

Package ‘SPEM’

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Type Package

Title S-system parameter estimation method

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Description This package can optimize the parameter in S-system models given time series data

License GPL-2

LazyLoad yes

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SPEM-package

S-system parameter estimation method package

Description

The function in this package allows for the computation of parameters in the n-gene S-system from time series data.

Details

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Author(s)

Yang, X-Y, Dent, J. E. and Nardini, C.

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row_optimize

Calculate parameters for one row

Description

This function calculates parameters for a single row in the expression data. If a large-size dataset will be calculated, this function is recommended.

Usage

```
## S4 method for signature 'ExpressionSet'  
row_optimize(TS_eSet,S,beta, sparsity = 0.2, lbH = -3, ubH = 3, lbB = 0, ubB = 10)
```

Arguments

| | |
|----------|---|
| TS_eSet | Time series data in ExpressionSet class assayData: Matrix with n metabolite in row and m time points in column. phenoData: Dataframe includes label "time", which represents the time points. |
| S | Slope of the row you want to calculated. You can either input a vector with length equal to the rows of assayData of TS_eSet, or use s_diff function in this package to calculate it. |
| beta | Initial beta. |
| sparsity | A threshold used to control the sparsity of reconstructed matrix. Values whose absolute value smaller than sparsity will be set to zero. |
| lbH | Lower boundary value of h. |
| ubH | Upper boundary value of h. |
| lbB | Lower boundary value of beta. |
| ubB | Upper boundary value of beta. |

Details

In this SPEM package, we aim to reconstruct gene networks from time-series expression data using the S-system model. The input dataset should be as an ExpressionSet data container, describing, in assayData, expression data for n genes (rows) and m time points (columns), along with a vector of length m, which records the exact values of time points, thus showing the sample intervals in phenoData. SPEM will calculate the parameters alpha, g, beta and h of the S-system function set that best fits the dataset.

In this function, user can calculate one row at a time. This function offers a parallel calculation option for users.

Value

This function return a vector bind with c(alpha, \$g_i\$, beta, \$h_i\$, Initial Beta, error).

Methods

signature(TS_eSet = "ExpressionSet") This method is created for the function row_optimize.

Author(s)

Yang, X-Y, Dent, Jennifer E. and Nardini, C.

Examples

```
#####Load the SOS pathway data #####
data(sos)

#####Set Slope and Initial Beta #####

Slope<- s_diff(sos)
S<- Slope[1,] #S is the slope of the row you want to calculate. You can either input a vector yourself.
```

```
beta<- runif(n=1,min=1,max=10)

#####Set parameters #####
sparsity<- 0.2
lbH<- -3
ubH<- 3
lbB<- 0
ubB<- 10

#####Calculate results #####

result_r<-row_optimize(sos,S,beta,sparsity,lbH,ubH,lbB,ubB)
```

sos

SOS pathway time series data

Description

In this package we offer the SOS data obtained from Uri Alon's lab (<http://www.weizmann.ac.il/mcb/UriAlon/>). SOS response is a general DNA repair system in bacteria which allows survival after DNA damage. This SOS dataset is taken from real experiment expression data in *Escherichia coli*. It contains 8 genes under Experiment 3 (UV light intensities, 4:20 Jm⁻²).

Usage

```
data(sos)
```

Format

sos.data is time series gene expression value data in ExpressionSet Class. assayData: Matrix with expression values of 8 genes in SOS pathway of *Escherichia coli*. These expression levels are observed at 50 time points. phenoData: Sample data.frame includes label "time", which represents the value of time points.

References

M. Ronen, R. Rosenberg, B. I. Shraiman, and U. Alon. Assigning numbers to the arrows: parameterizing a gene regulation network by using accurate expression kinetics. Proceedings of the National Academy of Sciences of the United States of America, Aug. 2002. PMID: 12145321.

Examples

```
data(sos)
```

SPEM

*S-system parameter estimation method***Description**

This function calculates parameters of S-system from entire time series matrix.

Usage

```
## S4 method for signature 'ExpressionSet'
SPEM(TS_eSet, n = 3, sparsity = 0.2, lbH = -3, ubH = 3, lbB = 0, ubB = 10)
```

Arguments

| | |
|----------|--|
| TS_eSet | Time series data in ExpressionSet class. assayData: Matrix with n metabolite in row and m time points in column. phenoData: phenoData type. The sample data.frame should include the label "time", which represents the values of time points. |
| n | Positive integer, SPEM will guess initial beta n times. |
| sparsity | A positive number. In order to force the interaction matrix to be sparse, interactions with absolute value smaller than "sparsity" will be set to zero. |
| lbH | Lower boundary value of h. |
| ubH | Upper boundary value of h. |
| lbB | Lower boundary value of beta. |
| ubB | Upper boundary value of beta. |

Details

In this SPEM package, we aim to reconstruct gene networks from time-series expression data using the S-system model. The input dataset should be as an ExpressionSet data container, describing, in assayData, expression data for n genes (rows) and m time points (columns), along with a vector of length m, which records the exact values of time points, thus showing the sample intervals in phenoData. SPEM will calculate the parameters alpha, G, beta and H of the S-system function set that best fits the dataset.

Value

| | |
|-------------------|--|
| alpha, G, beta, H | Parameters of the reconstructed S-system. |
| IniBeta | Guess of the IniBeta value (Picked randomly by SPEM itself). |
| error | Regression error. |

Methods

signature(TS_eSet = "ExpressionSet") This method is created for function SPEM.

Author(s)

Yang, X-Y., Dent, Jennifer E. and Nardini, C.

Examples

```
#####Generate Toy Model #####
#####
# If you want to calculate SOS dataset in this package, please read our vignette###
#Real dataset takes a long time to calculate. You may want to try function 'row_optimize' to compute it in parallel##

toy_expression_data<-matrix(data=abs(rnorm(12)),nrow=3,ncol=4, dimnames=list(paste("G",c(1:3),sep=''), paste("t",c(1:4),sep='')),
toy_timepoints_data<-data.frame(index=c(1:4), label=paste("tp",c(0,2,4,6),sep='_'), time=c(0,2,4,6),row.names=paste("G",c(1:3),sep='')),
toy_varMetadata<-data.frame(LabelDescription=c("Index number", "Label Detail", "Time points values"),row.names=c("Index number", "Label Detail", "Time points values")),
toy_phenoData<-new("AnnotatedDataFrame", data=toy_timepoints_data,varMetadata=toy_varMetadata)
toy_ExpressionSet<-new("ExpressionSet", exprs=toy_expression_data,phenoData=toy_phenoData)

#####Set parameters #####
n<- 1
sparsity<- 0.2
lbH<- -3
ubH<- 3
lbB<- 0
ubB<- 10
#####Calculate results #####

result<-SPEM(toy_ExpressionSet,n,sparsity,lbH,ubH,lbB,ubB)
```

s_diff

Calculate slopes from time points and time series matrix.

Description

This function allows users calculate slopes from time points and time series data.

Usage

```
## S4 method for signature 'ExpressionSet'
s_diff(TS_eSet)
```

Arguments

TS_eSet Time series data in ExpressionSet class. assayData: Matrix with n metabolite in row and m time points in column. phenoData: phenoData type. The sample data.frame should include the label "time", which represents the values of time points.

Value

This function directly return a slope matrix.

Methods

signature(TS_eSet = "ExpressionSet") This method is created for function *s_diff*.

Author(s)

Yang, X-Y, Dent, Jennifer E. and Nardini, C.

Examples

```
#####Load the SOS pathway data #####  
data(sos)  
  
#####Calculate results #####  
  
Slope<-s_diff(sos)
```

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