Package ‘SPEM’

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Description This package can optimize the parameter in S-system models given time series data
License GPL-2
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R topics documented:

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### Description

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

### Details
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

```r
## 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  
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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**

```r
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**


**Examples**

```r
data(sos)
```

---

**SPEM**  
*S-system parameter estimation method*

**Description**

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

**Usage**

```r
## 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
/toquotesingle/var_row_optimize/toquotesingle/var
to calculate it in parallel

toy_expression_data<-matrix(data=abs(rnorm(12)),nrow=3,ncol=4, dimnames=list(paste("G",c(1:3),sep="\""), past("tp",c(0,2,4,6),sep='_\"")), time=c(0,2,4,6),row.names=paste("tp",c(0,2,4,6),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("tp",c(0,2,4,6),sep='_\""))
toy_varMetadata<-data.frame(labelDescription=c("Index number","Label Detail", "Time points values"),row.names=c("index","label","time"))
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)
**Description**

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

**Usage**

```r
## 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**

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

#########Calculate results #######
Slope<-s_diff(sos)
```
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