

Package: EpiViz (via r-universe)

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Type Package

Title An implementation of Circos plots for epidemiologists

Version 0.0.1

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Description An implementation of Circos plots for epidemiologists in
R. It takes the Circlize package and adapts it for use by
epidemiologists. Circos plots provide an informative way of
plotting greater than 50 plotting points. A legend can be
plotted automatically and customised.

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Encoding UTF-8

LazyData true

Imports circlize (>= 0.4.6), dplyr (>= 0.8.3), ComplexHeatmap (>=
1.20.0), grid

Depends R (>= 3.1.2), graphics, grDevices

BugReports <https://github.com/mattlee821/EpiViz/issues>

URL <https://github.com/mattlee821/EpiViz>

RoxygenNote 7.2.2

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

RemoteUrl <https://github.com/mattlee821/EpiViz>

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circos_plot	<i>Create a Circos plot with up to 3 tracks using points, lines or bars</i>
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Description

Create a Circos plot with up to 3 tracks using points, lines or bars

Usage

```
circos_plot(  
  track_number,  
  track1_data,  
  track2_data,  
  track3_data,  
  track1_type,  
  track2_type,  
  track3_type,  
  label_column,  
  section_column,  
  order = TRUE,  
  order_column,  
  estimate_column,  
  pvalue_column,  
  pvalue_adjustment,  
  lower_ci,  
  upper_ci,  
  lines_column,  
  lines_type = "o",  
  bar_column,  
  histogram_column,  
  histogram_binsize = 0.01,  
  histogram_densityplot = FALSE,  
  legend = FALSE,  
  pvalue_legend = FALSE,  
  track1_label = NA,  
  track2_label = NA,  
  track3_label = NA,  
  pvalue_label = NA,  
  circle_size = 25,  
  track1_height = 0.2,  
  track2_height = 0.2,  
  track3_height = 0.2,  
  equal_axis = FALSE,  
  origin = 0,  
  colours = c("#00378f", "#ffc067", "#894300")  
)
```

Arguments

<code>track_number</code>	The number of tracks you want your circos plot to have. Maximum number of tracks is 3.
<code>track1_data</code>	The data frame of your first track.
<code>track2_data</code>	The data frame of your second track.
<code>track3_data</code>	The data frame of your third track.
<code>track1_type</code>	The type of plot for the first track. One of "scatter", "lines", "bar" and "histogram".
<code>track2_type</code>	The type of plot for the second track. One of "scatter", "lines", "bar" and "histogram".
<code>track3_type</code>	The type of plot for the third track. One of "scatter", "lines", "bar" and "histogram".
<code>label_column</code>	The column in your data frames that you will use as the labels for the circos plot. This will likely be the column with your exposure/outcome name in. Labels go on the outside of the plot.
<code>section_column</code>	The column in your data frames that you will use to group/section your data/plot by.
<code>order</code>	Do you want MR Viz to organise your columns alphabetically. Default is TRUE
<code>order_column</code>	If order = FALSE what column do you want to order your sections by
<code>estimate_column</code>	The column in your data frames with the estimates in.
<code>pvalue_column</code>	The column in your data frames with the p-values in.
<code>pvalue_adjustment</code>	The threshold you want to set your p-value 'significance' threshold too. This can be in the format of a single value or a function e.g. 0.05/22. The p-value threshold is only used for scatter plots.
<code>lower_ci</code>	The column in your data frames with the lower confidence intervals in.
<code>upper_ci</code>	The column in your data frames with the upper confidence intervals in.
<code>lines_column</code>	The column in your data frames that you want to plot as lines.
<code>lines_type</code>	The type of line plot you want. "l" = straight lines; "o" = straight lines with points; "s" = boxed lines; "h" = vertical lines. Default is "o".
<code>bar_column</code>	The column in your data frames that you want to plot as bars.
<code>histogram_column</code>	The column in your data frames that you want to plot as histograms.
<code>histogram_binsize</code>	The binsize of the histogram. Default is 0.01.
<code>histogram_densityplot</code>	Do you want your histogram to be a density plot or not. Default is FALSE.
<code>legend</code>	Do you want a legend = TRUE or FALSE. FALSE by default

pvalue_legend	Do you want a p-value legend icon (defalut = FALSE)
track1_label	What do you want the label for the first track to be e.g. "Body Mass Index"
track2_label	What do you want the label for the first track to be e.g. "Corondary Heart Disease"
track3_label	What do you want the label for the first track to be e.g. "Breast Cancer"
pvalue_label	What do you want the label for the p-value to read e.g. "p-value <= 0.05"
circle_size	The size of the circos plot. Smaller numbers make larger circos plots. Default is 25. You will need to adjust this number a few times to get the perfect size for your specific circos plot requirements. If you have long labels then try 25. If your labels are short try 1-10.
track1_height	Size of the track as a percent of the whole circle. Default is 20 percent (0.20)
track2_height	Size of the track as a percent of the whole circle. Default is 20 percent (0.20)
track3_height	Size of the track as a percent of the whole circle. Default is 20 percent (0.20). It is sometimes worth increasing the size of track 3 to 30 percent
equal_axis	Do you want your tracks to share the same axis (Defalut = FALSE), if TRUE it will use the minimmum and maximum from the upper and lower confidence intervals to calculate the axis for each track. This ONLY applies to 'points' all other plot types are independent of each track.
origin	Where do you want your X axis line drawn, e.g. 0 for continuous outcomes and 1 for binary outcomes when using beta and odds ratios respectively. Default is 0
colours	list of colours for each track. Use ""

Examples

```

circos_plot(track_number = 3,
track1_data = EpiViz_data1,
track2_data = EpiViz_data2,
track3_data = EpiViz_data3,
track1_type = "points",
track2_type = "lines",
track3_type = "bar",
label_column = 1,
section_column = 9,
estimate_column = 2,
pvalue_column = 3,
pvalue_adjustment = 1,
lower_ci = 4,
upper_ci = 5,
lines_column = 2,
lines_type = "o",
bar_column = 2,
legend = FALSE,

```

```
pvalue_legend = FALSE,
circle_size = 25)
```

EpiViz_data1	<i>Example data: Mendelian randomization results from an analysis of BMI measured in European men and women and 123 metabolites</i>
--------------	---

Description

A simulated dataset of linear regression results for 123 outcomes.

Usage

```
EpiViz_data1
```

Format

A simulated data frame with 123 rows and 8 variables imitating a traditional epidemiology results file from a linear regression:

label The name of the outcomes

beta Effect estimates

pvalue Pvalues of the effect estimates and standard errors

lower_confidence_interval Lower confidence interval bound

upper_confidence_interval Upper confidence interval bound

exposure The exposure used in the Mendelian randomization analysis

label_units The name of the outcomes with units

class The groups which the outcomes can be put into

subclass The subgroups which the outcomes can be put into ...

EpiViz_data2	<i>Example data: Mendelian randomization results from an analysis of BMI measured in European men and 123 metabolites</i>
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Description

A simulated dataset of linear regression results for 123 outcomes.

Usage

```
EpiViz_data2
```

Format

A simulated data frame with 123 rows and 8 variables imitating a traditional epidemiology results file from a linear regression:

label The name of the outcomes

beta Effect estimates

pvalue Pvalues of the effec estimates and standard errors

lower_confidence_interval Lower confidence interval bound

upper_confidence_interval Upper confidence interval bound

exposure The exposure used in the Mendelian randomization alaysis

label_units The name of the outcomes with units

class The groups which the outcomes can be put into

subclass The subgroups which the outcomes can be put into ...

EpiViz_data3	<i>Example data: Mendelian randomization results from an analysis of BMI measured in European women and 123 metabolites</i>
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Description

A simulated dataset of linear regression results for 123 outcomes.

Usage

EpiViz_data3

Format

A simulated data frame with 123 rows and 8 variables imitating a traditional epidemiology results file from a linear regression:

label The name of the outcomes

beta Effect estimates

pvalue Pvalues of the effec estimates and standard errors

lower_confidence_interval Lower confidence interval bound

upper_confidence_interval Upper confidence interval bound

exposure The exposure used in the Mendelian randomization alaysis

label_units The name of the outcomes with units

class The groups which the outcomes can be put into

subclass The subgroups which the outcomes can be put into ...

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