Package 'ReConPlot'

September 13, 2023

Title ReConPlot: REarrangement and COpy Number PLOT.

Version 0.2

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.

License free for academic use only. If you are not a member of a public funded academic and/or education and/or research institution you must obtain a commercial license from EMBL Enterprise Management GmbH (EMBLEM); please email EMBLEM (info@embl-em.de).

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Imports tidyverse,
   cowplot,
   scales

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,
  size_gene_label = 1.5,
  colour_band1 = "grey86",
  colour_band2 = "antiquewhite1",
  colour_DEL = "orange",
  colour_h2hINV = "forestgreen",
  colour_DUP = "darkblue",
  colour_t2tINV = "black",
  colour_TRA = "darkgray",
  color_minor_cn = "#8491B4B2",
  upper_limit_karyotype = -0.2,
  karyotype_rel_size = 0.2,
  custom_annotation = NULL,
  ann_dot_col = "black",
  ann_dot_size = 0.5,
  ann_y_title = "",
  ann_rel_size = 0.4,
  curvature_intrachr_SVs = -0.15,
  curvature_interchr_SVs = -0.08,
  max.cn = 8,
  npc_now = 0.00625 * 3,
  scale_ticks = 20000000,
  size_interchr_SV_tip = 0.2,
  label_interchr_SV = FALSE,
  size_sv_line = 0.1,
  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).
size_text	Size of the plot text. Defaults to 5pt (use 5-7pt for publication-ready figures).

size_gene_label

Size of the gene label text. Defaults to 1.5.

colour_band1	Colour of the first background horizontal stripe. Defaults to "grey86".
colour_band2	Colour of the second background horizontal stripe. Defaults to "antiquewhite1".
colour_DEL	Colour of the arcs representing deletions (DEL). Defaults to "orange".
colour_h2hINV	Colour of the arcs representing head-to-head inversions (h2hINV). Defaults to "forestgreen".
colour_DUP	Colour of the arcs representing duplications (DUP). Defaults to "darkblue".
colour_t2tINV	Colour of the arcs representing tail-to-tail inversions (t2tINV). Defaults to "black".
colour_TRA	Colour of the arcs representing translocations (TRA). Defaults to "darkgray".
color_minor_cn	Colour for the horizontal bars representing the minor copy number values. Defaults to "#8491B4B2".

upper_limit_karyotype

Upper limit in y-axis for karyotype ideogram. Defaults to -0.2 .

karyotype_rel_size

Size of the karyotype ideogram, relative to the CN y axis. Defaults to .2.

custom_annotation

Dataframe with custom annotation. Must contain columns "chr", "pos" and "y". Defaults to NULL.

ann_dot_col	Colour of the dots in annotation plot. Defaults to "0.5."black".
ann_dot_size	Size of the dots in annotation plot. Defaults to 0.5.
ann_y_title	Label for Y-axis in annotation plot. Defaults to "".
ann_rel_size	Size of the annotation plot, relative to the main plot. Defaults to 0.4.
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.cn	Cap on the total copy number. Defaults to 8.
npc_now	Controls spacing, needed to find SV partners on different chromosomes in the plot. Not recommended to change. Defaults to .00625 * 3.
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).
label_interchr_SV	
	Flag to annotate the second chromosome of interchromosomal SVs involving chromosomes not shown. Defaults to FALSE.
size_sv_line	Linewidth for SVs. Defaults to .1.
genome_version	Reference genome used. Can be either hg19, hg38, T2T, mm10 or mm39. Defaults to "hg38".

Examples

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

Index