Package ‘EGRNi’

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Type Package

Title Ensemble Gene Regulatory Network Inference

Version 0.1.6

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Description Gene regulatory network constructed using combined score obtained from individual network inference method. The combined score measures the significance of edges in the ensemble network. Fisher's weighted method has been implemented to combine the outcomes of different methods based on the probability values. The combined score follows chi-square distribution with 2n degrees of freedom. <doi:10.22271/09746315.2020.v16.i3.1358>.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Imports fdrtool, gdata, MASS, readr, stats

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NeedsCompilation no

Repository CRAN

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Contents

`CRN` *Correlation based network*

Description

Correlation based network

Usage

```
CRN(x)
```

Arguments

`x`	microarray dataset with genes in columns and samples in rows.

Value

s matrix containing connectivity scores

Examples

```
library(EGRNi)
data(gene_exp)
t_geneexp<-t(gene_exp)
CRN(t_geneexp)
```

Edg2Fw *To compute F score from edge scores*

Description

Edg2Fw computes the F-score from edge score using Fisher's weighted method. One pair of genes with k numbers of edge scores obtained from k numbers of independent method are combined using the probability value. The weight matrix w contains the weight for k number of methods.

Usage

```
Edg2Fw(s, w, k)
```

Arguments

`s`	Matrix containing edge scores obtained from k numbers of methods with gene pairs in row and edge scores in column
`w`	Matrix containing weight for all individual methods
`k`	Numbers of independent methods considered for computing edge scores

Details

Edg2Fw function generates mixture distribution based on edge score for each method given column wise in s matrix. The probability value for each pair of gene obtained from mixture distribution are combined using Fisher's weighted method. The combined score Fw follows chi-square distribution with 2k degrees of freedom.

Value

Fw_sum matrix containing F score for significant gene pairs

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A. (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

Examples

```
#load "EGRNi" library and Edge score data
library(EGRNi)
data(Edgescore)
data(weight)
Edg2Fw(Edgescore, weight, 4)
```

`Edgescore` *Edge score obtained from 4 different methods for Ensemble Gene Regulatory Network Inference*

Description

Edge score obtained from 4 different methods for Ensemble Gene Regulatory Network Inference

Usage

```
Edgescore(path)
```

Arguments

`path`	path to file name

Value

a `tibble`

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

`EGRN` *Ensemble Gene Regulatory Network Inference*

Description

EGRN computes F-score from probability values obtained individual method for each edge. The F-score follows ch-square distribution with 2k degrees of freedom, where k is the number of individual methods consider for ensemble study.The EGRN combines the outcomes obtained from four methods i.e. correlation, principal component regression, partial least square regression and ridge regression.The function EGRN has been implemented using Fisher's weighted method.

Usage

```
EGRN(x, n, w)
```

Arguments

`x`	Matrix containing gene expression data with genes in row and samples in column
`n`	Number of Bootstrap samples to obtain estimate of mean connectivity score and mean square error
`w`	Matrix containing weight for all individual methods

Details

The function works step-by-step as follows:The input gene expression data is considered for withdrawing n number of bootstrap samples to obtain the estimate of pairwise connectivity score for all possible pairs of genes in the dataset. The t-test statistic is calculated for each pair of genes and performed probability value and false discovery rate calculation from mixture distribution. The p-values for each edge are further used for computing F-score using fisher's weighted method. The fisher's weighted method provides the F-score which follows chi-square distribution with degrees of freedom twice the number of individual methods considered for ensemble study. The EGRN provides the network file as output containing the interacting pair of genes in row with final score.

Value

Fw_sum matrix containing F score for significant gene pairs

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A. (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

Examples

```
#load "EGRNi" library and gene expression data
library(EGRNi)
data(gene_exp)
data(weight)
EGRN(gene_exp[1:50,], 2, weight)
```

`F_score` *To compute F score using probability value*

Description

F_score computes the combined edge score from multiple probability values of edges obtained from independent methods. The probability score follows uniform distribution [0,1].The F score follows chi-square distribution with 2k degrees of freedom.

Usage

```
F_score(p, w, k)
```

Arguments

`p`	Matrix containing probability values of edges for each method column wise having gene pairs in row
`w`	Matrix containing weight for all individual methods
`k`	Numbers of independent methods considered for computing edge scores

Details

F_score function generates mixture distribution based on probability value for each method given column wise in p matrix. The probability value for each pair of gene are combined using Fisher's weighted method. The combined score Fw follows chi-square distribution with 2k degrees of freedom. The F_score provides the network file as output containing the interacting pair of genes in row with final score.

Value

Fw_sum matrix containing F score for significant gene pairs

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A. (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

Examples

```
#load "EGRNi" library and probability value data
library(EGRNi)
data(pvalue)
data(weight)
F_score(pvalue, weight, 4)
```

`gene_exp` *Gene expression data for Ensemble Gene Regulatory Network Inference*

Description

Gene expression data for Ensemble Gene Regulatory Network Inference

Usage

```
gene_exp(path)
```

Arguments

`path`	path to file name

Value

a `tibble`

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

`IntsctEdg2Fw` *To compute F score for significant edges from individual methods*

Description

IntsctEdg2Fw computes the Fw score using Fisher's weighted method for the significant edges obtained in k numbers of individual methods. The probability values are combined to compute the Fw score which follows chi-square distribution. The significant edges (>fdr) are selected using intersection.

Usage

```
IntsctEdg2Fw(s, w, k, fdr)
```

Arguments

`s`	Matrix containing edge scores obtained from k numbers of methods with gene pairs in row and edge scores in column
`w`	Matrix containing weight for all individual methods
`k`	Numbers of independent methods considered for computing edge scores
`fdr`	Cut-off for selecting significant edges

Details

IntsctEdg2Fw function generates mixture distribution based on edge score for each method given column wise in s matrix. The probability value for each pair of gene obtained from mixture distribution are combined using Fisher's weighted method. The combined score Fw follows chi-square distribution with 2k degrees of freedom.

Value

Fw matrix containing F score for significant gene pairs

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A. (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

Examples

```
#load "EGRNi" library and Edge score data
library(EGRNi)
data(Edgescore)
data(weight)
IntsctEdg2Fw(Edgescore,weight, k=4, fdr=0.1)
```

`PCN` *Principal component regression based network*

Description

Principal component regression based network

Usage

```
PCN(x)
```

Arguments

`x`	microarray dataset with genes in columns and samples in rows.

Value

s matrix containing connectivity scores

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

Examples

```
library(EGRNi)
data(gene_exp)
t_geneexp<-t(gene_exp)
PCN(t_geneexp)
```

`PLSN` *Partial least square based network*

Description

Partial least square based network

Usage

```
PLSN(x)
```

Arguments

`x`	microarray dataset with genes in columns and samples in rows.

Value

s matrix containing connectivity scores

Examples

```
library(EGRNi)
data(gene_exp)
t_geneexp<-t(gene_exp)
PLSN(t_geneexp)
```

`pvalue` *Probability values for Ensemble Gene Regulatory Network Inference*

Description

Probability values for Ensemble Gene Regulatory Network Inference

Usage

```
pvalue(path)
```

Arguments

`path`	path to file name

Value

a `tibble`

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

`RidgN` *Ridge regression based network*

Description

Ridge regression based network

Usage

```
RidgN(x)
```

Arguments

`x`	microarray dataset with genes in columns and samples in rows.

Value

s matrix containing connectivity scores

Examples

```
library(EGRNi)
data(gene_exp)
t_geneexp<-t(gene_exp)
RidgN(t_geneexp)
```

`weight` *Weights for Ensemble Gene Regulatory Network Inference*

Description

Weights for Ensemble Gene Regulatory Network Inference

Usage

```
weight(path)
```

Arguments

`path`	path to file name

Value

a `tibble`

Author(s)

Chiranjib Sarkar(cschiranjib9@gmail.com)

References

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A (2020). An ensemble approach for gene regulatory network study in rice blast. Journal of Crop and Weed , 16 , 1-8.

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