

# Package ‘SUITOR’

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**Title** Selecting the number of mutational signatures through cross-validation

**Version** 1.13.0

**Date** 2022-05-10

**Description** An unsupervised cross-validation method to select the optimal number of mutational signatures. A data set of mutational counts is split into training and validation data. Signatures are estimated in the training data and then used to predict the mutations in the validation data.

**Imports** stats, utils, graphics, ggplot2, BiocParallel

**Depends** R (>= 4.2.0)

**License** GPL-2

**bioViews** Genetics, Software, SomaticMutation

**Suggests** devtools, MutationalPatterns, RUnit, BiocManager, BiocGenerics, BiocStyle, knitr, rmarkdown

**NeedsCompilation** yes

**BugReports** <https://github.com/wheelerb/SUITOR/issues>

**VignetteBuilder** knitr

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SUITOR-package	<i>Number of mutational signatures</i>
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### Description

To select the number of mutational signatures through cross-validation.

### Details

SUITOR (Selecting the nUmber of mutatIonal signaTures thrOugh cRoss-validation), an unsupervised cross-validation method that requires little assumptions and no numerical approximations to select the optimal number of signatures without overfitting the data. The full dataset of mutation counts is split into a training set and a validation set; for a given number of signatures, these signatures are estimated in the training set and then they are used to predict the mutations in the validation set. Multiple candidate numbers of signatures are considered; and the number of signatures which predicts most closely the mutations in the validation set is selected.

The two main functions in this package are `suitor` and `suitorExtractWH`.

### Author(s)

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### References

Lee, D., Wang, D., Yang, X., Shi, J., Landi, M., Zhu, B. (2021) SUITOR: selecting the number of mutational signatures through cross-validation. bioRxiv, doi: <https://doi.org/10.1101/2021.07.28.454269>.

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getSummary	<i>Compute summary results</i>
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## Description

Compute summary results and the optimal rank from the matrix containing all results.

## Usage

```
getSummary(obj, NC, NR=96)
```

## Arguments

obj	Matrix containing all results in the return list from <a href="#">suiTor</a> .
NC	The number of columns in data when <a href="#">suiTor</a> was called.
NR	The number of rows in data when <a href="#">suiTor</a> was called. The default is 96.

## Details

The input matrix `obj` must have column 1 as the rank, column 2 as the value of `k` in `1:k.fold`, column 4 as the training errors, and column 5 as the testing errors.

## Value

A list containing the objects:

- `rank`: The optimal rank
- `all.results`: Matrix containing training and testing errors for all values of seeds, ranks, folds. NA values appear for runs in which the EM algorithm did not converge.
- `summary`: Data frame of summarized results for each possible rank created from `all.results`. The `MSErr` column is defined as `sqrt({fold1 + ... +foldK}/{nrow(data)*ncol(data)})`

## Author(s)

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## See Also

[plotErrors](#)

## Examples

```
data(SimData, package="SUITOR")
data(results, package="SUITOR")
ret <- getSummary(results$all.results, ncol(SimData))
ret$summary
ret$rank
```

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<code>plotData</code>	<i>Example data for plotting</i>
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## Description

A data frame with columns Rank, Type, and MSErr

## See Also

[suiTor](#)

## Examples

```
data(plotData, package="SUITOR")
plotData
```

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<code>plotErrors</code>	<i>Plot train and test errors</i>
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## Description

Plot train and test errors

## Usage

```
plotErrors(x)
```

## Arguments

`x` Data frame of summary results in the return list from [suiTor](#) or from [getSummary](#), or a data frame with columns Rank, Type, and MSErr.

## Details

The optimal rank is the minimum at which the test error is attained, and appears as a red dot on the graph.

## Value

NULL

## Author(s)

Donghyuk Lee <dhyuklee@pusan.ac.kr> and Bin Zhu <bin.zhu@nih.gov>

**Examples**

```
data(plotData, package="SUITOR")
plotErrors(plotData)
```

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**results***suitor return object***Description**

An object returned from the `suitor` function for examples

**See Also**[suitor](#)**Examples**

```
data(results, package="SUITOR")
results
```

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**SimData***Data for examples***Description**

Example input data and results

**Details**

Contains an example input data object of size 96 by 300. It is generated by `rpois` with mean `WH` where `W` (96 by 8) is profile of 8 signatures (SBS 4, 6, 7a, 9, 17b, 22, 26, 39) obtained from <https://cancer.sanger.ac.uk/cosmic/signatures/SBS> and `H` (8 by 300) is rounded integer generated from a uniform distribution between 0 and 100 with some randomly selected cells being set to zero.

**See Also**[suitor](#)**Examples**

```
data(SimData, package="SUITOR")
# Display a subset of data objects
SimData[1:5, 1:5]
```

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suitor	<i>suitor</i>
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## Description

Selecting the number of mutational signatures through cross-validation

## Usage

```
suitor(data, op=NULL)
```

## Arguments

data	Data frame or matrix containing mutational signatures. This object must contain non-negative values
op	List of options (see details). The default is NULL.

## Details

The algorithm finds the optimal rank by applying k-fold cross validation.

### Options list op:

Name	Description	Default Value
em.eps	EM algorithm stopping tolerance	1e-5
get.summary	0 or 1 to create summary results	1
k.fold	Number of folds	10
max.iter	Maximum number of iterations in EM algorithm	2000
max.rank	Maximum rank	10
min.rank	Minimum rank	1
min.value	Minimum value of matrix before factorizing	1e-4
BPPARAM	See <a href="#">BiocParallelParam</a>	NULL
n.starts	Number of starting points	30
plot	0 or 1 to produce an error plot	1
print	0 or 1 to print info	1
kfold.vec	Vector of values in 1:k.fold when running on a cluster	NULL

## Parallel computing

The BiocParallel package is used for parallel computing. If BPPARAM = NULL, then BPPARAM will be set to [SerialParam](#).

## Utilizing a cluster

When running on a cluster, the option get.summary should be set to 0. For fastest running jobs, set the options min.rank = max.rank, kfold.vec to a single integer in 1:k.fold, and n.starts to 1.

**Value**

A list containing the objects:

- `rank`: The optimal rank
- `all.results`: Matrix containing training and testing errors for all values of seeds, ranks, folds.
- `summary`: Data frame of summarized results for each possible rank created from `all.results`. The `MSerr` column is defined as `sqrt({fold1 + ... +foldK}/{nrow(data)*ncol(data)})`

**Author(s)**

Donghyuk Lee <dhyuklee@pusan.ac.kr> and Bin Zhu <bin.zhu@nih.gov>

**See Also**

[getSummary](#), [plotErrors](#)

**Examples**

```
data(SimData, package="SUITOR")

# Using the default options will take several minutes to run
ret <- suitor(SimData)
```

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*suitorExtractWH*

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*suitorExtractWH*

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**Description**

Extract the matrix of activities (exposures) and matrix of signatures

**Usage**

```
suitorExtractWH(data, rank, op=NULL)
```

**Arguments**

<code>data</code>	Data frame or matrix containing mutational signatures. This object must contain non-negative values
<code>rank</code>	Integer $> 0$
<code>op</code>	List of options (see details). The default is <code>NULL</code> .

**Details**

**Options list `op`:**

Name	Description	Default Value
min.value	Minimum value of matrix before factorizing	1e-4
BPPARAM	See <a href="#">BiocParallelParam</a>	NULL
n.starts	Number of starting points	30
print	0 or 1 to print info	1

### Parallel computing

The BiocParallel package is used for parallel computing. If BPPARAM = NULL, then BPPARAM will be set to [SerialParam](#).

### Value

A list containing the objects:

- $H$ : Matrix of activities (exposures)
- $W$ : Matrix of signatures

### Author(s)

Donghyuk Lee <dhyuklee@pusan.ac.kr> and Bin Zhu <bin.zhu@nih.gov>

### See Also

[suitor](#)

### Examples

```
data(SimData, package="SUITOR")
suitorExtractWH(SimData, 2)
```

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