Package ‘circlize’

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Title    Circular Visualization
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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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Circular visualization in R

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:
add_transparency

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

# There is no example
NULL

---

**add_transparency**  
*Add transparency to colors*

### Description

Add transparency to colors

### Usage

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

### Arguments

- **col**
  A vector of colors.
- **transparency**
  Transparency, numeric value between 0 and 1.

### Value

A vector of colors.

### Examples

```
add_transparency("red", 0.5)
add_transparency(1, 0.5)
add_transparency("#FF000080", 0.2)
```
adjacencyList2Matrix  Convert adjacency list to 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)
adjacencyList2Matrix(df)
adjacencyList2Matrix(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)
adjacencyMatrix2List(mat)
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 = dffrom[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**

```
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,
```

```r```
row.col = NULL,
column.col = NULL,
order = NULL,
directional = 0,
xmax = NULL,
symmetric = FALSE,
keep.diagonal = FALSE,
direction.type = "diffHeight",
diffHeight = mm_h(2),
link.target.prop = TRUE,
target.prop.height = mm_h(1),
reduce = 1e-5,
self.link = 2,
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,
link.zindex = NULL,
link.overlap = FALSE,
scale = FALSE,
group = NULL,
big.gap = 10,
small.gap = 1,
...)

Arguments

x a matrix or a data frame. The function will pass all argument to chordDiagramFromMatrix or chordDiagramFromDataFrame depending on the type of x. Also format of other arguments depends on the type of x. If it is in the form of a matrix, it should be an adjacency matrix. If it is in the form of a data frame, it should be an adjacency list.

grid.col pass to chordDiagramFromMatrix or chordDiagramFromDataFrame

grid.border pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
transparency       pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
col               pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
row.col           pass to chordDiagramFromMatrix
column.col        pass to chordDiagramFromMatrix 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
link.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.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/), especially useful when the table represents information of directional relations. This function visualize tables in a circular way.

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

Value

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

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

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,
)```
chordDiagramFromDataFrame

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.on.top = 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 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 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 num-
ber 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.# -link.decreasing

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.on.top
    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,
chordDiagramFromMatrix

  link.zindex = NULL,
  link.overlap = FALSE,
  scale = FALSE,
  group = NULL,
  big.gap = 10,
  small.gap = 1,
  ...)

Arguments

  mat          A table which represents as a numeric matrix.
  grid.col    Grid colors which correspond to matrix rows/columns (or sectors). The length
              of the vector should be either 1 or length(union(rownames(mat),colnames(mat))).
              It’s preferred that grid.col is a named vector of which names correspond to
              sectors. If it is not a named vector, the order of grid.col corresponds to order
              of sectors.
  grid.border border for grids. If it is NULL, the border color is same as grid color.
  transparency Transparency of link colors, 0 means no transparency and 1 means full trans-
                    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 generate colors according to values in mat, or a single value which means
              colors for all links are the same, or a three-column data frame in which the first
              two columns correspond to row names and columns and the third column is
              colors. You may use colorRamp2 to generate a function which maps values to
              colors.
  row.col      Colors for links. Links from the same row in mat will have the same color.
              Length should be same as number of rows in mat. This argument only works
              when col is set to NULL.
  column.col   Colors for links. Links from the same column in mat will have the same color.
              Length should be same as number of columns in mat. This argument only works
              when col and row.col is set to NULL.
  order        Order of sectors. Default order is union(df[[1]],df[[2]]).
  directional  Whether links have directions. 1 means the direction is from the first column
              in df to the second column, -1 is the reverse, 0 is no direction, and 2 for two
              directional. Same setting as link.border.
  xmax         maximum value on x-axes, the value should be a named vector.
  direction.type type for representing directions. Can be one or two values in "diffHeight"
              and "arrows". If the value contains "diffHeight", different heights of the links
              are used to represent the directions for which starting root has long height to
              give people feeling that something is coming out. If the value contains "ar-
              rows", users can customize arrows with following arguments. Same setting
              as link.border. Note if you want to set both diffHeight and arrows for
              certain links, you need to embed these two options into one string such as
              "diffHeight+arrows".
diffHeight  The difference of height between two 'roots' if directional is set to TRUE. If the value is set to a positive value, start root is shorter than end root and if it is set to a negative value, start root is longer than the end root.

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.
chordDiagramFromMatrix

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

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

Description

Draw arrow which is parallel to the circle

Usage

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 \texttt{mm_y/cm_y/inches_y} in absolute units.

If you see points overflow warnings, you can set \texttt{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),
```


col = color[CELL_META$sector.numeric.index]
circos.text(CELL_META$xcenter, CELL_META$ycenter, CELL_META$sector.index,
            facing = "downward")
}, bg.border = NA, track.height = 0.3)
circos.clear()

---

circos.axis  *Draw x-axis*

**Description**

Draw x-axis

**Usage**

```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 neither.
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

```r
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

```r
# Draw barplots

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

if(FALSE) {
  ############### real-time clock #################
  factors = letters[1]
  
circos.par("gap.degree" = 0, "cell.padding" = c(0, 0, 0, 0), "start.degree" = 90)
circos.initialize(sectors, xlim = c(0, 12))
circos.trackPlotRegion(sectors, ylim = c(0, 1), bg.border = NA)
circos.axis(sector.index = "a", major.at = 0:12, labels = "",
  direction = "inside", major.tick.length = mm_y(3))
circos.text(1:12, rep(0.5, 12), 1:12, facing = "downward")

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

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

    sec.degree = 90 - sec/60 * 360
    arrows(0, 0, cos(sec.degree/180*pi)*0.8, sin(sec.degree/180*pi)*0.8)

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

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

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

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()
circos.boxplot

Draw boxplots

Description

Draw boxplots

Usage

```r
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

- **value**: 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

```r
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)
```
```r
}
}
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
```

---

**circos.clear**  
*Reset the circular layout parameters*

**Description**

Reset the circular layout parameters

**Usage**

```r
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**

```r
# 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
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 = "#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 = "normal", border = NA,
            col = rand_color(100, luminosity = "bright", transparency = 0.75))
    })
circos.initialize(c("a"), xlim = c(0, 1))
circos.dendrogram

Add circular dendrograms
Description

Add circular dendrograms

Usage

```r
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, \ldots, \( n-0.5 \). 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

```r
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

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 plots 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

```r
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

bed  A data frame in bed format, the matrix should be stored from the fourth column.
col  Colors for the heatmaps. The value can be a matrix or a color mapping function generated by colorRamp2.
na_col  Color for NA values.
numeric.column  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.
border  Border of the heatmap grids.
border_lwd  Line width for borders of heatmap grids.
border_lty  Line style for borders of heatmap grids.
connection_height

- Height of the connection lines. If it is set to NULL, no connection will be drawn.
  Use `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 correspondence 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

Add an ideogram track

Description

Add an ideogram track

Usage

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

```r
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.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`.
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.

**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**

```r
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()
```
circos.genomicLines

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`
lty Settings are similar as col. Pass to circos.lines.
type There is an additional option segment which plot segment lines from start position to end position. Settings are similar as col. Pass to circos.lines.
area Settings are similar as col. Pass to circos.lines.
area.baseline Deprecated, use baseline instead.
baseline Settings are similar as col. Pass to circos.lines.
border Settings are similar as col. Pass to circos.lines.
pt.col Settings are similar as col. Pass to circos.lines.
cex Settings are similar as col. Pass to circos.lines.
pch Settings are similar as col. Pass to circos.lines.
... Mysterious parameters.

Details

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

The function behaves 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

```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, ...) {
```
circos.genomicLink

Add links from two sets of genomic positions

Description
Add links from two sets of genomic positions

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

Arguments
region1 A 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.
Add points to a plotting region, specifically for genomic graphics

Usage

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

region  A data frame contains 2 columns which correspond to start positions and end positions.
value   A data frame contains values and other information.
numeric.column  Which column in value data frame should be taken as y-value. If it is not defined, the whole numeric columns in value will be taken.
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

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

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

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

bed1 = generateRandomBed(nr = 100)
bed2 = generateRandomBed(nr = 100)
bed_list = list(bed1, bed2)
# data frame list
circos.genomicTrack(bed_list, panel.fun = function(region, value, ...) {
  cex = (value[[1]] - min(value[[1]]))/(max(value[[1]]) - min(value[[1]]))
  i = getI(...)
  circos.genomicPoints(region, value, cex = cex, pch = 16, col = i, ...)
})

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

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

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

circos.clear()

circos.genomicPosTransformLines

Add genomic position transformation lines between tracks

Description

Add genomic position transformation lines between tracks

Usage

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

Arguments

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

Details

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

Examples

# 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 \( \log_{10}(\text{dist}+1) \), and if `normalize_to_width` is TRUE, the value should correspond to \( \log_2(\text{rel}\_\text{dist}) \).
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.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()

---

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

**Description**

Draw rectangle-like grid, specifically for genomic graphics

**Usage**

circos.genomicRect(
  region,
  value = NULL,
  ytop = NULL,
  ybottom = NULL,
  ytop.column = NULL,
  ybottom.column = NULL,
  sector.index = get.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.
circos.genomicRect

- **col**: The length of col can be either one or number of rows of region. Pass to `circos.rect`.
- **border**: Settings are similar as col. Pass to `circos.rect`.
- **lty**: Settings are similar as col. Pass to `circos.rect`.
- **Mysterious parameters.**

**Details**

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

```r
circo.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circo.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"))
circo.genomicTrack(bed_list, stack = TRUE,
  panel.fun = function(region, value, ...) {
    circo.genomicRect(region, value, col = f(value[[1]]),
                      border = NA, ...)
    i = getI(...)
    cell.xlim = get.cell.meta.data("cell.xlim")
    circo.lines(cell.xlim, c(i, i), lty = 2, col = "+00000+")
  })

circo.genomicTrack(bed_list, ylim = c(0, 3),
  panel.fun = function(region, value, ...) {
    i = getI(...) 
    circo.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")
    circo.lines(cell.xlim, c(i, i), lty = 2, col = "+00000")
  })

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

circo.genomicTrack(bed_list, panel.fun = function(region, value, ...) {
  i = getI(...)
  circo.genomicRect(region, value, col = i, border = NA, ...)
})
```
Draw text in a cell, specifically for genomic graphics

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.

facing Passing to circos.text. Settings are similar as col.

niceFacing Should the facing of text be adjusted to fit human eyes?

direction Deprecated, use facing instead.

adj Pass to circos.text. Settings are similar as col.

cex Pass to circos.text. Settings are similar as col.

col Pass to circos.text. The length of col can be either one or number of rows of region.

font Pass to circos.text. Settings are similar as col.

padding pass to posTransform if it is set as posTransform.text.

extend pass to posTransform if it is set as posTransform.text.

align_to pass to posTransform if it is set as posTransform.text.

... Mysterious parameters.

Details

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

Examples

circos.par("track.height" = 0.1, cell.padding = c(0, 0, 0, 0))
circos.initializeWithIdeogram(plotType = 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()
**Description**

Create a track for genomic graphics

**Usage**

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

**Arguments**

... Pass to `circos.genomicTrackPlotRegion`.

**Details**

shortcut function of `circos.genomicTrackPlotRegion`.

**Examples**

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

---

**Description**

Create a track for genomic graphics

**Usage**

```r
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 note it is different from that in circos.trackPlotRegion. In this function, there are two arguments (region and value) plus .... In them, region is a two-column data frame with start positions and end positions in current genomic category (e.g. chromosome). value is a data frame which is derived from data but excluding the first three columns. Rows in value correspond to rows in region. ... is mandatory and is used to pass internal parameters to other functions. The definition of value will be different according to different input data (data frame or list of data frame) and different settings (stacked or not), please refer to 'details' section and vignettes to detailed explanation.

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

circos.heatmap(mat, split = NULL, col, na.col = "grey",
cell.border = NA, cell.lty = 1, cell.lwd = 1,
bg.border = NA, bg.lty = par("lty"), bg.lwd = par("lwd"),
ignore.white = is.na(cell.border),
cluster = TRUE, clustering.method = "complete", distance.method = "euclidean",
dend.callback = function(dend, m, si) reorder(dend, rowMeans(m)),
dend.side = c("none", "outside", "inside"), dend.track.height = 0.1,
rownames.side = c("none", "outside", "inside"), rownames.cex = 0.5,
rownames.font = par("font"), rownames.col = "black",
show.sector.labels = FALSE, 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.

**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/](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

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()
circos.info

Get information of the circular plot

Description

Get information of the circular plot

Usage

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

Arguments

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

# 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
```

---

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

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**

```r
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.
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
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

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))

---
circos.lines  Add lines to the plotting region

Description
Add lines to the plotting region

Usage

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`.
- **border**: color for border of the area.
- **pt.col**: If type is "o", point color.
- **cex**: If type is "o", point size.
- **pch**: If type is "o", point type.

Details

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

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

Examples

```r
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 = '/quotesingle.l'/", sector.index = "a", facing = "outside")

circos.lines(sort(runif(10) * 10), runif(10) * 8, sector.index = "b", type = "o")
circos.text(5, 9, "type = '/quotesingle.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 = '/quotesingle.h'/", sector.index = "c", facing = "outside")
```
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 inferred.
h.ratio        systematically change the link height. The value is between 0 and 1.
w               Since the link is a Bezier curve, it controls the shape of Bezier curve.
h2             Height of the bottom edge of the link if it is a ribbon.
w2             Shape of the bottom edge of the link if it is a ribbon.
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

---

circos.nested  Nested zooming with two circular plots

Description

Nested zooming with two circular plots

Usage

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

Arguments

f1  A self-defined function for making the first circular plot. The function should have no argument.
f2  A self-defined function for making the second circular plot. The function should have no argument.
correspondance  A six-column data frame which contains correspondance between the coordinates in two circular plots
connection_height
The height of the connection track, measured as the percent to the radius of the unit circle. The value can be specified by `uh` or `convert_height` with absolute units.

connection_col
Filled color of the connection track. The value can be a vector with same length as number of rows of `correspondance`

connection_border
Border color of the connection track.

connection_lty
Line style of the connection track borders

connection_lwd
Line width of the connection track borders

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

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

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

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

Author(s)
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See Also

Examples
```r
# There is no example
NULL
```
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 ($2\pi$) 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.
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

Add points to a plotting region

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, measued in the data coordinate in the cell.
y  Position of the center of the raster image, measued 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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>facing</td>
<td>Facing of the raster image.</td>
</tr>
<tr>
<td>niceFacing</td>
<td>Facing of text. Please refer to vignette for different settings.</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>scaling</td>
<td>Scaling factor to resize the raster image.</td>
</tr>
</tbody>
</table>

### Examples

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

if(FALSE) {
  # NOTE: following takes quite a long time to run
  load(system.file("extdata", "doodle.RData", package = "circlize"))
circos.par("cell.padding" = c(0, 0, 0, 0))
circos.initialize(letters[1:16], xlim = c(0, 1))
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  img = img_list[[CELL_META$sector.numeric.index]]
  circos.raster(img, CELL_META$xcenter, CELL_META$ycenter, width = 1,
                height = 1, facing = "bending.inside")
}, track.height = 0.25, bg.border = NA)
circos.track(ylim = c(0, 1), panel.fun = function(x, y) {
  img = img_list[[CELL_META$sector.numeric.index + 16]]
  circos.raster(img, CELL_META$xcenter, CELL_META$ycenter, width = 1,
                height = 1, facing = "bending.inside")
}, track.height = 0.25, bg.border = NA)
circos.clear()
}
```

### See Also

**Usage**

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

**Arguments**

- `xleft`: x for the left bottom points
- `ybottom`: y for the left bottom points
- `xright`: x for the right top points
- `ytop`: y for the right top points
- `sector.index`: Index for the sector
- `track.index`: Index for the track
- `rot`: Rotation of the rectangles. The value is measured clockwise in degree. Rotation is relative to the center of the rectangles.
- `...`: pass to `polygon`

**Details**

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

This function can be vectorized.

**Examples**

```r
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()
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

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

# 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()
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**: The base line to draw area, pass to `circos.lines`.
circos.trackPlotRegion

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)

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

# There is no example
NULL
**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

\[
\begin{align*}
\text{pch} &= \text{par("pch")}, \\
\text{col} &= \text{par("col")}, \\
\text{cex} &= \text{par("cex")}, \\
\text{bg} &= \text{par("bg")}, \\
\text{factors} &= \text{sectors}
\end{align*}
\]

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

```r
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  \textit{Draw text in cells among the whole track}

Description

Draw text in cells among the whole track
Usage

circos.trackText(
  sectors,
  x, y,
  labels,
  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"),
  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**

```
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**

```
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**

```
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

```r
circos.initialize(letters[1:8], xlim = c(0, 1))

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

```r
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

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

Arguments

...  All pass to `circos.axis`.

Details

This function is identical to `circos.axis`.

Examples

```r
# There is no example
NULL
```
**circos.yaxis**  Draw y-axis

**Description**

Draw y-axis

**Usage**

```r
circos.yaxis(
    side = c("left", "right"),
    at = NULL,
    labels = TRUE,
    tick = TRUE,
    sector.index = get.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>
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**

```r
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**

```r
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.
- **col_fun**: 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)
col_fun = colorRamp2(c(0, 0.5, 1), c("blue", "white", "red"))
col = col_fun(x)
col2value(col, col_fun = col_fun)
col2value("red", col_fun = col_fun)

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

---

**Description**

Color interpolation

**Usage**

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

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

Details

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

Value

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

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

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.
**convert_length**

**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**

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

**Description**

Convert units

**Usage**

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

**Arguments**

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

**Details**

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

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

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.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>
See Also

For pre-defined units, users can use `cm_x`, `mm_x` and `inches_x`. `convert_y` converts on y direction.


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()
```

---

**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())
```
cytoband.col

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

Describe

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**

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

Examples

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

genomicDensity

Calculate genomic region density

Description

Calculate genomic region density

Usage

```r
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.
get.all.sector.index

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()
bend <- subset(bed, chr == "chr1")
head(genomicDensity(bed))
head(genomicDensity(bed, count_by = "number"))
```

get.all.track.index

Get index for all sectors

Description

Get index for all sectors

Usage

get.all.track.index()

Details

It simply returns a vector of all track index.

Examples

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

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.
get.current.chromosome

    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()

get.current.chromosome

    Get current chromosome name

Description

    Get current chromosome name

Usage

    get.current.chromosome()

Details

    The function is same as get.current.sector.index and should only be put inside panel.fun when using circos.genomicTrackPlotRegion.

Examples

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

Get current sector index

Description
Get current sector index

Usage
get.current.sector.index()

Value
Simply returns the name of current sector

Examples
# There is no example
NULL

get.current.track.index

Get current track index

Description
Get current track index

Usage
get.current.track.index()

Value
Simply returns the numeric index for the current track.

Examples
# There is no example
NULL
getI

Which data that panel.fun is using

Description
Which data that panel.fun is using

Usage
getI(...)

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

Details
The function should only be put inside panel.fun when using \texttt{circos.genomicTrackPlotRegion}. If stack is set to \texttt{TRUE} in \texttt{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

get_most_inside_radius

Get the inside radius of the most inner track

Description
Get the inside radius of the most inner track

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

Convert units

Description

Convert units

Usage

inches_h(h)

Arguments

h

The height in numeric.

Details

See explanations in `convert_length` page.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# see examples in `convert_length` page
NULL

inches_x

Convert unit on x direction in data coordinate

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`. 
inches_y

Details
See explanations in convert_x page.

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

Examples
# see examples in `convert_x` page
NULL

inches_y  Convert unit on y direction in data coordinate

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  \hspace{1cm} \textit{Convert units} \\

\textbf{Description} \\
Convert units

\textbf{Usage} \\
inch_h(...) \\

\textbf{Arguments} \\
... \hspace{1cm} \text{pass to} \ inches_h \\

\textbf{Details} \\
This function is the same as \textit{inches_h}.

\textbf{Examples} \\
# There is no example 
NULL

inch_x  \hspace{1cm} \textit{Convert unit on x direction in data coordinate} \\

\textbf{Description} \\
Convert unit on x direction in data coordinate

\textbf{Usage} \\
inch_x(...) \\

\textbf{Arguments} \\
... \hspace{1cm} \text{pass to} \ inches_x. \\

\textbf{Details} \\
This function is the same as \textit{inches_x}.

\textbf{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

    # 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**

```r
mm_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
```

**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`. 
posTransform.default  Genomic position transformation function

Description

Genomic position transformation function

Usage

posTransform.default(region, ...)

Arguments

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

Details

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

For details why need to use position transformation, please refer to circos.genomicPosTransformLines.

Examples

# There is no example
NULL

posTransform.text  Genomic position transformation function specifically for text

Description

Genomic position transformation function specifically for text
Usage

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

Arguments

region Genomic positions at a single chromosome. It is a data frame with two columns which are start position and end position.
y positions of texts
labels text labels
cex text size
font text font style
sector.index sector index
track.index track index
padding padding of text
extend extend to allow labels to be put in an 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

# There is no example
NULL
Description

Print CELL META

Usage

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

Arguments

x   input
...
  additional parameters

Examples

# There is no example
NULL

Description

Calculate inter-distance of genomic regions

Usage

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

Arguments

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

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

### rand_color

#### Generate random colors

**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>
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"))
```

---

**read.chromInfo**

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

**Description**

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

**Usage**

```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.
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

```r
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

```r
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 the 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
df <- 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
df <- NULL
sectors = letters[1:8]
circos.initialize(sectors, 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

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

### show.index

**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.
Examples

# There is no example
NULL

ux

Convert unit on x direction in data coordinate

Description

Convert unit on x direction in data coordinate

Usage

ux(...)  

Arguments

... pass to convert_x.

Details

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.
$.CELL_META

Details

Please do not use this function. Use mm_y/cm_y/inches_y instead.

Examples

# There is no example
NULL

$.CELL_META  Easy to way to get meta data in the current cell

Description

Easy to way to get meta data in the current cell

Usage

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

Arguments

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

Details

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

See Also

get.cell.meta.data

Examples

# There is no example
NULL
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