

Package ‘dpcid’

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Contents

crit.dpcid	2
cv.lambda1	3
dpcid	5
dpcid_core	7
dpcid_l1_core	9
lshr.cov	11

Index 13

crit.dpcid	<i>Akaike information criterion (AIC) and Bayesian information criterion (BIC) for the DPCID</i>
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Description

crit.dpcid returns the AIC values corresponding to the given lambda1 and lambda2 values for the DPCID.

Usage

```
crit.dpcid(A,B,l1,seq_l2,wd1,wd2,rho1_init,rho2_init,niter=1000,tol=1e-6,scaling=FALSE)
```

Arguments

A	An observed dataset from the first condition.
B	An observed dataset from the second condition.
l1	The selected lambda1 in cv.lambda1.
seq_l2	A sequence of tuning parameter lambda2 for the fusion penalty
wd1	The estimate of diagonal elements of the precision matrix of the first condition.
wd2	The estimate of diagonal elements of the precision matrix of the second condition.
rho1_init	An initial value for the partial correlation matrix of the first condition.
rho2_init	An initial value for the partial correlation matrix of the second condition.
niter	A total number of iterations in the block-wise coordinate descent.
tol	A tolerance for the convergence.
scaling	a logical flag for scaling variable to have unit variance. Default is FALSE.

Details

crit.dpcid needs the estimates of the diagonal elements of two precision matrices.

Value

aic	A vector of aic values corresponding to a given sequence of tuning paramters.
bic	A vector of bic values corresponding to a given sequence of tuning paramters.

References

Yu, D., Lee, S. H., Lim, J., Xiao, G., Craddock, R. C., and Biswal, B. B. (2018). Fused Lasso Regression for Identifying Differential Correlations in Brain Connectome Graphs. *Statistical Analysis and Data Mining*, 11, 203–226.

Examples

```

library(MASS)

## True precision matrix
omega1 <- matrix(0,5,5)
omega1[1,2] <- omega1[1,3] <- omega1[1,4] <- 1
omega1[2,3] <- omega1[3,4] <- 1.5
omega1 <- t(omega1) + omega1
diag(omega1) <- 3

omega2 <- matrix(0,5,5)
omega2[1,3] <- omega2[1,5] <- 1.5
omega2[2,3] <- omega2[2,4] <- 1.5
omega2 <- t(omega2) + omega2
diag(omega2) <- 3

Sig1 = solve(omega1)
Sig2 = solve(omega2)
X1 = mvrnorm(50,rep(0,5),Sig1)
X2 = mvrnorm(50,rep(0,5),Sig2)

A = scale(X1,center=TRUE,scale=FALSE)
B = scale(X2,center=TRUE,scale=FALSE)

shr_res = lshr.cov(A)
PM1 = shr_res$shr_inv

shr_res = lshr.cov(B)
PM2 = shr_res$shr_inv

wd1 = diag(PM1)
wd2 = diag(PM2)

rho1_init = -(1/sqrt(wd1))*PM1
rho1_init = t( 1/sqrt(wd1)*t(rho1_init))
diag(rho1_init) = 1

rho2_init = -(1/sqrt(wd2))*PM2
rho2_init = t( 1/sqrt(wd2)*t(rho2_init))
diag(rho2_init) = 1

l1 = 0.3
seq_l2 = seq(0.1,1,by=0.2)

crit =crit.dpcid(A,B,l1,seq_l2,wd1,wd2,rho1_init,rho2_init)
crit$aic
crit$bic

```

Description

K-fold crossvalidation for the choice of the lambda1.

Usage

```
cv.lambda1(A,B, nfold,seq_lambda1,niter=1000,tol=1e-6,scaling=FALSE)
```

Arguments

A	An observed dataset from the first condition.
B	An observed dataset from the second condition.
nfold	the number of folds in the crossvalidation(i.e., K in K-fold cross validation)
seq_lambda1	A sequence of tuning parameters for the ridge penalty
niter	A total number of iterations in the block-wise coordinate descent.
tol	A tolerance for the convergence.
scaling	a logical flag for scaling variable to have unit variance. Default is FALSE.

Details

cv.lambda1 returns a vector of the K-fold crossvalidated errors and matrices of the initial estimates of the precision matrices.

Value

cv	A vector of crossvalidated errors corresponding to a given sequence of tuning paramters.
pm1	A matrix of the inverse of the linear shrinkage covariance estimates for the first condition.
pm2	A matrix of the inverse of the linear shrinkage covariance estimates for the second condition.

References

Yu, D., Lee, S. H., Lim, J., Xiao, G., Craddock, R. C., and Biswal, B. B. (2018). Fused Lasso Regression for Identifying Differential Correlations in Brain Connectome Graphs. *Statistical Analysis and Data Mining*, 11, 203–226.

Examples

```
library(MASS)

## True precision matrix
omega1 <- matrix(0,5,5)
omega1[1,2] <- omega1[1,3] <- omega1[1,4] <- 1
omega1[2,3] <- omega1[3,4] <- 1.5
omega1 <- t(omega1) + omega1
diag(omega1) <- 3
```

```

omega2 <- matrix(0,5,5)
omega2[1,3] <- omega2[1,5] <- 1.5
omega2[2,3] <- omega2[2,4] <- 1.5
omega2 <- t(omega2) + omega2
diag(omega2) <- 3

Sig1 = solve(omega1)
Sig2 = solve(omega2)
X1 = mvrnorm(50,rep(0,5),Sig1)
X2 = mvrnorm(50,rep(0,5),Sig2)

nfold = 5
seq_lam1 = seq(0.5,3,by=0.5)
cv_vec = cv.lambda1(X1,X2,nfold,seq_lam1,niter=1000,tol=1e-6)$cv

```

dpcid	<i>Differential partial correlation identification with the ridge and the fusion penalties</i>
-------	--

Description

DPCID is a procedure for the differential partial correlation identification with the ridge and the fusion penalties. This function conducts the two stage procedure (diagonal and partial correlation steps).

Usage

```
dpcid(A,B,lambda1,lambda2,niter=1000,tol=1e-6,scaling=FALSE)
```

Arguments

A	An observed dataset from the first condition.
B	An observed dataset from the second condition.
lambda1	A tuning parameter for the ridge penalty.
lambda2	A a tuning parameter for the fusion penalty between two precision matrices.
niter	A total number of iterations in the block-wise coordinate descent.
tol	A tolerance for the convergence.
scaling	a logical flag for scaling variable to have unit variance. Default is FALSE.

Details

In the first step (`lshr.cov`), each precision matrix is estimated from the optimal linear shrinkage covariance matrix. In the second step (`dpcid_core`), two partial correlation matrices are jointly estimated with a given tuning parameters `lambda1` and `lambda2` and fixed diagonal elements of two precision matrices.

Value

rho1	An estimated partial correlation matrix of the first condition.
rho2	An estimated partial correlation matrix of the second condition.
wd1	A vector of estimated diagonal elements of the first precision matrices.
wd2	A vector of estimated diagonal elements of the second precision matrices.
diff_edge	An index matrix of different edges between two conditions.
n_diff	The number of different edges between two conditions.

References

Yu, D., Lee, S. H., Lim, J., Xiao, G., Craddock, R. C., and Biswal, B. B. (2018). Fused Lasso Regression for Identifying Differential Correlations in Brain Connectome Graphs. *Statistical Analysis and Data Mining*, 11, 203–226.

Examples

```
library(MASS)

## True precision matrix
omega1 <- matrix(0,5,5)
omega1[1,2] <- omega1[1,3] <- omega1[1,4] <- 1
omega1[2,3] <- omega1[3,4] <- 1.5
omega1 <- t(omega1) + omega1
diag(omega1) <- 3

omega2 <- matrix(0,5,5)
omega2[1,3] <- omega2[1,5] <- 1.5
omega2[2,3] <- omega2[2,4] <- 1.5
omega2 <- t(omega2) + omega2
diag(omega2) <- 3

Sig1 = solve(omega1)
Sig2 = solve(omega2)
X1 = mvrnorm(50,rep(0,5),Sig1)
X2 = mvrnorm(50,rep(0,5),Sig2)

lambda1 = 0.2
lambda2 = 0.2

res = dpcid(X1,X2,lambda1,lambda2,niter=1000,tol=1e-6)
```

dpcid_core	<i>Identification of two partial correlation matrices having sparse differences</i>
------------	---

Description

dpcid_core estimates two partial correlation matrices by applying the regression approach with the ridge penalty and the fusion penalty.

Usage

```
dpcid_core(A,B,lambda1,lambda2,wd1,wd2,rho1_init,rho2_init,niter=1000,tol=1e-6)
```

Arguments

A	An observed dataset from the first condition.
B	An observed dataset from the second condition.
lambda1	A tuning parameter for the ridge penalty.
lambda2	A a tuning parameter for the fusion penalty between two precision matrices.
wd1	The estimate of diagonal elements of the precision matrix of the first condition.
wd2	The estimate of diagonal elements of the precision matrix of the second condition.
rho1_init	An initial value for the partial correlation matrix of the first condition.
rho2_init	An initial value for the partial correlation matrix of the second condition.
niter	A total number of iterations in the block-wise coordinate descent.
tol	A tolerance for the convergence.

Details

Dpcid_core is the partial correaltion step of the differential partial correlation identification method by Yu et al.(2018). The dpcid_core estimates two partial correlation matrices with the estimated diagonal elements of two precision matrices from the optimal linear shrinkage estimates. The estimated precision matrices by the optimal linear shrinkage estimates can simply be used as the initial values of PM1 and PM2 in the dpcid_core.

Value

rho1	An estimated partial correlatioin matrix of the first condition.
rho2	An estimated partial correlatioin matrix of the second condition.
resid1	Residuals of the first condtion.
resid2	Residuals of the second condtion.

References

Yu, D., Lee, S. H., Lim, J., Xiao, G., Craddock, R. C., and Biswal, B. B. (2018). Fused Lasso Regression for Identifying Differential Correlations in Brain Connectome Graphs. *Statistical Analysis and Data Mining*, 11, 203–226.

Examples

```
library(MASS)

## True precision matrix
omega1 <- matrix(0,5,5)
omega1[1,2] <- omega1[1,3] <- omega1[1,4] <- 1
omega1[2,3] <- omega1[3,4] <- 1.5
omega1 <- t(omega1) + omega1
diag(omega1) <- 3

omega2 <- matrix(0,5,5)
omega2[1,3] <- omega2[1,5] <- 1.5
omega2[2,3] <- omega2[2,4] <- 1.5
omega2 <- t(omega2) + omega2
diag(omega2) <- 3

Sig1 = solve(omega1)
Sig2 = solve(omega2)
X1 = mvrnorm(50,rep(0,5),Sig1)
X2 = mvrnorm(50,rep(0,5),Sig2)

A = scale(X1,center=TRUE,scale=FALSE)
B = scale(X2,center=TRUE,scale=FALSE)

lambda1 = 1
lambda2 = 1

shr_res = lshr.cov(A)
PM1 = shr_res$shr_inv

shr_res = lshr.cov(B)
PM2 = shr_res$shr_inv

wd1 = diag(PM1)
wd2 = diag(PM2)

rho1_init = -(1/sqrt(wd1))*PM1
rho1_init = t( 1/sqrt(wd1)*t(rho1_init))
diag(rho1_init) = 1

rho2_init = -(1/sqrt(wd2))*PM2
rho2_init = t( 1/sqrt(wd2)*t(rho2_init))
diag(rho2_init) = 1

res = dpcid_core(A, B, lambda1, lambda2, wd1,wd2, rho1_init, rho2_init)
```

dpcid_l1_core	<i>Identification of two partial correlation matrices having sparse differences</i>
---------------	---

Description

dpcid_core estimates two partial correlation matrices by applying the regression approach with the lasso penalty and the fusion penalty.

Usage

```
dpcid_l1_core(A,B,lambda1,lambda2,wd1,wd2,rho1_init,rho2_init,niter=1000,tol=1e-6)
```

Arguments

A	An observed dataset from the first condition.
B	An observed dataset from the second condition.
lambda1	A tuning parameter for the lasso penalty.
lambda2	A a tuning parameter for the fusion penalty between two precision matrices.
wd1	The estimate of diagonal elements of the precision matrix of the first condition.
wd2	The estimate of diagonal elements of the precision matrix of the second condition.
rho1_init	An initial value for the partial correlation matrix of the first condition.
rho2_init	An initial value for the partial correlation matrix of the second condition.
niter	A total number of iterations in the block-wise coordinate descent.
tol	A tolerance for the convergence.

Details

Dpcid_l1_core is the partial correlation step of the differential partial correlation identification method with the lasso penalty instead of the ridge penalty by Yu et al.(2018). The dpcid_l1_core estimates two partial correlation matrices with the estimated diagonal elements of two precision matrices from the optimal linear shrinkage estimates. The estimated precision matrices by the optimal linear shrinkage estimates can simply be used as the initial values of PM1 and PM2 in the dpcid_core.

Value

rho1	An estimated partial correlatioin matrix of the first condition.
rho2	An estimated partial correlatioin matrix of the second condition.
resid1	Residuals of the first condntion.
resid2	Residuals of the second condntion.

References

Yu, D., Lee, S. H., Lim, J., Xiao, G., Craddock, R. C., and Biswal, B. B. (2018). Fused Lasso Regression for Identifying Differential Correlations in Brain Connectome Graphs. *Statistical Analysis and Data Mining*, 11, 203–226.

Examples

```
library(MASS)

## True precision matrix
omega1 <- matrix(0,5,5)
omega1[1,2] <- omega1[1,3] <- omega1[1,4] <- 1
omega1[2,3] <- omega1[3,4] <- 1.5
omega1 <- t(omega1) + omega1
diag(omega1) <- 3

omega2 <- matrix(0,5,5)
omega2[1,3] <- omega2[1,5] <- 1.5
omega2[2,3] <- omega2[2,4] <- 1.5
omega2 <- t(omega2) + omega2
diag(omega2) <- 3

Sig1 = solve(omega1)
Sig2 = solve(omega2)
X1 = mvrnorm(50,rep(0,5),Sig1)
X2 = mvrnorm(50,rep(0,5),Sig2)

A = scale(X1,center=TRUE,scale=FALSE)
B = scale(X2,center=TRUE,scale=FALSE)

lambda1 = 1
lambda2 = 1

shr_res = lshr.cov(A)
PM1 = shr_res$shr_inv

shr_res = lshr.cov(B)
PM2 = shr_res$shr_inv

wd1 = diag(PM1)
wd2 = diag(PM2)

rho1_init = -(1/sqrt(wd1))*PM1
rho1_init = t( 1/sqrt(wd1)*t(rho1_init))
diag(rho1_init) = 1

rho2_init = -(1/sqrt(wd2))*PM2
rho2_init = t( 1/sqrt(wd2)*t(rho2_init))
diag(rho2_init) = 1

res = dpcid_l1_core(A, B, lambda1, lambda2, wd1,wd2, rho1_init, rho2_init)
```

lshr.cov	<i>Linear shrinkage estimates of covariance and inverse covariance matrix</i>
----------	---

Description

Linear shrinkage estimates of covariance and inverse covariance matrix.

Usage

```
lshr.cov(X, scaling=FALSE)
```

Arguments

X	An observed dataset from a specific condition.
scaling	a logical flag for scaling variable to have unit variance. Default is FALSE.

Details

shr_covp returns the optimal linear shrinkage parameter, the linear shrinkage estimates of the covariance and the precision matrix.

Value

shr_cov	Linear shrinkage estimate of the covariance matrix.
shr_inv	Linear shrinkage estimate of the inverse covariance matrix.

References

Ledoit, O. and M.~Wolf, M. (2004). A well-conditioned estimator for large-dimensional covariance matrices, *Journal of Multivariate Analysis*, 88, 365–411.

Yu, D., Lee, S. H., Lim, J., Xiao, G., Craddock, R. C., and Biswal, B. B. (2018). Fused Lasso Regression for Identifying Differential Correlations in Brain Connectome Graphs. *Statistical Analysis and Data Mining*, 11, 203–226.

Examples

```
library(MASS)

## True precision matrix
omega <- matrix(0,5,5)
omega[1,2] <- omega[1,3] <- omega[1,4] <- 1
omega[2,3] <- omega[3,4] <- 1.5
omega <- t(omega) + omega
diag(omega) <- 3
```

```
Sig = solve(omega)
X = mvrnorm(50, rep(0, 5), Sig)
lshr.cov(X)
```

Index

`crit.dpcid`, 2
`cv.lambda1`, 3

`dpcid`, 5
`dpcid_core`, 7
`dpcid_l1_core`, 9

`lshr.cov`, 11