ShatterSeek documentation

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`CNVsegs-class` *Class to store CNV data*

Description

Class to store CNV data

Arguments

`chrom`	(character): chromosome (also in Ensembl notation)
`start`	(numeric): start position for the CN segment
`end`	(numeric): end position for the CN segment
`CN`	(numeric): integer total copy number (e.g. 2 for unaltered chromosomal regions)

Value

an instance of the class 'CNVsegs' that contains CNV data. Required format by the function shatterseek

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`SVs-class` *Class to store SV data*

Description

Class to store SV data

Arguments

`chrom1`	(character): chromosome for the first breakpoint
`pos1`	(character): position for the first breakpoint
`chrom2`	(character): chromosome for the second breakpoint
`pos2`	(character): position for the second breakpoint
`SVtype`	(character): type of SV, encoded as: DEL (deletion-like; +/-), DUP (duplication-like; -/+), h2hINV (head-to-head inversion; +/+), and t2tINV (tail-to-tail inversion; -/-).
`strand1`	(e.g. + for DEL)
`strand2`	(e.g. - for DEL)

Value

an instance of the class 'SVs' that contains SV data. Required format by the function shatterseek

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`chromoth-class` *chromoth objects*

Description

The chromoth object is an object returned by the function shatterseek.

Details

This object stores the results returned by the function shatterseek. This object may be coerced to a data.frame using `as(object,"data.frame")`. The obtained `data.frame` object contains 5 columns, "chrom", The "chrom" column is the chromosome name. The "clusterSize" column is the maximum cluster size that

Accessors

In the following, x is a chromoth object.

`getSVs(x)`: Get the structrual variations; Note that since shatterseek first try to filter possible false structrual variations, the structrual variations returned by this function might be different from the structrual variations provided to shatterseek.

`getSegs(x)`: Get the copy number segmentation.

Author(s)

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See Also

plot.chromoth, shatterseek

`plot_chromothripsis` *Plot chromothripsis regions This function serves to plot chromothripsis regions in order to facilitate the revision of candidate chromothripsis regions*

Description

Plot chromothripsis regions This function serves to plot chromothripsis regions in order to facilitate the revision of candidate chromothripsis regions

Usage

```
plot_chromothripsis(ShatterSeek_output, chr = chr, BAF = NULL,
  sample_name = "", DEL_color = "darkorange1", DUP_color = "blue1",
  t2tINV_color = "forestgreen", h2hINV_color = "black", arc_size = 0.2)
```

Arguments

ShatterSeek_output	the output of the function shatterseek
chr	chromosome for which the plot will be generated (note that only the region where there is a cluster of interleaved SVs will be shown)
sample_name	name of the sample to be shown in the table
DEL_color	colour to show the deletion-like SVs
DUP_color	colour to show the duplication-like SVs
t2tINV_color	colour to show the t2tINV SVs
h2hINV_color	colour to show the h2hINV SVs
arc_size	size of the arcs representing intrachromosomal SVs

Value

a list containing ggplot objects (chromosome ideogram, SVs, CN profile, and table with information about the region)

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shatterseek *The main function of the package shatterSeek*

Description

Detect chromothripsis events from structural variations and copy number variation data

Usage

```
shatterseek(SV.sample,seg.sample)
```

Arguments

SV.sample	A SVs object that stores all the structural variations of the sample. To detect clusters of interleaved SVs, ShatterSeek only considers structural variations with two breakpoints on the same chromosome. Inter-chromosomal structural variations are used in the subsequent steps to detect multichromosomal events and to evaluate the set of statistical criteria described in the tutorial.
seg.sample	A CNVsegs object that contains the copy number segmentation results for the sample.

Value

A chromoth object.

References

Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Cortes-Ciriano et al. 2018

See Also

plot_chromothripsis

Examples

```
data(DO17373)
SV_data <- SVs(chrom1=as.character(SV_DO17373$chrom1),
   pos1=as.numeric(SV_DO17373$start1),
   chrom2=as.character(SV_DO17373$chrom2),
   pos2=as.numeric(SV_DO17373$end2),
   SVtype=as.character(SV_DO17373$svclass),
   strand1=as.character(SV_DO17373$strand1),
   strand2=as.character(SV_DO17373$strand2))

CN_data <- CNVsegs(chrom=as.character(SCNA_DO17373$chromosome),
   start=SCNA_DO17373$start,
   end=SCNA_DO17373$end,
   total_cn=SCNA_DO17373$total_cn)

chromothripsis <- shatterseek(SV.sample=SV_data, seg.sample=CN_data)
plots_chr3 = plot_chromothripsis(ShatterSeek_output = chromothripsis,chr = "3", sample_name="DO17373")
```

Index

chromoth, *3*
chromoth *(*chromoth-class*)*, 2
chromoth-class, 2
class:chromoth *(*chromoth-class*)*, 2
CNVsegs, *3*
CNVsegs *(*CNVsegs-class*)*, 1
CNVsegs-class, 1

getSegs *(*chromoth-class*)*, 2
getSVs *(*chromoth-class*)*, 2

plot.chromoth, *2*
plot_chromothripsis, 2, *4*

shatterseek, *2*, 3
SVs, *3*
SVs *(*SVs-class*)*, 1
SVs-class, 1