

# Package ‘BioCircos’

March 19, 2019

**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

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**Repository** CRAN

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BioCircos	<i>BioCircos</i>
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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,
  SNPmouseoverOutDisplay = TRUE, SNPmouseoverOutColor = "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

<code>tracklist</code>	A list of tracks to display.
<code>genome</code>	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.
<code>yChr</code>	A logical stating if the Y chromosome should be displayed. Used only when genome is set to 'hg19'.
<code>genomeFillColor</code>	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.
<code>chrPad</code>	Distance between chromosomes.
<code>displayGenomeBorder</code> , <code>genomeBorderColor</code> , <code>genomeBorderSize</code>	Should the reference genome have borders? If yes specify the color, in RGB hexadecimal format, and the thickness.
<code>genomeTicksDisplay</code> , <code>genomeTicksLen</code> , <code>genomeTicksColor</code> , <code>genomeTicksTextSize</code> , <code>genomeTicksTextColor</code> , <code>genomeTicksTextColor</code>	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?
<code>genomeLabelDisplay</code> , <code>genomeLabelTextSize</code> , <code>genomeLabelTextColor</code> , <code>genomeLabelDx</code> , <code>genomeLabelDy</code> , <code>genomeLabelAngle</code>	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.
<code>zoom</code>	Is zooming and moving in the visualization allowed?
<code>TEXTModuleDragEvent</code>	Are text annotations draggable?
<code>SNPMouseOverDisplay</code>	Display the tooltip when mouse hover on a SNP point.
<code>SNPMouseOverColor</code>	Color of the SNP point when hovered by the mouse, in hexadecimal RGB format.
<code>SNPMouseOverCircleSize</code>	Size of the SNP point when hovered by the mouse.
<code>SNPMouseOverCircleOpacity</code>	Opacity of the SNP point when hovered by the mouse.
<code>SNPMouseOutDisplay</code>	Hide tooltip when mouse is not hovering a SNP point anymore.
<code>SNPMouseOutColor</code>	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")
```

### 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	<i>Create a track with arcs to be added to a BioCircos tracklist</i>
-------------------	--

---

**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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