

# Package ‘SparseSignatures’

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**Title** SparseSignatures

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GenomicRanges, IRanges, BSgenome,  
BSgenome.Hsapiens.1000genomes.hs37d5, GenomeInfoDb, ggplot2,  
gridExtra

**Suggests** BiocGenerics, BiocStyle, testthat, knitr,

**Name** An R package for the extraction of sparse mutational signatures  
from whole genome sequencing data

## Description

Point mutations occurring in a genome can be divided into 96 categories based on the base being mutated, the base it is mutated into and its two flanking bases. Therefore, for any patient, it is possible to represent all the point mutations occurring in that patient’s tumor as a vector of length 96, where each element represents the count of mutations for a given category in the patient. A mutational signature represents the pattern of mutations produced by a mutagen or mutagenic process inside the cell. Each signature can also be represented by a vector of length 96, where each element represents the probability that this particular mutagenic process generates a mutation of the 96 above mentioned categories. In this R package, we provide a set of functions to extract and visualize the mutational signatures that best explain the mutation counts of a large number of patients.

**Encoding** UTF-8

**LazyData** TRUE

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**URL** <https://github.com/danro9685/SparseSignatures>

**BugReports** <https://github.com/danro9685/SparseSignatures>

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---

as.alpha

*as.alpha*

---

### Description

Return the discovered alpha values from an input object as the one generated by the function nmf.LassoK.

### Usage

```
as.alpha(nmf.LassoK.result)
```

**Arguments**

`nmf.LassoK.result`  
discovered signatures into an object as the one generated by the function `nmf.LassoK`

**Value**

A matrix with alpha values

**Examples**

```
data(nmf_LassoK_example)
res = as.alpha(nmf_LassoK_example)
```

---

`as.alpha.in.range`      *as.alpha.in.range*

---

**Description**

Return the discovered alpha values for a given configuration from an input object as the one generated by the function `evaluate.lambda.range`.

**Usage**

```
as.alpha.in.range(lambda.range.result, lambda_value = 0.2)
```

**Arguments**

`lambda.range.result`  
discovered signatures into an object as the one generated by the function `evaluate.lambda.range`

`lambda_value`      value of LASSO used for the estimation whose configuration has to be returned

**Value**

A matrix with alpha values

**Examples**

```
data(lambda_range_example)
res = as.alpha.in.range(lambda_range_example, lambda_value=0.10)
```

---

`as.beta`*as.beta*

---

**Description**

Return the discovered signatures (beta values) from an input object as the one generated by the function `nmf.LassoK`.

**Usage**

```
as.beta(nmf.LassoK.result)
```

**Arguments**

`nmf.LassoK.result`

discovered signatures into an object as the one generated by the function `nmf.LassoK`

**Value**

A matrix with beta values

**Examples**

```
data(nmf_LassoK_example)
res = as.beta(nmf_LassoK_example)
```

---

`as.beta.in.range`*as.beta.in.range*

---

**Description**

Return the discovered signatures (beta values) for a given configuration from an input object as the one generated by the function `evaluate.lambda.range`.

**Usage**

```
as.beta.in.range(lambda.range.result, lambda_value = 0.2)
```

**Arguments**

`lambda.range.result`

discovered signatures into an object as the one generated by the function `evaluate.lambda.range`

`lambda_value`

value of LASSO used for the estimation whose configuration has to be returned

**Value**

A matrix with beta values

**Examples**

```
data(lambda_range_example)
res = as.beta.in.range(lambda_range_example, lambda_value=0.10)
```

---

```
as.loglik.progression  as.loglik.progression
```

---

**Description**

Return the log-likelihood values for each iteration during the estimation of the signatures from an input object as the one generated by the function `nmf.LassoK`.

**Usage**

```
as.loglik.progression(nmf.LassoK.result)
```

**Arguments**

`nmf.LassoK.result`  
discovered signatures into an object as the one generated by the function `nmf.LassoK`

**Value**

A vector with log-likelihood values for each iteration during the estimation of the signatures

**Examples**

```
data(nmf_LassoK_example)
res = as.loglik.progression(nmf_LassoK_example)
```

---

```
as.loglik.progression.in.range
as.loglik.progression.in.range
```

---

**Description**

Return the log-likelihood values for a given configuration for each iteration during the estimation of the signatures from an input object as the one generated by the function `evaluate.lambda.range`.

**Usage**

```
as.loglik.progression.in.range(lambda.range.result, lambda_value = 0.2)
```

**Arguments**

`lambda.range.result`  
discovered signatures into an object as the one generated by the function `evaluate.lambda.range`

`lambda_value` value of LASSO used for the estimation whose configuration has to be returned

**Value**

A vector with log-likelihood values for each iteration during the estimation of the signatures

**Examples**

```
data(lambda_range_example)
res = as.loglik.progression.in.range(lambda_range_example, lambda_value=0.10)
```

---

`as.mean.squared.error`    *as.mean.squared.error*

---

**Description**

Return the mean squared error between the observed counts and the predicted ones for all the configurations considered during cross validation. This function expects an input object as the one generated by the function `nmf.LassoCV`.

**Usage**

```
as.mean.squared.error(nmf.LassoCV.result)
```

**Arguments**

`nmf.LassoCV.result`  
 results of cross validation into an object as the one generated by the function `nmf.LassoCV`

**Value**

A list with distributions and median values of the mean squared error values computed between the observed counts and the predicted ones at each iteration of cross validation

**Examples**

```
data(cv_example)
res = as.mean.squared.error(cv_example)
```

---

`as.starting.beta`    *as.starting.beta*

---

**Description**

Return the initial values of beta used for the estimation of the signatures from an input object as the one generated by the function `nmf.LassoK`.

**Usage**

```
as.starting.beta(nmf.LassoK.result)
```

### Arguments

`nmf.LassoK.result`  
discovered signatures into an object as the one generated by the function `nmf.LassoK`

### Value

A matrix with the initial values of beta used for the estimation of the signatures

### Examples

```
data(nmf_LassoK_example)
res = as.starting.beta(nmf_LassoK_example)
```

---

```
as.starting.beta.in.range
  as.starting.beta.in.range
```

---

### Description

Return the initial values of beta used for the estimation of the signatures for a given configuration from an input object as the one generated by the function `evaluate.lambda.range`.

### Usage

```
as.starting.beta.in.range(lambda.range.result, lambda_value = 0.2)
```

### Arguments

`lambda.range.result`  
discovered signatures into an object as the one generated by the function `nmf.LassoK`

`lambda_value` value of LASSO used for the estimation whose configuration has to be returned

### Value

A matrix with the initial values of beta used for the estimation of the signatures

### Examples

```
data(lambda_range_example)
res = as.starting.beta.in.range(lambda_range_example, lambda_value=0.10)
```

---

background	<i>germline replication error</i>
------------	-----------------------------------

---

**Description**

germline replication error estimated in Rahbari, Raheleh, et al. (2016).

**Usage**

```
data(background)
```

**Format**

vector of rates

**Value**

vector of rates for the 96 trinucleotides

**Source**

Rahbari, Raheleh, et al. "Timing, rates and spectra of human germline mutation." *Nature genetics* 48.2 (2016): 126.

---

cv_example	<i>example of results obtained with the function nmf.LassoCV on the counts input from Nik-Zainal, Serena, et al. (2016).</i>
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---

**Description**

example of results obtained with the function nmf.LassoCV on the counts input from Nik-Zainal, Serena, et al. (2016).

**Usage**

```
data(cv_example)
```

**Format**

results obtained with the function nmf.LassoCV on the counts input from Nik-Zainal, Serena, et al. (2016)

**Value**

results obtained with the function nmf.LassoCV on the counts input from Nik-Zainal, Serena, et al. (2016)



---

```
evaluate.lambda.range evaluate.lambda.range
```

---

## Description

Estimate the range of lambda values to be considered in the signature inference. Note that too small values of lambda result in dense signatures, but too large values lead to bad fit of the counts.

## Usage

```
evaluate.lambda.range(x, K = 6, beta = NULL,
  background_signature = NULL, nmf_runs = 10, lambda_values = c(0.1,
  0.2, 0.3, 0.4, 0.5), iterations = 20, max_iterations_lasso = 10000,
  num_processes = Inf, seed = NULL, verbose = TRUE)
```

## Arguments

x	count matrix.
K	numeric value (greater than 1) indicating the number of signatures to be discovered.
beta	starting beta for the estimation. If it is NULL, starting beta is estimated by NMF.
background_signature	background signature to be used. If not provided, a warning is thrown.
nmf_runs	number of iteration of NMF to be performed for a robust estimation of starting beta. If beta is not NULL, this parameter is ignored.
lambda_values	range of values of LASSO to be used between 0 and 1. This value should be greater than 0. 1 is the value of LASSO that would shrink all the signatures to 0 within one step. The higher lambda_rate is, the sparser are the resulting signatures, but too large values result in a poor fit of the counts.
iterations	Number of iterations to be performed. Each iteration correspond to a first step where the counts are fitted and a second step where sparsity is enhanced.
max_iterations_lasso	Number of maximum iterations to be performed during the sparsification.
num_processes	Number of processes to be used during parallel execution. If executing in single process mode, this is ignored.
seed	Seed for reproducibility.
verbose	boolean; Shall I print all messages?

## Value

A list corresponding to results of the function nmf.LassoK for each value of lambda to be tested. This function allows to test a good range of lambda values to be considered. One should keep in mind that too small values generate dense solution, while too high ones leads to poor fit. This behavior is resampled in the values of loglik\_progression, which should be increasing: too small values of lamda results in unstable log-likelihood through the iterations, while too large values make log-likelihood drop.

---

```
import.counts.data    import.counts.data
```

---

### Description

Import point mutations data to build the count matrix to extract mutational signatures.

### Usage

```
import.counts.data(input, bsg, mutation_categories)
```

### Arguments

input	either a data.frame/data.table object or a file with 5 columns: sample name, chromosome, position, ref, alt.
bsg	a BSgenome object for the reference genome. Chromosome names have to match the input table.
mutation_categories	array with the 96 mutational categories to be considered. It is provided along with the package by data(mutation_categories).

### Value

A count matrix to extract mutational signatures

### Examples

```
data(ssm560_reduced)
library("BSgenome.Hsapiens.1000genomes.hs37d5")
bsg = BSgenome.Hsapiens.1000genomes.hs37d5
data(mutation_categories)
imported_data = import.counts.data(input=ssm560_reduced,bsg=bsg,mutation_categories=mutation_categories)
```

---

```
lambda_range_example    example of results obtained with the function evaluate.lambda.range on the counts input from Nik-Zainal, Serena, et al. (2016).
```

---

### Description

example of results obtained with the function evaluate.lambda.range on the counts input from Nik-Zainal, Serena, et al. (2016).

### Usage

```
data(lambda_range_example)
```

### Format

results obtained with the function evaluate.lambda.range on the counts input from Nik-Zainal, Serena, et al. (2016)

**Value**

results obtained with the function `evaluate.lambda.range` on the counts input from Nik-Zainal, Serena, et al. (2016)

---

mutation_categories	<i>trinucleotides mutation categories</i>
---------------------	---

---

**Description**

96 trinucleotides mutation categories

**Usage**

```
data(mutation_categories)
```

**Format**

matrix of 96 trinucleotides mutation categories

**Value**

matrix of 96 trinucleotides mutation categories

---

<code>nmf.LassoCV</code>	<i>nmf.LassoCV</i>
--------------------------	--------------------

---

**Description**

Perform the discovery by cross validation of  $K$  (unknown) somatic mutational signatures given a set of observations  $x$ . The estimation can slow down because of memory usage, when a high number of cross validation repetitions is asked and when the grid search is performed for a lot of configurations. In this case, we advise to split the computation into multiple smaller sets.

**Usage**

```
nmf.LassoCV(x, K = 3:10, starting_beta = NULL,
  background_signature = NULL, nmf_runs = 10, lambda_values = c(0.1,
  0.2, 0.3), cross_validation_entries = 0.05,
  cross_validation_iterations = 5, cross_validation_repetitions = 10,
  iterations = 20, max_iterations_lasso = 10000, num_processes = Inf,
  seed = NULL, verbose = TRUE)
```

**Arguments**

x	count matrix.
K	a range of numeric value (each of them greater than 1) indicating the number of signatures to be discovered.
starting_beta	a list of starting beta value for each configuration of K. If it is NULL, starting betas are estimated by NMF.
background_signature	background signature to be used. If not provided, a warning is thrown.
nmf_runs	number of iteration of NMF to be performed for a robust estimation of starting beta. If beta is not NULL, this parameter is ignored.
lambda_values	range of values of LASSO to be used between 0 and 1. This value should be greater than 0. 1 is the value of LASSO that would shrink all the signatures to 0 within one step. The higher lambda_rate is, the sparser are the resulting signatures, but too large values result in a poor fit of the counts.
cross_validation_entries	Percentage of cells in the count matrix to be replaced by 0s.
cross_validation_iterations	For each configuration, the first time the signatures are discovered form a matrix with a ercentage of values replaced by 0s. This may result in a poor. This parameter is the number of restarts to be performed to improve this estimate.
cross_validation_repetitions	Number of time cross-validation should be repeated. Higher values result in better estimate, but are computationally expensive.
iterations	Number of iterations to be performed. Each iteration correspond to a first step where the counts are fitted and a second step where sparsity is enhanced.
max_iterations_lasso	Number of maximum iterations to be performed during the sparsification.
num_processes	Number of processes to be used during parallel execution. If executing in single process mode, this is ignored.
seed	Seed for reproducibility.
verbose	boolean; Shall I print all messages?

**Value**

A list corresponding with 3 elements: `grid_search`, `starting_beta` and `mean_squared_error`. Here, `grid_search` provides all the results of the executions within the grid search; `starting_beta` is the set of initial values of beta used for each configuration and `mean_squared_error` is the mean squared error between the observed counts and the predicted ones for each configuration.

---

nmf.LassoK

*nmf.LassoK*


---

**Description**

Perform the discovery of K somatic mutational signatures given a set of observed counts x.

**Usage**

```
nmf.LassoK(x, K, beta = NULL, background_signature = NULL,
           nmf_runs = 10, lambda_rate = 0.2, iterations = 20,
           max_iterations_lasso = 10000, num_processes = Inf, parallel = NULL,
           seed = NULL, verbose = TRUE)
```

**Arguments**

x	count matrix.
K	numeric value (greater than 1) indicating the number of signatures to be discovered.
beta	starting beta for the estimation. If it is NULL, starting beta is estimated by NMF.
background_signature	background signature to be used. If not provided, a warning is thrown.
nmf_runs	number of iteration of NMF to be performed for a robust estimation of starting beta. If beta is not NULL, this parameter is ignored.
lambda_rate	value of LASSO to be used between 0 and 1. This value should be greater than 0. 1 is the value of LASSO that would shrink all the signatures to 0 within one step. The higher lambda_rate is, the sparser are the resulting signatures, but too large values result in a poor fit of the counts.
iterations	Number of iterations to be performed. Each iteration correspond to a first step where the counts are fitted and a second step where sparsity is enhanced.
max_iterations_lasso	Number of maximum iterations to be performed during the sparsification.
num_processes	Number of processes to be used during parallel execution. If executing in single process mode, this is ignored.
parallel	Cluster object for parallel execution.
seed	Seed for reproducibility.
verbose	boolean; Shall I print all messages?

**Value**

A list with the discovered signatures. It includes 5 elements: alpha: matrix of the discovered alpha values beta: matrix of the discovered signatures starting\_beta: initial signatures on which the method has been applied best\_loglik: log-likelihood of the best signatures configuration loglik\_progression: log-likelihood values during the iterations. This values should be increasing, if not the selected value of lambda is too high

**Examples**

```
data(starting_betas_example)
beta = starting_betas_example[["5_signatures", "Value"]]
res = nmf.LassoK(x=patients, K=5, beta=beta, background=background, lambda_rate=0.10, iterations=5, num_processes=5)
```

---

nmf_LassoK_example	<i>example of results obtained with the function nmf.LassoK on the counts input from Nik-Zainal, Serena, et al. (2016).</i>
--------------------	---

---

**Description**

example of results obtained with the function nmf.LassoK on the counts input from Nik-Zainal, Serena, et al. (2016).

**Usage**

```
data(nmf_LassoK_example)
```

**Format**

results obtained with the function nmf.LassoK on the counts input from Nik-Zainal, Serena, et al. (2016)

**Value**

results obtained with the function nmf.LassoK on the counts input from Nik-Zainal, Serena, et al. (2016)

---

patient.plot	<i>patient.plot</i>
--------------	---------------------

---

**Description**

Plot the counts for a patient.

**Usage**

```
patient.plot(countMatrix, patientName, xlabels = TRUE, freq = FALSE)
```

**Arguments**

countMatrix	count matrix as the one generated by the import.data function.
patientName	name of the patient. This should match a rowname of the countMatrix.
xlabels	boolean value; shall I display x labels?
freq	boolean value; shall I display rates instead of counts?

**Value**

A ggplot2 object

**Examples**

```
data(patients)
patient.plot(countMatrix=patients,patientName="PD18775a")
```

---

patients	<i>point mutations for 560 breast tumors</i>
----------	--

---

**Description**

dataset of counts of the point mutations detected in 560 breast tumors published in Nik-Zainal, Serena, et al. (2016).

**Usage**

```
data(patients)
```

**Format**

counts of the point mutations

**Value**

counts of point mutations for 560 tumors and 96 trinucleotides

**Source**

Nik-Zainal, Serena, et al. "Landscape of somatic mutations in 560 breast cancer whole-genome sequences." Nature 534.7605 (2016): 47.

---

signatures.plot	<i>signatures.plot</i>
-----------------	------------------------

---

**Description**

Plot the discovered signatures.

**Usage**

```
signatures.plot(beta, useColNames = TRUE, mutation_categories = NULL,
  firstBackground = TRUE, xlabel = TRUE)
```

**Arguments**

beta	discovered signatures
useColNames	boolean value; shall I use the colnames from beta as names for the signatures?
mutation_categories	if useColNames is FALSE, the trinucleotides categories to be considered can be specified. An example is provided in the package and can be loaded by data(mutation_categories)
firstBackground	boolean value; shall I display the background signature as the first element?
xlabels	boolean value; shall I display x labels?

**Value**

A ggplot2 object

**Examples**

```
data(nmf_LassoK_example)
beta = as.beta(nmf_LassoK_example)
signatures.plot(beta=beta)
```

---

ssm560_reduced	<i>a reduced version of the point mutations for 560 breast tumors in the format compatible with the import function</i>
----------------	---

---

**Description**

reduced version of the dataset of counts of the point mutations detected in 560 breast tumors published in Nik-Zainal, Serena, et al. (2016).

**Usage**

```
data(ssm560_reduced)
```

**Format**

reduced version of the counts of the point mutations in the format compatible with the import function

**Value**

reduced version of the counts of point mutations for 560 tumors and 96 trinucleotides in the format compatible with the import function

**Source**

Nik-Zainal, Serena, et al. "Landscape of somatic mutations in 560 breast cancer whole-genome sequences." Nature 534.7605 (2016): 47.

---

starting.betas.estimation	<i>starting.betas.estimation</i>
---------------------------	----------------------------------

---

**Description**

Perform a robust estimation of the starting beta for the nmfLasso method

**Usage**

```
starting.betas.estimation(x, K = 3:10, background_signature = NULL,
  nmf_runs = 10, num_processes = Inf, seed = NULL, verbose = TRUE)
```



**Arguments**

x	count matrix.
K	range of numeric values (each of them greater than 1) indicating the number of signatures to be discovered.
background_signature	background signature to be used. If not provided, a warning is thrown.
nmf_runs	number of iteration of NMF to be performed for a robust estimation of starting beta. If beta is not NULL, this parameter is ignored.
num_processes	Number of processes to be used during parallel execution. If executing in single process mode, this is ignored.
seed	Seed for reproducibility.
verbose	boolean; Shall I print all messages?

**Value**

A list of starting beta values for each configuration of K.

---

starting\_betas\_example

*example of results obtained with the function starting.betas.estimation on the counts input from Nik-Zainal, Serena, et al. (2016).*

---

**Description**

example of results obtained with the function starting.betas.estimation on the counts input from Nik-Zainal, Serena, et al. (2016).

**Usage**

```
data(starting_betas_example)
```

**Format**

results obtained with the function starting.betas.estimation on the counts input from Nik-Zainal, Serena, et al. (2016)

**Value**

results obtained with the function starting.betas.estimation on the counts input from Nik-Zainal, Serena, et al. (2016)

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