Package 'svaRetro'

January 20, 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

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R topics documented:

`rtDetect` *Detecting retrotranscript insertion in nuclear genomes.*

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 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 *svaRetro: a package for retrotransposed transcript detection*

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")‘

`%na%` *Replaces the NA values in a with corresponding values in b*

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.

`%null%` *Uses b if a is NULL*

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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