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 stand-
alone 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

LazyData true

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

Imports RColorBrewer, htmlwidgets, jsonlite, plyr, grDevices

NeedsCompilation no

Author Loan Vulliard [trl, cre],
Xiaowei Chen [aut],
Ya Cui [aut]

Maintainer Loan Vulliard <lvulliard@cemm.at>

Repository CRAN

Date/Publication 2019-03-19 16:23:26 UTC

R topics documented:

BioCircos   *BioCircos*

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: ",
```

```
ARCMouseOverTooltipsHtml02 = "<br/>Start: ",
ARCMouseOverTooltipsHtml03 = "<br/>End: ",
ARCMouseOverTooltipsHtml04 = "<br/>",
ARCMouseOverTooltipsHtml05 = "",
ARCMouseOverTooltipsBorderWidth = "1px", LINKMouseOverDisplay = TRUE,
LINKMouseOverStrokeColor = "#FF00FF", LINKMouseOverOpacity = 0.9,
LINKMouseOutDisplay = TRUE, LINKMouseOutStrokeColor = "none",
LINKMouseOverTooltipsHtml01 = "Fusion: ",
LINKMouseOverTooltipsHtml02 = "",
LINKMouseOverTooltipsBorderWidth = "1px",
LINKMouseOverStrokeWidth = 5, LINKMouseOutStrokeWidth = "none",
BARMouseOutDisplay = TRUE, BARMouseOutColor = "none",
BARMouseOverDisplay = TRUE, BARMouseOverColor = "#FF0000",
BARMouseOverOpacity = 0.9,
BARMouseOverTooltipsHtml01 = "Chromosome: ",
BARMouseOverTooltipsHtml02 = "<br/>Start: ",
BARMouseOverTooltipsHtml03 = " End: ",
BARMouseOverTooltipsHtml04 = "<br/>",
BARMouseOverTooltipsHtml05 = "<br/>Value: ",
BARMouseOverTooltipsHtml06 = "",
BARMouseOverTooltipsBorderWidth = "1px",
HEATMAPMouseOutDisplay = TRUE, HEATMAPMouseOutColor = "none",
HEATMAPMouseOverDisplay = TRUE, HEATMAPMouseOverColor = "#FF0000",
HEATMAPMouseOverOpacity = 0.9,
HEATMAPMouseOverTooltipsHtml01 = "Chromosome: ",
HEATMAPMouseOverTooltipsHtml02 = "<br/>Start: ",
HEATMAPMouseOverTooltipsHtml03 = " End: ",
HEATMAPMouseOverTooltipsHtml04 = "<br/>",
HEATMAPMouseOverTooltipsHtml05 = "<br/>Value: ",
HEATMAPMouseOverTooltipsHtml06 = "",
HEATMAPMouseOverTooltipsBorderWidth = "1px",
LINEMouseOutDisplay = TRUE, LINEMouseOutLineOpacity = "none",
LINEMouseOutLineStrokeColor = "none",
LINEMouseOutLineStrokeWidth = "none", LINEMouseOverDisplay = T,
LINEMouseOverLineOpacity = 1,
LINEMouseOverLineStrokeColor = "#FF0000",
LINEMouseOverLineStrokeWidth = "none",
LINEMouseOverTooltipsHtml01 = "Line",
LINEMouseOverTooltipsBorderWidth = 0, CNVMouseOutDisplay = TRUE,
CNVMouseOutColor = "none", CNVMouseOutArcOpacity = 1,
CNVMouseOutArcStrokeColor = "none", CNVMouseOutArcStrokeWidth = 0,
CNVMouseOverDisplay = TRUE, CNVMouseOverColor = "#FF0000",
CNVMouseOverArcOpacity = 0.9, CNVMouseOverArcStrokeColor = "#F26223",
CNVMouseOverArcStrokeWidth = 3,
CNVMouseOverTooltipsHtml01 = "Chromosome: ",
CNVMouseOverTooltipsHtml02 = "<br>Start: ",
CNVMouseOverTooltipsHtml03 = "<br>End: ",
CNVMouseOverTooltipsHtml04 = "<br>Value: ",
```

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

Arguments

tracklist   A list of tracks to display.

genome   A list of chromosome lengths to be used as reference for the visualization or
                   'hg19' to use the chromosomes 1 to 22 and the sexual chromosomes according
                   to the hg19 reference.

yChr   A logical stating if the Y chromosome should be displayed. Used only when
                   genome is set to 'hg19'.

genomeFillColor
                   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
                   character 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.

genomeTicksDisplay, genomeTicksLen, genomeTicksColor, genomeTicksTextSize, genomeTicksTextColor, genom
                   Should the refence 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?

genomeLabelDisplay, genomeLabelTextSize, genomeLabelTextColor, genomeLabelDx, genomeLabelDy, genomeLab
                   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".

SNPMouseOverTooltipsHtml01

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

SNPMouseOverTooltipsHtml02

> Label displayed in tooltip in second position, before genomic position.

SNPMouseOverTooltipsHtml03

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

SNPMouseOverTooltipsHtml04

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

SNPMouseOverTooltipsHtml05

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

SNPMouseOverTooltipsBorderWidth

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

ARCMouseOverDisplay

> Display the tooltip when mouse hover on an arc.

ARCMouseOverColor

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

ARCMouseOverArcOpacity

> Opacity of the arc when hovered by the mouse.

ARCMouseOutDisplay

> Hide tooltip when mouse is not hovering an arc anymore.

ARCMouseOutColor

> 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".

ARCMouseOverTooltipsHtml01

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

ARCMouseOverTooltipsHtml02

> Label displayed in tooltip in second position, before genomic position.

ARCMouseOverTooltipsHtml03

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

ARCMouseOverTooltipsHtml04

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

ARCMouseOverTooltipsHtml05

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

ARCMouseOverTooltipsBorderWidth

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

LINKMouseOverDisplay

> Display the tooltip when mouse hover on a link.

LINKMouseOverStrokeColor

> Color of the link when hovered.

LINKMouseOverOpacity

> Opacity of the link when hovered.

LINKMouseOutDisplay

> Hide tooltip when mouse is not hovering a link anymore.

LINKMouseOutStrokeColor

> 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")
```

BioCircos-shiny   *Shiny bindings for BioCircos*

Description

Output and render functions for using BioCircos within Shiny applications and interactive Rmd
documents.

Usage

```
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

```
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

```
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

```
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

```
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

```
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 pa-
                   rameter.

...   Ignored

Examples

```
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

```
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

```
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), 2e+6*(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, gene2Na
	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

```
start_chromosomes <- 1:5
end_chromosomes <- 2*10:6
start_pos <- 2.5e+7*2:6
end_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()

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

## 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).

Index