

# Package ‘nemTar’

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**Type** Package

**Title** A method for singlaing network inference from (epi)genetic aberration profiles

**Version** 0.1.0

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**Description** The package 'nemTar' are the extension of classic nest effects models(NEMs)

**Depends** R (*i*= 3.5.0),  
nem (*i*= 2.60.0),  
dplyr (*i*= 0.8.5)

**License** GPL (*i*= 2)

**Encoding** UTF-8

**LazyData** true

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

**biocViews**

**Imports** methods

**RoxygenNote** 7.1.1

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compute_WIG	<i>Calculating the weightheted information gain(WIG) of each S-genes</i>
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### Description

Calculating the weightheted information gain(WIG) of each S-genes

### Usage

```
compute_WIG(post_prob, path_affected, num_sgene)
```

### Arguments

post_prob	a list of the probablitiy that an E-gene is affected by an S-gene with respect to a specific pathway
path_affected	a list of the E-genes that are affected by the S-genes and are realted to a specific pathway
num_sgene	a numeric of the number of S-genes

### Value

a list contains the probability of the uniform distribution before the nertwork inference, and the WIG profiles of every S-gene,as well as the WIGs of S-genes

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nem_Tar_greedy	<i>Inferring the signaling network from (epi)genetic aberrations and effect reporter gene profiles based on greedy hill climbing methods</i>
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### Description

Inferring the signaling network from (epi)genetic aberrations and effect reporter gene profiles based on greedy hill climbing methods

### Usage

```
nem_Tar_greedy(D, Sgenes, S_pattern, initial = NULL, control, verbose = TRUE)
```

### Arguments

D	an E-gene observation matrix with the dimension of p(number of samples) × n(number of effect reporter genes)
Sgenes	a character vector of S-genes
S_pattern	a binary matrix showing the state of whether signaling components(S-genes)are perturbed, with the dimension of m × m
initial	the initial state of the S-gene graph
control	a list contains necessary parameters for implementing the methods,the details could be referred to <a href="#">nem</a>
verbose	a logic to whether present the execution process

**Value**

a list contains the network inference results, please also refer to [nem](#)

**See Also**

[nem\\_Tar\\_triples](#) [nem](#)

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nem_Tar_triples	<i>Inferring the signaling network from (epi)genetic aberrations and effect reporter gene profiles based on triple relation inference methods</i>
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**Description**

Inferring the signaling network from (epi)genetic aberrations and effect reporter gene profiles based on triple relation inference methods

**Usage**

```
nem_Tar_triples(D, Sgenes, S_pattern, control, verbose = TRUE)
```

**Arguments**

D	an E-gene observation matrix with the dimension of p(number of samples) × n(number of effect reporter genes)
Sgenes	a character vector of S-genes
S_pattern	a binary matrix showing the state of whether signaling components(S-genes)are perturbed, with the dimension of m × m(m is the number of S-genes)
control	a list contains necessary parameters for implementing the methods,as nemTar is developed based on nem, the users of nemTar should apply the function <code>nem::set.default.parameters(Sgenes,type="mLL",para=para)</code> , para is a vector of length two:false positive rate and false negative rate.
verbose	a logic to whether present the execution process

**Value**

a list contains the network inference results using triple relation, please also refer to the [nem](#)

**See Also**

[nem\\_Tar\\_greedy](#) [nem](#)

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path_post	<i>To dissect the influenced E-genes and the probability of influence under the assumption of nested effects for a specific pathway</i>
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### Description

To dissect the influenced E-genes and the probability of influence under the assumption of nested effects for a specific pathway

### Usage

```
path_post(nemTar_rslt, path_list, Sgenes)
```

### Arguments

nemTar_rslt	the output of the signaling network inferred by nemTar
path_list	a character of the the signature genes of an pathway
Sgenes	a character of the S-genes within the signaling network

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permu_test	<i>Employing the permutation test</i>
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### Description

Employing the permutation test

### Usage

```
permu_test(path_post, nem_rslt, path_list, sampling_times)
```

### Arguments

path_post	the influenced E-genes and the probability of influence under the assumption of nested effects
nem_rslt	the output of the signaling network inferred by nemTar
path_list	a character of the the signature genes of an pathway
sampling_times	a numeric number indicating the times of sampling

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sampleData2	<i>Generation of the data for sampling in the simulation of the cancer multi-omics samples</i>
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### Description

Generation of the data for sampling in the simulation of the cancer multi-omics samples

### Usage

```
sampleData2(  
  Phi,  
  S_obs,  
  p,  
  m,  
  type = "binary",  
  typeI.err = typeI.err,  
  typeII.err = typeII.err  
)
```

### Arguments

Phi	adjacency matrix
S_obs	binary matrix indicating the observation of S-genes' states
p	number of samples(patients) to sample
m	number of E-genes to sample
type	an integer,represents the number of row within the raw image
typeI.err	simulated type I error for binary data
typeII.err	simulated type II error for binary data

### See Also

[sampleData](#)

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WIGsig_test	<i>The statistical significance test based on the bootstrap of WIGs</i>
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### Description

The statistical significance test based on the bootstrap of WIGs

### Usage

```
WIGsig_test(sample_WIG0, WIG, sampling_times)
```

### Arguments

sample_WIG0	the background distribution of the WIG from the sampling of WIG
WIG	the pathway-specific WIGcalculated using <code>compute_WIG</code>
sampling_times	a numeric number indicating the times of sampling

**Value**

the statistical significance(BH-adjusted p-value)

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WIG_double	<i>Calculating the weigheted information gain(WIG) of combinational perturbation of 2 S-genes</i>
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**Description**

Calculating the weigheted information gain(WIG) of combinational perturbation of 2 S-genes

**Usage**

```
WIG_double(path_post, num_sgene)
```

**Arguments**

path_post	the influenced E-genes and the probalility of influence under the assumption of nested effects
num_sgene	a numeric of the number of S-genes

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WIG_sample	<i>Sampling of the WIG to measure the statistical significance</i>
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**Description**

Sampling of the WIG to measure the statistical significance

**Usage**

```
WIG_sample(path_post, nem_rslt, path_list, num_sgene, sampling_times)
```

**Arguments**

path_post	the influenced E-genes and the probalility of influence under the assumption of nested effects
nem_rslt	the output of the signaling network inferred by nemTar
path_list	a character of the the signature genes of an pathway
num_sgene	a numeric of the number of S-genes
sampling_times	a numeric number indicating the times of sampling

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