

# Package ‘lollipop’

January 26, 2023

**Type** Package

**Title** Plot Variants and Somatic Mutations

**Version** 0.2.2

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**Description** Draw lollipop using GRanges objects. this package was designed only for drawing lollipop. 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

**RoxygenNote** 7.2.3

**NeedsCompilation** no

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**Repository** CRAN

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## R topics documented:

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lollipop

*Lolliplots***Description**

Plot variants and somatic mutations. Jianhong Ou and Lihua Julie Zhu (2019)<doi:10.1038/s41592-019-0430-y>

**Usage**

```
lollipop(
  SNP.gr,
  features = NULL,
  ranges = NULL,
  type = "circle",
  newpage = TRUE,
  ylab = TRUE,
  ylab.gp = gpar(col = "black"),
  yaxis = TRUE,
  yaxis.gp = gpar(col = "black"),
  xaxis = TRUE,
  xaxis.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 <a href="#">GRanges</a> , <a href="#">GRangesList</a> or a list of <a href="#">GRanges</a> . All the width of <a href="#">GRanges</a> must be 1.   |
| features                    | A object of <a href="#">GRanges</a> , <a href="#">GRangesList</a> or a list of <a href="#">GRanges</a> . The metadata 'featureLayerID' are used for drawing features in different layers. See details in vignette. |
| ranges                      | A object of <a href="#">GRanges</a> or <a href="#">GRangesList</a> .   |
| 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.   |

|                               |  |
|-------------------------------|--|
| <code>xaxis</code>            | 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.   |
| <code>legend</code>           | If it is a list with named color vectors, a legend will be added.  |
| <code>cex</code>              | <code>cex</code> will control the size of circle.  |
| <code>dashline.col</code>     | color for the dashed line.   |
| <code>jitter</code>           | jitter the position of nodes or labels.  |
| <code>rescale</code>          | logical(1), character(1), numeric vector, or a dataframe with <code>rescale</code> from and to. Rescale the x-axis or not. if dataframe is used, <code>colnames</code> must be <code>from.start</code> , <code>from.end</code> , <code>to.start</code> , <code>to.end</code> . And the from scale must cover the whole plot region. The <code>rescale</code> 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. |
| <code>label_on_feature</code> | Labels of the feature directly on them. Default FALSE.   |
| <code>...</code>              | 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

```
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),
```

```
label.parameter.rot=45)  
lollipop(SNP.gr, features, type="pie")
```

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