

# Package ‘SigsPack’

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**Type** Package

**Title** Mutational Signature Estimation for Single Samples

**Version** 1.20.0

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**Description** Single sample estimation of exposure to mutational signatures. Exposures to known mutational signatures are estimated for single samples, based on quadratic programming algorithms. Bootstrapping the input mutational catalogues provides estimations on the stability of these exposures. The effect of the sequence composition of mutational context can be taken into account by normalising the catalogues.

**License** GPL-3

**Encoding** UTF-8

**Depends** R (>= 3.6)

**biocViews** SomaticMutation, SNP, VariantAnnotation, BiomedicalInformatics, DNaseq

**Imports** quadprog (>= 1.5-5), methods, Biobase, BSgenome (>= 1.46.0), VariantAnnotation (>= 1.24.5), Biostrings, GenomeInfoDb, GenomicRanges, rtracklayer, SummarizedExperiment, graphics, stats, utils

**Suggests** IRanges, BSgenome.Hsapiens.UCSC.hg19, BiocStyle, knitr, rmarkdown

**VignetteBuilder** knitr

**BugReports** <https://github.com/bihealth/SigsPack/issues>

**URL** <https://github.com/bihealth/SigsPack>

**Collate** bootstrap\_mut\_catalogues.R cosmicSigs.R sigProfilerExome.R sigProfiler20190522.R create\_mut\_catalogues.R decomposeQP.R get\_context\_freq.R hg19context\_freq.R normalize.R plot\_bootstrapped\_exposure.R signature\_exposure.R summarize\_exposures.R vcf2mut\_cat.R

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bootstrap\_mut\_catalogues

*Bootstraps a given mutational catalogue*

---

### Description

Bootstraps a given mutational catalogue by replicating samples from the original catalogue's distribution of mutational features. The output can be input to `signature_exposure`.

### Usage

```
bootstrap_mut_catalogues(n, original, m = NULL)
```

### Arguments

<code>n</code>	Amount of bootstrapped replicates that are created (they will by default have the same amount of mutations as the original catalogue)
<code>original</code>	Mutational catalogue (matrix) of a sample that is taken as the distribution from which the replicates are sampled
<code>m</code>	Amount of mutations the replicates are supposed to have (e.g. if this differs from the original or if the original is provided as probabilities instead of total counts)

### Value

matrix containing the mutational catalogues of the replicates

## Examples

```
data(cosmicSigs)
reps <- bootstrap_mut_catalogues(n = 150, original = create_mut_catalogues(
  10, 500)[["catalogues"]][,1])
```

---

cosmicSigs

*COSMIC Signature Profiles*

---

## Description

COSMIC Signature Profiles

## Usage

```
cosmicSigs
```

## Format

A matrix with 30 rows and 96 columns containing the signature profiles of the 30 consensus signatures as reported on COSMIC.

**Signature N** The profile of signature N representing the relative proportions of mutations generated by each signature based on the trinucleotide frequencies of the reference human genome version GRCh37.#'

## Source

[https://cancer.sanger.ac.uk/cancergenome/assets/signatures\\_probabilities.txt](https://cancer.sanger.ac.uk/cancergenome/assets/signatures_probabilities.txt)

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create\_mut\_catalogues *Creates simulated mutational catalogues*

---

## Description

Creates mutational catalogues from chosen mutational signature profiles to gain simulated data sampled from a distribution with known signature contribution

## Usage

```
create_mut_catalogues(n, m, P = get(utils::data("cosmicSigs", package =
  "SigsPack")), sig_set = NULL, c_exposure = NULL)
```

**Arguments**

n	Amount of mutational catalogues that will be created
m	Amount of mutations that each catalogues will have
P	Matrix (f x k) containing the signature profiles of k signatures which will be used to create the catalogues k is the amount of signature profiles that P contains f is the amount of features that the profiles are defined on (default: COSMIC signature matrix 96 x 30) (optional)
sig_set	Numeric vector containing the index of the columns from P (which are the signature profiles) that will be used to create the catalogues (optional). Defaults to all columns of P.
c_exposure	Numeric vector specifying the contribution of each signature to the distribution each sample is drawn from. Samples will have an appr. exposure of c_exposure[idx] to signature sig_set[idx] (if sum(c_exposure)==1). (optional) Default: random exposure.

**Value**

List containing a matrix (f x n) with the simulated catalogues and a matrix (k x n) detailing the signature exposure of each catalogue

**Examples**

```
data(cosmicSigs)
sim_data <- create_mut_catalogues(10, 300, cosmicSigs, c(2,6,15,27))
sim_data <- create_mut_catalogues(1000, 500)
sim_data <- create_mut_catalogues(1, 500, sig_set = c(1,4,29), c_exposure = c(0.25, 0.65, 0.1))
```

---

decomposeQP

*decomposeQP function*


---

**Description**

This function is taken from the package 'SignatureEstimation' by Xiaoqing Huang and Damian Wojtowicz (source: <https://www.ncbi.nlm.nih.gov/CBBresearch/Przytycka/index.cgi#signatureestimation>) The function allows to get the optimal solution by using dual method to solve the quadratic programming problem.

**Usage**

```
decomposeQP(m, P, ...)
```

**Arguments**

m	observed tumor profile vector for a single patient/sample, 96 by 1. m is normalized.
P	signature profile matrix, 96 by N (N = # signatures, COSMIC: N=30)
...	control parameter that can be passed into the solve.QP function

**Value**

matrix containing estimated signature exposures

**Examples**

```
data(cosmicSigs)
mut_cat<- (create_mut_catalogues(1,500)[['catalogues']])/500
decomposeQP(mut_cat, cosmicSigs)
```

---

get_context_freq	<i>Extract occurrence of tri-nucleotide contexts</i>
------------------	--

---

**Description**

Extracts the frequencies of the tri-nucleotide contexts in a given region of the genome. These frequencies are needed to normalize a mutational catalogue. The output can be input to `normalize()`.

**Usage**

```
get_context_freq(genome, region = NULL)
```

**Arguments**

genome	a BSgenome object
region	a GRanges object, path, URL, connection or BEDFile object.

**Value**

matrix containing the frequencies of the trinucleotide contexts

**Examples**

```
gr<-GenomicRanges::GRanges(seqnames=c("chr1"),
                             ranges=IRanges::IRanges(start=c(100000),end=c(1000000)),
                             strand=c("+"))
get_context_freq(BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19, gr)
get_context_freq(BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19)

## Not run:
get_context_freq(BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19, 'example.bed')

## End(Not run)
```

---

hg19context_freq	<i>Trinucleotide frequencies of the human reference genome hg19</i>
------------------	---

---

**Description**

Trinucleotide frequencies of the human reference genome hg19

**Usage**

```
hg19context_freq
```

**Format**

A numeric vector with 32 elements

**Trinucleotide** The frequency of a certain trinucleotide context in the genome.

**Source**

BSgenome.Hsapiens.UCSC.hg19

---

normalize	<i>Normalize mutational catalogues</i>
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**Description**

Normalizes the catalogues to a target distribution (e.g. to match the distribution of the reference signatures).

**Usage**

```
normalize(mut_cat, source_context,
  target_context = get(utils::data("hg19context_freq", package =
    "SigsPack")))
```

**Arguments**

mut_cat	mutational catalogues (96 by n, n being the amounts of catalogues) that will be normalized. The tri-nucleotide contexts are expected to be in the default lexicographical order (see simulated data or cosmicSigs)
source_context	Distribution of tri-nucleotides in the source region.
target_context	Distribution of tri-nucleotides in the target region. Defaults to the context frequencies of BSgenome.Hsapiens.UCSC.hg19 since that corresponds to the COSMIC signatures

**Value**

mutational catalogues (96 by n, n being the amounts of catalogues) normalized to match the target distribution (context)

**Note**

The output from `get_context_freq()` can be used as input to this function

**Examples**

```
# this is a toy example:
#create mutational catalogue:
sim_data <- create_mut_catalogues(1, 500)[['catalogues']]
# get trinucleotide frequencies for the genome:
genome_context <- get_context_freq(BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19)
#get trinucleotide frequencies for a specific region:
gr<-GenomicRanges::GRanges(seqnames=c("chr1"),
                           ranges=IRanges::IRanges(start=c(100000),end=c(1000000)),
                           strand=c("+"))
region_context<-get_context_freq(BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19, gr)
#normalize data:
normalized_mut_cat <- normalize(sim_data, region_context, genome_context)

## Not run:
# get the tri-nucleotide distribution of an exome region
exome_contexts <- get_context_freq(BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19,
                                  'example_exome.bed')

# normalize the mutational catalogue to match the COSMIC signatures
normalized_mut_cat <- normalize(mut_cat, exome_contexts, hg19context_freq)

## End(Not run)
```

---

plot\_bootstrapped\_exposure

*Plot signature exposure estimation for several samples*

---

**Description**

Creates a boxplot illustrating the results of the signature estimation for several mutational catalogues (e.g. bootstrapped re-samples or a cohort). The plot shows the distribution of estimated signature exposure for all the catalogues, highlighting the one of the original mutational catalogue if one is provided.

**Usage**

```
plot_bootstrapped_exposure(bootstrapped_exposure,
                           original_estimation = NULL, title = NULL, box_col = NULL,
                           point_col = NULL, sig_names = NULL, sample_names = NULL)
```

**Arguments**

bootstrapped\_exposure

matrix (n by k) containing the signature exposure of several mutational catalogues (bootstrapped re-samples) n is the amount of re-samples k is the amount of signature profiles that P contains

original_estimation	matrix (n by k) containing the signature exposure of one or several mutational catalogues (typically, the original sample) that will be displayed on top of the boxplots
title	character, title of the plot
box_col	color option of the boxplot
point_col	color option of the points that indicate the exposure of the original profile(s). Should be a vector, if several original profiles are plotted
sig_names	character vector, names of the signatures to be displayed as x-axis labels
sample_names	character vector, names of the original profile(s)

**Value**

Displays a boxplot

**Note**

The function can of course also be used to plot the distribution of estimated signature exposures in a cohort instead of one bootstrapped sample.

**Examples**

```
# prepare input
data(cosmicSigs)
mut_cat <- create_mut_catalogues(4,400)
exposures <- signature_exposure(bootstrap_mut_catalogues(
  1000, mut_cat[['catalogues']][,1]))[['exposures']]
original_exposure <- signature_exposure(mut_cat[['catalogues']])[['exposures']]

plot_bootstrapped_exposure(exposures, as.matrix(original_exposure[,1]))

plot_bootstrapped_exposure(exposures, as.matrix(original_exposure),
  title='Example', box_col='grey')
```

---

signature\_exposure      *Estimates the signature exposure of a mutational catalogue*

---

**Description**

Estimates the signature exposure of a mutational catalogue by reconstructing it from a chosen set of signatures, by default, the used method is quadratic programming

**Usage**

```
signature_exposure(mut_cat, P = get(utils::data("cosmicSigs", package =
  "SigsPack")), sig_set = NULL, FUN = decomposeQP, ...)
```



**Arguments**

mut_cat	matrix (f by n) containing one or several mutational catalogues of samples whose signature exposures are to be estimated f is the amount of features that the profiles are defined on n is the number of catalogues
P	Matrix (f by k) containing the signature profiles of k signatures whose exposure is to be found k is the amount of signature profiles that P contains f is the amount of features that the profiles are defined on (default: COSMIC signature matrix 96 x 30)
sig_set	Numeric vector containing the index of the columns from the signature matrix (which are the signature profiles) that will be used reconstruct the mutational catalogue.
FUN	Function to estimate the signature exposure. Default: Quadratic programming (P has to be of full rank to use this method)
...	control parameters that will be passed to FUN

**Value**

List of the estimated signature exposure, the reconstructed profile of the sample, the cosine similarity between the two and the error

**Examples**

```
data(cosmicSigs)
signature_exposure(create_mut_catalogues(10,500)[['catalogues']])
signature_exposure(create_mut_catalogues(10,500)[['catalogues']], sig_set = c(2,7,16,28,30))
signature_exposure(as.matrix(create_mut_catalogues(10,500)[['catalogues']][,1]))
```

---

sigProfiler20190522    *COSMIC v3 whole genome SBS Signature Profiles*

---

**Description**

COSMIC v3 whole genome SBS Signature Profiles

**Usage**

```
sigProfiler20190522
```

**Format**

A matrix with 96 rows and 67 columns containing the signature profiles of the 67 consensus signatures as reported on COSMIC version 3.

**SBS<N>** The profile of signature SBS<N> representing the relative proportions of mutations generated by each signature based on the trinucleotide frequencies of the reference human genome version GRCh37. The signature profiles have been normalised for mutational catalogues collected on WGS data.

**Source**

<https://cancer.sanger.ac.uk/cosmic/signatures/SBS/>

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sigProfilerExome	<i>COSMIC v3 exome SBS Signature Profiles</i>
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**Description**

COSMIC v3 exome SBS Signature Profiles

**Usage**

```
sigProfilerExome
```

**Format**

A matrix with 96 rows and 67 columns containing the signature profiles of the 67 consensus signatures as reported on COSMIC version 3.

**SBS<N>** The profile of signature SBS<N> representing the relative proportions of mutations generated by each signature based on the trinucleotide frequencies of the reference human genome version GRCh37. The signature profiles have been normalised for mutational catalogues collected on exome datasets.

**Source**

<https://cancer.sanger.ac.uk/cosmic/signatures/SBS/>

---

summarize_exposures	<i>Signature exposure analysis of a mutational catalogue</i>
---------------------	--

---

**Description**

Bootstraps a mutational catalogue and details the results about the signature estimation in a table and a boxplot

**Usage**

```
summarize_exposures(mut_cat, P = get(utils::data("cosmicSigs", package =
  "SigsPack")), plotting = TRUE, m = NULL)
```

**Arguments**

mut_cat	mutational catalogue (96 by 1)
P	Matrix (f x k) containing the signature profiles of k signatures whose exposure is to be found k is the amount of signature profiles that P contains f is the amount of features that the profiles are defined on (default: COSMIC signature matrix 96 by 30)
plotting	boolean, TRUE by default, if True, a boxplot showing the distribution of estimated signature exposure for all the re-samples, highlighting the one of the original mutational catalogue, thus providing insights on the reliability of the estimates
m	numeric, amount of mutations in the profile (needed for bootstrapping in case mut_cat doesn't contain absolute counts.)

**Value**

table (k by 6) containing statistics for each signature about the estimated exposure over 1000 bootstrapped resamples - original exposure estimated exposure of the original mutational profile - min minimum estimated exposure to this signature - 1. quartile - median - 3. quartile - max maximum estimated exposure to this signature

if the plotting option is chosen, a boxplot will also be displayed

**Examples**

```
summarize_exposures(create_mut_catalogues(10,500)[['catalogues']][,1], plotting=FALSE)
```

---

vcf2mut_cat	<i>Derive the mutational catalogue from a vcf</i>
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---

**Description**

Creates a matrix containing the mutational catalogue from a vcf file or object. The result can be input to the analysis functions of this package.

**Usage**

```
vcf2mut_cat(vcf, genome, name = NULL, seqs = NULL)
```

**Arguments**

vcf	*.vcf file or a vcf object containing variant calling data for one patient
genome	a BSgenome object corresponding to the genome the variants were called on
name	optional, a sample name
seqs	optional, a character vector containing the names of the sequences that are to be included in the mutational profile. If none is given everything will be included

**Value**

mutational catalogue (matrix) of a patient containing SNV absolute counts (in the 96 trinucleotide context) format: 1 by 96

**Note**

The execution can take some time, depending on the size of the vcf

**Examples**

```
## Not run:  
vcf2mut_cat('test.vcf', BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19)  
  
## End(Not run)
```

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