Package ‘GeneClusterNet’

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Title Gene Expression Clustering and Gene Network
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Author Yaqun Wang, Zhengyang Shi and Xiang Zhan
Maintainer Yaqun Wang <yw505@sph.rutgers.edu>
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Description

GeneClusterNet is a contributed R package for reconstructing gene regulatory network from time course gene expression data based on clustering of dynamic gene expressions. It provides functions for gene expression clustering, deciding the optimal number of clusters based on Bayesian Information Criterion (BIC), interpolating expression data for unevenly spaced measurements to have expression data as measured at even time intervals, and applying Dynamic Bayesian Network model to reconstruct gene regulatory networks. It also includes functions for displaying and visualizing clusters and networks.

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Author(s)

Yaqun Wang, Zhengyang Shi and Xiang Zhan

Maintainer: Yaqun Wang <yw505@sph.rutgers.edu>
GeneCluster

References


R package G1DBN available at https://cran.r-project.org/package=G1DBN

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Description

Providing functional clustering of time course gene expressions by using the Legendre orthogonal polynomials (LOP) to model cluster-specific curves for each cluster.

Usage

GeneCluster(mExpression, times, NumberOfCluster, orderLOP)

Arguments

mExpression a gene expression matrix with $p$ columns (length of time vector) and $n$ rows (number of genes).

times time vector specifies the time points of measurements.

NumberOfCluster number of cluster ($J$)

orderLOP order of Legendre Polynomials ($r$)

Value

A list that contains $MeanExpression$ is the matrix with $J$ rows ($J$ is number of Cluster) and $n$ columns (length of time vector), each rows is the mean expression of a cluster. $LOPCoefficient$ is the coefficient matrix of LOP with $J$ rows and $r+1$ columns.$Classifications$ indicates the cluster label for each of genes. A list of Plots, first plot is the mean expression plot for every clusters and each of the rest plots displays the trajectories of gene expressions in each cluster.

Author(s)

Yaqun Wang <yw505@sph.rutgers.edu>, Zhengyang Shi
References


Examples

```r
# load the package
library(GeneClusterNet)

# Set the number of Clusters is 3 and order of Legendre Polynomials is 5.
set.seed(1234)
data(mExpression)
Sample=mExpression[sample(1:nrow(mExpression),50,replace=FALSE),]
GeneCluster(Sample, times=c(1:18), NumberOfCluster=3,orderLOP=5)
```

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Description

Given time course expressions of \( n \) genes, time vector, order of Legendre Polynomials and a range of cluster numbers, e.g. from 1 to 15, the function can identify the optimal number of clusters, which has the smallest BIC value.

Usage

`GeneClusterBIC(mExpression, times, G = c(1:15), orderLOP)`

Arguments

- **mExpression**: a gene expression matrix with \( p \) columns (length of time vector) and \( n \) rows (number of genes).
- **times**: time vector specifies the time points of measurements.
- **G**: range of number of clusters
- **orderLOP**: order of Legendre Polynomials

Value

A list of BIC corresponds to every number of clusters and the optimal BIC. A plot shows the smallest BIC.
Author(s)
Yaqun Wang <yw505@sph.rutgers.edu>, Zhengyang Shi

References


Examples

# load the package
library(GeneClusterNet)
set.seed(1234)
data(mExpression)
Sample=mExpression[sample(1:nrow(mExpression),50,replace=FALSE),]
GeneClusterBIC(Sample, times=c(1:18), G=c(1:5), orderLOP=5)

Description
To perform the dynamic Bayesian network analysis, the time points of gene expression measurements have to be evenly spaced. If the original time points in a dataset are not even, this function can not only interpolate measurements to have evenly spaced time course gene expressions, but also allow users to specify the number of time points.

Usage
GeneClusterInterp(LOPCoefficient, OriginalTime, outLen = 20)

Arguments
LOPCoefficient coefficient matrix of LOP.
OriginalTime time vector
outLen number of new time points.

Value
A matrix with J + 1 rows (J is number of Cluster) and outLen columns (number of equal time space). The first row of it provides the new time vector.
**Author(s)**

Yaqun Wang <yw505@sph.rutgers.edu>, Zhengyang Shi

**References**


**Examples**

```r
# load the package
library(GeneClusterNet)
set.seed(1234)
data(mExpression)
sample=mExpression[sample(1:nrow(mExpression),50,replace=FALSE),]
LOPCoefficient =GeneCluster (Sample, times=c(1:18), NumberOfCluster=3,orderLOP=5)$LOPCoefficient
GeneClusterInterp (LOPCoefficient, OriginalTime=c(1:18),outLen=20)
```

**Description**

This function clusters gene expressions and makes inference of gene regulatory network with dynamic Bayesian network method based on G1DBN. It integrates the analyses of GeneCluster, GeneClusterBIC, GeneClusterInterp and G1DBN.

**Usage**

```r
GeneClusterNet(mExpression, times, orderLOP, alpha1 = 0.5, alpha2 = 0.05,
realign = F, cutoff = c(lowCut = -0.35, upCut = 0.2),
NumberOfCluster = 0, sLabels = NULL)
```

**Arguments**

- `mExpression` a gene expression matrix with \( p \) columns (length of time vector) and \( n \) rows (number of genes).
- `times` time vector
- `orderLOP` order of Legendre Polynomials
- `alpha1` threshold that use for edge selection in the 1st order dependence score matrix \( S_1 \) and its default setting is 0.5. See [https://cran.r-project.org/web/packages/G1DBN/G1DBN.pdf](https://cran.r-project.org/web/packages/G1DBN/G1DBN.pdf).
threshold that use for edge selection in the score matrix S2 and its default setting is 0.05. See https://cran.r-project.org/web/packages/G1DBN/G1DBN.pdf

default is FALSE, realign is true, the cutoff variable indicates a cutoff range.
cutoff range for determining the time of initial up or down regulation.

number of cluster. if it is set to zero, the function will determine the optimal number of gene expression clusters automatically.

default is NULL, the user could specify the cluster labels when number of cluster is specified.

Value

A score matrix and an adjacency matrix. It also creates a list of plots same as the function GeneCluster. In addition, it creates a plot of gene regulatory network.

Author(s)

Yaqun Wang <yw505@sph.rutgers.edu>, Zhengyang Shi

References


R package G1DBN available at https://cran.r-project.org/package=G1DBN

Examples

# load the package
library(GeneClusterNet)
set.seed(1234)
data(mExpression)
Sample=mExpression[sample(1:nrow(mExpression),50,replace=FALSE),]
GeneClusterNet (Sample, times=c(1:18), orderLOP=5 ,alpha1=0.5, alpha2=0.05,NumberOfCluster = 3)
mExpression

Usage

data("mExpression")

References


Examples

# load the package
library(GeneClusterNet)

data(mExpression)

# first 5 rows
Sample=mExpression[1:5,]

plot(1:18,Sample[,1],type="l", ylim=c(min(Sample),max(Sample)),xlab="Time",ylab="Expression",lwd=2)
color=1
for (i in 2:5){
  color=color+1
  lines(1:18,Sample[i,],col=color,lwd=2)
}
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