

# Package ‘ifCNVR’

February 15, 2022

**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

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**Repository** CRAN

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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)
```

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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))
```

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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")
```

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calculateScore	<i>calculate Score</i>
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### 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="-")
```

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CreateReadsMatrix      *CreateReadsMatrix*

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## 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      *generateReport*

---

**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()
```

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normalizeReads      *normalizeReads*

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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)
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**Value**

a normalized reads matrix

**Examples**

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

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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 ...

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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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