Package ‘lolliplot’

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Type Package
Title Plot Variants and Somatic Mutations
Version 0.2.2
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Description Draw lolliplot using GRanges objects. this package was designed only for drawing lolliplot. So, it’s faster than 'trackViewer', but un-related functions has been derived.
Depends R (>= 3.5.0)
Imports methods, scales, grDevices, IRanges, grid, grImport, GenomicRanges
Suggests knitr, rmarkdown
License GPL (>= 2)
Encoding UTF-8
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### lolliplot

#### Description


#### Usage

```r
tolliplot(
  SNP.gr,
  features = NULL,
  ranges = NULL,
  type = "circle",
  newpage = TRUE,
  ylab = TRUE,
  ylab.gp = gpar(col = "black"),
  xaxis = TRUE,
  xaxis.gp = gpar(col = "black"),
  yaxis = TRUE,
  yaxis.gp = gpar(col = "black"),
  legend = NULL,
  cex = 1,
  dashline.col = "gray80",
  jitter = c("node", "label"),
  rescale = FALSE,
  label_on_feature = FALSE,
  ...
)
```

#### Arguments

- **SNP.gr**: A object of `GRanges`, `GRangesList` or a list of `GRanges`. All the width of `GRanges` must be 1.
- **features**: A object of `GRanges`, `GRangesList` or a list of `GRanges`. The metadata 'featureLayerID' are used for drawing features in different layers. See details in vignette.
- **ranges**: A object of `GRanges` or `GRangesList`.
- **type**: character. Could be circle, pie, pin, pie.stack or flag.
- **newpage**: Plot in the new page or not.
- **ylab**: Plot ylab or not. If it is a character vector, the vector will be used as ylab.
- **ylab.gp, xaxis.gp, yaxis.gp**: An object of class gpar for ylab, xaxis or yaxis.
- **yaxis**: Plot yaxis or not.
xaxis
Plot xaxis or not. If it is a numeric vector with length greater than 1, the vector
will be used as the points at which tick-marks are to be drawn. And the names of
the vector will be used to as labels to be placed at the tick points if it has names.

legend
If it is a list with named color vectors, a legend will be added.

cex
cex will control the size of circle.

dashline.col
color for the dashed line.

jitter
jitter the position of nodes or labels.

rescale
logical(1), character(1), numeric vector, or a dataframe with rescale from and
to. Rescale the x-axis or not. If dataframe is used, colnames must be from.start,
from.end, to.start, to.end. And the from scale must cover the whole plot region.
The rescale parameter can be set as "exon" or "intron" to emphasize "exon" or
"intron" region. The "exon" or "intron" can be followed with an integer e.g.
"exon_80", or "intron_99". The integer indicates the total percentage of "exon"
or "intron" region. Here "exon" indicates all regions in features. And "intron"
indicates all flank regions of the features.

label_on_feature
Labels of the feature directly on them. Default FALSE.
... not used.

Details
In SNP.gr and features, metadata of the GRanges object will be used to control the color, fill, border,
alpha, shape, height, cex, dashline.col, data source of pie if the type is pie. And also the controls
for labels by name the metadata start as label.parameter.<properties> such as label.parameter.rot,
label.parameter.gp. The parameter is used for grid.text. The metadata `featureLayerID` for features
are used for drawing features in different layers. The metadata `SNPsideID` for SNP.gr are used for
determining the side of lollipops. And the `SNPsideID` could only be 'top' or 'bottom'.

Value
No return value, called for side effects

Examples
```r
SNP <- c(10, 100, 105, 108, 400, 410, 420, 600, 700, 805, 840, 1400, 1402)
x <- sample.int(100, length(SNP))
SNP.gr <- GenomicRanges::GRanges("chr1", IRanges::IRanges(SNP, width=1, names=paste0("snp", SNP)),
   value1=x, value2=100-x)
SNP.gr$color <- rep(list(c("red", "blue")), length(SNP))
SNP.gr$border <- sample.int(7, length(SNP), replace=TRUE)
features <- GenomicRanges::GRanges("chr1", IRanges::IRanges(
c(1, 501, 1001),
   width=c(120, 500, 405),
   names=paste0("block", 1:3)),
   color="black",
   fill=c("#FF8833", "#51C6E6", "#DFA32D"),
   height=c(0.1, 0.05, 0.08),
   ... not used.
```
lollipo\text{\texttt{t}}(\texttt{SNP.gr, features, type="pie"})

lollipo\text{\texttt{t}}(\texttt{SNP.gr, features, label parameter rot=45})
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