

Package: BioCircos (via r-universe)

October 29, 2024

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

Repository <https://lvulliard.r-universe.dev>

RemoteUrl <https://github.com/lvulliard/biocircos.r>

RemoteRef HEAD

RemoteSha 99db76448f1f62da1115fa973962939d3039b4dc

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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 = 0.028,
  genomeLabelDy = "-0.55em", 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", 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	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 adde
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.
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 = "", maxRadius = 0.9, minRadius = 0.5, ...)
```

Arguments

trackname	The name of the new track.
chromosomes	A vector containing the chromosomes on which each arcs are 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 arcs begin or end. 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.
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))
```

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