Package 'BioCircos'

January 20, 2025

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)

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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

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Repository CRAN

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Contents

`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`, `genomeTicksScale`	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`, `genomeLabelOrientation`	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 format.
`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 parameter.
`...`	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`, `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

```
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).

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