

# Package ‘mSigAct’

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**Title** mutational Signature Activity analysis ('mSigAct')

**Version** 2.0.10.9001

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**Description** Analyze the “activities” of mutational signatures in one or more mutational spectra. 'mSigAct' stands for mutational Signature Activity. mSigAct can estimate (conservatively) whether there is evidence that a particular set of mutational signatures is present in a spectrum. It can also determine a \*minimal\* subset of signatures needed to plausibly reconstruct an observed spectrum. This sparse assign signatures functionality is \*deliberately biased\* toward using as few signatures as possible. This package does not provide all-purpose estimation for signature attribution.

**License** GPL-3

**URL** <https://github.com/steverozen/mSigAct>

**BugReports** <https://github.com/steverozen/mSigAct/issues>

**Encoding** UTF-8

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**VignetteBuilder** knitr

**biocViews**

**Imports** dplyr,  
ICAMS,  
ICAMSxtra,  
lsa,  
nloptr,  
philentropy,  
quadprog,  
rlang,  
stats,  
sets,  
tibble,  
utils

**Remotes** github::steverozen/ICAMS@master,  
github::steverozen/ICAMSxtra@master

**Suggests** BSgenome.Hsapiens.1000genomes.hs37d5,  
devtools,  
htmlwidgets,  
knitr,  
PCAWG7,  
profvis,  
rmarkdown,  
testthat (>= 2.1.0),  
usethis

**R topics documented:**

cossim . . . . .	2
DefaultManyOpts . . . . .	3
ExposureProportions . . . . .	3
g_ineq_for_ObjFnBinomMaxLH2 . . . . .	4
LLHSpectrumMAP . . . . .	5
LLHSpectrumNegBinom . . . . .	6
MAPAssignActivity . . . . .	6
MAPAssignActivity1 . . . . .	8
ObjFnBinomMaxLHMustRound . . . . .	10
ObjFnBinomMaxLHNoRoundOK . . . . .	10
ObjFnBinomMaxLHRound . . . . .	11
OneMAPAssignTest . . . . .	11
OptimizeExposure . . . . .	12
OptimizeExposureQP . . . . .	13
OptimizeExposureQPBootstrap . . . . .	14
PCAWGMAPTest . . . . .	15
PossibleArtifacts . . . . .	16
RareSignatures . . . . .	16
ReconstructSpectrum . . . . .	17
SignaturePresenceTest . . . . .	17
SignaturePresenceTest1 . . . . .	18
SparseAssignActivity . . . . .	18
<b>Index</b>	<b>20</b>

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cossim	<i>Cosine similarity with useful argument types..</i>
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---

**Description**

Calls `cosine`.

**Usage**

`cossim(v1, v2)`

**Arguments**

- `v1` A vector or single-column matrix
- `v2` A vector or single-column matrix

---

DefaultManyOpts	<i>Set default options for many functions, especially <code>nloptr</code>.</i>
-----------------	--

---

## Description

Set default options for many functions, especially `nloptr`.

## Usage

```
DefaultManyOpts()
```

## Value

A list with the following elements

**global.opts** A sub-list with several options for `nloptr`, q.v., for the global optimization phase, including `eval_f`, the objective function.

**local.opts** A sub-list with several options for `nloptr`, q.v., for the local optimization phase, including `eval_f`, the objective function and the inequality constraint function `eval_g_ineq`

**nbinom.size** The dispersion parameter for the negative binomial distribution; smaller is more dispersed. See `NegBinomial`.

**trace** If > 0 print progress messages.

---

ExposureProportions

*Return the proportions of tumors of a given cancer type that have a particular signature*

---

## Description

Return the proportions of tumors of a given cancer type that have a particular signature

## Usage

```
ExposureProportions(
  mutation.type,
  cancer.type,
  all.sigs = NULL,
  drop.sigs.no.info = TRUE,
  must.include = character(),
  must.include.prop = 0.1
)
```

**Arguments**

<code>mutation.type</code>	A character string, one of "SBS96", "SBS192", "ID", "DBS78".
<code>cancer.type</code>	A character string.
<code>all.sigs</code>	An optional matrix of known signatures, with column names being signature ids. Only used to drop signatures not present in <code>all.sigs</code> .
<code>drop.sigs.no.info</code>	If TRUE, drop signatures not present in the column names of <code>all.sigs</code> .
<code>must.include</code>	A character vector of signature IDs that must be included, even if they have not previously been observed in that cancer type. The associated proportion is specified by <code>must.include.prop</code> .
<code>must.include.prop</code>	The value used for the expected proportion of signatures in <code>must.include</code> but not previously observed in the given <code>cancer.type</code> .

**Value**

A numerical vector of the proportion of tumors of type `cancer.type` with each signature for those signatures observed in `cancer.type`. The names are the signature ids.

---

`g_ineq_for_ObjFnBinomMaxLH2`

*Function to constrain the sum of estimated exposures to the number of mutations in the spectrum.*

---

**Description**

See [nloptr](#) to understand how this function is used.

**Usage**

```
g_ineq_for_ObjFnBinomMaxLH2(exp, spectrum, sigs, nbinom.size)
```

**Arguments**

<code>exp</code>	A numeric vector of exposures.
<code>spectrum</code>	The observed spectrum we are trying to reconstruct.
<code>sigs</code>	The signatures with which we are trying to reconstruct the spectrum. (Ignored in this function but used by <a href="#">nloptr</a> .)
<code>nbinom.size</code>	Dispersion parameter. (Ignored in this function but used by <a href="#">nloptr</a> .)

---

LLHSpectrumMAP	<i>Likelihood that 1 observed spectrum was generated from a vector of expected mutation counts using prior information of the signature presence proportions</i>
----------------	--

---

## Description

Likelihood that 1 observed spectrum was generated from a vector of expected mutation counts using prior information of the signature presence proportions

## Usage

```
LLHSpectrumMAP (
  spectrum,
  expected.counts,
  nbinom.size,
  model,
  sigs.presence.prop,
  verbose = FALSE
)
```

## Arguments

spectrum	An observed spectrum (a numeric vector).
expected.counts	A vector of (integer) expected mutation counts, one expected count for each mutation type. We want to know the likelihood that this model generated the observed spectrum, assuming each mutational types generates counts according to a negative binomial distribution with the given expected.counts (argument mu to <a href="#">NegBinomial</a> ) and dispersion parameter nbinom.size.
nbinom.size	The dispersion parameter for the negative binomial distribution; smaller is more dispersed. See <a href="#">NegBinomial</a> .
model	Names of sigs present in the MAP exposure. Do not use indices.
sigs.presence.prop	The proportions of samples that contain each signature. A numerical vector (values between 0 and 1), with names being a superset of model.
verbose	If TRUE print messages under some circumstances.

## Value

$\log(\text{likelihood}(\text{spectrum} \mid \text{expected.counts})) + \log(\text{probability}(\text{model} \mid \text{sigs.presence.prop}))$ , or, in more detail, the sum of the negative binomial likelihoods that each element of the spectrum (i.e., the count for each mutation type e.g. ACT > AAT) was generated from the expected count for that mutation type plus the probability of the signature model used in the reconstruction given the prior sigs.presence.prop.

---

LLHSpectrumNegBinom

*Likelihood that 1 observed spectrum was generated from a vector of expected mutation counts.*

---

### Description

Likelihood that 1 observed spectrum was generated from a vector of expected mutation counts.

### Usage

```
LLHSpectrumNegBinom(spectrum, expected.counts, nbinom.size, verbose = FALSE)
```

### Arguments

spectrum	An observed spectrum (a numeric vector)
expected.counts	A vector of (integer) expected mutation counts, one expected count for each mutation type. We want to know the likelihood that this model generated the observed spectrum, assuming each mutational types generates counts according to a negative binomial distribution with the given expected.counts (argument mu to <a href="#">NegBinomial</a> ) and dispersion parameter nbinom.size.
nbinom.size	The dispersion parameter for the negative binomial distribution; smaller is more dispersed. See <a href="#">NegBinomial</a> .
verbose	If TRUE print messages under some circumstances.

### Value

`log(likelihood(spectrum | expected.counts))`, or, in more detail, the sum of the negative binomial likelihoods that each element of the spectrum (i.e., the count for each mutation type e.g. ACT > AAT) was generated from the expected count for that mutation type.

---

MAPAssignActivity    *Find Maximum A Posteriori (MAP) assignment of signature exposures that explain multiple spectra*


---

### Description

Find Maximum A Posteriori (MAP) assignment of signature exposures that explain multiple spectra

### Usage

```
MAPAssignActivity(
  spectra,
  sigs,
  sigs.presence.prop,
  output.dir,
  max.level = 5,
  p.thresh = 0.05,
```

```

m.opts = DefaultManyOpts(),
num.parallel.samples = 5,
mc.cores.per.sample = min(20, 2^max.level),
max.subsets = 1000,
max.presence.proportion = 0.99,
progress.monitor = NULL,
seed = NULL
)

```

## Arguments

<code>spectra</code>	The spectra (multiple spectra) to be reconstructed.
<code>sigs</code>	A numerical matrix, possibly an <a href="#">ICAMS</a> catalog.
<code>sigs.presence.prop</code>	The proportions of samples that contain each signature. A numerical vector (values between 0 and 1), with names being a subset of <code>colnames(sigs)</code> .
<code>output.dir</code>	Directory path to save the output file.
<code>max.level</code>	The maximum number of signatures to try removing.
<code>p.thresh</code>	If the p value for a better reconstruction with as opposed to without a set of signatures is > than this argument, then we can use exposures without this set.
<code>m.opts</code>	See <a href="#">DefaultManyOpts</a> .
<code>num.parallel.samples</code>	The (maximum) number of samples to run in parallel. On Microsoft Windows machines it is silently changed to 1. Each sample in turn can require multiple cores, as governed by <code>mc.cores.per.sample</code> .
<code>mc.cores.per.sample</code>	The maximum number of cores to use for each sample. On Microsoft Windows machines it is silently changed to 1.
<code>max.subsets</code>	The maximum number of subsets that can be tested for removal from the set of signatures.
<code>max.presence.proportion</code>	The maximum value of the proportion of tumors that must have a given signature.
<code>progress.monitor</code>	Function called at the start of each new level (number of signatures to try excluding). Must take named arguments <code>value</code> and <code>detail</code> , and no others. Designed for a <a href="#">AsyncProgress</a> progress bar function.
<code>seed</code>	Random seed; set this to get reproducible results. (The numerical optimization is in two phases; the first, global phase might rarely find different optima depending on the random seed.)

## Value

A list of lists containing output for each sample in `spectra`. Each sublist has the following elements

**MAP** A 2-column `tibble` with the attributions with the highest MAP found. Column 1 contains signature ids; column 2 contains the associated counts.

**MAP.row** A 1-row `tibble` with various information on the selected exposure.

**best.sparse** A 2-column tibble with the most-sparse attributions with the highest MAP, in the same format as element MAP.

**best.sparse.row** A 1-row tibble with various information on the most-sparse exposure with the best MAP.

**all.tested** A tibble of all the search results.

**messages** Possibly empty character vector with messages.

**success** TRUE if search was successful, FALSE otherwise.

**time.for.MAP.assign** Value from `system.time` for `MAPAssignActivityInternal`.

**MAP.recon** Reconstruction based on MAP.

**sparse.MAP.recon** Reconstruction based on `best.sparse`.

**MAP.distances** Various distances and similarities between `spect` and `MAP.recon`.

**sparse.MAP.distances** Various distances and similarities between `spect` and `sparse.MAP.recon`.

These elements will be NULL if `max.subsets` is exceeded.

---

MAPAssignActivity1 *Find a Maximum A Posteriori (MAP) assignment of signature exposures that explain one spectrum.*

---

## Description

Find a Maximum A Posteriori (MAP) assignment of signature exposures that explain one spectrum.

## Usage

```
MAPAssignActivity1(
  spect,
  sigs,
  sigs.presence.prop,
  max.level = 5,
  p.thresh = 0.05,
  m.opts = DefaultManyOpts(),
  max.mc.cores = min(20, 2^max.level),
  max.subsets = 1000,
  max.presence.proportion = 0.99,
  progress.monitor = NULL,
  seed = NULL
)
```

## Arguments

<code>spect</code>	A single spectrum.
<code>sigs</code>	A numerical matrix, possibly an <a href="#">ICAMS</a> catalog.
<code>sigs.presence.prop</code>	The proportions of samples that contain each signature. A numerical vector (values between 0 and 1), with names being a subset of <code>colnames(sigs)</code> .
<code>max.level</code>	The maximum number of signatures to try removing.



<code>p.thresh</code>	If the p value for a better reconstruction with as opposed to without a set of signatures is > than this argument, then we can use exposures without this set.
<code>m.opts</code>	See <a href="#">DefaultManyOpts</a> .
<code>max.mc.cores</code>	The maximum number of cores to use. On Microsoft Windows machines it is silently changed to 1.
<code>max.subsets</code>	The maximum number of subsets that can be tested for removal from the set of signatures.
<code>max.presence.proportion</code>	The maximum value of the proportion of tumors that must have a given signature.
<code>progress.monitor</code>	Function called at the start of each new level (number of signatures to try excluding). Must take named arguments <code>value</code> and <code>detail</code> , and no others. Designed for a <a href="#">AsyncProgress</a> progress bar function.
<code>seed</code>	Random seed; set this to get reproducible results. (The numerical optimization is in two phases; the first, global phase might rarely find different optima depending on the random seed.)

## Value

A list with the elements

**MAP** A 2-column `tibble` with the attributions with the highest MAP found. Column 1 contains signature ids; column 2 contains the associated counts.

**MAP.row** A 1-row `tibble` with various information on the selected exposure.

**best.sparse** A 2-column `tibble` with the most-sparse attributions with the highest MAP, in the same format as element `MAP`.

**best.sparse.row** A 1-row `tibble` with various information on the most-sparse exposure with the best MAP.

**all.tested** A `tibble` of all the search results.

**messages** Possibly empty character vector with messages.

**success** TRUE if search was successful, FALSE otherwise.

**time.for.MAP.assign** Value from `system.time` for [MAPAssignActivityInternal](#).

**MAP.recon** Reconstruction based on `MAP`.

**sparse.MAP.recon** Reconstruction based on `best.sparse`.

**MAP.distances** Various distances and similarities between `spect` and `MAP.recon`.

**sparse.MAP.distances** Various distances and similarities between `spect` and `sparse.MAP.recon`.

These elements will be NULL if `max.subsets` is exceeded.

---

ObjFnBinomMaxLHMustRound

*A deprecated negative binomial maximum likelihood objective function.*

---

### Description

Use [ObjFnBinomMaxLHRound](#) instead.

### Usage

```
ObjFnBinomMaxLHMustRound(exp, spectrum, sigs, nbinom.size)
```

### Arguments

<code>exp</code>	A vector of exposures ("activities").
<code>spectrum</code>	The spectrum to assess.
<code>sigs</code>	The matrix of signatures.
<code>nbinom.size</code>	The dispersion parameter for the negative binomial distribution; smaller is more dispersed. See <a href="#">NegBinomial</a> .

### Details

This function will lead to errors in some situations when the rounded reconstructed signature contains 0s for mutations classes for which the target spectrum is > 0.

---

ObjFnBinomMaxLHNoRoundOK

*A deprecated negative binomial maximum likelihood objective function.*

---

### Description

Use [ObjFnBinomMaxLHRound](#) instead.

### Usage

```
ObjFnBinomMaxLHNoRoundOK(exp, spectrum, sigs, nbinom.size)
```

### Arguments

<code>exp</code>	A vector of exposures ("activities").
<code>spectrum</code>	The spectrum to assess.
<code>sigs</code>	The matrix of signatures.
<code>nbinom.size</code>	The dispersion parameter for the negative binomial distribution; smaller is more dispersed. See <a href="#">NegBinomial</a> .

### Details

This function rounds sometimes, which leads to minor differences in log likelihoods of reconstructed spectra ([LLHSpectrumNegBinom](#)) compared to the value returned by this function.

---

ObjFnBinomMaxLHRound

*The preferred negative binomial maximum likelihood objective function.*


---

## Description

Can be used as the objective function for [SparseAssignActivity](#), [SparseAssignActivity1](#), and [SignaturePresenceTest1](#). (Internally used by [nloptr](#).)

## Usage

```
ObjFnBinomMaxLHRound(exp, spectrum, sigs, nbinom.size)
```

## Arguments

exp	A vector of exposures ("activities").
spectrum	The spectrum to assess.
sigs	The matrix of signatures.
nbinom.size	The dispersion parameter for the negative binomial distribution; smaller is more dispersed. See <a href="#">NegBinomial</a> .

## Value

$-1 * \log(\text{likelihood}(\text{spectrum} \mid \text{reconstruction}))$

[nloptr](#) minimizes the objective function, so the lower the objective function, the better.

---

OneMAPAssignTest     *Run one test of [MAPAssignActivity1](#).*


---

## Description

Run one test of [MAPAssignActivity1](#).

## Usage

```
OneMAPAssignTest (
  spect,
  reference.exp,
  cancer.type,
  mutation.type,
  exposure.mutation.type,
  max.subsets = 1000,
  max.level = 5,
  max.mc.cores = 100,
  m.opts = DefaultManyOpts(),
  out.dir = NULL,
  p.thresh,
```

```

    max.presence.proportion,
    sigs.prop = NULL,
    sigs = NULL
)

```

### Arguments

<code>spect</code>	A single spectrum.
<code>reference.exp</code>	Compare the inferred exposures to this.
<code>cancer.type</code>	Character string from a fixed set indicating different cancer types, used to look up the set of signatures known in that cancer type and the proportion of cancers of that type that have the signature. TODO: provide information on how to find the allowed cancer types.
<code>mutation.type</code>	One of "SBS96", "SBS192", "ID", "DBS78".
<code>exposure.mutation.type</code>	One of "SBS96", "ID", "DBS78".
<code>max.subsets</code>	The maximum number of subsets that can be tested for removal from the set of signatures.
<code>max.level</code>	The maximum number of signatures to try removing.
<code>max.mc.cores</code>	The maximum number of cores to use. On Microsoft Windows machines it is silently changed to 1.
<code>m.opts</code>	See <a href="#">DefaultManyOpts</a> .
<code>out.dir</code>	If non-NULL create this directory if necessary and put results there.
<code>p.thresh</code>	If the p value for a better reconstruction with than without a set of signatures is > than <code>p.thresh</code> , then we can use exposures without this set.
<code>max.presence.proportion</code>	The maximum value of the proportion of tumors that must have a given signature. Used so that it is possible to exclude a signature from a spectrum, e.g. perhaps all examples of tumor types have SBS5, but we want to allow a small chance that SBS5 is not present.
<code>sigs.prop</code>	The proportions of samples that contain each signature. A numerical vector (values between 0 and 1), with names being signature identifiers. Can be the return value from <a href="#">ExposureProportions</a> .
<code>sigs</code>	Matrix of signatures.

---

OptimizeExposure	<i>Optimize the reconstruction of a spectrum from a set of signatures.</i>
------------------	--

---

### Description

Optimize the reconstruction of a spectrum from a set of signatures.

### Usage

```
OptimizeExposure(spectrum, sigs, m.opts, ...)
```

**Arguments**

<code>spectrum</code>	The spectrum to be reconstructed.
<code>sigs</code>	The available signatures.
<code>m.opts</code>	Options that govern the numerical optimization. For documentation see <a href="#">DefaultManyOpts</a> .
<code>...</code>	Additional arguments for <code>eval_f</code> .

**Value**

A list with elements	
<code>loglh</code>	The log likelihood of the best solution (set of exposures) found.
<code>exposure</code>	The vector of exposures that generated <code>loglh</code> , i.e. the number of mutations ascribed to each signature.
<code>objective</code>	The final value of the objective function.
<code>solution</code>	The optimum exposures. Deprecated.
<code>warnings</code>	A character vector of warnings.
<code>global.search.diagnostics</code>	Diagnostics from <a href="#">nloptr</a> .
<code>local.search.diagnostics</code>	Diagnostics from <a href="#">nloptr</a> .

---

OptimizeExposureQP *Quadratic programming optimization of signature activities*

---

**Description**

Quadratic programming optimization of signature activities

**Usage**

```
OptimizeExposureQP(spectrum, signatures)
```

**Arguments**

<code>spectrum</code>	Mutational signature spectrum as a numeric vector or single column data frame or matrix.
<code>signatures</code>	Matrix or data frame of signatures from which reconstruct <code>spectrum</code> . Rows are mutation types and columns are signatures. Should have column names for interpretable results. Cannot be a vector because the column names are needed.

**Value**

A vector of exposures with names being the colnames from `signatures`. Code adapted from `SignatureEstimation::decomposeQP`.

---

OptimizeExposureQPBootstrap

*Bootstrap `OptimizeExposureQP` and filter exposures by confidence intervals*


---

## Description

Bootstrap `OptimizeExposureQP` and filter exposures by confidence intervals

## Usage

```
OptimizeExposureQPBootstrap(
  spectrum,
  signatures,
  num.replicates = 10000,
  conf.int = 0.95,
  mc.cores = 10,
  seed = NULL
)
```

## Arguments

<code>spectrum</code>	Mutational signature spectrum as a numeric vector or single column data frame or matrix.
<code>signatures</code>	Matrix or data frame of signatures from which reconstruct <code>spectrum</code> . Rows are mutation types and columns are signatures. Should have column names for interpretable results. Cannot be a vector because the column names are needed.
<code>num.replicates</code>	Number of bootstrap replicates.
<code>conf.int</code>	Discard signatures with <code>conf.int</code> that overlaps 0.
<code>mc.cores</code>	The maximum number of cores to use. On MS Windows machines it defaults to 1.
<code>seed</code>	Random seed; set this to get reproducible results.

#' @return A list with elements

`exposure` The vector of exposures that generated `loglh`, i.e. the number of mutations ascribed to each signature. The names of `exposure` are a subset of the `colnames(signatures)`.

`euclidean.dist` The final value of the objective function.

`cosine.sim` The cosine similarity between `spectrum` and the reconstruction based on signatures.

If the spectrum has 0 mutations, no bootstrapping is done, and in the return value all `signatures` have 0 exposures, `euclidean.dist` is 0, and `cosine.sim` is NaN.

PCAWGMAPTest

Run [MAPAssignActivity1](#) on one sample from the PCAWG platinum data set.

## Description

Run [MAPAssignActivity1](#) on one sample from the PCAWG platinum data set.

Run [MAPAssignActivity1](#) on one sample from the PCAWG platinum data set with artifact signatures removed.

## Usage

```
PCAWGMAPTest (
  cancer.type,
  sample.index,
  mutation.type,
  max.level = 5,
  max.mc.cores,
  out.dir = NULL,
  p.thresh = 0.01,
  m.opts = DefaultManyOpts(),
  max.presence.proportion = 0.99,
  sigs.prop = NULL
)
```

```
PCAWGMAPTest (
  cancer.type,
  sample.index,
  mutation.type,
  max.level = 5,
  max.mc.cores,
  out.dir = NULL,
  p.thresh = 0.01,
  m.opts = DefaultManyOpts(),
  max.presence.proportion = 0.99,
  sigs.prop = NULL
)
```

## Arguments

<code>cancer.type</code>	A cancer type from the PCAWG exposures matrix.
<code>sample.index</code>	The index of the sample within the exposures matrix.
<code>mutation.type</code>	One of "SBS96", "SBS192", "ID", "DBS78"
<code>max.level</code>	The maximum number of signatures to try removing.
<code>max.mc.cores</code>	The maximum number of cores to use. On Microsoft Windows machines it is silently changed to 1.
<code>out.dir</code>	If non-NULL create this directory if necessary and put results there.

<code>p.thresh</code>	If the p value for a better reconstruction with than without a set of signatures is > than <code>p.thresh</code> , then we can use exposures without this set.
<code>m.opts</code>	See <a href="#">DefaultManyOpts</a> .
<code>max.presence.proportion</code>	The maximum value of the proportion of tumors that must have a given signature. Used so that it is possible to exclude a signature from a spectrum, e.g. perhaps all examples of tumor types have SBS5, but we want to allow a small chance that SBS5 is not present.
<code>sigs.prop</code>	The proportions of samples that contain each signature. A numerical vector (values between 0 and 1), with names being signature identifiers. Can be the return value from <a href="#">ExposureProportions</a> .

**Value**

See [OneMAPAssignTest](#).

A list with two elements, each the result for one call to [OneMAPAssignTest](#).

---

<code>PossibleArtifacts</code>	<i>Return a character vector of the IDs of possible SBS96 signature artifacts.</i>
--------------------------------	--

---

**Description**

Return a character vector of the IDs of possible SBS96 signature artifacts.

**Usage**

```
PossibleArtifacts()
```

---

<code>RareSignatures</code>	<i>Return a character vector of the IDs of rare SBS96 signatures.</i>
-----------------------------	---

---

**Description**

Return a character vector of the IDs of rare SBS96 signatures.

**Usage**

```
RareSignatures()
```



---

ReconstructSpectrum

*Given signatures (sigs) and exposures (exp), return a spectrum or spectra*

---

## Description

Given signatures (sigs) and exposures (exp), return a spectrum or spectra

## Usage

```
ReconstructSpectrum(sigs, exp, use.sig.names = FALSE)
```

## Arguments

sigs	Signature as a matrix or or data frame, with each row one mutation type (g.e. CCT > CAT or CC > TT) and each column a signature.
exp	The exposures for one or more samples as a matrix or data.frame, with each row a signature and each column a sample.
use.sig.names	If TRUE check that rownames (exp) is a subset of colnames (sigs), and use only the columns in sigs that are present in exp.

## Details

Does not care or check if colSums (sigs) == 1. Error checking is minimal since this function is called often.

---

SignaturePresenceTest

*Test whether a given signature is plausibly present in a catalog.*

---

## Description

Test whether a given signature is plausibly present in a catalog.

## Usage

```
SignaturePresenceTest (
  spectra,
  sigs,
  target.sig.index,
  m.opts = NULL,
  mc.cores = 10
)
```

**Arguments**

spectra	The catalog (matrix) to analyze. This could be an <a href="#">ICAMS</a> catalog or a numerical matrix.
sigs	A catalog of signatures from which to choose. This could be an <a href="#">ICAMS</a> catalog or a numerical matrix.
target.sig.index	The index of the signature the presence of which we want to test.
m.opts	If NULL use the return from calling <a href="#">DefaultManyOpts</a> . For documentation see <a href="#">DefaultManyOpts</a> .
mc.cores	Number of cores to use. Always silently changed to 1 on Microsoft Windows.

---

SignaturePresenceTest1

*Test whether a given signature is plausibly present in a spectrum.*

---

**Description**

For backward compatibility. See also [AnySigSubsetPresent](#).

**Usage**

```
SignaturePresenceTest1(spectrum, sigs, target.sig.index, m.opts)
```

**Arguments**

spectrum	The spectrum to analyze.
sigs	A catalog of signatures from which to choose.
target.sig.index	The index of the signature the presence of which we want to test.
m.opts	For documentation see <a href="#">DefaultManyOpts</a> .

---

SparseAssignActivity

*Find known signatures that can most sparsely reconstruct each spectrum in a catalog.*

---

**Description**

Find known signatures that can most sparsely reconstruct each spectrum in a catalog.

**Usage**

```
SparseAssignActivity(
  spectra,
  sigs,
  max.level = 5,
  p.thresh = 0.05,
  m.opts = NULL,
  num.parallel.samples = 5,
  mc.cores.per.sample = min(20, 2^max.level)
)
```

**Arguments**

<code>spectra</code>	The spectra (multiple spectra) to be reconstructed.
<code>sigs</code>	The known signatures to use in reconstruction.
<code>max.level</code>	The largest number of signatures to consider discarding in the reconstruction.
<code>p.thresh</code>	The maximum p value based on which it is decided to retain a signature in a reconstruction.
<code>m.opts</code>	For documentation see <a href="#">DefaultManyOpts</a> .
<code>num.parallel.samples</code>	The (maximum) number of samples to run in parallel; each sample in turn can require multiple cores, as governed by <code>mc.cores.per.sample</code> .
<code>mc.cores.per.sample</code>	The maximum number of cores to use for each sample. On Microsoft Windows machines it is silently changed to 1.

**Value**

A list with the inferred exposure matrix as element `exposure`.

# Index

AnySigSubsetPresent, [18](#)  
AsyncProgress, [7](#), [9](#)  
  
cosine, [2](#)  
cossim, [2](#)  
  
DefaultManyOpts, [3](#), [7](#), [9](#), [12](#), [13](#), [16](#), [18](#),  
[19](#)  
  
ExposureProportions, [3](#), [12](#), [16](#)  
  
g\_ineq\_for\_ObjFnBinomMaxLH2, [4](#)  
  
ICAMS, [7](#), [8](#), [18](#)  
  
LLHSpectrumMAP, [5](#)  
LLHSpectrumNegBinom, [6](#), [10](#)  
  
MAPAssignActivity, [6](#)  
MAPAssignActivity1, [8](#), [11](#), [15](#)  
MAPAssignActivityInternal, [8](#), [9](#)  
  
NegBinomial, [3](#), [5](#), [6](#), [10](#), [11](#)  
nloptr, [3](#), [4](#), [11](#), [13](#)  
  
ObjFnBinomMaxLHMustRound, [10](#)  
ObjFnBinomMaxLHNoRoundOK, [10](#)  
ObjFnBinomMaxLHRound, [10](#), [11](#)  
OneMAPAssignTest, [11](#), [16](#)  
OptimizeExposure, [12](#)  
OptimizeExposureQP, [13](#), [14](#)  
OptimizeExposureQPBootstrap, [14](#)  
  
PCAWGMAPTest, [15](#)  
PossibleArtifacts, [16](#)  
  
RareSignatures, [16](#)  
ReconstructSpectrum, [17](#)  
  
SignaturePresenceTest, [17](#)  
SignaturePresenceTest1, [11](#), [18](#)  
SparseAssignActivity, [11](#), [18](#)  
SparseAssignActivity1, [11](#)