Package ‘SPEM’

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Date 2013-1-12
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Description This package can optimize the parameter in S-system models given time series data
License GPL-2
LazyLoad yes
biocViews Network, NetworkInference, Software
NeedsCompilation no

R topics documented:

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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
row_optimize

Package: SPEM
Type: Package
Version: 1.0
Date: 2013-01-13
License: GPL-2
LazyLoad: yes

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

```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, Sg_iS, beta, Sh_iS, 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

Examples
data(sos)

### S4 method for signature 'ExpressionSet'

SPEM(TS_eSet, n = 3, sparsity = 0.2, lbH = -3, ubH = 3, lbB = 0, ubB = 10)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TS_eSet</td>
<td>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 &quot;time&quot;, which represents the values of time points.</td>
</tr>
<tr>
<td>n</td>
<td>Positive integer, SPEM will guess initial beta n times.</td>
</tr>
<tr>
<td>sparsity</td>
<td>A positive number. In order to force the interaction matrix to be sparse, interactions with absolute value smaller than &quot;sparsity&quot; will be set to zero.</td>
</tr>
<tr>
<td>lbH</td>
<td>Lower boundary value of h.</td>
</tr>
<tr>
<td>ubH</td>
<td>Upper boundary value of h.</td>
</tr>
<tr>
<td>lbB</td>
<td>Lower boundary value of beta.</td>
</tr>
<tr>
<td>ubB</td>
<td>Upper boundary value of beta.</td>
</tr>
</tbody>
</table>
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

```r
# 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 '/quotesingle.Var/quotesingle.Var Var row_optimize'/quotesingle.Var/quotesingle.Var 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("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)
```
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

```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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