Package ‘BioCircos’

October 12, 2022

**Title**  Interactive Circular Visualization of Genomic Data using 'htmlwidgets' and 'BioCircos.js'

**Version**  0.3.4

**Description**  Implement in 'R' interactive Circos-like visualizations of genomic data, to map information such as genetic variants, genomic fusions and aberrations to a circular genome, as proposed by the 'JavaScript' library 'BioCircos.js', based on the 'JQuery' and 'D3' technologies. The output is by default displayed in standalone HTML documents or in the 'RStudio' viewer pane. Moreover it can be integrated in 'R Markdown' documents and 'Shiny' applications.

**Depends**  R (>= 3.1.0)

**License**  GPL-2 | file LICENSE

**Encoding**  UTF-8

**URL**  https://github.com/lvulliard/BioCircos.R

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**VignetteBuilder**  knitr

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BioCircos

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Description

Interactive circular visualization of genomic data using ‘htmlwidgets’ and ‘BioCircos.js’

Usage

BioCircos(tracklist = BioCircosTracklist(), genome = "hg19",
yChr = TRUE, genomeFillColor = "Spectral", chrPad = 0.04,
displayGenomeBorder = TRUE, genomeBorderColor = "#000",
genomeBorderSize = 0.5, genomeTicksDisplay = TRUE,
genomeTicksLen = 5, genomeTicksColor = "#000",
genomeTicksTextSize = "0.6em", genomeTicksTextColor = "#000",
genomeTicksScale = 3e+07, genomeLabelDisplay = TRUE,
genomeLabelTextSize = "10pt", genomeLabelTextColor = "#000",
genomeLabelDx = 0, genomeLabelDy = 10, genomeLabelOrientation = 0,
zoom = TRUE, TEXTModuleDragEvent = FALSE,
SNPMouseOverDisplay = TRUE, SNPMouseOverColor = "FF0000",
SNPMouseOverCircleSize = 3, SNPMouseOverCircleOpacity = 0.9,
SNPMouseOutDisplay = TRUE, SNPMouseOutColor = "none",
SNPMouseOverTooltipsHtml01 = "Chromosome: ",
SNPMouseOverTooltipsHtml02 = "<br/>Position: ",
SNPMouseOverTooltipsHtml03 = "<br/>Value: ",
SNPMouseOverTooltipsHtml04 = "<br/>",
SNPMouseOverTooltipsHtml05 = "",
SNPMouseOverTooltipsBorderWidth = "1px", ARCMouseOverDisplay = TRUE,
ARCMouseOverColor = "FF0000", ARCMouseOverArcOpacity = 0.9,
ARCMouseOutDisplay = TRUE, ARCMouseOutColor = "none",
ARCMouseOverTooltipsHtml01 = "Chromosome: ",

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CNVMouseOverTooltipsHtml05 = "",
CNVMouseOverTooltipsBorderWidth = "1px", width = NULL,
height = NULL, elementId = NULL, ...

Arguments

tracklist A list of tracks to display.
geno A list of chromosome lengths to be used as reference for the visualization or
'cg19' to use the chromosomes 1 to 22 and the sexual chromosomes according
to the cg19 reference.
yChr A logical stating if the Y chromosome should be displayed. Used only when
geno is set to 'cg19'.
genoFillColor The color to display in each chromosome. Can be a RColorBrewer palette name
used to generate one color per chromosome, or a character object or vector of
color objects stating RGB values in hexadecimal format or base R colors. If
the vector is shorter than the reference genome, values will be repeated.
chrPad Distance between chromosomes.
displayGenomeBorder, genomeBorderColor, genomeBorderSize
    Should the reference genome have borders? If yes specify the color, in RGB
    hexadecimal format, and the thickness.
genoTicksDisplay, genoTicksLen, genoTicksColor, genoTicksTextSize, genoTicksTextColor, geno
    Should the reference genome have ticks, of which length, color (in hexadecimal
    RGB format), with labels in which font size and color, and spaced by how many
    bases?
genoLabelDisplay, genoLabelTextSize, genoLabelTextColor, genoLabelDx, genoLabelDy, genoLabel
    Should the reference genome have labels on each chromosome, in which font
    size and color? Moreover rotation and radius shifts for the label texts can be
    added, and the angle between the radius and the label changed.
zoom Is zooming and moving in the visualization allowed?
TEXTModuleDragEvent
    Are text annotations draggable?
SNPMouseOverDisplay
    Display the tooltip when mouse hover on a SNP point.
SNPMouseOverColor
    Color of the SNP point when hovered by the mouse, in hexadecimal RGB for-
    mat.
SNPMouseOverCircleSize
    Size of the SNP point when hovered by the mouse.
SNPMouseOverCircleOpacity
    Opacity of the SNP point when hovered by the mouse.
SNPMouseOutDisplay
    Hide tooltip when mouse is not hovering a SNP point anymore.
SNPMouseOutColor
    Color of the SNP point when mouse is not hovering a SNP point anymore, in
    hexadecimal RGB format. To revert back to original color, use the value "none".
SNPMouseOver TooltipsHtml01
Label displayed in tooltip in first position, before chromosome number.

SNPMouseOver TooltipsHtml02
Label displayed in tooltip in second position, before genomic position.

SNPMouseOver TooltipsHtml03
Label displayed in tooltip in third position, before value.

SNPMouseOver TooltipsHtml04
Label displayed in tooltip in fourth position, before SNP labels if any.

SNPMouseOver TooltipsHtml05
Label displayed in tooltip in fifth position, after SNP labels if any.

SNPMouseOver TooltipsBorderWidth
The thickness of the tooltip borders, with units specified (such as em or px).

ARCMouseOver Display
Display the tooltip when mouse hover on an arc.

ARCMouseOver Color
Color of the arc when hovered by the mouse, in hexadecimal RGB format.

ARCMouseOver Arc Opacity
Opacity of the arc when hovered by the mouse.

ARCMouseOut Display
Hide tooltip when mouse is not hovering an arc anymore.

ARCMouseOut Color
Color of the arc when mouse is not hovering an arc anymore, in hexadecimal RGB format. To revert back to original color, use the value "none".

ARCMouseOver TooltipsHtml01
Label displayed in tooltip in first position, before chromosome number.

ARCMouseOver TooltipsHtml02
Label displayed in tooltip in second position, before genomic position.

ARCMouseOver TooltipsHtml03
Label displayed in tooltip in third position, before value.

ARCMouseOver TooltipsHtml04
Label displayed in tooltip in fourth position, before ARC labels if any.

ARCMouseOver TooltipsHtml05
Label displayed in tooltip in fifth position, after ARC labels if any.

ARCMouseOver TooltipsBorderWidth
The thickness of the tooltip borders, with units specified (such as em or px).

LINKMouseOver Display
Display the tooltip when mouse hover on a link.

LINKMouseOver Stroke Color
Color of the link when hovered.

LINKMouseOver Opacity
Opacity of the link when hovered.

LINKMouseOut Display
Hide tooltip when mouse is not hovering a link anymore.

LINKMouseOut Stroke Color
Color of the link when mouse is not hovering anymore, in hexadecimal RGB format. To revert back to original color, use the value "none".
LINKMouseOverTooltipsHtml01
Label displayed in tooltip in first position, before label.
LINKMouseOverTooltipsHtml02
Label displayed in tooltip in second position, after label.
LINKMouseOverTooltipsBorderWidth
The thickness of the tooltip borders, with units specified (such as em or px).
LINKMouseOverStrokeWidth
Thickness of the link when hovered.
LINKMouseOutStrokeWidth
Thickness of the link when mouse is not hovering a link anymore.
BARMouseOutDisplay
Hide tooltip when mouse is not hovering a bar anymore.
BARMouseOutColor
Color of the bar when mouse is not hovering anymore, in hexadecimal RGB format. To revert back to original color, use the value "none".
BARMouseOverDisplay
Display the tooltip when mouse hover on a bar.
BARMouseOverColor
Color of the bar when hovered.
BARMouseOverOpacity
Opacity of the bar when hovered.
BARMouseOverTooltipsHtml01
Label displayed in tooltip in first position, before chromosome number.
BARMouseOverTooltipsHtml02
Label displayed in tooltip in second position, before start position.
BARMouseOverTooltipsHtml03
Label displayed in tooltip in second position, before end position.
BARMouseOverTooltipsHtml04
Label displayed in tooltip in third position, before labels if any.
BARMouseOverTooltipsHtml05
Label displayed in tooltip in fourth position, before values.
BARMouseOverTooltipsHtml06
Label displayed in tooltip in fifth position, after values.
BARMouseOverTooltipsBorderWidth
The thickness of the tooltip borders, with units specified (such as em or px).
HEATMAPMouseOutDisplay
Hide tooltip when mouse is not hovering a box anymore.
HEATMAPMouseOutColor
Color of the box when mouse is not hovering anymore, in hexadecimal RGB format. To revert back to original color, use the value "none".
HEATMAPMouseOverDisplay
Display the tooltip when mouse hover on a box.
HEATMAPMouseOverColor
Color of the box when hovered.
HEATMAPMouseOverOpacity
  Opacity of the box when hovered.
HEATMAPMouseOverTooltipsHtml01
  Label displayed in tooltip in first position, before chromosome number.
HEATMAPMouseOverTooltipsHtml02
  Label displayed in tooltip in second position, before start position.
HEATMAPMouseOverTooltipsHtml03
  Label displayed in tooltip in second position, before end position.
HEATMAPMouseOverTooltipsHtml04
  Label displayed in tooltip in third position, before labels if any.
HEATMAPMouseOverTooltipsHtml05
  Label displayed in tooltip in fourth position, before values.
HEATMAPMouseOverTooltipsHtml06
  Label displayed in tooltip in fifth position, after values.
HEATMAPMouseOverTooltipsBorderWidth
  The thickness of the tooltip borders, with units specified (such as em or px).
LINEMouseOutDisplay
  Hide tooltip when mouse is not hovering a line anymore.
LINEMouseOutLineOpacity
  Opacity of the line when mouse is not hovering a link anymore.
LINEMouseOutLineStrokeColor
  Color of the line when mouse is not hovering anymore, in hexadecimal RGB format. To revert back to original color, use the value "none".
LINEMouseOutLineStrokeWidth
  Thickness of the line when mouse is not hovering a link anymore.
LINEMouseOverDisplay
  Display the tooltip when mouse hover on a line.
LINEMouseOverLineOpacity
  Opacity of the line when hovered by the mouse, in hexadecimal RGB format.
LINEMouseOverLineStrokeColor
  Color of the line when hovered by the mouse, in hexadecimal RGB format.
LINEMouseOverLineStrokeWidth
  Width of the line when hovered by the mouse, in hexadecimal RGB format.
LINEMouseOverTooltipsHtml01
  Label displayed in tooltip.
LINEMouseOverTooltipsBorderWidth
  The thickness of the tooltip borders, with units specified (such as em or px).
CNVMouseOutDisplay
  Hide tooltip when mouse is not hovering an arc anymore.
CNVMouseOutColor
  Color of the line when mouse is not hovering anymore, in hexadecimal RGB format. To revert back to original color, use the value "none".
CNVMouseOutArcOpacity
  Opacity of the arc when not hovered by the mouse anymore.
CNVMouseOutArcStrokeColor
   Color of the arc’s stroke when not hovered by the mouse anymore.

CNVMouseOutArcStrokeWidth
   Width of the arc’s stroke when not hovered by the mouse anymore.

CNVMouseOverDisplay
   Display the tooltip when mouse hover on an arc.

CNVMouseOverColor
   Color of the arc when hovered by the mouse, in hexadecimal RGB format.

CNVMouseOverArcOpacity
   Opacity of the arc when hovered by the mouse.

CNVMouseOverArcStrokeColor
   Color of the arc’s stroke when hovered by the mouse, in hexadecimal RGB format.

CNVMouseOverArcStrokeWidth
   Width of the arc’s stroke when hovered by the mouse.

CNVMouseOverTooltipsHtml01
   Label displayed in tooltip in first position, before chromosome number.

CNVMouseOverTooltipsHtml02
   Label displayed in tooltip in second position, before starting position.

CNVMouseOverTooltipsHtml03
   Label displayed in tooltip in second position, before ending position.

CNVMouseOverTooltipsHtml04
   Label displayed in tooltip in third position, before value.

CNVMouseOverTooltipsHtml05
   Label displayed in tooltip in third position, after value.

CNVMouseOverTooltipsBorderWidth
   The thickness of the tooltip borders, with units specified (such as em or px).

width, height
   Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended.

elementId
   the name of the HTML id to be used to contain the visualization.

... Ignored

Examples

BioCircos(yChr = FALSE, chrPad = 0, genomeFillColor = "Blues")
BioCircosArcTrack

Usage

```r
BioCircosOutput(outputId, width = "100\%", height = "400px")
renderBioCircos(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

- `outputId`: output variable to read from
- `width, height`: Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended.
- `expr`: An expression that generates a BioCircos
- `env`: The environment in which to evaluate expr.
- `quoted`: Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.

BioCircosArcTrack  
*Create a track with arcs to be added to a BioCircos tracklist*

Description

Arcs are defined by beginning and ending genomic coordinates

Usage

```r
BioCircosArcTrack(trackname, chromosomes, starts, ends,
colors = "#40B9D4", labels = "", opacities = 1, maxRadius = 0.9,
minRadius = 0.5, ...)
```

Arguments

- `trackname`: The name of the new track.
- `chromosomes`: A vector containing the chromosomes on which each arc is found. Values should match the chromosome names given in the genome parameter of the BioCircos function.
- `starts, ends`: Vectors containing the coordinates on which each arc begins or ends. Values should be inferior to the chromosome lengths given in the genome parameter of the BioCircos function.
- `colors`: The colors for each arc. Can be a RColorBrewer palette name used to generate one color per arc, or a character object or vector of character objects stating RGB values in hexadecimal format or base R colors. If the vector is shorter than the number of arcs, values will be repeated.
- `labels`: One or multiple character objects to label each arc.
- `opacities`: One or multiple opacity values for the arcs, between 0 and 1.
- `minRadius, maxRadius`: Where the track should begin and end, in proportion of the inner radius of the plot.
- `...`: Ignored
Examples

```r
BioCircos(BioCircosArcTrack('ArcTrack', chromosomes = 1:5, starts = 2e+7*1:5, ends = 2.5e+7*2:6))
```

---

**BioCircosBackgroundTrack**

*Create a background track to be added to a BioCircos tracklist*

---

**Description**

Simple background to display behind another track

**Usage**

```r
BioCircosBackgroundTrack(trackname, fillColors = "#EEEEFF", borderColors = "#000000", maxRadius = 0.9, minRadius = 0.5, borderSize = 0.3, ...)
```

**Arguments**

- `trackname` : The name of the new track.
- `fillColors` : The color of the background element, in hexadecimal RGB format.
- `borderColors` : The color of the background borders, in hexadecimal RGB format.
- `minRadius`, `maxRadius` : Where the track should begin and end, in proportion of the inner radius of the plot.
- `borderSize` : The thickness of the background borders.
- `...` : Ignored

**Examples**

```r
BioCircos(BioCircosBackgroundTrack('bgTrack', fillColors="#FFEEEE", borderSize = 1))
```
BioCircosBarTrack

Create a track with a bar plot to be added to a BioCircos tracklist

Description

Bins are defined by a genomic range and associated with a numerical value.

Usage

BioCircosBarTrack(trackname, chromosomes, starts, ends, values,
labels = "", maxRadius = 0.9, minRadius = 0.5, color = "#40B9D4",
range = 0, ...)

Arguments

trackname The name of the new track.
chromosomes A vector containing the chromosomes on which each bar is found. Values should match the chromosome names given in the genome parameter of the BioCircos function.
starts, ends Vectors containing the coordinates on which each bin begins or ends.
values A vector of numerical values associated with each bin, used to determine the height of each bar on the track.
labels One or multiple character objects to label each bar.
minRadius, maxRadius Where the track should begin and end, in proportion of the inner radius of the plot.
color The color for the bars, in hexadecimal RGB format.
range Vector of values to be mapped to the minimum and maximum radii of the track. Default to 0, mapping the minimal and maximal values input in the values parameter.
... Ignored

Examples

BioCircos(BioCircosBarTrack('BarTrack', chromosomes = 1:3, starts = 1e+7*2:4, ends = 2.5e+7*2:4,
values = 1:3, labels = c('A', 'B', 'C'), range = c(0,4)) + BioCircosBackgroundTrack('BGTrack'))
**BioCircosCNVTrack**

Create a track with concentric arcs to be added to a BioCircos tracklist

**Description**

Arcs are defined by a genomic range and radially associated with a numerical value.

**Usage**

```r
BioCircosCNVTrack(trackname, chromosomes, starts, ends, values,
                   maxRadius = 0.9, minRadius = 0.5, width = 1, color = "#40B9D4",
                   range = 0, ...)
```

**Arguments**

- **trackname**  
The name of the new track.
- **chromosomes**  
A vector containing the chromosomes on which each arc is found. Values should match the chromosome names given in the genome parameter of the BioCircos function.
- **starts, ends**  
Vectors containing the coordinates on which each arc begins or ends.
- **values**  
A vector of numerical values associated with each bin, used to determine the height of each bar on the track.
- **minRadius, maxRadius**  
Where the track should begin and end, in proportion of the inner radius of the plot.
- **width**  
The thickness of the arc.
- **color**  
The color for the arcs, in hexadecimal RGB format.
- **range**  
Vector of values to be mapped to the minimum and maximum radii of the track. Default to 0, mapping the minimal and maximal values input in the values parameter.
- **...**  
Ignored

**Examples**

```r
BioCircos(BioCircosCNVTrack('BarTrack', chromosomes = 1:3, starts = 1e+7*2:4, ends = 2.5e+7*2:4,
                             values = 1:3, color = "#BB0000", maxRadius = 0.85, minRadius = 0.55)
           + BioCircosBackgroundTrack('BGTrack'))
```
BioCircosHeatmapTrack

Create a heatmap track to be added to a BioCircos tracklist

Description

Heatmaps are defined by the genomic range and the color-associated numerical value of each box of the heatmap layer.

Usage

```r
BioCircosHeatmapTrack(trackname, chromosomes, starts, ends, values, 
labels = "", maxRadius = 0.9, minRadius = 0.5, 
color = c("#40B9D4", "#F8B100"), range = 0, ...)```

Arguments

- **trackname**: The name of the new track.
- **chromosomes**: A vector containing the chromosomes on which each box is found. Values should match the chromosome names given in the genome parameter of the BioCircos function.
- **starts, ends**: Vectors containing the coordinates on which each box begins or ends.
- **values**: A vector of numerical values associated with each box, used to determine the height of each bar on the track.
- **labels**: One or multiple character objects to label each bar.
- **minRadius, maxRadius**: Where the track should begin and end, in proportion of the inner radius of the plot.
- **color**: A vector of the colors in hexadecimal RGB format to be mapped to the minimum and maximum values of the track. Colors of intermediate values will be linearly interpolated between this two colors.
- **range**: A vector of the values to be mapped to the minimum and maximum colors of the track. Default to 0, mapping the minimal and maximal values input in the values parameter.
- **...**: Ignored

Examples

```r
BioCircos(BioCircosHeatmapTrack("HmTrack", chromosomes = 1:3, starts = 1e+7*2:4, ends = 2.5e+7*2:4, 
values = 1:3, labels = c('A ', 'B ', 'C ')))```
BioCircosLineTrack  

Create a track with lines to be added to a BioCircos tracklist

Description

Lines are defined by genomic coordinates and values of an ordered set of points, that will define the edges of the segments.

Usage

BioCircosLineTrack(trackname, chromosomes, positions, values,
        color = "#40B9D4", width = 2, maxRadius = 0.9, minRadius = 0.5,
        range = 0, ...)

Arguments

trackname  
The name of the new track.

chromosomes  
A vector containing the chromosomes on which each vertex is found. Values should match the chromosome names given in the genome parameter of the BioCircos function.

positions  
A vector containing the coordinates on which each vertex are found. Values should be inferior to the chromosome lengths given in the genome parameter of the BioCircos function.

values  
A vector of numerical values associated with each vertex, used to determine the radial coordinate of each vertex on the visualization.

color  
The color of the line in hexadecimal RGB format.

width  
The line width.

minRadius, maxRadius  
Where the track should begin and end, in proportion of the inner radius of the plot.

range  
Vector of values to be mapped to the minimum and maximum radii of the track. Default to 0, mapping the minimal and maximal values input in the values parameter.

...  
Ignored

Examples

BioCircos(BioCircosLineTrack('LnId', rep(1,30), 2e6*(1:100), log(1:100))
+ BioCircosBackgroundTrack('BGId'))
BioCircosLinkTrack  

Create an inner track with links to be added to a BioCircos tracklist

Description

Links are defined by beginning and ending genomic coordinates of the 2 regions to linked, such as the positions linked in genomic fusions.

Usage

BioCircosLinkTrack(trackname, gene1Chromosomes, gene1Starts, gene1Ends, gene2Chromosomes, gene2Starts, gene2Ends, color = "#40B9D4", labels = "", maxRadius = 0.4, width = "0.1em", gene1Names = "", gene2Names = "", displayAxis = TRUE, axisColor = "#B8B8B8", axisWidth = 0.5, axisPadding = 0, displayLabel = TRUE, labelColor = "#000000", labelSize = "1em", labelPadding = 3, ...)

Arguments

trackname  The name of the new track.
gene1Chromosomes, gene1Starts, gene1Ends, gene1Names, gene2Chromosomes, gene2Starts, gene2Ends, gene2Names  Vectors with the chromosomes, genomic coordinates of beginning and end, and names of both genes to link. Chromosomes and positions should respect the chromosome names and lengths given in the genome parameter of the BioCircos function.
color  The color for the links, in hexadecimal RGB format.
labels  A vector of character objects to label each link.
maxRadius  Where the track should end, in proportion of the inner radius of the plot.
width  The thickness of the links.
displayAxis  Display additional axis (i.e. circle) around the track.
axisColor, axisWidth, axisPadding  Color, thickness and padding of the additional axis.
displayLabel  Display labels of the track.
labelColor, labelSize, labelPadding  Color, font size and padding of the labels around the track.
...  Ignored

Examples

```R
start_chromosomes <- 1:5
dend_chromosomes <- 2:10:6
start_pos <- 2.5e+7*2:6
dend_pos <- 2e+7*1:5
BioCircos(BioCircosLinkTrack('LinkTrack', start_chromosomes, start_pos, start_pos+1, end_chromosomes, end_pos, end_pos+1, color = '#FF00FF'))
```
BioCircosSNPTrack

Create a track with SNPs to be added to a BioCircos tracklist

Description

SNPs are defined by genomic coordinates and associated with a numerical value

Usage

BioCircosSNPTrack(trackname, chromosomes, positions, values,
  colors = "#40B9D4", labels = "", size = 2, shape = "circle",
  opacities = 1, maxRadius = 0.9, minRadius = 0.5, range = 0, ...)

Arguments

- **trackname**: The name of the new track.
- **chromosomes**: A vector containing the chromosomes on which each SNP are found. Values should match the chromosome names given in the genome parameter of the BioCircos function.
- **positions**: A vector containing the coordinates on which each SNP are found. Values should be inferior to the chromosome lengths given in the genome parameter of the BioCircos function.
- **values**: A vector of numerical values associated with each SNPs, used to determine the radial coordinates of each point on the visualization.
- **colors**: The colors for each point. Can be a RColorBrewer palette name used to generate one color per point, or a character object or vector of character objects stating RGB values in hexadecimal format or base R colors. If the vector is shorter than the number of points, values will be repeated.
- **labels**: One or multiple character objects to label each point.
- **size**: The size of each point.
- **shape**: Shape of the points. Can be "circle" or "rect".
- **opacities**: One or multiple opacity values for the points, between 0 and 1.
- **minRadius, maxRadius**: Where the track should begin and end, in proportion of the inner radius of the plot.
- **range**: Vector of values to be mapped to the minimum and maximum radii of the track. Default to 0, mapping the minimal and maximal values input in the values parameter.
- **...**: Ignored

Examples

BioCircos(BioCircosSNPTrack('SNPTrack', chromosomes = 1:3, positions = 1e+7*2:4,
  values = 1:3, colors = "Accent", labels = c('A', 'B', 'C')) + BioCircosBackgroundTrack('BGTrack'))
BioCircosTextTrack

Create a Text track to be added to a BioCircos tracklist

Description

Simple text annotation displayed in the visualization

Usage

BioCircosTextTrack(trackname, text, x = -0.15, y = 0, size = "1.2em",
weight = "bold", opacity = 1, color = "#000000", ...)

Arguments

- **trackname**: The name of the new track.
- **text**: The text to be displayed.
- **x, y**: Coordinates of the lower left corner of the annotation, in proportion of the inner radius of the plot.
- **size**: Font size, with units specified (such as em or px).
- **weight**: Font weight. Can be "normal", "bold", "bolder" or "lighter".
- **opacity**: Font opacity.
- **color**: Font color, in hexadecimal RGB format.
- **...**: Ignored

Examples

BioCircos(BioCircosTextTrack('textTrack', 'Annotation', color = 'DD2222', x = -0.3))

BioCircosTracklist

Create a list of BioCircos tracks

Description

This allows the use of the `+` and `-` operator on these lists

Usage

BioCircosTracklist()

```r
## S3 method for class 'BioCircosTracklist'
x + ...
```

```r
## S3 method for class 'BioCircosTracklist'
x - ...
```
Arguments

- x: The tracklist on which other tracks should be added or removed.
- . . .: The tracks to add (as tracklists) or to remove (as track names).
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