

# Package ‘svaRetro’

April 10, 2022

**Type** Package

**Title** Retrotransposed transcript detection from structural variants

**Version** 1.0.0

**Date** 2021-04-15

**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\_14

**git\_last\_commit** c7b9142

**git\_last\_commit\_date** 2021-10-26

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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 maxium distance allowed on the reference genome between the paired exon boundries. |
| minscore | The minimum proportion of intronic deletions of a transcript should be identi-fied.    |

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 retro-posed transcripts respectively. 'exon' and 'txs' in the metadata columns report exon\_id and tran-script\_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.

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*%null%*

**Value**

An un-null object.

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