Package ‘FacPad’

February 19, 2015

Type Package

Title Bayesian Sparse Factor Analysis model for the inference of pathways responsive to drug treatment

Version 3.0

Date 2014-03-25

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Depends R (>= 2.12.1),Rlab,MASS

Description
This method tries to explain the gene-wise treatment response ratios in terms of the latent pathways. It uses bayesian sparse factor modeling to infer the loadings (weights) of each pathway on its associated probesets as well as the latent factor activity levels for each treatment.

License GPL (>= 2)

LazyLoad yes

NeedsCompilation no

Repository CRAN

Date/Publication 2014-03-28 00:31:36

R topics documented:

`FacPad-package` *Sparse factor modeling for the inference of drug-responsive pathways*

Description

This method tries to explain the gene-wise treatment response ratios in terms of the latent pathways. It uses bayesian sparse factor modeling to infer the loadings (weights) of each pathway on its associated probesets as well as the latent factor activity levels for each treatment.

Details

Package:	FacPad
Type:	Package
Version:	2.0
Date:	2014-03-25
License:	GPL (>= 2)
LazyLoad:	yes

install.packages("FacPad")

Author(s)

Haisu Ma<haisu.ma.pku.2008@gmail.com>

Examples

```
data(matrixY)
data(matrixL)
result<-gibbs_sampling(matrixY,matrixL,max_iter=30,
thin=10,file_name="test_30iter.RData")

result2<-gibbs2(matrixY,matrixL,eta0=0.2,eta1=0.2,
max_iter=50,thin=10,file_name="test_v2_50iter.RData")
```

`gibbs2` *A Collapsed Gibbs Sampling Algorithm for the Inference of Sparse Bayesian Factor Models_version2*

Description

In each iteration, the algorithm iteratively updates each entry in the binary matrix Z, loading matrix W and factor activity matrix X, as well as other model parameters.

Usage

```
gibbs2(matrixY, matrixL,eta0,eta1,alpha_tau = 1,
beta_tau = 0.01, tau_sig = 1, max_iter = 10000,
thin = 10, alpha_sigma = 0.7, beta_sigma = 0.3, file_name)
```

Arguments

`matrixY`	The input treatment response matrix. It has dimension G by J,where G is the number of probesets and J is the number of different treatments. The (g,j)-th entry represents the ratio of the expression of the g-th probeset after and before the j-th treatment.
`matrixL`	The binary probeset-pathway association matrix.It has dimension G by K. If the (g,k)-th entry has value 1, it indicates that the g-th probeset is involved in the k-th pathway; and the (g,k)-th entry takes value 0 if there is no association relationship.
`eta0`	The bernoulli probability of entries in matrix Z taking a non-zero value given that the corresponding entry in matrix L is zero
`eta1`	The bernoulli probability of entries in matrix Z taking the value zero given that the corresponding entry in matrix L is one
`alpha_tau`	The alpha parameter of Gamma distribution used for the simulation of noise, default value=1
`beta_tau`	The beta parameter of Gamma distribution used for the simulation of noise, default value=0.01
`tau_sig`	Pre-defined precision of each entry in the factor loadings matrixW, default value=0
`max_iter`	The number of iterations of the collaped Gibbs sampling algorithm, default=10000
`thin`	The number of iteration cycle for the record of Gibbs samples. For the convenience of storage, the result of the Gibbs sampling will be kept every other "thin" iterations to alliviate the auto-correlation problem between adjacent interations of the Gibbs sampling process
`alpha_sigma`	the alpha parameter for the Gamma prior for matrixW
`beta_sigma`	The beta parameter for the Gamma prior for matrixW
`file_name`	name of the file saving the result

Value

The algorithm will store the inferred binary indicator matrix Z, loading matrix W and factor activity matrix X (as well as tau_g if not pre-difined) in each thinned iteration and write them into .RData file with name defined by the user.

Author(s)

Haisu Ma<haisu.ma@yale.edu>

Examples

```
data(matrixY)
data(matrixL)
result<-gibbs2(matrixY,matrixL,eta0=0.2,eta1=0.2,
max_iter=50,thin=10,file_name=”test_v2_50iter.RData”)
```

`gibbs_sampling` *A Collapsed Gibbs Sampling Algorithm for the Inference of Sparse Bayesian Factor Models*

Description

In each iteration, the algorithm iteratively updates each entry in the loading matrix W and factor activity matrix X, as well as other model parameters.

Usage

```
gibbs_sampling(matrixY, matrixL, alpha_tau = 1,
beta_tau = 0.01, tau_sig = 1, max_iter = 10000,
thin = 10, alpha_sigma = 0.7, beta_sigma = 0.3, file_name)
```

Arguments

`matrixY`	The input treatment response matrix. It has dimension G by J,where G is the number of probesets and J is the number of different treatments. The (g,j)-th entry represents the ratio of the expression of the g-th probeset after and before the j-th treatment.
`matrixL`	The binary probeset-pathway association matrix.It has dimension G by K. If the (g,k)-th entry has value 1, it indicates that the g-th probeset is involved in the k-th pathway; and the (g,k)-th entry takes value 0 if there is no association relationship.
`alpha_tau`	The alpha parameter of Gamma distribution used for the simulation of noise, default value=1
`beta_tau`	The beta parameter of Gamma distribution used for the simulation of noise, default value=0.01
`tau_sig`	Pre-defined precision of each entry in the factor loadings matrixW, default value=0
`max_iter`	The number of iterations of the collaped Gibbs sampling algorithm, default=10000
`thin`	The number of iteration cycle for the record of Gibbs samples. For the convenience of storage, the result of the Gibbs sampling will be kept every other "thin" iterations to alliviate the auto-correlation problem between adjacent interations of the Gibbs sampling process
`alpha_sigma`	the alpha parameter for the Gamma prior for matrixW
`beta_sigma`	The beta parameter for the Gamma prior for matrixW
`file_name`	name of the file saving the result

Value

The algorithm will store the inferred loading matrix W and factor activity matrix X (as well as tau_g if not pre-difined) in each thinned iteration and write them into .RData file with name defined by the user.

Author(s)

Haisu Ma<haisu.ma@yale.edu>

Examples

```
data(matrixY)
data(matrixL)
result<-gibbs_sampling(matrixY,matrixL,max_iter=50,thin=10,
file_name="test_50iter.RData")
```

`matrixL` *Pathway structure matrix L*

Description

A binary matrix of dimension G by K. Entries of 1 indicate the presence of a probeset-pathway association relationship, whereas entries of 0 indicate the opposite.

Usage

```
data(matrixL)
```

Format

The format is: num [1:50, 1:5] 0 0 0 0 1 0 0 0 0 1 ...

Details

matrix L determines the sparsity strcuture of the loading matrix W. The binary association information can be extracted from many pathway databases, such as KEGG, BioCarta, etc.

Examples

```
data(matrixL)
```

`matrixY` *The treatment response matrix*

Description

A numeric matrix of dimension G by J, where G is the total number of probesets measured by the microarray platform and J is the total number of treatments. Each entry of matrixY is the ratio of the probeset expression after and before treatment.

Usage

```
data(matrixY)
```

Format

The format is: num [1:50, 1:10] 0.6691 1.9856 -2.6227 0.0386 0.4526 ...

Examples

```
data(matrixY)
```

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