

# Package ‘svaNUMT’

May 22, 2022

**Type** Package

**Title** NUMT detection from structural variant calls

**Version** 1.2.0

**Date** 2022-03-07

**Description** svaNUMT contains functions for detecting NUMT events from structural variant calls. It takes structural variant calls in GRanges of breakend notation and identifies NUMTs by nuclear-mitochondrial breakend junctions. The main function reports candidate NUMTs if there is a pair of valid insertion sites found on the nuclear genome within a certain distance threshold. The candidate NUMTs are reported by events.

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**Depends** GenomicRanges, rtracklayer, VariantAnnotation, StructuralVariantAnnotation, BiocGenerics, Biocstrings, R (>= 4.0)

**Imports** assertthat, stringr, dplyr, methods, rlang, GenomeInfoDb, S4Vectors, GenomicFeatures

**Suggests** TxDb.Hsapiens.UCSC.hg19.knownGene, BSgenome.Hsapiens.UCSC.hg19, ggplot2, devtools, testthat (>= 2.1.0), roxygen2, knitr, readr, plyranges, circlize, IRanges, SummarizedExperiment, rmarkdown

**RoxygenNote** 7.1.2

**Encoding** UTF-8

**VignetteBuilder** knitr

**biocViews** DataImport, Sequencing, Annotation, Genetics, VariantAnnotation

**BugReports** <https://github.com/PapenfussLab/svaNUMT/issues>

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

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

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numtDetect	<i>Detecting nuclear mitochondria fusion events.</i>
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### Description

Detecting nuclear mitochondria fusion events.

### Usage

```
numtDetect(
  gr,
  numtS,
  genomeMT,
  max_ins_dist = 10,
  maxgap_numtS = 10,
  min_len = 20,
  min.Align = 0.8
)
```

### Arguments

<code>gr</code>	A GRanges object
<code>numtS</code>	A GRanges object of known NUMT sites.
<code>genomeMT</code>	A genome object of the mitochondria.
<code>max_ins_dist</code>	The maximum distance allowed on the reference genome between the paired insertion sites. Only intra-chromosomal NUMT events are supported. Default value is 10.
<code>maxgap_numtS</code>	The maximum distance allowed between the insertion sequence loci and known NUMTs.
<code>min_len</code>	The minimum length allowed of the insertion sequences. Default value is 20.
<code>min.Align</code>	The minimum alignment score allowed between the insertion sequence and MT genome.

## Details

Nuclear mitochondrial fusion (NUMT) is a common event found in human genomes. This function searches for NUMT events by identifying breakpoints supporting the fusion of nuclear chromosome and mitochondrial genome. Only BND notations are supported at the current stage. Possible linked nuclear insertion sites are reported by chromosome in GRanges format.

## Value

A nested list of GRanges objects of candidate NUMTs.

## Examples

```
vcf.file <- system.file("extdata", "MT.vcf", package = "svaNUMT")
vcf <- VariantAnnotation::readVcf(vcf.file, "hg19")
gr <- breakpointRanges(vcf, nominalPosition=TRUE)
numtS <- readr::read_table(system.file("extdata", "numtS.txt", package = "svaNUMT"), col_names = FALSE)
colnames(numtS) <- c("bin", "seqnames", "start", "end", "name", "score", "strand")
numtS <- `seqlevelsStyle`-(GRanges(numtS), "NCBI")
genome <- BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19
genomeMT <- genome$chrMT
numt.gr <- numtDetect(gr, numtS, genomeMT, max_ins_dist=20)
```

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svaNUMT

*svaNUMT: a package for NUMT detection*

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## Description

svaNUMT contains functions for detecting NUMT events from structural variant calls. svaNUMT contains functions for detecting NUMT events from structural variant calls. It takes structural variant calls in GRanges of breakend notation and identifies NUMTs by nuclear-mitochondrial break-end junctions. The main function reports candidate NUMTs if there is a pair of valid insertion sites found on the nuclear genome within a certain distance threshold. The candidate NUMTs are reported by events.

## Details

For more details on the features of StructuralVariantAnnotation, read the vignette: `'browseVignettes(package = "svaNUMT")'`

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