Package 'CISE'

April 5, 2018

Type Package

Title Common and Individual Structure Explained for Multiple Graphs

Version 0.1.0

Description Specific dimension reduction methods for replicated graphs
(multiple undirected graphs repeatedly measured on a common set of
nodes). The package contains efficient procedures for estimating
a shared baseline propensity matrix and graph-specific low rank
matrices. The algorithm uses block coordinate descent algorithm to
solve the model, which alternatively performs L2-penalized logistic
regression and multiple partial eigenvalue decompositions, as described
in the paper Wang et al. (2017) <arXiv:1707.06360>.

Depends R (>= 3.3.0)

Imports far, gdata, glmnet (>= 2.0-13), MASS, Matrix (>= 1.2-12),
rARPACK (>= 0.11-0)

URL https://arxiv.org/abs/1707.06360

License GPL-2

LazyData true

RoxygenNote 6.0.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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A   *Adjacency matrices of binary brain networks for 212 subjects*

Description

Data from Human Connectome Project (HCP). The brain is segmented into 68 regions. Each subject's binary network consists of a collection of inter- connections among those brain regions, with ones indicate a connection between a pair of regions and zeros indicate no connection.

Usage

```
data(A)
```

Format

An object of class array of dimension 68 x 68 x 212.

Source

[Github](#)

References

Wang et al. (2017) ([Arxiv](#))

MGRAF1   *First variant of M-GRAF model*

Description

MGRAF1 returns the estimated common structure Z and subject-specific low rank components Q_i and Λ_i for multiple undirected graphs.

Usage

```
MGRAF1(A, K, tol, maxit)
```

Arguments

A	Binary array with size VxVxn storing the VxV symmetric adjacency matrices of n graphs.
K	An integer that specifies the latent dimension of the graphs
tol	A numeric scalar that specifies the convergence threshold of CISE algorithm. CISE iteration continues until the absolute percent change in joint log-likelihood is smaller than this value. Default is tol = 0.01.
maxit	An integer that specifies the maximum number of iterations. Default is maxit = 5.

Details

The subject-specific deviation D_i is decomposed into

$$D_i = Q_i * \Lambda_i * Q_i^\top,$$

where each Q_i is a VxK orthonormal matrix and each Λ_i is a KxK diagonal matrix.

Value

A list is returned containing the ingredients below from M-GRAF1 model corresponding to the largest log-likelihood over iterations.

Z	A numeric vector containing the lower triangular entries in the estimated matrix Z.
Lambda	Kxn matrix where each column stores the diagonal entries in Λ_i.
Q	VxKxn array containing the estimated VxK orthonormal matrix Q_i, i=1,...,n.
D_LT	Lxn matrix where each column stores the lower triangular entries in $D_i = Q_i * \Lambda_i * Q_i^\top$; L=V(V-1)/2.
LL_max	Maximum log-likelihood across iterations.
LL	Joint log-likelihood at each iteration.

Examples

```
data(A)
n = dim(A)[3]
subs = sample.int(n=n,size=30)
A_sub = A[ , , subs]
res = MGRAF1(A=A_sub, K=3, tol=0.01, maxit=5)
```

MGRAF2	*Second variant of M-GRAF model*

Description

MGRAF2 returns the estimated common structure Z and Λ that are shared by all the subjects as well as the subject-specific low rank matrix Q_i for multiple undirected graphs.

Usage

```
MGRAF2(A, K, tol, maxit)
```

Arguments

A	Binary array with size VxVxn storing the VxV symmetric adjacency matrices of n graphs.
K	An integer that specifies the latent dimension of the graphs
tol	A numeric scalar that specifies the convergence threshold of CISE algorithm. CISE iteration continues until the absolute percent change in joint log-likelihood is smaller than this value. Default is tol = 0.01.
maxit	An integer that specifies the maximum number of iterations. Default is maxit = 5.

Details

The subject-specific deviation D_i is decomposed into

$$D_i = Q_i * \Lambda * Q_i^\top,$$

where each Q_i is a VxK orthonormal matrix and Λ is a KxK diagonal matrix.

Value

A list is returned containing the ingredients below from M-GRAF2 model corresponding to the largest log-likelihood over iterations.

Z	A numeric vector containing the lower triangular entries in the estimated matrix Z.
Lambda	Kx1 vector storing the diagonal entries in Λ.
Q	VxKxn array containing the estimated VxK orthonormal matrix Q_i, i=1,...,n.
D_LT	Lxn matrix where each column stores the lower triangular entries in $D_i = Q_i * \Lambda * Q_i^\top$; L=V(V-1)/2.
LL_max	Maximum log-likelihood across iterations.
LL	Joint log-likelihood at each iteration.

Examples

```
data(A)
n = dim(A)[3]
subs = sample.int(n=n,size=30)
A_sub = A[ , , subs]
res = MGRAF2(A=A_sub, K=3, tol=0.01, maxit=5)
```

MGRAF3	*Third variant of M-GRAF model*

Description

`MGRAF3` returns the estimated common structure Z and Q that are shared by all the subjects as well as the subject-specific low rank matrix Λ_i for multiple undirected graphs.

Usage

```
MGRAF3(A, K, tol, maxit)
```

Arguments

A	Binary array with size VxVxn storing the VxV symmetric adjacency matrices of n graphs.
K	An integer that specifies the latent dimension of the graphs
tol	A numeric scalar that specifies the convergence threshold of CISE algorithm. CISE iteration continues until the absolute percent change in joint log-likelihood is smaller than this value. Default is tol = 0.01.
maxit	An integer that specifies the maximum number of iterations. Default is maxit = 5.

Details

The subject-specific deviation D_i is decomposed into

$$D_i = Q * \Lambda_i * Q^\top,$$

where Q is a VxK orthonormal matrix and each Λ_i is a KxK diagonal matrix.

Value

A list is returned containing the ingredients below from M-GRAF3 model corresponding to the largest log-likelihood over iterations.

Z	A numeric vector containing the lower triangular entries in the estimated matrix Z.
Lambda	Kxn matrix where each column stores the diagonal entries in Λ_i.

Q	VxK orthonormal matrix
LL_max	Maximum log-likelihood across iterations.
LL	Joint log-likelihood at each iteration.

Examples

```
data(A)
n = dim(A)[3]
subs = sample.int(n=n,size=30)
A_sub = A[ , , subs]
res = MGRAF3(A=A_sub, K=3, tol=0.01, maxit=5)
```

VSPLOT   *Visuospatial processing ability for 212 subjects*

Description

Data from Human Connectome Project (HCP). Visuospatial processing is commonly assessed using the Variable Short Penn Line Orientation Test (VSPLOT), where two line segments are presented on the screen and participants are asked to rotate a movable line so that it is parallel to the fixed line. The data contains an indicator of high/low visuospatial processing score for 212 subject. The order of the subjects is in the same order as in the array of adjacency matrices data(A).

Usage

```
data(VSPLOT)
```

Format

An object of class character of length 212.

Source

Github

References

Wang et al. (2017) (Arxiv)

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