

# Package ‘selectKSigs’

June 7, 2023

**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** 1.12.0

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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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R topics documented:

|                                     |           |
|-------------------------------------|-----------|
| calcPMSLikelihood . . . . .         | 2         |
| Calculate_Likelihood_test . . . . . | 3         |
| convertFromTurbo_F . . . . .        | 3         |
| convertFromTurbo_Q . . . . .        | 4         |
| convertToTurbo_F . . . . .          | 4         |
| convertToTurbo_Q . . . . .          | 5         |
| cv_PMSignature . . . . .            | 5         |
| getBG . . . . .                     | 6         |
| getCounts . . . . .                 | 6         |
| getExposures . . . . .              | 7         |
| getFeatures . . . . .               | 7         |
| getFeatureVec . . . . .             | 8         |
| getK . . . . .                      | 8         |
| getLL . . . . .                     | 9         |
| getLogLikelihoodC . . . . .         | 9         |
| getSamplelist . . . . .             | 10        |
| getSamplelistG . . . . .            | 11        |
| getSignatures . . . . .             | 11        |
| getTranscription . . . . .          | 12        |
| select_kth_fold . . . . .           | 12        |
| splitG . . . . .                    | 13        |
| <b>Index</b>                        | <b>14</b> |

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

---

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

---

|                    |                                                                   |
|--------------------|-------------------------------------------------------------------|
| convertFromTurbo_Q | <i>Restore the converted parameter <math>Q</math> for turboEM</i> |
|--------------------|-------------------------------------------------------------------|

---

**Description**

Restore the converted parameter  $Q$  for turboEM

**Usage**

```
convertFromTurbo_Q(turboQ, signatureNum, sampleNum)
```

**Arguments**

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

**Value**

a vector

---

|                  |                                                                       |
|------------------|-----------------------------------------------------------------------|
| convertToTurbo_F | <i>Convert the parameter <math>F</math> so that turboEM can treat</i> |
|------------------|-----------------------------------------------------------------------|

---

**Description**

Convert the parameter  $F$  so that turboEM can treat

**Usage**

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

**Arguments**

|              |                                                                                     |
|--------------|-------------------------------------------------------------------------------------|
| vF           | $F$ (converted to a vector)                                                         |
| fdim         | a vector specifying the number of possible values for each mutation signature       |
| signatureNum | the number of mutation signatures                                                   |
| isBackground | 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> |
|------------------|----------------------------------------------------------|

---

**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

---

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

---

**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)
```

---

**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

---

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

---

**Description**

Get a matrix of mutational exposures of signatures

**Usage**

```
getExposures(object)
```

**Arguments**

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

**Value**

a matrix of mutational exposures of signatures

---

|             |                                          |
|-------------|------------------------------------------|
| getFeatures | <i>Get a vector of possible features</i> |
|-------------|------------------------------------------|

---

**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

---

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

---

**Description**

Get a matrix of feature vector list

**Usage**

```
getFeatureVec(object)
```

**Arguments**

|        |                               |
|--------|-------------------------------|
| object | the MutationFeatureData class |
|--------|-------------------------------|

**Value**

a matrix of feature vector list

---

|      |                                     |
|------|-------------------------------------|
| getK | <i>Get the number of signatures</i> |
|------|-------------------------------------|

---

**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

---

|       |                                        |
|-------|----------------------------------------|
| getLL | <i>Get the values of loglikelihood</i> |
|-------|----------------------------------------|

---

**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

---

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

---

**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> |
|---------------|----------------------------|

---

**Description**

Get the sample list

**Usage**

```
getSamplelist(object)
```

**Arguments**

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

**Value**

the sample list of named elements.

---

|                |                            |
|----------------|----------------------------|
| getSamplelistG | <i>Get the sample list</i> |
|----------------|----------------------------|

---

**Description**

Get the sample list

**Usage**

```
getSamplelistG(object)
```

**Arguments**

|        |                               |
|--------|-------------------------------|
| object | the MutationFeatureData class |
|--------|-------------------------------|

**Value**

the sample list of named elements.

---

|               |                                                        |
|---------------|--------------------------------------------------------|
| getSignatures | <i>Get an array of signature feature distributions</i> |
|---------------|--------------------------------------------------------|

---

**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

---

|                  |                                                            |
|------------------|------------------------------------------------------------|
| getTranscription | <i>Get the status of specifying the transcription bias</i> |
|------------------|------------------------------------------------------------|

---

**Description**

Get the status of specifying the transcription bias

**Usage**

```
getTranscription(object)
```

**Arguments**

object                    the MutationFeatureData class

**Value**

the status of specifying the transcription bias

---

|                 |                                              |
|-----------------|----------------------------------------------|
| select_kth_fold | <i>Output the training data or test data</i> |
|-----------------|----------------------------------------------|

---

**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.

---

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

---

**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)
```

# Index

calcPMSLikelihood, [2](#)  
Calculate\_Likelihood\_test, [3](#)  
convertFromTurbo\_F, [3](#)  
convertFromTurbo\_Q, [4](#)  
convertToTurbo\_F, [4](#)  
convertToTurbo\_Q, [5](#)  
cv\_PMSignature, [5](#)  
  
getBG, [6](#)  
getCounts, [6](#)  
getExposures, [7](#)  
getFeatures, [7](#)  
getFeatureVec, [8](#)  
getK, [8](#)  
getLL, [9](#)  
getLogLikelihoodC, [9](#)  
getSamplelist, [10](#)  
getSamplelistG, [11](#)  
getSignatures, [11](#)  
getTranscription, [12](#)  
  
select\_kth\_fold, [12](#)  
splitG, [13](#)