

# Package ‘selectKSigs’

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**Type** Package

**Title** Selecting the number of mutational signatures using a  
perplexity-based measure and cross-validation

**Depends** R(>= 3.6)

**Imports** HiLDA, magrittr, gtools, methods, Rcpp

**Suggests** knitr, rmarkdown, testthat, BiocStyle, ggplot2, dplyr, tidyr

**Version** 1.17.0

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**Description** A package to suggest the number of mutational signatures in a  
collection of somatic mutations using calculating the cross-validated  
perplexity score.

**URL** <https://github.com/USCbiostats/selectKSigs>

**BugReports** <https://github.com/USCbiostats/HiLDA/selectKSigs>

**License** GPL-3

**biocViews** Software, SomaticMutation, Sequencing, StatisticalMethod,  
Clustering

**RoxygenNote** 7.1.2

**LinkingTo** Rcpp

**VignetteBuilder** knitr

**Encoding** UTF-8

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**Author** Zhi Yang [aut, cre],  
Yuichi Shiraishi [ctb]

**Maintainer** Zhi Yang <[zyang895@gmail.com](mailto:zyang895@gmail.com)>

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calcPMSLikelihood	<i>A function for calculating the log-likelihood from the data and parameters</i>
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Description

A function for calculating the log-likelihood from the data and parameters

Usage

calcPMSLikelihood(p, y)

Arguments

- p            this variable includes the parameters for mutation signatures and membership parameters
- y            this variable includes the information on the mutation features, the number of mutation signatures specified and so on

Value

a value

---

`Calculate_Likelihood_test`*Output the maximum potential scale reduction statistic of all parameters estimated*

---

**Description**

Output the maximum potential scale reduction statistic of all parameters estimated

**Usage**

```
Calculate_Likelihood_test(train, test, paramG)
```

**Arguments**

<code>train</code>	a <code>MutationFeatureData</code> S4 class output of training data.
<code>test</code>	a <code>MutationFeatureData</code> S4 class output of test data.
<code>paramG</code>	an <code>estimatedParameters</code> S4 class with estimated parameters

**Value**

the likelihood of the test data

---

`convertFromTurbo_F`      *Restore the converted parameter F for turboEM*

---

**Description**

Restore the converted parameter F for turboEM

**Usage**

```
convertFromTurbo_F(turboF, fdim, signatureNum, isBackground)
```

**Arguments**

<code>turboF</code>	F (converted for turboEM)
<code>fdim</code>	a vector specifying the number of possible values for each mutation signature
<code>signatureNum</code>	the number of mutation signatures
<code>isBackground</code>	the logical value showing whether a background mutation features is included or not

**Value**

a vector

---

<code>convertFromTurbo_Q</code>	<i>Restore the converted parameter <math>Q</math> for turboEM</i>
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**Description**

Restore the converted parameter  $Q$  for turboEM

**Usage**

`convertFromTurbo_Q(turboQ, signatureNum, sampleNum)`

**Arguments**

- |                           |                                   |
|---------------------------|-----------------------------------|
| <code>turboQ</code>       | $Q$ (converted for turboEM)       |
| <code>signatureNum</code> | the number of mutation signatures |
| <code>sampleNum</code>    | the number of cancer genomes      |

**Value**

a vector

---

<code>convertToTurbo_F</code>	<i>Convert the parameter <math>F</math> so that turboEM can treat</i>
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**Description**

Convert the parameter  $F$  so that turboEM can treat

**Usage**

`convertToTurbo_F(vF, fdim, signatureNum, isBackground)`

**Arguments**

- |                           |   |
|---------------------------|---|
| <code>vF</code>           | $F$ (converted to a vector)   |
| <code>fdim</code>         | a vector specifying the number of possible values for each mutation signature       |
| <code>signatureNum</code> | the number of mutation signatures   |
| <code>isBackground</code> | the logical value showing whether a background mutaiton features is included or not |

**Value**

a vector

---

convertToTurbo_Q	<i>Convert the parameter Q so that turboEM can treat</i>
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**Description**

Convert the parameter Q so that turboEM can treat

**Usage**

```
convertToTurbo_Q(vQ, signatureNum, sampleNum)
```

**Arguments**

vQ	Q (converted to a vector)
signatureNum	the number of mutation signatures
sampleNum	the number of cancer genomes

**Value**

a vector

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cv_PMSignature	<i>Output the maximum potential scale reduction statistic of all parameters estimated</i>
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**Description**

Output the maximum potential scale reduction statistic of all parameters estimated

**Usage**

```
cv_PMSignature(inputG, Kfold = 3, nRep = 3, Klimit = 8)
```

**Arguments**

inputG	a MutationFeatureData S4 class.
Kfold	an integer number of the number of cross-validation folds.
nRep	an integer number of replications.
Klimit	an integer of the maximum value of number of signatures.

**Value**

a matrix of measures

**Examples**

```
load(system.file("extdata/sample.rdata", package = "selectKSigs"))
results <- cv_PMSignature(G, Kfold = 3)
```

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**getBG***Get the status of using the background signature*

---

**Description**

Get the status of using the background signature

**Usage**

```
getBG(object)
```

**Arguments**

object                      the EstimatedParameters class (the result of pmgetSignature)

**Value**

the status of using the background signature

---

**getCounts***Get the count data in a matrix*

---

**Description**

Get the count data in a matrix

**Usage**

```
getCounts(object)
```

**Arguments**

object                      the MutationFeatureData class

**Value**

the count data in a matrix

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getExposures	<i>Get a matrix of mutational exposures of signatures</i>
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---

**Description**

Get a matrix of mutational exposures of signatures

**Usage**

```
getExposures(object)
```

**Arguments**

object	the EstimatedParameters class (the result of pmgetSignature)
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**Value**

a matrix of mutational exposures of signatures

---

getFeatures	<i>Get a vector of possible features</i>
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**Description**

Get a vector of possible features

**Usage**

```
getFeatures(object)
```

**Arguments**

object	the EstimatedParameters class (the result of pmgetSignature)
--------	--

**Value**

a vector of possible features

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getFeatureVec	<i>Get a matrix of feature vector list</i>
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---

**Description**

Get a matrix of feature vector list

**Usage**

```
getFeatureVec(object)
```

**Arguments**

object            the MutationFeatureData class

**Value**

a matrix of feature vector list

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getK	<i>Get the number of signatures</i>
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**Description**

Get the number of signatures

**Usage**

```
getK(object)
```

**Arguments**

object            the EstimatedParameters class (the result of pmgetSignature)

**Value**

the number of signatures in pmgetSignature in HiLDA



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getLL	<i>Get the values of loglikelihood</i>
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**Description**

Get the values of loglikelihood

**Usage**

```
getLL(object)
```

**Arguments**

object                the EstimatedParameters class (the result of pmgetSignature)

**Value**

likelihood values estimated by pmgetSignature in HiLDA

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getLogLikelihoodC	<i>Calculate the value of the log-likelihood for given parameters</i>
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**Description**

Calculate the value of the log-likelihood for given parameters

**Usage**

```
getLogLikelihoodC(
  vPatternList,
  vSparseCount,
  vF,
  vQ,
  fdim,
  signatureNum,
  sampleNum,
  patternNum,
  samplePatternNum,
  isBackground,
  vF0
)
```

**Arguments**

vPatternList	The list of possible mutation features (converted to a vector)
vSparseCount	The table showing (mutation feature, sample, the number of mutation) (converted to a vector)
vF	F (converted to a vector)
vQ	Q (converted to a vector)
fdim	a vector specifying the number of possible values for each mutation signature
signatureNum	the number of mutation signatures
sampleNum	the number of cancer genomes
patternNum	the number of possible combinations of all the mutation features
samplePatternNum	the number of possible combination of samples and mutation patterns
isBackground	the logical value showing whether a background mutation features is included or not
vF0	a background mutation features

**Value**

a value

---

getSamplelist	<i>Get the sample list</i>
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**Description**

Get the sample list

**Usage**

```
getSamplelist(object)
```

**Arguments**

object	the EstimatedParameters class (the result of pmgetSignature)
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**Value**

the sample list of named elements.

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getSamplelistG	<i>Get the sample list</i>
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**Description**

Get the sample list

**Usage**

```
getSamplelistG(object)
```

**Arguments**

object	the MutationFeatureData class
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**Value**

the sample list of named elements.

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getSignatures	<i>Get an array of signature feature distributions</i>
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**Description**

Get an array of signature feature distributions

**Usage**

```
getSignatures(object)
```

**Arguments**

object	the EstimatedParameters class (the result of pmgetSignature)
--------	--

**Value**

an array of signature feature distributions

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getTranscription	<i>Get the status of specifying the transcription bias</i>
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**Description**

Get the status of specifying the transcription bias

**Usage**

```
getTranscription(object)
```

**Arguments**

object	the MutationFeatureData class
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**Value**

the status of specifying the transcription bias

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select_kth_fold	<i>Output the training data or test data</i>
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**Description**

Output the training data or test data

**Usage**

```
select_kth_fold(inputG, k, f_s, folds, include)
```

**Arguments**

inputG	a MutationFeatureData S4 class output by the pmsignature.
k	an integer number of the number of cross-validation folds.
f_s	a primary key of combining the feature pattern and sample ID.
folds	the assignment to each fold.
include	a boolean indicator of whether to include kth fold or not.

**Value**

a MutationFeatureData S4 class of either include or exclude kth fold.

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splitG	<i>Output the maximum potential scale reduction statistic of all parameters estimated</i>
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**Description**

Output the maximum potential scale reduction statistic of all parameters estimated

**Usage**

```
splitG(inputG, Kfold = 3)
```

**Arguments**

inputG	a MutationFeatureData S4 class output by the pmsignature.
Kfold	an integer number of the number of cross-validation folds.

**Value**

a matrix made of perplexity from the results of cross-validation.

**Examples**

```
load(system.file("extdata/sample.rdata", package = "selectKSigs"))
G_split <- splitG(G, Kfold = 3)
```

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