Package 'ReConPlot'

February 11, 2023

Title ReConPlot: REarrangement and COpy Number PLOT.

Version 0.1

Description ReConPlot provides functionalities to depict copy number and structural rearrangement profiles, including inter- and intrachromosomal structural variants. These functionalities are particularly useful to study complex genomic rearrangements in cancer genomes.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2.9000

Depensds R (>= 4.1.0),ggplot2,dplyr,tidyr,grid,gridExtra,ggthemes,karyoploteR,cowplot,ggplotify

R topics documented:

`ReConPlot` *Function to plot genomic rearrangements (allele-specific copy number profiles and structural variants)*

Description

This function generates publication-quality plots for copy number and structural variation profiles, which are particularly useful in the context of cancer genome analysis projects.

Usage

```
ReConPlot(
  sv,
  cnv,
  title = "",
  genes = NULL,
  chr_selection = NULL,
  scaling_cn_SVs = 1/5,
  scale_separation_SV_type_labels = 1/22,
```

```
  pos_SVtype_description = 5000000,
  window = 10000000,
  xscale = 10 * 10^6,
  percentage_increase_y_axis = 0.1,
  legend_SV_types = TRUE,
  size_chr_labels = 7,
  size_title = 7,
  size_text = 5,
  lower_limit_karyotype = -0.7,
  upper_limit_karyotype = -0.2,
  colour_band2 = "antiquewhite1",
  colour_band1 = "grey86",
  colour_DEL = "orange",
  colour_h2hINV = "forestgreen",
  colour_DUP = "darkblue",
  colour_t2tINV = "black",
  colour_TRA = "darkgray",
  size_gene_label = 1.5,
  color_minor_cn = "#8491B4B2",
  curvature_intrachr_SVs = -0.15,
  curvature_interchr_SVs = -0.08,
  max.cnv = 8,
  npc_now = 0.00625 * 3,
  scale_ticks = 20000000,
  size_interchr_SV_tip = 0.2,
  genome_version = "hg38"
)
```

Arguments

sv	Dataframe with SV information. Required, no default value.
cnv	Dataframe with copy number information. Required, no default value.
title	Title of the plot. Defaults to "".
genes	Vector of genes (HUGO gene names) to be shown on the plot. Defaults to NULL.
chr_selection	Chromosomes, start and end positions to be depicted. Defaults to NULL.
scaling_cn_SVs	Relative dimension of the panel representing the SVs with respect to the copy number profile. Defaults to 1/6.
scale_separation_SV_type_labels	Separatation (denoted as a fraction of the y axis XXX) between the SV labels/legend. Defaults to 1/18.
pos_SVtype_description	Position for the SV labels/legend on the y axis. Defaults to 1000000.
window	extra spacing on the x axis around the leftmost and rightmost breakpoints detected in the chromosomes selected unless a specific start and end positions for the plot are input.
xscale	Scale for the x axis. Defaults to 10*10^6 to put the x axis in Mbp.
percentage_increase_y_axis	Relative percentage to increase the distance of the y axis. XX

legend_SV_types
: Whether to show the legend for the SV types or not. Defaults to TRUE.

size_chr_labels
: Size of the chromsosome labels. Defaults to 7pt (use 5-7pt for publication-ready figures).

size_title
: Size of the plot title. Defaults to 7pt (use 5-7pt for publication-ready figures).

colour_band2
: Colour of the second background horizintal stripe. Defaults to "antiquewhite1"

colour_band1
: Colour of the first background horizintal stripe. Defaults to "grey86"

colour_DEL
: Colour of the arcs representing deletions (DEL)

colour_h2hINV
: Colour of the arcs representing head-to-head inversions (h2hINV).

colour_DUP
: Colour of the arcs representing duplications (DUP).

colour_t2tINV
: Colour of the arcs representing tail-to-tail inversions (t2tINV).

size_gene_label
: Size of the gene labels. Defaults to 2.2.

color_minor_cn
: Colour for the horizontal bars representing the minor copy number values.

curvature_intrachr_SVs
: Curvature for the arcs represeting intrachromosomal SVs. Defaults to -0.15

curvature_interchr_SVs
: Curvature for the arcs represeting interchromosomal SVs. Defaults to -0.08

max.cnv
: Cap on the total copy number (for the minor we do not need as the minor will never be very high). Defaults to 10.

scale_ticks
: Spacing of breaks in the x axis (in bp). Defaults to 20000000 (i.e., 20Mb).

size_interchr_SV_tip
: Size of the line indicating interchromosomal SVs involving chromosomes not shown (that is, not included in chr_selection).

genome_version
: Reference genome used. Can be either hg19, hg38 or T2T (for T2T-CHM13v1.1).

Examples

```
Please the tutorial of the package.
```