1e7, n.window = NULL, overlap = TRUE, chr.len = NULL)
\end{verbatim}

\textbf{Arguments}

\begin{verbatim}
region \hspace{1cm} \text{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 \hspace{1cm} \text{Window size to calculate genomic density}
n.window \hspace{1cm} \text{number of windows, if it is specified, window.size is ignored}
overlap \hspace{1cm} \text{Whether two neighbouring windows have half overlap}
chr.len \hspace{1cm} \text{the chromosome length. The value should be named vector}
\end{verbatim}

\textbf{Details}

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

\textbf{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.
get.all.sector.index

References


Examples

```r
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

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

Details

It simply returns a vector of all sector index.

References


Examples

```r
## 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**  
```r
get.all.track.index()
```

**Details**  
It simply returns a vector of all track index.

**Examples**  
```r
## 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**  
```r
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
get.cell.meta.data

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


See Also

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

Examples

```r
def = letters[1:4]
circos.initialize(def, 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**


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

**Value**

Simply returns the name of current sector

**Examples**

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

**Description**

Get current track index

**Usage**

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

**Value**

Simply returns the numeric index for the current track.

**Examples**

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

**getI**

*Which data that panel.fun is using*

**Description**

Which data that panel.fun is using

**Usage**

```r
geti(...)```

**Arguments**

```r
...  # Invisible arguments that users do not need to care```
highlight.chromosome

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


Examples

```r
# 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

Examples

## Not run:

```r
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)
```

### Description

Highlight sectors and tracks
highlight.sector

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 absolute 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()
posTransform.default  

Genomic position transformation function

Description
Genomic position transformation function

Usage
posTransform.default(region, ...)

Arguments

region  
Genomic positions at a single chromosome. It is a data frame with two columns which are start position and end position.

...  
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

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[l]),  
border = f(value[l]), 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)

---

posTransform.text  Genomic position transformation function specifically for text

**Description**

Genomic position transformation function specifically for text

**Usage**

```r
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
The `extend` parameter extends labels 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

```r
## 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)
```
```r
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
```
print.CELL_META

Description
Print CELL_META

Usage
## S3 method for class 'CELL_META'
print(x, ...)
**rainfallTransform**

**Arguments**

- `x` input
- `...` additional parameters

**Examples**

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

---

**rainfallTransform**  *Calculate inter-distance of genomic regions*

**Description**

Calculate inter-distance of genomic regions

**Usage**

```r
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**

rand_color

Examples

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

---

**rand_color**  
*Generate random colors*

### Description

Generate random colors

### Usage

```r
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"))

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

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
```r
reverse.circlize

Value

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

chr chromosome  Sorted chromosome names

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

References


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

```r
df(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()
```

Description

Set flag to current cell

Usage

```r
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

```r
df(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**


**Examples**

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

---

smartAlign  

*Adjust positions of text*

**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

Convert units

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

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

Description

Convert unit on y direction in data coordinate

Usage

```c
uy(…)
```

Arguments

```c
… pass to convert_y
```

Details

This function is same as convert_y.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

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

Easy to way to get meta data in the current cell

Usage

```r
## 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

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