

Package ‘ifCNVR’

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Title Isolation-Forest Based 'CNV' Detection from 'NGS' Data

Version 0.1.0

URL <https://github.com/SimCab-CHU/ifCNVR>

Description Automatically detects Copy Number Variations (CNV) from Next Generation Sequencing data using a machine learning algorithm, Isolation forest. More details about the method can be found in the paper by Cabello-Aguilar (2022) <[doi:10.1101/2022.01.03.474771](https://doi.org/10.1101/2022.01.03.474771)>.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Imports data.table, rmarkdown, isotree

Depends R (>= 2.10)

NeedsCompilation no

Author Simon Cabello-Aguilar [aut, cre]
(<<https://orcid.org/0000-0002-2904-7430>>)

Maintainer Simon Cabello-Aguilar <s-cabelloaguilar@chu-montpellier.fr>

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abSamples	<i>abSamples</i>
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Description

abSamples

Usage

```
abSamples(readsMatrix, conta = "auto", q = 0.99, verbose = TRUE)
```

Arguments

readsMatrix	a matrix of the number of reads per target
conta	a parameter for the isotree function
q	quantile
verbose	a boolean

Value

the aberrant and normal samples

Examples

```
readsMatrix = data.frame(targets=paste0("target_",seq(1,50)), matrix(runif(500),nrow=50,ncol=10))
abSamples(readsMatrix)
```

abTargets	<i>abTargets</i>
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Description

abTargets

Usage

```
abTargets(readsMatrix, abSamples, opt = "regular", pred = 0.6)
```

Arguments

readsMatrix	the reads matrix
abSamples	the abSamples list result of the abSamples function
opt	"regular" or "extensive" a parameter
pred	a threshold on the isolation forest outlier prediction (range=[0,1])

Value

a list of dataframes of the targets tagged as outliers

Examples

```
abTargets(readsMatrixExample, abSamples(readsMatrixExample))
```

calculateRatio	<i>calculate Ratio</i>
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Description

calculate Ratio

Usage

```
calculateRatio(readsMatrix, abSamples, roi, soi)
```

Arguments

readsMatrix	the reads matrix
abSamples	the abSamples list result of the abSamples function
roi	the region of interest
soi	the sample of interest

Value

the ratio associated with the abTargets

Examples

```
calculateRatio(readsMatrixExample, abSamples(readsMatrixExample), "EGFR-Ex20", "sample_2")
```

calculateScore	<i>calculate Score</i>
----------------	------------------------

Description

calculate Score

Usage

```
calculateScore(  
  readsMatrix,  
  abSamples,  
  abTargets,  
  roi = "Gene",  
  sep = "-",  
  thrScore = 7  
)
```

Arguments

readsMatrix	a reads matrix with samples in columns and targets in lines (the first column are the targets)
abSamples	the abSamples list result of the abSamples function
abTargets	a list of dataframes of the targets tagged as outliers result of the abTargets() function
roi	the region of interest (Gene or Gene-Exon)
sep	a character the separator between roi in the bed file
thrScore	(default 0) a threshold on the localization score

Value

the score associated with the abSamples in the desired roi

Examples

```
abS <- abSamples(readsMatrixExample)  
abT <- abTargets(readsMatrixExample, abSamples(readsMatrixExample))  
calculateScore(readsMatrixExample, abS, abT, sep="-")
```

CreateReadsMatrix *CreateReadsMatrix*

Description

CreateReadsMatrix

Usage

```
CreateReadsMatrix(  
  bamPath,  
  bedFile,  
  bedtoolsPath,  
  outputFile = "n",  
  verbose = TRUE  
)
```

Arguments

bamPath	a path leading to the .bam and .bai files
bedFile	a path leading to the .bed file (Warning replace chrX by X in the position)
bedtoolsPath	the path leading to bedtools
outputFile	(optional) a path leading to a text file
verbose	a boolean

Value

a reads matrix

Examples

```
bamPath <- system.file("extdata/",package = "ifCNVR")  
bed <- system.file("bedFile.bed",package = "ifCNVR")  
bedtools <- 'n'  
readsMatrix <- CreateReadsMatrix(bamPath, bed, bedtools)
```

generateReport	<i>generateReport</i>
----------------	-----------------------

Description

generateReport

Usage

```
generateReport(outputFile = "n", readsMatrix, resTable, CNVpos)
```

Arguments

outputFile	a path to the html output file
readsMatrix	the reads matrix
resTable	the table result of the CalculateScore() function
CNVpos	the CNVpos list result of the abSamples function

Value

a html report

Examples

```
generateReport()
```

normalizeReads	<i>normalizeReads</i>
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Description

normalizeReads

Usage

```
normalizeReads(readsMatrix)
```

Arguments

readsMatrix	a reads matrix with samples in columns and targets in lines (the first column are the targets)
-------------	--

Value

a normalized reads matrix

Examples

```
normReads <- normalizeReads(readsMatrixExample)
```

readsMatrixExample	<i>Example dataset</i>
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Description

A dataset for the examples

Usage

```
readsMatrixExample
```

Format

A data frame with 11 rows and 6 variables:

targets the targets

sample_1 the number of reads in sample 1

sample_2 the number of reads in sample 2

sample_3 the number of reads in sample 3

sample_4 the number of reads in sample 4

sample_5 the number of reads in sample 5 ...

scoring	<i>scoring</i>
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Description

scoring

Usage

```
scoring(k, n, N)
```

Arguments

k number of modified targets on the region

n number of targets on the region

N number of targets in the panel

Value

the confidence score

Examples

```
scoring(10,20,150)
```


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