

# Package: svaRetro (via r-universe)

October 11, 2026

**Type** Package

**Title** Retrotransposed transcript detection from structural variants

**Version** 1.19.0

**Date** 2026-02-18

**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, AnnotationDbi, assertthat, Biostrings, stringr, dplyr, methods, rlang, S4Vectors, Seqinfo, GenomeInfoDb, GenomicFeatures, utils

**Suggests** TxDb.Hsapiens.UCSC.hg19.knownGene, org.Hs.eg.db, 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>

**Config/pak/sysreqs**  
make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

**Repository** <https://bioc.r-universe.dev>

**Date/Publication** 2026-04-28 12:56:48 UTC

**RemoteUrl** <https://github.com/bioc/svaRetro>  
**RemoteRef** HEAD  
**RemoteSha** 6a5d754c5d5483237e572c0102dbeb7c083539b1

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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> |
|--------|----------------------------|

---

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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|          |                                                                |
|----------|----------------------------------------------------------------|
| 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`*svaRetro: a package for retrotransposed transcript detection*

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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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