

Package ‘svaRetro’

May 16, 2024

Type Package

Title Retrotransposed transcript detection from structural variants

Version 1.10.0

Date 2022-02-10

Description svaRetro contains functions for detecting retrotransposed transcripts (RTs) from structural variant calls. It takes structural variant calls in GRanges of breakend notation and identifies RTs by exon-exon junctions and insertion sites. The candidate RTs are reported by events and annotated with information of the inserted transcripts.

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Depends GenomicRanges, rtracklayer, BiocGenerics,
StructuralVariantAnnotation, R (>= 4.0)

Imports VariantAnnotation, assertthat, Biostrings, stringr, dplyr,
methods, rlang, GenomicFeatures, GenomeInfoDb, S4Vectors, utils

Suggests TxDb.Hsapiens.UCSC.hg19.knownGene, ggplot2, devtools,
testthat (>= 2.1.0), roxygen2, knitr, BiocStyle, plyranges,
circlize, tictoc, IRanges, stats, SummarizedExperiment,
rmarkdown

RoxygenNote 7.1.1

Encoding UTF-8

VignetteBuilder knitr

biocViews DataImport, Sequencing, Annotation, Genetics,
VariantAnnotation, Coverage, VariantDetection

BugReports <https://github.com/PapenfussLab/svaRetro/issues>

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Author Ruining Dong [aut, cre] (<<https://orcid.org/0000-0003-1433-0484>>)

Maintainer Ruining Dong <lnyidrn@gmail.com>

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`.combineMatchingTranscripts`
Combining matching transcripts

Description

Combining matching transcripts

Usage

```
.combineMatchingTranscripts(gr, names)
```

Arguments

| | |
|--------------------|----------------------------|
| <code>gr</code> | A GRanges object |
| <code>names</code> | A vector of granges names. |

Details

This is an internal function used to merge all overlapping transcripts of a breakpoint into one vector.

Value

A list of vectors. Each vector is named with the name of the corresponding granges.

.scoreByTranscripts *Ranking matching transcripts*

Description

Ranking matching transcripts

Usage

```
.scoreByTranscripts(genes, transcripts.col)
```

Arguments

genes TxDb object of genes. hg19 and hg38 are supported in the current version.
transcripts.col A vector of transcript names.

Details

This is an internal function which returns overlapping transcript names with ranking scores. The ranking score is the proportion of exon-exon fusions (intronic deletion events) detected for a given transcript.

Value

A dataframe with two columns, tx_name and score.

.txs2genesym *Adding gene symbol annotations*

Description

Adding gene symbol annotations

Usage

```
.txs2genesym(txs, unique.genesyms = TRUE)
```

Arguments

txs A list of transcript ids in UCSC format.
unique.genesyms TRUE or FALSE. If TRUE, the converted gene symbols will remove duplicates.

Details

This is an internal function which takes a list of txs in UCSC id format as input and convert the txs to gene symbol.

Value

A list of names in gene symbols

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|----------|--|
| rtDetect | <i>Detecting retrotranscript insertion in nuclear genomes.</i> |
|----------|--|

Description

Detecting retrotranscript insertion in nuclear genomes.

Usage

```
rtDetect(gr, genes, maxgap = 100, minscore = 0.4)
```

Arguments

| | |
|----------|--|
| gr | A GRanges object |
| genes | TxDb object of genes. hg19 and hg38 are supported in the current version. |
| maxgap | The maximum distance allowed on the reference genome between the paired exon boundaries. |
| minscore | The minimum proportion of intronic deletions of a transcript should be identified. |

Details

This function searches for retroposed transcripts by identifying breakpoints supporting intronic deletions and fusions between exons and remote loci. Only BND notations are supported at the current stage.

Value

A GRangesList object, named insSite and rt, reporting breakpoints supporting insert sites and retroposed transcripts respectively. 'exon' and 'txs' in the metadata columns report exon_id and transcript_name from the 'genes' object.

Examples

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
genes <- TxDb.Hsapiens.UCSC.hg19.knownGene
vcf.file <- system.file("extdata", "diploidSV.vcf",
                        package = "svaRetro")
vcf <- VariantAnnotation::readVcf(vcf.file, "hg19")
gr <- breakpointRanges(vcf, nominalPosition=TRUE)
rt <- rtDetect(gr, genes, maxgap=30, minscore=0.6)
```

| | |
|----------|---|
| svaRetro | <i>svaRetro: a package for retrotransposed transcript detection</i> |
|----------|---|

Description

svaRetro contains functions for detecting retrotransposed transcripts from structural variant calls.

Details

For more details on the features of StructuralVariantAnnotation, read the vignette: `'browseVignettes(package = "svaRetro")'`

| | |
|-------------------|---|
| <code>%na%</code> | <i>Replaces the NA values in a with corresponding values in b</i> |
|-------------------|---|

Description

Replaces the NA values in a with corresponding values in b

Usage

```
a %na% b
```

Arguments

a, b objects to be tested or coerced.

Value

The altered object.

| | |
|---------------------|----------------------------|
| <code>%null%</code> | <i>Uses b if a is NULL</i> |
|---------------------|----------------------------|

Description

Uses b if a is NULL

Usage

```
a %null% b
```

Arguments

a, b objects to be tested or coerced.

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%null%

Value

An un-null object.

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