Package 'nemTar'

January 30, 2021

Type Package

Title A method for singlaing network inference from (epi)genetic aberration profiles **Version**
0.1.0

Author Yuchen ZHANG

Maintainer Yuchen ZHANG <yuczhang9@163.com> Xin WANG <xin.wang@cityu.edu.hk>

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

Depends R (>= 3.5.0),

nem (>= 2.60.0),

dplyr (<= 0.8.5)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Suggests knitr,
rmarkdown

VignetteBuilder knitr

biocViews

Imports methods

RoxygenNote 7.1.1

R topics documented:

---

compute_WIG	*Calculating the weigheted information gain(WIG) of each S-genes*

Description

Calculating the weigheted 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

---

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

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) $\times$ 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 $\times$ 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 nem
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

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

Description

Inferring the signaling network from (epi)genetic aberrations and effect reporter gene profiles based on triple realtion 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 nem::set.default.parameters(Sgenes,type="mLL",para=para), 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

---

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

Description

To dissect the influenced E-genes and the probalility 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

---

permu_test	*Employing the permuation test*

Description

Employing the permuation 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

---

sampleData2	*Generation of the data for sampling in the simulation of the cancer multi-omics samples*

Description

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

Usage

```
sampleData2(
  Phi,
  S_obs,
  p,
  m,
  uninformative = 0,
  type = "binary",
  typeI.err = typeI.err,
  typeII.err = typeII.err
)
```

Arguments

Phi	adjacency matrix
S_obs	binary matrix inddicating 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

WIGsig_test	*The statistical significance test based on the bootstrap of WIGs*

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 `compute_WIG`
sampling_times	a numeric number indicating the times of sampling

Value

the statistical significance(BH-adjusted p-value)

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

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

WIG_sample	*Sampling of the WIG to measure the statistical significance*

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

Index