

# Package ‘svaRetro’

June 30, 2022

**Type** Package

**Title** Retrotransposed transcript detection from structural variants

**Version** 1.2.0

**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>

**git\_branch** RELEASE\_3\_15

**git\_last\_commit** 7ec810b

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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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