Package ‘SomaticSignatures’

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Type   Package
Title   Somatic Signatures
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Description The SomaticSignatures package identifies mutational signatures of single nucleotide variants (SNVs). It provides a infrastructure related to the methodology described in Nik-Zainal (2012, Cell), with flexibility in the matrix decomposition algorithms.
URL   https://github.com/juliangehring/SomaticSignatures
Imports S4Vectors, IRanges, GenomeInfoDb, Biostrings, ggplot2, ggbio, reshape2, NMF, pcaMethods, Biobase, methods, proxy
Depends R (>= 3.1.0), VariantAnnotation, GenomicRanges
Suggests testthat, knitr, parallel,
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ByteCompile TRUE
License MIT + file LICENSE
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R topics documented:

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Description
Cluster the mutational spectrum by sample or motif.

Usage
clusterSpectrum(m, by = c("sample", "motif"), distance = "Cosine", ...)

Arguments
m Mutational spectrum matrix
by Dimension to cluster by.
distance Distance function used in the clustering.
... Additional arguments passed to 'hclust'.

Details
Hierarchical clustering of the motif matrix aka mutational spectrum.

Value
An 'hclust' object.

See Also
hclust
dist
**Decomposition Functions for Somatic Signatures**

**Description**

Estimate somatic signatures from sequence motifs with a selection of statistical methods.

**Usage**

```r
nmfDecomposition(x, r, ..., includeFit = FALSE)
pcaDecomposition(x, r, ..., includeFit = FALSE)
```

**Arguments**

- `x` GRanges object [required]
- `r` Number of signatures [integer, required]
- `...` Additional arguments passed to `NMF::nmf` or `pcaMethods::pca`.
- `includeFit` Include the fit object returned by the low-level decomposition function in the output.

**Details**

The `nmfDecomposition` and `pcaDecomposition` functions estimate a set of `r` somatic signatures using the NMF or PCA, respectively.

In previous versions of the package, these functions were known as `nmfSignatures` and `pcaSignatures`, respectively. While they are still available, we recommend using the new naming convention.

**Value**

The `signature` functions return a list with the elements:

- `wMatrix` of the form `motif x signature`
- `hMatrix` of the form `sample x signature`
- `vMatrix` of the form `motif x sample`, containing the reconstruction of `m` from `w` and `h`.
- `mInput matrix m`
- `rNumber of signatures`
- `fitFit object returned by the low-level decomposition function, if `includeFit` is true.

**See Also**

- `NMF` package
- `pcaMethods` package
- `prcomp`
**gcContent**  
*GC Content*

**Description**

Compute the GC content for regions of a reference sequence.

**Usage**

\[ \text{gcContent(regions, ref)} \]

**Arguments**

- **regions**: GRanges object with the regions for which the GC content should be computed.
- **ref**: Reference sequence object, as a 'BSgenome' or 'FaFile' object.

**Value**

A numeric vector with the GC content [0,1] for each region.

**Examples**

```r
library(BSgenome.Hsapiens.1000genomes.hs37d5)
regs = GRanges(c("1", "2"), IRanges(1e7, width = 100))
gc = gcContent(regs, BSgenome.Hsapiens.1000genomes.hs37d5)
```

**GRanges-converters**  
*GRanges converter functions*

**Description**

A set of utilities functions to convert and extract data in 'GRanges' objects.

**Usage**

- **ncbi(x)**
- **ucsc(x)**
- **seqchar(x)**

**Arguments**

- **x**: A 'GRanges' object or one inheriting from the 'GRanges' class [required].
hs-chrs

Details

- granges: Extracts only the `GRanges` information by dropping the metadata columns of the object. The `seqinfo` slot is kept.
- ncbi, ucsc: Shorthand for converting the seqnames notation to 'UCSC' (e.g. 'chr1', 'chrM') or 'NCBI' (e.g. '1', 'MT') notation, respectively. This also sets the `genome` slot in the `seqinfo` field to 'NA'.
- seqchar: Extracts the `seqnames` as a character vector.

Value

For `ncbi`, `ucsc`: An object of the same class as the input.
For `seqchar`: A character vector with `seqnames`.

See Also

seqnames, mcols
seqlevelsStyle

Examples

```r
mutect_path = system.file("examples", "mutect.tsv", package = "SomaticSignatures")
vr1 = readMutect(mutect_path, strip = TRUE)

## extract the GRanges
gr = granges(vr1)

## convert back and forth
gr_ncbi = ncbi(gr)
gr_ucsc = ucsc(gr_ncbi)

identical(gr, gr_ucsc)

## extract the seqnames as a character vector
seq_chars = seqchar(gr)
```

---

 hs-chrs | Human Chromosome Names
---|---

Description

List human chromosome names.

Usage

hsToplevel()
hsAutosomes()
hsAllosomes()
hsLinear()
kmerFrequency

Value

Character vector with chromosome names (NCBI notation).

Examples

hsToplevel()
hsAutosomes()
hsAllosomes()
hsLinear()

kmerFrequency  Kmer Frequency

Description

Estimate the occurrence frequency of k-mers in a reference sequence.

Usage

kmerFrequency(ref, n = 1e4, k = 1, ranges = as(seqinfo(ref), "GRanges"))

Arguments

ref  A 'BSgenome' or 'FaFile' object matching the respective reference sequence [required].
n  The number of samples to draw [integer, default: 1e4].
k  The 'k'-mer size of the context, including the variant position [integer, default: 3].
ranges  Ranges in respect to the reference sequence to sample from [GRanges, default: take from the 'seqinfo' slot].

Details

The k-mer frequency is estimated by random sampling of `n` locations across the specified `ranges` of the reference sequence.

Value

A named vector, with names corresponding to the k-mer and values to the frequency.

Examples

library(BSgenome.Hsapiens.1000genomes.hs37d5)
kmer_freq = kmerFrequency(BSgenome.Hsapiens.1000genomes.hs37d5, 1e2, 3)
kmers-data

**Description**

3mer base frequencies of human whole-genome and whole-exome sampling, based on the hg19/GRCh37 reference sequence.

For details, see the `inst/scripts/kmers-data.R` script.

**Value**

Vectors with frequency of k-mers.

**See Also**

kmerFrequency

**Examples**

```r
data(kmers, package = "SomaticSignatures")
```

motif-functions

**Description**

Tabulate somatic motifs by a grouping variable.

**Usage**

```r
motifMatrix(vr, group = "sampleNames", normalize = TRUE)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>vr</td>
<td>GRanges object [required]</td>
</tr>
<tr>
<td>group</td>
<td>Grouping variable name [character, default: 'sampleNames']</td>
</tr>
<tr>
<td>normalize</td>
<td>Normalize to frequency</td>
</tr>
</tbody>
</table>

**Details**

The `motifMatrix` function transforms the metadata columns of a `VRanges` object, as returned by the `mutationContext` function, to a matrix of the form `motifs x groups`. This constitutes the bases for the estimation of the signatures. By default (with `normalize` set to TRUE), the counts are transformed to frequencies, such that the sum of frequencies of each group equal 1. Otherwise (with `normalize` set to FALSE), the counts for each motif in a group is returned.
Value

Occurrence matrix with motifs in rows and samples in columns.

See Also

'mutationContext', 'mutationContextMutect'

Examples

data(sca_motifs_tiny)
motifMatrix(sca_motifs_tiny, group = "study")

Description

Summary and plotting function for characterizing the distributions of mutations along the genome.

Usage

mutationDistance(x)

plotRainfall(x, group, size = 2, alpha = 0.5, space.skip = 0, ...)

Arguments

x A 'GRanges' or 'VRanges' object [required].
group The variable name for color groups [optional].
size Point size [default: 2]
alpha Alpha value for points [default: 0.5]
space.skip Space between chromosomes, as defined by 'plotGrandLinear' [default: 0]
... Additional arguments passed to 'plotGrandLinear'

Value

- mutationDensity The position-sorted GRanges `x` with the additional column `distance`, specifying the distance from the previous mutation (or the beginning of the chromosome if it happens to be the first mutation on the chromosome.)
- plotRainfall Object of class 'ggbio', as returned by 'plotGrandLinear'.

See Also

plotGrandLinear from the 'ggbio' package
Examples

```r
library(GenomicRanges)
library(IRanges)

set.seed(1)
chr_len = 100
gr = GRanges(rep(1:3, each = 10),
IRanges(start = sample.int(chr_len, 30, replace = FALSE), width = 1),
mutation = sample(c("A", "C", "G", "T"), 30, replace = TRUE))
seqlengths(gr) = rep(chr_len, 3)
p = plotRainfall(gr)
print(p)
```

mutational-normalization

Normalize Somatic Motifs

Description

Normalize somatic motifs, to correct for biases between samples.

Usage

```
normalizeMotifs(x, norms)
```

Arguments

- `x`: Matrix, as returned by `motifMatrix` [required]
- `norms`: Vector with normalization factors [required]. The names must match the base sequence names in `x`.

Value

A matrix as `x` with normalized counts.

See Also

`motifMatrix`
mutational-plots  Mutational Plots

Description
Plots for variant analysis

Usage
plotVariantAbundance(x, group = NULL, alpha = 0.5, size = 2)

Arguments
- x: A VRanges object [required].
- group: Grouping variable, refers to a column name in 'x'. By default, no grouping is performed.
- alpha: Alpha value for data points.
- size: Size value for data points.

Details
The 'plotVariantAbundance' shows the variant frequency in relation to the total coverage at each variant position. This can be useful for examining the support of variant calls.

Value
A 'ggplot' object.

mutational-signatures  Estimate Somatic Signatures

Description
Estimate somatic signatures from sequence motifs with a selection of statistical methods.

Usage
identifySignatures(m, nSigs, decomposition = nmfDecomposition, ...)

Arguments
- m: Motif matrix, as returned by 'motifMatrix' [required].
- nSigs: Number of signatures [integer, required].
- decomposition: Function to apply for the matrix decomposition. The methods NMF and PCA are already implemented in the functions 'nmfDecomposition' and 'pcaDecomposition', respectively.
- ...: Additional arguments passed to the 'decomposition' function.
'identifySignatures' estimate a set of 'r' somatic signatures, based on a matrix decomposition method (such as NMF, PCA).

Value
An object of class 'MutationalSignatures'.

See Also
The predefined decomposition functions: nmfDecomposition and pcaDecomposition
mutationContext, mutationContextMutect
motifMatrix
MutationalSignatures class

Examples
data("sca_mm", package = "SomaticSignatures")
sigs = identifySignatures(sca_mm, 5)

Description
Object representing of somatic signatures.

Usage

## S4 method for signature 'MutationalSignatures'
signatures(object)

## S4 method for signature 'MutationalSignatures'
samples(object)

## S4 method for signature 'MutationalSignatures'
observed(object)

## S4 method for signature 'MutationalSignatures'
fitted(object)

## S4 method for signature 'MutationalSignatures'
show(object)

Arguments

object 'MutationalSignatures' object
Value

```R
help("MutationalSignatures")
```

See Also

`identifySignatures`

---

**mutationContext**  
*mutationContext functions*

### Description

Extract the sequence context surrounding SNVs from a genomic reference.

### Usage

```r
mutationContext(vr, ref, k = 3, strand = FALSE, unify = TRUE, check = FALSE)
mutationContextMutect(vr, k = 3, unify = TRUE)
```

### Arguments

- **vr**  
  'VRanges' with SNV substitutions, with 'ref' and 'alt' columns filled [required].  
  Each element of 'ref' and 'alt' have be a single base from the DNA bases (A,C,G,T). For 'mutationContextMutect', an object as returned by the 'read-Mutect' function.

- **ref**  
  A 'BSgenome', 'FastaFile' or 'TwoBitfile' object representing the reference sequence [required]. More generally, any object with a defined 'getSeq' method can be used.

- **k**  
  The 'k'-mer size of the context, including the variant position [integer, default: 3]. The variant will be located at the middle of the k-mer which requires 'k' to be odd.

- **strand**  
  Should all variants be converted to the 'plus' strand? [logical, default: FALSE].

- **unify**  
  Should the alterations be converted to have a C/T base pair as a reference alleles? [logical, default: TRUE]

- **check**  
  Should the reference base of 'vr' be checked against 'ref' [logical, default: TRUE]? In case the two references do not match, a warning will be printed.

### Details

The somatic motifs of a SNV, composed out of (a) the base change and (b) the sequence context surrounding the variant, is extracted from a genomic sequence with the 'mutationContext' function.

Different types of classes that represent the genomic sequence can used together with the 'mutationContext' function: 'BSgenome', 'FastaFile' and 'TwoBitFile' objects are supported through Bioconductor by default. See the vignette for examples discussing an analysis with non-reference genomes.

For mutect variant calls, all relevant information is already contained in the results and somatic motifs can constructed by using the 'mutationContextMutect' function, without the need for the reference sequence.
numberSignatures

Value

The original 'VRanges' object 'vr', with the additional columns

alteration DNAStringSet with 'ref|alt'.
context DNAStringSet with '..N..' of length 'k', where N denotes the variant position.

See Also

readMutect for mutationContextMutect
'showMethods("getSeq")' for genomic references that can be used

Examples

mutect_path = system.file("examples", "mutect.tsv", package = "SomaticSignatures")
vr1 = readMutect(mutect_path)
ct1 = mutationContextMutect(vr1)

table(numberSignatures = assessNumberSignatures(m, nSigs, decomposition = nmfDecomposition, ..., nReplicates = 1))
plotNumberSignatures(gof)

Arguments

m Mutational spectrum matrix, same as used for 'identifySignatures'.
nSigs Vector of integers with the numbers of signatures that should be tested. See the 'nSigs' argument for 'identifySignatures'.
decomposition Function to apply for the matrix decomposition. See the 'decomposition' argument for 'identifySignatures'.
... Additional arguments passed to the 'decomposition' function. See the '...' argument for 'identifySignatures'.
nReplicates How many runs should be used for assessing a value of 'nSigs'? For decomposition methods with random seeding, values greater than 1 should be used.
gof Data frame, as returned of 'assessNumberSignatures'.

Description

Assessment of the number of signatures in the data.

Usage

assessNumberSignatures(m, nSigs, decomposition = nmfDecomposition, ..., nReplicates = 1)
plotNumberSignatures(gof)
Details

Compute the decomposition for a given number of signatures, and assess the goodness of the reconstruction between the observed and fitted mutational spectra $M$ and $V$, respectively. The residual sum of squares (RSS)

$$RSS = \sum_{i,j} (M_{ij} - V_{ij})^2$$

and the explained variance

$$evar = 1 - \frac{RSS}{\sum_{i,j} V_{ij}^2}$$

are used as summary statistics which can generally applied to all decomposition approaches.

The 'plotNumberSignatures' function visualizes the results of the 'assessNumberSignatures' analysis. Statistics of the individual runs are shown as gray crosses, whereas the mean across the runs is depicted in red.

If a decomposition method uses random seeding and hence recomputing the decomposition of the same data can yield different results, evaluating the summary statistics will give more reliable estimates of the number of signatures. This applies to some NMF algorithms, for example. Methods with a deterministic decomposition, such as the standard PCA, do not need this, since repeated computations will yield the same decomposition. This behaviour is controlled by the 'nReplicates' parameter, where the default of '1' corresponds to a single run.

In practice, these summary statistics should not be trusted blindly, but rather interpreted together with biological knowledge and scientific reasoning. For a discussion of the interpretation of these statistics with special focus on the NMF decomposition, please refer to the references listed below.

Value

- assessNumberSignatures: A data frame with the RSS and explained variance for each run
- plotNumberSignatures: A ggplot object

References


See Also

identifySignatures
rss and evar functions of the NMF package.

Examples

data("sca_mm", package = "SomaticSignatures")
nSigs = 2:8
stat = assessNumberSignatures(sca_mm, nSigs, nReplicates = 3)
plotNumberSignatures(stat)
readMutect

Description

Import 'mutect' calls.

Usage

readMutect(file, columns, strip = FALSE)

Arguments

- **file**: Location of the mutect tsv files [character, required]
- **columns**: Names of columns to import from the file [character vector, optional, default: missing]. If missing, all columns will be imported.
- **strip**: Should additional columns be imported? [logical, default: FALSE]. If TRUE, return only the bare 'VRanges' object.

Details

The 'readMutect' function imports the mutational calls of a '*.tsv' file returned by the 'mutect' caller to a 'VRanges' object. For a description of the information of the columns, please refer to the mutect documentation.

Value

A 'VRanges' object, with each row corresponding to one variant in the original file.

References


http://www.broadinstitute.org/cancer/cga/mutect_run

Examples

```r
mutect_path = system.file("examples", "mutect.tsv", package = "SomaticSignatures")
vr1 = readMutect(mutect_path)
vr2 = readMutect(mutect_path, strip = TRUE)
```
sca-data  

SomaticCancerAlterations Results

Description

Motif matrix and 5 estimated signatures (NMF) from the somatic variant calls in the 'SomaticCancerAlterations' package. For details, see the vignette of the 'SomaticSignatures' package.

See Also

SomaticCancerAlterations package

Examples

data(sca_motifs_tiny, package = "SomaticSignatures")
data(sca_mm, package = "SomaticSignatures")
data(sca_sigs, package = "SomaticSignatures")

signature-plots  

Plot Mutational Signatures

Description

Visualize estimated signatures, sample contribution, and mutational spectra.

Usage

plotObservedSpectrum(s, colorby = c("sample", "alteration"))
plotFittedSpectrum(s, colorby = c("sample", "alteration"))

plotMutationSpectrum(vr, group, colorby = c("sample", "alteration"), normalize = TRUE)

plotSignatureMap(s)
plotSignatures(s, normalize = FALSE, percent = FALSE)

plotSampleMap(s)
plotSamples(s, normalize = FALSE, percent = FALSE)

Arguments

s  MutationalSignatures object [required]
vr  VRanges object
colorby  Which variable to use for the coloring in the spectra representation.
normalize  Plot relative contributions (TRUE) instead of absolute (FALSE) ones.
percent  Display the results as fraction (FALSE) or percent (TRUE).
group  Charactering string that represents the variable name used for grouping.
Details

With the plotting function, the obtained signatures and their ocurrence in the samples can be visualized either as a heatmap (’plotSignatureMap’, ’plotSampleMap’) or a barchart (’plotSignature’, ’plotSamples’).

Since the plotting is based on the ’ggplot2’ framework, all properties of the plots can be fully controlled by the user after generating the plots. Please see the examples for some customizations and the ’ggplot2’ documentation for the entire set of options.

Value

A ’ggplot’ object, whose properties can further be changed

See Also

See the ’ggplot2’ package for customizing the plots.

Examples

data("sca_sigs", package = "SomaticSignatures")

plotSamples(sigs_nmf)

plotSignatures(sigs_nmf, normalize = TRUE)

## customize the plots ##
p = plotSamples(sigs_nmf)

library(ggplot2)

## (re)move the legend
p = p + theme(legend.position = "none")

## change the axis labels
p = p + xlab("Studies")

## add a title
p = p + ggtitle("Somatic Signatures in TGCA WES Data")

## change the color scale
p = p + scale_fill_brewer(palette = "Blues")

## decrease the size of x-axis labels
p = p + theme(axis.text.x = element_text(size = 9))

p

signatures21-data 21 Signatures

Description

Published signatures, taken from ftp://ftp.sanger.ac.uk/pub/cancer/AlexandrovEtAl/signatures.txt

References

SomaticSignatures

Examples

```r
data(signatures21, package = "SomaticSignatures")
head(signatures21)
```

---

**Description**

Identifying somatic signatures of single nucleotide variants. This package provides a infrastructure related to the methodology described in Nik-Zainal (2012, Cell), with flexibility in the matrix decomposition algorithms.

**Details**

The 'SomaticSignatures' package offers the framework for identifying mutational signatures of single nucleotide variants (SNVs) from high-throughput experiments. In the concept of mutational signatures, a base change resulting from an SNV is regarded in terms of motifs which embeds the variant in the context of the surrounding genomic sequence. Based on the frequency of such motifs across samples, mutational signatures and their occurrence in the samples can be estimated. An introduction into the methodology and a use case are illustrated in the vignette of this package.

**Author(s)**


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**References**


**Examples**

```r
vignette(package = "SomaticSignatures")
```
Description
Utility functions

Usage
```
dfConvertColumns(x, from = "character", to = "factor")
```

Arguments
- `x`: A 'data.frame' to convert [required].
- `from`: The class of the columns to be converted [default: 'character'].
- `to`: The class of the columns to be converted to [default: 'factor'].

Details
The `dfConvertColumns` converts all columns of a data frame with class `from` to the class `to`.

Value
A 'data.frame' object.
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