Package ‘circlize’

February 20, 2024

**Type** Package

**Title** Circular Visualization

**Version** 0.4.16

**Date** 2024-02-20

**Depends** R (>= 4.0.0), graphics

**Imports** GlobalOptions (>= 0.1.2), shape, grDevices, utils, stats, colorspace, methods, grid

**Suggests** knitr, dendextend (>= 1.0.1), ComplexHeatmap (>= 2.0.0), gridBase, png, markdown, bezier, covr, rmarkdown

**VignetteBuilder** knitr

**Description** Circular layout is an efficient way for the visualization of huge amounts of information. Here this package provides an implementation of circular layout generation in R as well as an enhancement of available software. The flexibility of the package is based on the usage of low-level graphics functions such that self-defined high-level graphics can be easily implemented by users for specific purposes. Together with the seamless connection between the powerful computational and visual environment in R, it gives users more convenience and freedom to design figures for better understanding complex patterns behind multiple dimensional data. The package is described in Gu et al. 2014 <doi:10.1093/bioinformatics/btu393>.

**URL** https://github.com/jokergoo/circlize,


**License** MIT + file LICENSE

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2024-02-20 10:30:02 UTC
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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`
- `circos.polygon`
- `circos.segments`
- `circos.text`
- `circos.axis, circos.xaxis, circos.yaxis`
- `circos.barplot`
- `circos.boxplot`
- `circos.violin`
- `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`

Draw circular heatmaps

- `circos.heatmap`

Functions to arrange circular layout:

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

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

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

Functions to initialize circos plot with genomic coordinates:

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

Functions to arrange genomic circular layout:

- `circos.genomicTrack`

Functions to add basic graphics in genomic scale:

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

Functions with specific purpose:
- `circos.genomicDensity`
- `circos.genomicRainfall`
- `circos.genomicIdeogram`
- `circos.genomicHeatmap`
- `circos.genomicLabels`

Finally, function that draws Chord diagram:

- `chordDiagram`

Please refer to the vignettes (https://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**

```r
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**

```r
add_transparency("red", 0.5)
add_transparency(1, 0.5)
add_transparency("#FF000080", 0.2)
```
adjacencyList2Matrix  
Convert adjacency list to an adjacency matrix

Description

Convert adjacency list to an adjacency matrix

Usage

adjacencyList2Matrix(lt, square = FALSE)

Arguments

lt  A data frame which contains adjacency list.
square  Should the returned matrix be a square matrix?

Examples

set.seed(123)
df = data.frame(from = sample(letters, 10, replace = TRUE),
                  to = sample(letters, 10, replace = TRUE),
                  value = 1:10)
adacencyList2Matrix(df)
adacencyList2Matrix(df, square = TRUE)

adjacencyMatrix2List  
Convert adjacency matrix to an adjacency list

Description

Convert adjacency matrix to an adjacency list

Usage

adjacencyMatrix2List(mat, keep.zero = FALSE)

Arguments

mat  A numeric matrix.
keep.zero  Whether to keep the interactions with value zero.

Examples

set.seed(999)
mat = matrix(sample(18, 18), 3, 6)
rownames(mat) = paste0("S", 1:3)
colnames(mat) = paste0("E", 1:6)
adacencyMatrix2List(mat)
arrange_links_evenly  Arrange links evenly on each sector

Description

Arrange links evenly on each sector

Usage

arrange_links_evenly(df, directional = 0)

Arguments

df  A data frame with two columns. The values should only contain sector names.
directional  Whether the links are directional.

Details

This function only deals with single-line links.

Value

A data frame with four columns of the sectors and the positions of the links.

Examples

sectors = letters[1:20]
df = data.frame(from = sample(sectors, 40, replace = TRUE),
             to = sample(sectors, 40, replace = TRUE),
             stringsAsFactors = FALSE)
df = unique(df)
df = df[!df$from == df$to, ]
circos.initialize(sectors, 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$sector.index)
})
df2 = arrange_links_evenly(df, directional = 1)
for(i in seq_len(nrow(df2))) {
    s1 = df$from[i]
    s2 = df$to[i]
    circos.link(df2[i, "sector1"], df2[i, "pos1"],
                df2[i, "sector2"], df2[i, "pos2"],
                directional = 1)
}

**calc_gap**  

*Calculate gaps to make two Chord diagrams in the same scale*

**Description**

Calculate gaps to make two Chord diagrams in the same scale.

**Usage**

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**

Both Chord diagrams should be both two-group Chord diagram.

**Value**

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

**Examples**

```r
set.seed(123)
mat1 = matrix(sample(20, 25, replace = TRUE), 5)
chordDiagram(mat1, directional = 1, grid.col = rep(1:5, 2), transparency = 0.5,
            big.gap = 10, small.gap = 1)
mat2 = mat1 / 2
gap = calc_gap(mat1, mat2, big.gap = 10, small.gap = 1)
chordDiagram(mat2, directional = 1, grid.col = rep(1:5, 2), transparency = 0.5,
            big.gap = gap, small.gap = 1)
```
### CELL_META

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

---

**Description**

Easy way to get meta data in the current cell

**Usage**

CELL_META

**Details**

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

**See Also**

`get.cell.meta.data`

**Examples**

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

x   a matrix or a data frame. The function will pass all argument to \texttt{chordDiagramFromMatrix} or \texttt{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 \texttt{chordDiagramFromMatrix} or \texttt{chordDiagramFromDataFrame}
grid.border   pass to \texttt{chordDiagramFromMatrix} or \texttt{chordDiagramFromDataFrame}
transparency  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
col  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
row.col  pass to chordDiagramFromMatrix
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
link.target.prop  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
target.prop.height  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
reduce  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
self.link  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
preAllocateTracks  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
annotationTrack  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
annotationTrackHeight  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.border  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.lwd  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.lty  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.auto  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
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.arr.col  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.largest.ontop  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.visible  pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.rank  This is argument is removed.
link.zindex  order to add links to the circle, a large value means to add it later.
link.overlap  pass to `chordDiagramFromMatrix` or `chordDiagramFromDataFrame`
scale  scale each sector to same width
group  It contains the group labels and the sector names are used as the names in the vector.
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/](http://circos.ca/intro/tabular_visualization/)), especially useful when the table represents information of directional relations. This function visualize tables in a circular way.

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

Value

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

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

See Also

Examples

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

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

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

---

**chordDiagramFromDataFrame**

*Plot Chord Diagram from a data frame*

**Description**

Plot Chord Diagram from a data frame

**Usage**

```r
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"),
  link.target.prop = TRUE,
  target.prop.height = mm_h(1),
  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.auto = TRUE,
)```
link.sort = "default",
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,
link.zindex = seq_len(nrow(df)),
link.overlap = FALSE,
scale = FALSE,
group = NULL,
big.gap = 10,
small.gap = 1,
plot = TRUE,
...)

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.

link.target.prop If the Chord diagram is directional, for each source sector, whether to draw bars that shows the proportion of target sectors.

target.prop.height The height of the bars when link.target.prop is turned on.

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.auto Ignored.

link.sort whether sort links on every sector based on the width of the links on it. The value can be logical. The value can also be string "default" which automatically adjusts link orders so that links have minimal overall intersections. The value can also be a string "asis" and it is only workable for input as a data frame so that the links have the same orders as in the original data frame. for link.sort

link.decreasing for link.sort
chordDiagramFromDataFrame

link.arr.length
pass to `circos.link`. The format of this argument is same as `link.lwd`.

link.arr.width
pass to `Arrowhead`. The format of this argument is same as `link.lwd`.

link.arr.type
pass to `circos.link`, same settings as `link.lwd`. Default value is `triangle`.

link.arr.col
color or the single line link which is put in the center of the belt. The format of this argument is same as `link.lwd`.

link.arr.lwd
line width of the single line link which is put in the center of the belt. The format of this argument is same as `link.lwd`.

link.arr.lty
line type of the single line link which is put in the center of the belt. The format of this argument is same as `link.lwd`.

link.largest.ontop
controls the order of adding links, whether based on the absolute value?

link.rank
This is argument is removed.

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.zindex
order to add links to the circle, a large value means to add it later.

link.overlap
if it is a directional Chord Diagram, whether the links that come or end in a same sector overlap?

scale
scale each sector to same width

group
It contains the group labels and the sector names are used as the names in the vector.

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.

plot
Internally used.

... 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`.

See Also

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 = mm_h(2),
  link.target.prop = TRUE,
  target.prop.height = mm_h(1),
  reduce = 1e-5,
  xmax = NULL,
  self.link = 2,
  symmetric = FALSE,
  keep.diagonal = FALSE,
  preAllocateTracks = NULL,
  annotationTrack = c("name", "grid", "axis"),
  annotationTrackHeight = mm_h(c(3, 2)),
  link.border = NA,
  link.lwd = par("lwd"),
  link.lty = par("lty"),
  link.auto = TRUE,
  link.sort = "default",
  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,
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(unique(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 the order of sectors.
- **grid.border**: Border for grids. If it is `NULL`, the border color is the same as the 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. `NA` also ignores this argument.
- **col**: Colors for links. It can be a matrix which corresponds to `mat`, or a function which generates colors according to values in `mat`, or a single value which means all links have the same color, 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 the same as the 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 the same as the 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 the 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.

link.target.prop  If the Chord diagram is directional, for each source sector, whether to draw bars that shows the proportion of target sectors.

target.prop.height  The height of the bars when link.target.prop is turned on.

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.auto  Ignored.

link.sort  whether sort links on every sector based on the width of the links on it. The value can be logical. The value can also be string "default" which automatically adjusts link orders so that links have minimal overall intersections. The value can also be a string "asis" and it is only workable for input as a data frame so that the links have the same orders as in the original data frame.

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  This is argument is removed.
link.zindex  order to add links to the circle, a large value means to add it later.
link.overlap  if it is a directional Chord Diagram, whether the links that come or end in a same sector overlap?
scale  scale each sector to same width
group  It contains the group labels and the sector names are used as the names in the vector.
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.

See Also


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

*Draw arrow which is parallel to the circle*

**Description**

Draw arrow which is parallel to the circle

**Usage**

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

**Arguments**

- **x1**: Start position of the arrow on the x-axis.
- **x2**: End position of the arrow on the x-axis. Note x2 should be larger than x1. The direction of arrows can be controlled by `arrow.position` argument.
- **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. If you want to the arrow in the reversed direction, set this value to "start".
- **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). For the values of width, arrow.head.Length, arrow.head.width, they can be set with mm_y/cm_y/inches_y in absolute units.

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

Author(s)

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See Also


Examples

```r
op = par(no.readonly = TRUE)
par(mfrow = c(1, 2))
circos.initialize(letters[1:4], xlim = c(0, 1))
col = rand_color(4)
tail = c("point", "normal", "point", "normal")
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
circos.arrow(x1 = 0, x2 = 1, y = 0.5, width = 0.4, 
arrow.head.width = 0.6, arrow.head.length = cm_x(1),
col = col[CELL_META$sector.numeric.index], 
tail = tail[CELL_META$sector.numeric.index]) 
}, bg.border = NA, track.height = 0.4)
circos.clear()
circos.initialize(letters[1:4], xlim = c(0, 1))
tail = c("point", "normal", "point", "normal")
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
circos.arrow(x1 = 0, x2 = 1, y = 0.5, width = 0.4, 
arrow.head.width = 0.6, arrow.head.length = cm_x(1),
col = col[CELL_META$sector.numeric.index], 
tail = tail[CELL_META$sector.numeric.index], 
arrow.position = "start") 
}, bg.border = NA, track.height = 0.4)
par(op)
```

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

---

**circos.axis**  
*Draw x-axis*

**Description**

Draw x-axis

**Usage**

```r
circos.axis(
    h = "top",
    major.at = NULL,
    labels = TRUE,
    major.tick = TRUE,
    sector.index = get.current.sector.index(),
    track.index = get.current.track.index(),
    labels.font = par("font"),
    labels.cex = par("cex"),
    labels.facing = "inside",
    labels.direction = NULL,
    labels.niceFacing = TRUE,
    direction = c("outside", "inside"),
    minor.ticks = 4,
    major.tick.length = mm_y(1),
    major.tick.percentage = 0.5,
    lwd = par("lwd"),
    col = par("col"),
    labels.col = par("col"),
    labels.pos.adjust = TRUE)
```

**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 will be no minor ticks either.
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.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.
major.tick.percentage  Not used any more, please directly use major.tick.length.
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 so that the first label align to its left and the last label align to its right if they exceed the range on axes. The value can be a vector of length two which correspond to the first label and the last label.

details
It only draws axes on x-direction.

see also

circos.yaxis draws axes on y-direction.


Examples

sectors = letters[1:8]
circos.par(points.overflow.warning = FALSE)
circos.initialize(sectors, xlim = c(0, 10))
circos.trackPlotRegion(sectors, 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(sectors, ylim = c(0, 10))
circos.axis(sector.index = "a")
circos.barplot

Draw barplots
Description

Draw barplots

Usage

circos.barplot(value, pos, bar_width = 0.6,
    col = NA, border = "black", lwd = par("lwd"), lty = par("lty"),
    sector.index = get.current.sector.index(),
    track.index = get.current.track.index())

Arguments

value A numeric vector or a matrix. If it is a matrix, columns correspond to the height of bars.
pos Positions of the bars.
bar_width Width of bars. It assumes the bars locating at x = 1, 2, ....
col Filled color of bars.
border Color for the border.
lwd Line width.
lty Line style.
sector.index Index of sector.
track.index Index of track.

Details

If the input variable is a matrix, it draws a stacked barplot.

Please note, the x-values of barplots are normally integer indices. Just be careful when initializing the circular layout.

Examples

circos.initialize(letters[1:4], xlim = c(0, 10))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
    value = runif(10)
    circos.barplot(value, 1:10 - 0.5, col = 1:10)
})
circos.track(ylim = c(-1, 1), panel.fun = function(x, y) {
    value = runif(10, min = -1, max = 1)
    circos.barplot(value, 1:10 - 0.5, col = ifelse(value > 0, 2, 3))
})
circos.clear()

circos.initialize(letters[1:4], xlim = c(0, 10))
circos.track(ylim = c(0, 4), panel.fun = function(x, y) {
    value = matrix(runif(10*4), ncol = 4)
    circos.barplot(value, 1:10 - 0.5, col = 2:5)
})
circos.clear()
Description

Draw boxplots

Usage

circos.boxplot(value, pos, outline = TRUE, box_width = 0.6,
               col = NA, border = "black", lwd = par("lwd"), lty = par("lty"),
               cex = par("cex"), pch = 1, pt.col = par("col"),
               sector.index = get.current.sector.index(),
               track.index = get.current.track.index())

Arguments

tvalue: A numeric vector, a matrix or a list. If it is a matrix, boxplots are made by columns (each column is a box).
pos: Positions of the boxes.
outline: Whether to draw outliers.
box_width: Width of boxes.
col: Filled color of boxes.
border: Color for the border as well as the quantile lines.
lwd: Line width.
lty: Line style

cex: Point size.
pch: Point type.
pt.col: Point color.
sector.index: Index of sector.
track.index: Index of track.

Details

Please note, the x-values of boxplots are normally integer indices. Just be careful when initializing the circular layout.

Examples

circos.initialize(letters[1:4], xlim = c(0, 10))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
    for(pos in seq(0.5, 9.5, by = 1)) {
        value = runif(10)
        circos.boxplot(value, pos)

}
)
circos.clear()
circos.initialize(letters[1:4], xlim = c(0, 10))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  value = replicate(runif(10), n = 10, simplify = FALSE)
circos.boxplot(value, 1:10 - 0.5, col = 1:10)
})
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.

Examples
# There is no example
NULL

circos.connect
Draw connecting lines/ribbons between two sets of points

Description
Draw connecting lines/ribbons between two sets of points
circos.connect

Usage

    circos.connect(x0, y0, x1, y1,
        sector.index = get.current.sector.index(),
        track.index = get.current.track.index(),
        type = c("normal", "segments", "bezier"),
        segments.ratio = c(1, 1, 1),
        col = par("col"),
        border = "black",
        lwd = par("lwd"),
        lty = par("lty"),
        ...
    )

Arguments

  x0             x coordinates for point set 1. The value can also be a two-column matrix.
  y0             y coordinates for point set 1.
  x1             x coordinates for point set 2. The value can also be a two-column matrix.
  y1             y coordinates for point set 2.
  sector.index   Index for the sector.
  track.index    Index for the track.
  type           Which type of connections. Values can be "normal", "segments" and "bezier".
  segments.ratio When type is set to segments, each connecting line is segmented into three parts. This argument controls the length of the three parts of sub-segments.
  col            Color of the segments.
  border         Border color of the links.
  lwd            Line width of the segments.
  lty            Line type of the segments.
  ...            Other arguments.

Examples

    circos.initialize(c("a"), xlim = c(0, 1))
    circos.track(ylim = c(0, 1), track.height = 0.7, bg.border = NA,
        panel.fun = function(x, y) {
            circos.lines(CELL_META$cell.xlim, rep(CELL_META$cell.ylim[1], 2), col = "#CCCCC"
            circos.lines(CELL_META$cell.xlim, rep(CELL_META$cell.ylim[2], 2), col = "#CCCCC"
            x0 = runif(100)
            x1 = runif(100)

            circos.connect(x0, 0, x1, 1,
                type = "normal", border = NA,
                col = rand_color(100, luminosity = "bright", transparency = 0.75)
            )
        }
    )
    circos.initialize(c("a"), xlim = c(0, 1))
```
circos.track(ylim = c(0, 1), track.height = 0.7, bg.border = NA,
panel.fun = function(x, y) {
  circos.lines(CELL_META$cell.xlim, rep(CELL_META$cell.ylim[1], 2), col = "#CCCCCC")
  circos.lines(CELL_META$cell.xlim, rep(CELL_META$cell.ylim[2], 2), col = "#CCCCCC")
  x0 = runif(100)
  x1 = runif(100)

  circos.connect(x0, 0, x1, 1,
     type = "bezier", border = NA,
     col = rand_color(100, luminosity = "bright", transparency = 0.75))
})
circos.initialize(c("a"), xlim = c(0, 1))
circos.track(ylim = c(0, 1), track.height = 0.7, bg.border = NA,
panel.fun = function(x, y) {
  circos.lines(CELL_META$cell.xlim, rep(CELL_META$cell ylim[1], 2), col = "#CCCCCC")
  circos.lines(CELL_META$cell.xlim, rep(CELL META$cell ylim[2], 2), col = "#CCCCCC")
  x0 = sort(runif(200))
  x1 = sort(runif(200))
  x1 = matrix(x1, ncol = 2, byrow = TRUE)

  circos.connect(x0, 0, x1, 1,
     type = "normal", border = NA,
     col = rand_color(100, luminosity = "bright", transparency = 0.5))
})
circos.initialize(c("a"), xlim = c(0, 1))
circos.track(ylim = c(0, 1), track.height = 0.7, bg.border = NA,
panel.fun = function(x, y) {
  circos.lines(CELL_META$cell.xlim, rep(CELL META$cell ylim[1], 2), col = "#CCCCCC")
  circos.lines(CELL_META$cell.xlim, rep(CELL META$cell ylim[2], 2), col = "#CCCCCC")
  x0 = sort(runif(500))
  x1 = sort(runif(500))
  x1 = matrix(x1, ncol = 2, byrow = TRUE)
  x1 = x1[nrow(x1),]

  l = abs(x0[, 1] - x1[, 1]) < 0.5
  circos.connect(x0[1 ,], 0, x1[1 ,], 1,
     type = "bezier", border = NA,
     col = rand_color(sum(l), luminosity = "bright", transparency = 0.5))
})
```

---

```
Add circular dendrograms
```
circos.dendrogram

Description

Add circular dendrograms

Usage

circos.dendrogram(
  dend,
  facing = c("outside", "inside"),
  max_height = NULL,
  use_x_attr = FALSE,
  sector.index = get.current.sector.index(),
  track.index = get.current.track.index())

Arguments

dend
A dendrogram object.
facing
Is the dendrograms facing inside to the circle or outside?
max_height
Maximum height of the dendrogram. This is important if more than one
dendrograms are drawn in one track and making them comparable. The height of a
dendrogram can be obtained by attr(dend, "height").
use_x_attr
Whether use the x attribute to determine node positions in the dendrogram, used
internally.
sector.index
Index of sector.
track.index
Index of track.

Details

Assuming there are n nodes in the dendrogram, the positions for leaves on x-axis are always 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.

See Also


Examples

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

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

suppressPackageStartupMessages(require(dendextend))
dend = color_branches(dend, k = 6, col = 1:6)
circos.trackPlotRegion(ylim = c(0, max_height), bg.border = NA,
  track.height = 0.4, panel.fun = function(x, y) {
    circos.dendrogram(dend, max_height = max_height)
  })
circos.clear()

---

**circos.genomicAxis**  
*Add genomic axes*

**Description**

Add genomic axes

**Usage**

```r
circos.genomicAxis(
  h = "top",
  major.at = NULL,
  labels = NULL,
  major.by = NULL,
  tickLabelsStartFromZero = TRUE,
  labels.cex = 0.4*par("cex"),
  sector.index = get.current.sector.index(),
  track.index = get.current.track.index(),
  ...
)
```

**Arguments**

- **h**  
  Position of the axes. "top" or "bottom".

- **major.at**  
  Major breaks. If `major.at` is set, `major.by` is ignored.

- **labels**  
  labels corresponding to `major.at`. If `labels` is set, `major.at` must be set.

- **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.
circos.genomicDensity

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.

See Also


Examples

circos.initializeWithIdeogram(chromosome.index = paste0("chr", 1:4), plotType = NULL)
circos.track(ylim = c(0, 1), panel.fun = function(x, y) circos.genomicAxis())
circos.track(ylim = c(0, 1), track.height = 0.1)
circos.track(track.index = get.current.track.index(), panel.fun = function(x, y) {
  circos.genomicAxis(h = "bottom", direction = "inside")
})
circos.clear()

circos.genomicDensity  Calculate and add genomic density track

Description

Calculate and add genomic density track

Usage

circos.genomicDensity(
data,
ylim.force = FALSE,
window.size = NULL,
overlap = TRUE,
count_by = c("percent", "number"),
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. If the input is a list of data frames, there will be multiple density plot in one same track.

ylim.force  Whether to force upper bound of ylim to be 1. Ignored if count_by is set to number.

window.size  Pass to genomicDensity.

overlap  Pass to genomicDensity.

count_by  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. If multiple sets of genomic regions are visualized in one single track, you should set the colors with transparency to distinguish them.

lwd  Width of lines, the same setting as col argument.

lty  Style of lines, the same setting as col argument.

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.

If you have multiple sets of genomic regions, you should make sure the density ranges for all sets are similar, or I suggest you should put them into different tracks. One example can be found in the "Examples" Section where the density range for bed_list[2] is too high compared to the range for bed_list[1], thus, it is better to put the two sets of regions into two separate tracks.

See Also


Examples

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()

############ draw the two densities in one track ############
circos.initializeWithIdeogram(plotType = c("axis", "labels"))
circos.genomicDensity(bed_list, col = c("#FF000080", "#0000FF80"), track.height = 0.2)
circos.clear()

---

circos.genomicHeatmap  Add heatmaps for selected regions

Description
Add heatmaps for selected regions

Usage
circos.genomicHeatmap(
  bed,
  col,
  na_col = "grey",
  numeric.column = NULL,
  border = NA,
  border_lwd = par("lwd"),
  border_lty = par("lty"),
  connection_height = mm_h(5),
  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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>bed</td>
<td>A data frame in bed format, the matrix should be stored from the fourth column.</td>
</tr>
<tr>
<td>col</td>
<td>Colors for the heatmaps. The value can be a matrix or a color mapping function generated by <code>colorRamp2</code>.</td>
</tr>
<tr>
<td>na_col</td>
<td>Color for NA values.</td>
</tr>
<tr>
<td>numeric.column</td>
<td>Column index for the numeric columns. The values can be integer index or character index. By default it takes all numeric columns from the fourth column.</td>
</tr>
<tr>
<td>border</td>
<td>Border of the heatmap grids.</td>
</tr>
<tr>
<td>border_lwd</td>
<td>Line width for borders of heatmap grids.</td>
</tr>
<tr>
<td>border_lty</td>
<td>Line style for borders of heatmap grids.</td>
</tr>
</tbody>
</table>
connection_height

Height of the connection lines. If it is set to NULL, no connection will be drawn. Use \texttt{mm_h/cm_h/inches_h} to set a height in absolute unit.

| line_col | Color of the connection lines. 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.

See Also


Examples

```r
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]])))
```

circos.genomicIdeogram

\textit{Add an ideogram track}

Description

Add an ideogram track

Usage

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

- **cytoband**: A data frame or a file path, pass to `read.cytoband`.
- **species**: Abbreviations of the genome, 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>

**See Also**


**Examples**

```r
circos.initializeWithIdeogram(plotType = c("labels", "axis"))
circos.track(ylim = c(0, 1))
circos.genomicIdeogram()  # put ideogram as the third track
```

---

**Description**

Initialize circular plot with any genomic data

**Usage**

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

data A data frame in bed format.
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.

See Also


Examples

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, tickLabelsStartFromZero = FALSE)
circos.clear()

circos.genomicInitialize(df, major.by = 5000)
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()

---
circos.genomicLabels  
*Add labels to specified genomic regions*

**Description**
Add labels to specified genomic regions

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

**Arguments**
- **bed**: A data frame in bed format.
- **labels**: A vector of labels corresponding to rows in bed.
- **labels.column**: If the label column is already in bed, the index for this column in bed.
circos.genomicLabels

facing  fFacing of the labels. The value can only be "clockwise" or "reverse.clockwise".
niceFacing  Whether automatically adjust the facing of the labels.
col  Color for the labels.
cex  Size of the labels.
font  Font of the labels.
padding  Padding of the labels, the value is the ratio to the height of the label.
connection_height  Height of the connection track.
line_col  Color for the connection lines.
line_lwd  Line width for the connection lines.
line_lty  Line type for the 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?
labels.side  Same as side. It will replace side in the future versions.
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.

This function creates two tracks, one for the connection lines and one for the labels.

See Also


Examples

circos.initializeWithIdeogram()
bed = generateRandomBed(nr = 50, fun = function(k) sample(letters, k, replace = TRUE))
bed[1, 4] = "aaaaa"
circos.genomicLabels(bed, labels.column = 4, side = "inside")
circos.clear()

circos.initializeWithIdeogram(plotType = NULL)
circos.genomicLabels(bed, labels.column = 4, side = "outside",
    col = as.numeric(factor(bed[[1]])), line_col = as.numeric(factor(bed[[1]])))
circos.genomicIdeogram()
circos.clear()
Add lines to a plotting region, specifically for genomic graphics

**Description**

Add lines to a plotting region, specifically for genomic graphics

**Usage**

```r
circos.genomicLines(
  region,
  value,
  numeric.column = NULL,
  sector.index = get.current.sector.index(),
  track.index = get.current.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 positions and end positions.

- **value**
  
  A data frame contains values and other information.

- **numeric.column**
  
  Which column in value data frame should be taken as y-value. If it is not defined, the whole numeric columns in value will be taken.

- **sector.index**
  
  Index of sector.

- **track.index**
  
  Index of track.

- **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`. 
### 44

**circos.genomicLines**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>lty</code></td>
<td>Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td><code>type</code></td>
<td>There is an additional option segment which plot segment lines from start position to end position. Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td><code>area</code></td>
<td>Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td><code>area.baseline</code></td>
<td>Deprecated, use <code>baseline</code> instead.</td>
</tr>
<tr>
<td><code>baseline</code></td>
<td>Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td><code>border</code></td>
<td>Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td><code>pt.col</code></td>
<td>Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td><code>cex</code></td>
<td>Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td><code>pch</code></td>
<td>Settings are similar as col. Pass to <code>circos.lines</code>.</td>
</tr>
<tr>
<td>...</td>
<td>Mysterious parameters.</td>
</tr>
</tbody>
</table>

**Details**

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


**Examples**

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

bed = generateRandomBed(nr = 100)
circos.genomicTrack(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.genomicTrack(bed_list, panel.fun = function(region, value, ...) {
  i = getI(...) 
  circos.genomicLines(region, value, col = i, ...)
})

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

bed = generateRandomBed(nr = 100, nc = 4)
circos.genomicTrack(bed, panel.fun = function(region, value, ...) {
```
```r
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 data frame in bed format.
- `region2` A data frame in bed format.
- `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`.

**Description**
Add links from two sets of genomic positions

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

### Description

Add points to a plotting region, specifically for genomic graphics

### Examples

```r
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()
```
Arguments

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

Details

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

The function behaviours differently from different formats of input, see the examples in the "Examples" Section or go to https://jokergoo.github.io/circlize_book/book/modes-of-input.html for more details.

Examples

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

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

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

bed1 = generateRandomBed(nr = 100)
bed2 = generateRandomBed(nr = 100)
bed_list = list(bed1, bed2)
# data frame list

cir<1>cos.genomicTrack(bed_list, panel.fun = function(region, value, ...) {
  cex = (value[[1]] - min(value[[1]]))/(max(value[[1]]) - min(value[[1]]))
  i = getI(...)
  cir<1>cos.genomicPoints(region, value, cex = cex, pch = 16, col = i, ...)
})

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

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

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

cir<1>cos.clear()

cir<1>cos.genomicPosTransformLines

Add genomic position transformation lines between tracks

Description

Add genomic position transformation lines between tracks

Usage

```r
cir<1>cos.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

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

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.

Examples

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

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.
pch Style of points.
cex Size of points.
normalize_to_width If it is TRUE, the value is the relative distance divided by the width of the region.
...
... Pass to circos.trackPlotRegion.

Details

This is high-level graphical function, which mean, it will create a new track.
Rainfall plot can be used to visualize distribution of regions. On the plot, y-axis corresponds to the distance to neighbour regions (log-based). So if there is a drop-down on the plot, it means there is a cluster of regions at that area.
On the plot, y-axis are log10-transformed.

See Also


Examples

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

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

```r
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()
```

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

**Description**

Draw rectangle-like grid, specifically for genomic graphics

**Usage**

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

**Arguments**

- `region`  
  A data frame contains 2 column which correspond to start positions and end positions.

- `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`  
  Index of sector.

- `track.index`  
  Index of track.

- `posTransform`  
  Self-defined function to transform genomic positions, see `posTransform.default` for explanation.
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.genomicTrack`. The function behaviours differently from different formats of input, see the examples in the "Examples" Section or go to [https://jokergoo.github.io/circlize_book/book/modes-of-input.html](https://jokergoo.github.io/circlize_book/book/modes-of-input.html) for more details.

**Examples**

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.genomicTrack(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.genomicTrack(bed_list, ylim = c(0, 3),
                   panel.fun = function(region, value, ...) {
                       i = getI(...)
                       circos.genomicRect(region, value, ytop = i+0.4, ybottom = i-0.4, col = f(value[[1]]),
                       border = NA, ...)
                       cell.xlim = get.cell.meta.data("cell.xlim")
                       circos.lines(cell.xlim, c(i, i), lty = 2, col = "#000000")
                   })

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

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

})
circos.clear()

circos.genomicText

**Draw text in a cell, specifically for genomic graphics**

**Description**

Draw text in a cell, specifically for genomic graphics

**Usage**

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

**Arguments**

- **region** A data frame contains 2 columns which correspond to start positions and end positions.
- **value** A data frame contains values and other information.
- **y** A vector or a single value indicating position of text.
- **labels** Labels of text corresponding to each genomic positions.
- **labels.column** If labels are in value, index of column in value.
numeric.column Which column in value data frame should be taken as y-value. If it is not defined, only the first numeric columns in value will be taken.

sector.index Index of sector.

track.index Index of track.

posTransform Self-defined function to transform genomic positions, see posTransform.default for explanation.

text Facing Passing to circos.text. Settings are similar as col.
niceFacing Should the facing of text be adjusted to fit human eyes?
direction Deprecated, use facing instead.
adj Pass to circos.text. Settings are similar as col.
cex Pass to circos.text. Settings are similar as col.
col Pass to circos.text. The length of col can be either one or number of rows of region.

font Pass to circos.text. Settings are similar as col.
padding pass to posTransform if it is set as posTransform.text.
extend pass to posTransform if it is set as posTransform.text.
align_to pass to posTransform if it is set as posTransform.text.

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

Examples

```r
circos.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(phenotype = NULL)

bed = generateRandomBed(nr = 20)

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

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

circos.clear()
```
circos.genomicTrack  Create a track for genomic graphics

Description
Create a track for genomic graphics

Usage
circos.genomicTrack(...)

Arguments
... Pass to circos.genomicTrackPlotRegion.

Details
shortcut function of circos.genomicTrackPlotRegion.

Examples
# There is no example
NULL

circos.genomicTrackPlotRegion  Create a track for genomic graphics

Description
Create a track for genomic graphics

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

- **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 not 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`.

See Also


Examples

# There is no example
NULL
Arguments

- **mat**: A matrix or a vector. The vector is transformed as a one-column matrix.
- **split**: A categorical variable. It splits the matrix into a list of matrices.
- **col**: If the values in the matrices are continuous, the color should be a color mapping generated by `colorRamp2`. If the values are characters, the color should be a named color vector.
- **na.col**: Color for NA values.
- **cell.border**: Border color of cells. A single scalar.
- **cell.lty**: Line type of cell borders. A single scalar.
- **cell.lwd**: Line width of cell borders. A single scalar.
- **bg.border**: Color for background border.
- **bg.lty**: Line type of the background border.
- **bg.lwd**: Line width of the background border.
- **ignore.white**: Whether to draw the white color?
- **cluster**: Whether to apply clustering on rows. The value can also be a dendrogram/hclust object or other objects that can be converted to with `as.dendrogram`.
- **clustering.method**: Clustering method, pass to `hclust`.
- **distance.method**: Distance method, pass to `dist`.
- **dend.callback**: A callback function that is applied to the dendrogram in every sector.
- **dend.side**: Side of the dendrograms relative to the heatmap track.
- **dend.track.height**: Track height of the dendrograms.
- **rownames.side**: Side of the row names relative to the heatmap track.
- **rownames.cex**: Cex of row names.
- **rownames.font**: Font of row names.
- **rownames.col**: Color of row names.
- **show.sector.labels**: Whether to show sector labels.
- **cell_width**: Relative widths of heatmap cells.
- **...**: Pass to `circos.track` which draws the heatmap track.

See Also

https://jokergoo.github.io/2020/05/21/make-circular-heatmaps/
Examples

```r
set.seed(123)
mat1 = rbind(cbind(matrix(rnorm(50*5, mean = 1), nr = 50),
               matrix(rnorm(50*5, mean = -1), nr = 50)),
             cbind(matrix(rnorm(50*5, mean = -1), nr = 50),
               matrix(rnorm(50*5, mean = 1), nr = 50))
)
rownames(mat1) = paste0("R", 1:100)
colnames(mat1) = paste0("C", 1:10)
mat1 = mat1[sample(100, 100), ] # randomly permute rows
split = sample(letters[1:5], 100, replace = TRUE)
spilt = factor(split, levels = letters[1:5])
col_fun1 = colorRamp2(c(-2, 0, 2), c("blue", "white", "red"))
circos.heatmap(mat1, split = split, col = col_fun1)
circos.clear()
```

---

**circos.heatmap.initialize**

*Initialize circular heatmaps*

**Description**

Initialize circular heatmaps

**Usage**

```r
circos.heatmap.initialize(mat, split = NULL, cluster = TRUE,
                          clustering.method = "complete", distance.method = "euclidean",
                          dend.callback = function(dend, m, si) reorder(dend, rowMeans(m)),
                          cell_width = rep(1, nrow(mat)))
```

**Arguments**

- `mat` A matrix or a vector. The vector is transformed as a one-column matrix.
- `split` A categorical variable. It splits the matrix into a list of matrices.
- `cluster` whether to apply clustering on rows. The value can also be a dendrogram/hclust object or other objects that can be converted to with `as.dendrogram`.
- `clustering.method` Clustering method, pass to `hclust`.
- `distance.method` Distance method, pass to `dist`.
- `dend.callback` A callback function that is applied to the dendrogram in every sector.
- `cell_width` Relative widths of heatmap cells.
circos.heatmap.link  

Draw a link between two matrix rows in the circular heatmap

Description

Draw a link between two matrix rows in the circular heatmap

Usage

circos.heatmap.link(row_from, row_to, ...)

Arguments

row_from  
The row index where the link starts. The value should be length 1. If you want to draw multiple links, put the function in a for loop.

row_to  
The row index where the link ends.

...  
Pass to circos.link.

Examples

```r
set.seed(123)
mat = matrix(rnorm(100*10), nrow = 100)
rownames(mat) = paste0("R", 1:100)
col_fun = colorRamp2(c(-2, 0, 2), c("blue", "white", "red"))
circos.heatmap(mat, col = col_fun, rownames.side = "outside")
circos.heatmap.link(10, 60)
circos.clear()

split = sample(letters[1:5], 100, replace = TRUE)
circos.heatmap(mat, col = col_fun, split = split, rownames.side = "outside")
circos.heatmap.link(10, 60)
circos.clear()
```
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`, `cell.width`, `cell.height`, `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.

See Also


Examples

```r
# There is no example
NULL
```
circos.initialize  Initialize the circular layout

Description

Initialize the circular layout

Usage

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

Arguments

- **sectors**: A factor variable or a character vector which represent data categories
- **factors**: The same as sectors. It will be removed in future versions.
- **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.
- **ring**: Whether the sector represented as a ring. If yes, there should only be one sector in the circle.

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.

**See Also**


**Examples**

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

---

```r
circos.initializeCircularGenome

*Initialize a layout for circular genome*

---

**Description**

Initialize a layout for circular genome

**Usage**

```r
circos.initializeCircularGenome(name, genome_size, plotType = "axis", ...)
```

**Arguments**

- `name`: Name of the genome (or the "chromosome name").
- `genome_size`: Size of the genome
- `plotType`: Pass to `circos.genomicInitialize`
- `...`: All goes to `circos.genomicInitialize`

**Examples**

```r
# There is no example
NULL
```
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 = usable_chromosomes(species),
  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.

See Also


Examples

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()

---

**circos.labels**  
*Add a label track*

**Description**  
Add a label track

**Usage**

```r
circos.labels(
  sectors, x, labels,
  facing = "clockwise",
  niceFacing = TRUE,
  col = par("col"),
  cex = 0.8,
  font = par("font"),
  padding = 0.4,
  connection_height = mm_h(5),
  line_col = par("col"),
  line_lwd = par("lwd"),
  line_lty = par("lty"),
  labels_height = min(c(cm_h(1.5), max(strwidth(labels, cex = cex, font = font)))),
  side = c("inside", "outside"),
  labels.side = side,
  track.margin = circos.par("track.margin")
)
```

**Arguments**

- **sectors**: A vector of sector names.
- **x**: Positions of the labels.
- **labels**: A vector of labels.
- **facing**: Facing of the labels. The value can only be "clockwise" or "reverse.clockwise".
- **niceFacing**: Whether automatically adjust the facing of the labels.
- **col**: Color for the labels.
- **cex**: Size of the labels.
- **font**: Font of the labels.
- **padding**: Padding of the labels, the value is the ratio to the height of the label.
- **connection_height**: Height of the connection track.
- **line_col**: Color for the connection lines.
circos.lines

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>line_lwd</td>
<td>Line width for the connection lines.</td>
</tr>
<tr>
<td>line_lty</td>
<td>Line type for the connection lines.</td>
</tr>
<tr>
<td>labels_height</td>
<td>Height of the labels track.</td>
</tr>
<tr>
<td>side</td>
<td>Side of the labels track, is it in the inside of the track where the regions are marked?</td>
</tr>
<tr>
<td>labels.side</td>
<td>Same as side. It will replace side in the future versions.</td>
</tr>
<tr>
<td>track.margin</td>
<td>Bottom and top margins.</td>
</tr>
</tbody>
</table>

Details

This function creates two tracks, one for the connection lines and one for the labels.

If two labels are too close and overlap, this function automatically adjusts the positions of neighbouring labels.

Examples

```r
circos.initialize(sectors = letters[1:8], xlim = c(0, 1))
circos.track(ylim = c(0, 1))
circos.labels(c("a", "a", "b", "b"), x = c(0.1, 0.12, 0.4, 0.6), labels = c(0.1, 0.12, 0.4, 0.6))
```

---

**Description**

Add lines to the plotting region

**Usage**

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

x  Data points on x-axis, measured in "current" data coordinate.
y  Data points on y-axis, measured in "current" data coordinate.
sector.index  Index for the sector.
track.index  Index for the track.
col  Line color.
lwd  Line width.
lty  Line style.
type  Line type, similar as type argument in lines, but only in c("l", "o", "h", "s")
straight  Whether draw straight lines between points.
area  Whether to fill the area below the lines. If it is set to TRUE, col controls the filled color in the area and border controls color of the line.
area.baseline  deprecated, use baseline instead.
baseline  The base line to draw areas. By default it is the minimal of y-range (bottom). It can be a string or a number. If a string, it should be one of bottom and top. This argument also works if type is set to h.
borders  color for border of the area.
pt.col  If type is "o", point color.
cex  If type is "o", point size.
pch  If type is "o", point type.

details

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

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

Examples

sectors = letters[1:9]
circos.par(points.overflow.warning = FALSE)
circos.initialize(sectors, xlim = c(0, 10))
circos.trackPlotRegion(sectors, 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 = 'c'", 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, baseline = '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,         
    inverse = FALSE,  
    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,
reduce_to_mid_line = FALSE)

Arguments

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

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.

See Also


Examples

# There is no example
NULL
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 \texttt{circos.par(start.degree = \ldots)} is not set in \texttt{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 \texttt{circos.clear} in either \texttt{f1()} or \texttt{f2()}. It will be called internally in \texttt{circos.nested}.

If \texttt{adjust.start.degree} is set to \texttt{TRUE}, \texttt{start.degree} should not be set in \texttt{f2()}. Also \texttt{canvas.xlim} and \texttt{canvas.ylim} are reset in \texttt{f2()}, they should not be set in \texttt{f2()} either.

Author(s)

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See Also


Examples

# There is no example
NULL
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.

circle.margin  Margin in the horizontal and vertical direction. The value should be a positive numeric vector and the length of it should be either 1, 2, or 4. When it has length of 1, it controls the margin on the four sides of the circle. When it has length of 2, the first value controls the margin on the left and right, and the second value controls the margin on the bottom and top side. When it has length of 4, the four values controls the margins on the left, right, bottom and top sides of the circle. So A value of c(x1, x2, y1, y2) means circos.par(canvas.xlim = c(-(1+x1), 1+x2), canvas.ylim = c(-(1+y1), 1+y2)).

canvas.xlim  The coordinate for the canvas. Because circlize draws everything (or almost everything) inside the unit circle, the default canvas.xlim and canvas.ylim for the canvas would be all c(-1, 1). However, you can set it to a more broad interval if you want to draw other things out of the circle. By choosing proper canvas.xlim and canvas.ylim, you can draw part of the circle. E.g. setting canvas.xlim to c(0, 1) and canvas.ylim to c(0, 1) would only draw circle in the region of (0, pi/2).

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

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

xaxis.clock.wise  The direction in the x-axes for all sectors. Default is TRUE.

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

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

See Also


Examples

circos.par
circos.points

Description

Add points to a plotting region

Usage

```r
circos.points(
  x, y,
  sector.index = get.current.sector.index(),
  track.index = get.current.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.

See Also

Examples

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

circos.polygon

Draw polygon

Description

Draw polygon

Usage

circos.polygon(
  x, y,
  sector.index = get.current.sector.index(),
  track.index = get.current.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.

Examples

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

circos.raster  

Add raster images

Description

Add raster images

Usage

circos.raster(
  image, x, y,
  width, height,
  facing = c("inside", "outside", "reverse.clockwise", "clockwise", "downward", "bending.inside", "bending.outside"),
  niceFacing = FALSE,
  sector.index = get.current.sector.index(),
  track.index = get.current.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.
circos.rect

Description

Draw rectangle-like grid
Usage

circos.rect(
    xleft, ybottom, xright, ytop,
    sector.index = get.current.sector.index(),
    track.index = get.current.track.index(),
    rot = 0,
    ...
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>xleft</td>
<td>x for the left bottom points</td>
</tr>
<tr>
<td>ybottom</td>
<td>y for the left bottom points</td>
</tr>
<tr>
<td>xright</td>
<td>x for the right top points</td>
</tr>
<tr>
<td>ytop</td>
<td>y for the right top points</td>
</tr>
<tr>
<td>sector.index</td>
<td>Index for the sector</td>
</tr>
<tr>
<td>track.index</td>
<td>Index for the track</td>
</tr>
<tr>
<td>rot</td>
<td>Rotation of the rectangles. The value is measured clockwise in degree. Rotation is relative to the center of the rectangles.</td>
</tr>
<tr>
<td>...</td>
<td>pass to polygon</td>
</tr>
</tbody>
</table>

Details

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

This function can be vectorized.

Examples

circos.initialize(c("a", "b", "c", "d"), xlim = c(0, 10))
circos.track(ylim = c(0, 10), panel.fun = function(x, y) {
    for(rot in seq(0, 360, by = 30)) {
        circos.rect(2, 2, 6, 6, rot = rot)
    }
}, track.height = 0.5)

---

circos.segments  
Draw segments through pairwise of points

Description

Draw segments through pairwise of points
Usage

circos.segments(
  x0, y0, x1, y1,
  sector.index = get.current.sector.index(),
  track.index = get.current.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

circos.initialize(letters[1:8], xlim = c(0, 1))
circos.track(ylim = c(0, 1), track.height = 0.3, panel.fun = function(x, y) {
  x = seq(0.2, 0.8, by = 0.2)
  y = seq(0.2, 0.8, by = 0.2)

circos.segments(x, 0.1, x, 0.9)
circos.segments(0.1, y, 0.9, y)
})
circos.clear()

circos.text  Draw text in a cell

Description

Draw text in a cell
Usage

circos.text(
  x, y,
  labels,
  sector.index = get.current.sector.index(),
  track.index = get.current.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.

See Also

Examples

```r
sectors = letters[1:4]
circos.par(points.overflow.warning = FALSE)
circos.initialize(sectors, xlim = c(0, 10))
circos.trackPlotRegion(sectors, ylim = c(0, 10),
  track.height = 0.5, panel.fun = function(x, y) {
    circos.text(3, 1, "inside", facing = "inside", cex = 0.8)
    circos.text(7, 1, "outside", facing = "outside", cex = 0.8)
    circos.text(0, 5, "reverse.clockwise", facing = "reverse.clockwise",
               adj = c(0.5, 0), cex = 0.8)
    circos.text(10, 5, "clockwise", facing = "clockwise", adj = c(0.5, 0),
               cex = 0.8)
    circos.text(5, 5, "downward", facing = "downward", cex = 0.8)
    circos.text(3, 9, "====bending.inside====", facing = "bending.inside",
               cex = 0.8)
    circos.text(7, 9, "====bending.outside====", facing = "bending.outside",
               cex = 0.8)
  })
circos.clear()
```

---

circos.track

Create plotting regions for a whole track

Description

Create plotting regions for a whole track

Usage

`circos.track(...)`

Arguments

`...`     Pass to `circos.trackPlotRegion`.

Details

Shortcut function of `circos.trackPlotRegion`.

Examples

```r
# 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**

```r
circos.trackHist(
  sectors,
  x,
  track.height = circos.par("track.height"),
  track.index = NULL,
  ylim = 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,
  factors = sectors)
```

**Arguments**

- **sectors**: A `factor` or a character vector which represents the categories of data.
- **factors**: The same as `sectors`. It will be removed in future versions.
- **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.
- **ylim**: Ranges on y-direction. By default, `ylim` is calculated automatically.
- **force.ylim**: Whether to force all cells in the track to share the same `ylim`.
- **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.

See Also


Examples

x = rnorm(1600)
sectors = sample(letters[1:16], 1600, replace = TRUE)
circos.initialize(sectors, x = x)
circos.trackHist(sectors, x = x, col = "#999999",
                border = "#999999")
circos.trackHist(sectors, x = x, bin.size = 0.1,
                col = "#999999", border = "#999999")
circos.trackHist(sectors, x = x, draw.density = TRUE,
                col = "#999999", border = "#999999")
circos.clear()
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(
  sectors,
  x, y,
  track.index = get.current.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"),
  factors = sectors)
```

Arguments
- **sectors**: A factor or a character vector which represents the categories of data.
- **factors**: The same as sectors. It will be removed in future versions.
- **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**: Controls the color of the line.
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`.

Examples

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

```
circos.trackPlotRegion

Create plotting regions for a whole track

Description

Create plotting regions for a whole track

Usage

circos.trackPlotRegion(
  sectors = 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},
  factors = sectors)
```
Arguments

sectors  
A factor or a character vector which represents categories of data, if it is NULL, then it uses all sector index.

factors  
The same as sectors. It will be removed in future versions.

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.

track.height  
Height of the track. It is the percentage to the radius of the unit circles. The value can be set by uh to an absolute unit. If updating a track (with proper track.index value), this argument is ignored.

track.margin  
only affect current track

cell.padding  
only affect current track

bg.col  
Background color for the plotting regions. It can be vector which has the same length of sectors.

bg.border  
Color for the border of the plotting regions. It can be vector which has the same length of sectors.

bg.lty  
Line style for the border of the plotting regions. It can be vector which has the same length of sectors.

bg.lwd  
Line width for the border of the plotting regions. It can be vector which has the same length of sectors.

panel.fun  
Panel function to add graphics in each cell, see "details" section and vignette for explanation.

Details

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

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

Since ranges for values on x-axis has already been defined by circos.initialize, only ranges for values on y-axis should be specified in this function. There are two ways to identify the ranges for values on y-axes either by y or ylim. If y is set, it must has the same length as factors and the ylim for each cell is calculated from y values. Also, the ylim can be specified from ylim which can be a two-element vector or a matrix which has two columns and the number of rows is the same as the length of the levels of the factors.
If there is no enough space for the new track or the new track overlaps with other tracks, there will be an error.

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

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

Panel

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

See vignette for examples of how to use this feature.

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()

circos.trackPoints

Add points to the plotting regions in a same track

Description

Add points to the plotting regions in a same track

Usage

circos.trackPoints(
    sectors,
    x, y,
    track.index = get.current.track.index(),
)
circos.trackText

pch = par("pch"),
col = par("col"),
cex = par("cex"),
bg = par("bg"),
factors = sectors)

Arguments
sectors A factor or a character vector which represents the categories of data
factors The same as sectors. It will be removed in future versions.
x Data points on x-axis
y Data points on y-axis
track.index Index for the track
pch Point type
col Point color
cex Point size
bg background color

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

Length of pch, col and cex can be one, length of levels of the factors or length of factors.
This function can be replaced by a for loop containing circos.points.

Examples

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

circos.trackText Draw text in cells among the whole track

Description
Draw text in cells among the whole track
Usage

circos.trackText(
  sectors,  # A factor or a character vector which represents the categories of data
  x, y,  # Data points on x-axis
  labels,  # Labels
  track.index = get.current.track.index(),  # Index for the track
  direction = NULL,  # deprecated, use facing instead.
  facing = c("inside", "outside", "reverse-clockwise", "clockwise",  # Facing of text
              "downward", "bending", "bending-inside", "bending-outside"),
  niceFacing = FALSE,  # Should the facing of text be adjusted to fit human eyes?
  adj = par("adj"),
  cex = 1,
  col = par("col"),
  font = par("font"),
  factors = sectors)

Arguments

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

Details

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

This function can be replaced by a for loop containing circos.text.

Examples

# There is no example
NULL
circos.triangle  

**Draw triangles**

**Description**

Draw triangles

**Usage**

```r
circos.triangle(x1, y1, x2, y2, x3, y3, ...)
```

**Arguments**

- `x1`: x-coordinates for the first point.
- `y1`: y-coordinates for the first point.
- `x2`: x-coordinates for the second point.
- `y2`: y-coordinates for the second point.
- `x3`: x-coordinates for the third point.
- `y3`: y-coordinates for the third point.
- `...`: Pass to `circos.polygon`.

**Examples**

```r
circos.initialize(c("a", "b", "c", "d"), xlim = c(0, 10))
circos.track(ylim = c(0, 10), panel.fun = function(x, y) {
  circos.triangle(c(2, 2), c(2, 8),
  c(8, 8), c(2, 8),
  c(5, 5), c(8, 2))
}, track.height = 0.5)
```

---

circos.update  

**Create plotting regions for a whole track**

**Description**

Create plotting regions for a whole track

**Usage**

```r
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.
Examples

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

---

circos.violin

**Draw violin plots**

Description

Draw violin plots

Usage

```r
circos.violin(value, pos, violin_width = 0.8,
    col = NA, border = "black", lwd = par("lwd"), lty = par("lty"),
    show_quantile = TRUE, pt.col = par("col"), cex = par("cex"), pch = 16,
    max_density = NULL, sector.index = get.current.sector.index(),
    track.index = get.current.track.index())
```

Arguments

- **value**: A numeric vector, a matrix or a list. If it is a matrix, boxplots are made by columns.
- **pos**: Positions of the boxes.
- **violin_width**: Width of violins.
- **col**: Filled color of boxes.
- **border**: Color for the border as well as the quantile lines.
- **lwd**: Line width.
- **lty**: Line style
- **show_quantile**: Whether to show the quantile lines.
- **cex**: Point size.
- **pch**: Point type.
- **pt.col**: Point color.
- **max_density**: The maximal density value across several violins. It is used to compare between violins.
- **sector.index**: Index of sector.
- **track.index**: Index of track.
Examples

circos.initialize(letters[1:4], xlim = c(0, 10))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  for(pos in seq(0.5, 9.5, by = 1)) {
    value = runif(10)
    circos.violin(value, pos)
  }
})
circos.clear()
circos.initialize(letters[1:4], xlim = c(0, 10))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  value = replicate(runif(10), n = 10, simplify = FALSE)
  circos.violin(value, 1:10 - 0.5, col = 1:10)
})
circos.clear()

circos.xaxis

Draw x-axis

description

Draw x-axis

Usage

circos.xaxis(...)

Arguments

All pass to circos.axis.

details

This function is identical to circos.axis.

Examples

# 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.current.sector.index(),
  track.index = get.current.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.
- **tick**: Whether to draw 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.niceFacing**: Should facing of axis labels be human-easy
- **tick.length**: length of the tick
- **lwd**: line width for ticks
- **col**: color for the axes
- **labels.col**: color for the labels
Details

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

Examples

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

sectors = letters[1:8]
circos.par(points.overflow.warning = FALSE)
circos.par(gap.degree = 8)
circos.initialize(sectors, xlim = c(0, 10))
circos.trackPlotRegion(sectors, 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)
```

---

**cm_h**

Convert units

Description

Convert units

Usage

`cm_h(h)`

Arguments

- `h` The height in numeric.

Details

See explanations in `convert_length` page.

Author(s)

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

**Examples**

```r
# see examples in `convert_length` page
NULL
```

---

**cm_x**

*Convert unit on x direction in data coordinate*

**Description**

Convert unit on x direction in data coordinate

**Usage**

```r
cm_x(x, sector.index = get.current.sector.index(),
    track.index = get.current.track.index(), ...)
```

**Arguments**

- `x` : The x-value in numeric.
- `sector.index` : Index of sector.
- `track.index` : Index of track.
- `...` : Pass to `convert_x`.

**Details**

See explanations in `convert_x` page.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# see examples in `convert_x` page
NULL
```
cm_y

Convert unit on y direction in data coordinate

Description

Convert unit on y direction in data coordinate

Usage

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

Arguments

- `y`: The y-value in numeric.
- `sector.index`: Index of sector.
- `track.index`: Index of track.

Details

See explanations in `convert_y` page.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# see examples in `convert_y` page
NULL
```

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 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 sRGB color space, value should be between 0 and 1.
- `b`: blue channel in sRGB color space, value should be between 0 and 1.
- `colFun`: the color mapping function generated by `colorRamp2`.

Details

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

Value

A vector of original numeric values.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

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

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

Description

Color interpolation

Usage

```r
colorRamp2(breaks, colors, transparency = 0, space = "LAB",
            hcl_palette = NULL, reverse = FALSE)
```
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", "LAB", "XYZ", "sRGB", "LUV", see color-class for detail.
hcl_palette Name of the HCL palette. Value should be supported in hcl.pals.
reverse Whether should the colors in hcl_palette be reversed.

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.

See Also

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

Examples

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

convert_height Convert units

Description

Convert units

Usage

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>

See Also

For pre-defined units, users can use cm_h, mm_h and inches_h.

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 coverts 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.

This function is mainly used in the radical 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

```r
sectors = letters[1:10]
circos.par(cell.padding = c(0, 0, 0, 0), track.margin = c(0, 0))
circos.initialize(sectors, xlim = cbind(rep(0, 10), runif(10, 0.5, 1.5)))
circos.track(ylim = c(0, 1), track.height = mm_h(5))
circos.par(track.margin = c(0, mm_h(2)))
circos.track(ylim = c(0, 1), track.height = cm_h(1))
circos.par(track.margin = c(0, mm_h(5)))
circos.track(ylim = c(0, 1), track.height = inch_h(1))
circos.clear()
```

---

**convert_x**

*Convert unit on x direction in data coordinate*

### Description

Convert unit on x direction in data coordinate

### Usage

```r
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.
**convert_y**

Convert unit on y direction in data coordinate

**Description**

Convert unit on y direction in data coordinate

**Usage**

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

**Examples**

```r
sectors = letters[1:10]
circos.par(cell.padding = c(0, 0, 0, 0), track.margin = c(0, 0))
circos.initialize(sectors, xlim = cbind(rep(0, 10), runif(10, 0.5, 1.5)))
circos.track(ylim = c(0, 1), track.height = mm_h(5),
  panel.fun = function(x, y) {
    circos.lines(c(0, 0 + mm_x(5)), c(0.5, 0.5), col = "blue")
  })
circos.par(track.margin = c(0, mm_h(2)))
circos.track(ylim = c(0, 1), track.height = cm_h(1),
  panel.fun = function(x, y) {
    xcenter = get.cell.meta.data("xcenter")
    circos.lines(c(xcenter, xcenter), c(0, cm_y(1)), col = "red")
  })
circos.par(track.margin = c(0, mm_h(5)))
circos.track(ylim = c(0, 1), track.height = inch_h(1),
  panel.fun = function(x, y) {
    line_length_on_x = cm_x(1*sqrt(2)/2)
    line_length_on_y = cm_y(1*sqrt(2)/2)
    circos.lines(c(0, line_length_on_x), c(0, line_length_on_y), col = "orange")
  })
circos.clear()
```
Arguments

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

Value

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

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

For pre-defined units, users can use `cm_y`, `mm_y` and `inches_y`. `convert_x` converts on x direction.


Examples

# see example on `convert_x` page
NULL

<table>
<thead>
<tr>
<th>cytoband.col</th>
<th>Assign colors to cytogenetic band (hg19) according to the Giemsa stain results</th>
</tr>
</thead>
</table>

Description

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

Usage

cytoband.col(x)

Arguments

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

Examples

# There is no example
NULL
degree

Mark the value as a degree value

Description

Mark the value as a degree value

Usage

degree(x)

Arguments

x  degree value

Value

a degree object

Examples

# There is no example
NULL

draw.sector

Draw sectors or rings in a circle

Description

Draw sectors or rings in a circle

Usage

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

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

Details

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

Examples

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

sectors = letters[1:8]
circos.initialize(sectors, xlim = c(0, 1))
for(i in 1:3) {
  circos.trackPlotRegion(ylim = c(0, 1))
}
circos.info(plot = TRUE)

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

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

draw.sector(get.cell.meta.data("cell.start.degree", sector.index = "e"),
           get.cell.meta.data("cell.end.degree", sector.index = "f"),
           get.cell.meta.data("cell.top.radius", track.index = 2),
           get.cell.meta.data("cell.bottom.radius", track.index = 3),
           col = "#0000FF40")
```
pos = circlize(c(0.2, 0.8), c(0.2, 0.8), sector.index = "h", track.index = 2)
draw.sector(pos[1, "theta"], pos[2, "theta"], pos[1, "rou"], pos[2, "rou"],
clock.wise = TRUE, col = "#00FFFF40")
circos.clear()

**fontsize**

Convert fontsize to cex

**Description**

Convert fontsize to cex

**Usage**

```
fontsize(x)
```

**Arguments**

- **x** value for fontsize

**Examples**

```r
# 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 `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 nr.

Examples

# There is no example
NULL

genomicDensity  Calculate genomic region density

Description

Calculate genomic region density

Usage

genomicDensity(
  region,
  window.size = 1e7,
  n.window = NULL,
  overlap = TRUE,
  count_by = c("percent", "number"),
  chr.len = NULL)

Arguments

region  Genomic positions. It can be a data frame with two columns which are start positions and end positions on a single chromosome. It can also be a bed-format data frame which contains the chromosome column.

window.size  Window size to calculate genomic density
	n.window  number of windows, if it is specified, window.size is ignored

overlap  Whether two neighbouring windows have half overlap

count_by  How to count the value for each window, percent: percent of the window covered by the input regions; number: number of regions that overlap to the window.

chr.len  the chromosome length. The value should be named vector

Details

It calculate the percent of each genomic windows that is covered by the input regions.
Value
If the input is a two-column data frame, the function returns a data frame with three columns: start
position, end position and the overlapping (value depends on the count_by argument). And if the
input is a bed-format data frame, there will be an additionally chromosome name column.

Examples
```r
bed = generateRandomBed()
blood = subset(bed, chr == "chr1")
head(genomicDensity(bed))
head(genomicDensity(bed, count_by = "number"))
```

---

**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.

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

---

**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.
get.cell.meta.data

Examples

# There is no example

NULL

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

Description

Get the meta data of a cell

Usage

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

Arguments

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

Details

The following meta information for a cell can be obtained:

sector.index  The name (index) for the sector
sector.numeric.index  Numeric index for the sector
track.index  Numeric index for the track
xlim  Minimal and maximal values on the x-axis
ylim  Minimal and maximal values on the y-axis
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. The values ignore the direction of the circular layout (i.e. whether it is clock wise or not).
yplot  Radius for top and bottom borders of the cell.
cell.width  Width of the cell, in degrees.
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.

See Also

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

Examples

sectors = letters[1:4]
circos.initialize(sectors, 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()

gc Neuroscience

Description

Get current chromosome name

Usage

gc Neuroscience() 

Details

The function is same as gc Neuroscience and should only be put inside panel.fun when using circos.genomicTrackPlotRegion.

Examples

# There is no example
NULL
get.current.track.index

Get current track index

Description
Get current track index

Usage
get.current.track.index()

Value
Simply returns the numeric index for the current track.

Examples
# There is no example
NULL
getI

Which data that panel.fun is using

Description

Which data that panel.fun is using

Usage

geti(...)

Arguments

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

Details

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

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

Examples

# There is no example
NULL

---

ger_most_inside_radius

Get the inside radius of the most inner track

Description

Get the inside radius of the most inner track

Usage

ger_most_inside_radius()

Examples

# There is no example
NULL
highlight.chromosome Highlight chromosomes

Description
Highlight chromosomes

Usage
highlight.chromosome(...)

Arguments
... pass to highlight.sector

Details
This is only a shortcut function of highlight.sector.

Examples
# There is no example
NULL

highlight.sector Highlight sectors and tracks

Description
Highlight sectors and tracks

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

**highlight.sector**

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`.

See Also


Examples

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

highlight.sector("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("f", "g", col = NA, border = "green",
  lwd = 2, track.index = c(2, 3))
highlight.sector(sectors, col = "#FFFF0040", track.index = 4)
circos.clear()
```
inches_x

Description

Convert unit on x direction in data coordinate

Usage

inches_x(x, sector.index = get.current.sector.index(),
          track.index = get.current.track.index(), ...)

Arguments

x          The x-value in numeric.
sector.index Index of sector.
track.index  Index of track.
...        Pass to convert_x.

Examples

# see examples in `convert_length` page
NULL
inches_y

Description
Convert unit on y direction in data coordinate

Usage
inches_y(y, sector.index = get.current.sector.index(),
track.index = get.current.track.index())

Arguments
y The y-value in numeric.
sector.index Index of sector.
track.index Index of track.

Details
See explanations in convert_y page.

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

Examples
# see examples in `convert_y` page
NULL
**inch_h**  
*Convert units*

**Description**  
Convert units

**Usage**  
```
inch_h(...)  
```

**Arguments**  
```
... pass to inches_h  
```

**Details**  
This function is the same as *inches_h*.

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

**inch_x**  
*Convert unit on x direction in data coordinate*

**Description**  
Convert unit on x direction in data coordinate

**Usage**  
```
inch_x(...)  
```

**Arguments**  
```
... pass to inches_x.  
```

**Details**  
This function is the same as *inches_x*.

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

Convert unit on y direction in data coordinate

Description

Convert unit on y direction in data coordinate

Usage

inch_y(...)

Arguments

... pass to inches_y

Details

This function is the same as inches_y.

Examples

# There is no example
NULL

mm_h

Convert units

Description

Convert units

Usage

mm_h(h)

Arguments

h The height in numeric.

Details

See explanations in convert_length page.

Author(s)

Zuguang Gu <z.gu@dkfz.de>
**Examples**

```r
# see examples in `convert_length` page
NULL
```

---

**mm_x**  
*Convert unit on x direction in data coordinate*

---

**Description**

Convert unit on x direction in data coordinate

**Usage**

```r
mm_x(x, sector.index = get.current.sector.index(), track.index = get.current.track.index(), ...)
```

**Arguments**

- `x`: The x-value in numeric.
- `sector.index`: Index of sector.
- `track.index`: Index of track.
- `...`: Pass to `convert_x`.

**Details**

See explanations in `convert_x` page.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# see examples in `convert_x` page
NULL
```
### mm_y

*Convert unit on y direction in data coordinate*

#### Description

Convert unit on y direction in data coordinate

#### Usage

\[
\text{mm}_y(y, \text{sector.index} = \text{get.current.sector.index}(), \\
\text{track.index} = \text{get.current.track.index}())
\]

#### Arguments

- **y**: The y-value in numeric.
- **sector.index**: Index of sector.
- **track.index**: Index of track.

#### Details

See explanations in `convert_y` page.

#### Author(s)

Zuguang Gu <z.gu@dkfz.de>

#### Examples

```r
# see examples in `convert_y` page
NULL
```

### names.CELL_META

*Names of all meta data in the current cell*

#### Description

Names of all meta data in the current cell

#### Usage

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

#### Arguments

- **x**: use `CELL_META`. 
Examples

names(CELL_META)

---

**posTransform.default**  *Genomic position transformation function*

Description

Genomic position transformation function

Usage

posTransform.default(region, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>region</td>
<td>Genomic positions at a single chromosome. It is a data frame with two columns which are start position and end position.</td>
</tr>
<tr>
<td>...</td>
<td>other arguments</td>
</tr>
</tbody>
</table>

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](#).

Examples

# There is no example
NULL

---

**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
- `cex` - text size
- `font` - text font style
- `sector.index` - sector index
- `track.index` - track index
- `padding` - padding of text
- `extend` - extend to allow labels to be put in a region which is wider than the current chromosome. The value should be a proportion value and the length is either one or two.
- `...` - other arguments

Details

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

Examples

```r
# There is no example
NULL
```
Description
Print CELL_META

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

Arguments
- `x`: input
- `...`: additional parameters

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

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.

Examples

```r
c Www = generateRandomBed()
c www = subset(www, chr == "chr1")
c head(rainfallTransform(www))
```

**Description**

Generate random colors

**Usage**

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

**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.
- `friendly`: If it is true, light random colors will not be generated.

**Details**

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

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>
read.chromInfo

Examples

```r
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))
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

```r
read.chromInfo(
  chromInfo = system.file(package = "circlize", "extdata", "chromInfo.txt"),
  species = NULL,
  chromosome.index = usable_chromosomes(species),
  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
read.cytoband

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 https://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 = usable_chromosomes(species),
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 reads the cytoband data, sorts the chromosome names, and calculates the length of each chromosome. By default, it is human hg19 cytoband data.

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

Value

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

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 transforms data points from polar coordinate system to a specified data coordinate system.
Value

A matrix with two columns (x and y)

Examples

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

---

**set.current.cell**

*Set flag to current cell*

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

*Set gaps between tracks*

**Description**

Set gaps between tracks.

**Usage**

```r
set_track_gap(gap = 0.02)
```

**Arguments**

- `gap`  
  Gap between two tracks. Use `mm_h/cm_h/inches_h` to set in absolute units.

**Examples**

```r
ccircos.initialize(letters[1:10], xlim = c(0, 1))
ccircos.track(ylim = c(0, 1))
set_track_gap(mm_h(2))
ccircos.track(ylim = c(0, 1))
ccircos.clear()
```

### 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**

```r
show.index()
```

**Details**

This function is deprecated, please use `circos.info` instead.

**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
Please do not use this function. Use mm_h/cm_h/inches_h’ instead.
**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**  
Please do not use this function. Use mm_x/cm_x/inches_x' instead.

**Examples**  
# There is no example
NULL

**uy**  
Convert unit on y direction in data coordinate

**Description**  
Convert unit on y direction in data coordinate

**Usage**  
uy(...)

**Arguments**  
... pass to convert_y.
$\textit{CELL\_META}$

Details

Please do not use this function. Use \texttt{\texttt{mm\_y/cm\_y/inches\_y'}} instead.

Examples

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

---

$\textit{CELL\_META}$  
\textit{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
## S3 method for class 'CELL\_META'
x$name
```

Arguments

- \texttt{x}  
  name of the variable should be "CELL\_META"
- \texttt{name}  
  name of the cell meta name

Details

The variable \texttt{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 \texttt{CELL\_META$sector.index}.

See Also

`get.cell.meta.data`

Examples

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