

Package ‘sveval’

December 13, 2018

Title SV evaluation

Version 0.0.0.9000

Description Evaluate SV in a call set against a truth set using overlap-based approaches and sequence comparison for insertions.

Depends R (\geq 3.4.4)

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Imports VariantAnnotation,
GenomicRanges,
magrittr,
dplyr,
rlang,
DelayedArray,
Biostrings,
parallel,
testthat

R topics documented:

filterSVs	2
readSVvcf	2
svevalOl	3

Index	4
--------------	-------------------

filterSVs	<i>Filter SVs for regions of interest</i>
-----------	---

Description

Filter SVs for regions of interest

Usage

```
filterSVs(sv.gr, regions.gr, ol.prop = 0.5)
```

Arguments

sv.gr	the input SVs (e.g. read from readSVvcf)
regions.gr	the regions of interest
ol.prop	minimum proportion of sv.gr that must overlap regions.gr. Default is 0.5

Value

a subset of sv.gr that overlaps regions.gr

Author(s)

Jean Monlong

readSVvcf	<i>Read SVs from a VCF file</i>
-----------	---------------------------------

Description

Read SVs from a VCF file

Usage

```
readSVvcf(vcf.file, keep.ins.seq = FALSE, sample.name = NULL)
```

Arguments

vcf.file	the path to the VCF file
keep.ins.seq	should it keep the inserted sequence? Default is FALSE.
sample.name	the name of the sample to use. If NULL (default), use first sample.

Value

a GRanges object with relevant information.

Author(s)

Jean Monlong

sveval0l

*SV evaluation based on overlap and variant size***Description**

SV evaluation based on overlap and variant size

Usage

```
sveval0l(calls.gr, truth.gr, max.ins.dist = 20, min.cov = 0.5,
min.del.rol = 0.1, ins.seq.comp = FALSE, nb.cores = 1,
min.size = 0, max.size = Inf, bed.regions = NULL,
bed.regions.ol = 0.5, sample.name = NULL, outfile = NULL,
out.bed.prefix = NULL)
```

Arguments

<code>calls.gr</code>	call set. A GRanges or the path to a VCF file.
<code>truth.gr</code>	truth set. A GRanges or the path to a VCF file.
<code>max.ins.dist</code>	maximum distance for insertions to be clustered. Default is 20.
<code>min.cov</code>	the minimum coverage to be considered a match. Default is 0.5
<code>min.del.rol</code>	minimum reciprocal overlap for deletions. Default is 0.1
<code>ins.seq.comp</code>	compare sequence instead of insertion sizes. Default is FALSE.
<code>nb.cores</code>	number of processors to use. Default is 1.
<code>min.size</code>	the minimum SV size to be considered. Default 0.
<code>max.size</code>	the maximum SV size to be considered. Default is Inf.
<code>bed.regions</code>	If non-NULL, a GRanges object or path to a BED file (no headers) with regions of interest.
<code>bed.regions.ol</code>	minimum proportion of sv.gr that must overlap regions.gr. Default is 0.5
<code>sample.name</code>	the name of the sample to use if VCF files given as input. If NULL (default), use first sample.
<code>outfile</code>	the TSV file to output the results. If NULL (default), returns a data.frame.
<code>out.bed.prefix</code>	prefix for the output BED files. If NULL (default), no BED output.

Value

a data.frame with TP, FP and FN for each SV type.

Author(s)

Jean Monlong

Index

`filterSVs`, [2](#)

`readSVvcf`, [2](#)

`sveval01`, [3](#)