

# Package ‘svaRetro’

November 23, 2024

**Type** Package

**Title** Retrotransposed transcript detection from structural variants

**Version** 1.13.0

**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>

**git\_url** <https://git.bioconductor.org/packages/svaRetro>

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`.combineMatchingTranscripts`  
*Combining matching transcripts*

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### 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.

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.scoreByTranscripts     *Ranking matching transcripts*

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### 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*

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### 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>
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**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)
```

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svaRetro	<i>svaRetro: a package for retrotransposed transcript detection</i>
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**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")’

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%na%	<i>Replaces the NA values in a with corresponding values in b</i>
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**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.

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%null%	<i>Uses b if a is NULL</i>
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**Description**

Uses b if a is NULL

**Usage**

```
a %null% b
```

**Arguments**

a, b                    objects to be tested or coerced.

**Value**

An un-null object.

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