

Package ‘fastCorrDiff’

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Type Package

Title Fast Differential Correlation Matrix Screening

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Description Fast spectral algorithms for differential analysis on large-scale correlation matrices of Li et. al. (2021) <[arXiv:2111.03721](https://arxiv.org/abs/2111.03721)> are implemented. The methods can identify a group of genes exhibiting differential correlation patterns between two groups. For high-dimensional matrices, compressed spectral screening methods are also provided based on random subsampling. The work to build this package is partially supported by the NSF grant DMS-2015298.

License GPL (>= 2)

Depends Matrix,irlba,plyr

Imports stats,RSpectra

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fastCorrDiff-package *Fast Differential Correlation Matrix Screening*

Description

Fast spectral algorithms for differential analysis on large-scale correlation matrices of Li et. al. (2021) <arXiv:2111.03721> are implemented. The methods can identify a group of genes exhibiting differential correlation patterns between two groups. For high-dimensional matrices, compressed spectral screening methods are also provided based on random subsampling. The work to build this package is partially supported by the NSF grant DMS-2015298.

Details

The DESCRIPTION file:

```
Package:      fastCorrDiff
Type:         Package
Title:        Fast Differential Correlation Matrix Screening
Version:      0.5
Date:         2021-11-10
Author:       Tianxi Li and Xiwei Tang
Maintainer:   Tianxi Li <tianxili@virginia.edu>
Description:  Fast spectral algorithms for differential analysis on large-scale correlation matrices of Li et. al. (2021) <arXiv:2111.03721>
License:      GPL (>= 2)
Depends:      Matrix,irlba,plyr
Imports:      stats,RSpectra
```

Index of help topics:

```
CaiSpectral      Spectral project algorithm of Cai et al (2017).
SS              Spectral screening of a differential
               correlation matrix
SS.boot         Bootstrapping function for spectral screening
fast.SS         Compressed spectral screening
fastCorrDiff-package Fast Differential Correlation Matrix Screening
```

The package for fast differential correlation/covariance analysis based on spectral methods. It includes the spectral screening and compressed spectral screening methods proposed in Li et al (2021) <arXiv:2111.03721> to identify a group of variables exhibiting differential correlation pattern between two settings. The methods are designed for a great scalability when the number of variables is large, such that computing the full correlation matrices is not feasible.

Author(s)

Tianxi Li and Xiwei Tang
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References

Tianxi Li, Xiwei Tang, and Ajay Chatrath. Compressed spectral screening for large-scale differential correlation analysis with application in selecting Glioblastoma gene modules. arXiv preprint arXiv:2111.03721, 2021.

T. T. Cai, T. Liang, A. Rakhlin, et al. Computational and statistical boundaries for submatrix localization in a large noisy matrix. *The Annals of Statistics*, 45(4):1403-1430, 2017.

Examples

```
X1 <- matrix(rnorm(200),10,20)
C1 <- cor(X1)
X2 <- matrix(rnorm(200),10,20)
C2 <- cor(X2)

D <- C1-C2

fit <- SS(D, 3, K.seq = FALSE, sv = FALSE)

fit$score
```

CaiSpectral

Spectral project algorithm of Cai et al (2017).

Description

Spectral projection algorithm of Cai et al (2017), which is based on the rank 1 spectral structure.

Usage

```
CaiSpectral(D)
```

Arguments

D The differential correlation matrix

Details

See the reference

Value

The spectral scores. It is recommended in the paper to use any two-class clustering algorithm to separate the variables.

Author(s)

Tianxi Li and Xiwei Tang Maintainer: Tianxi Li <tianxili@virginia.edu>

References

T. T. Cai, T. Liang, A. Rakhlin, et al. Computational and statistical boundaries for submatrix localization in a large noisy matrix. *The Annals of Statistics*, 45(4):1403-1430, 2017.

See Also

[fast.SS](#)

Examples

```
X1 <- matrix(rnorm(200),10,20)
C1 <- cor(X1)
X2 <- matrix(rnorm(200),10,20)
C2 <- cor(X2)

D <- C1-C2

fit <- CaiSpectral(D)

fit
```

fast.SS

Compressed spectral screening

Description

Compressed spectral screening for high-dimensional differential correlation matrices.

Usage

```
fast.SS(X1, X2, rho, K, K.seq = FALSE, sv = FALSE, tune = FALSE)
```

Arguments

X1	Matrix of the first group of observations. Each row is variable and each column is an observation. Note that this is different from the usual way of statistical data matrices, because usually number of variables is much larger than the number of observations in this case.
X2	Matrix of the second group of observations. Each row is variable and each column is an observation. Note that this is different from the usual way of statistical data matrices, because usually number of variables is much larger than the number of observations in this case.
rho	The sampling proportion for compressed screening.
K	The rank K or the maximum rank K to calculate the spectral scores

K.seq	logical value. If TRUE, then it returns the spectral screening scores for all rank from 1 to K. If FALSE (default), it returns the rank K result
sv	logical value. If TRUE, the square roots of singular values will be used in the score calculation.
tune	logical value. If TRUE, a cross-validation procedure will be called to estimate the the rank K by evaluating imputation errors of ten percent of additional sampled entries.

Details

This function can be used to tune the SS function as well. Also, the spectral projection method of Cai et al (2017) is also implemented as part of the function. So, it will return the scores by both compressed version of spectral screening and spectral projection. Notice that if one wants to analyze the Spearman's correlation, the input objects X1 and X2 should be the rank matrices instead of raw data matrices.

Value

SS	The result of the SS function on the incomplete correlation matrix
Cai	The result of the spectral projection of Cai et al (2017) on the incomplete correlation matrix
tune.error	The imputation error on hold-out entries
tune.time	Timing for the additional tuning step.

Author(s)

Tianxi Li and Xiwei Tang Maintainer: Tianxi Li <tianxili@virginia.edu>

References

Tianxi Li, Xiwei Tang, and Ajay Chatrath. Compressed spectral screening for large-scale differential correlation analysis with application in selecting Glioblastoma gene modules. arXiv preprint arXiv:2111.03721, 2021.

See Also

[SS](#)

Examples

```
X1 <- matrix(rnorm(200),10,20)
X2 <- matrix(rnorm(200),10,20)

fit <- fast.SS(X1, X2, 0.3, K=2)
fit$SS$score
```

SS *Spectral screening of a differential correlation matrix*

Description

The full matrix version of spectral screening method.

Usage

```
SS(D, K, K.seq = FALSE, sv = FALSE)
```

Arguments

D	The difference matrix of two correlation/covariance matrices
K	The rank K or the maximum rank K to calculate the spectral scores
K.seq	logical value. If TRUE, then it returns the spectral screening scores for all rank from 1 to K. If FALSE (default), it returns the rank K result
sv	logical value. If TRUE, the square roots of singular values will be used in the score calculation.

Details

This is the full version spectral screening method, which can be applicable to a few thousands of variables. If a tuning of K is needed, please use the fast.SS for tuning.

Value

R	The the singular vector matrix. Each row is for one variable.
R.sv	The R matrix scaled by sqrt of singular values
score	The spectral score for screening

Author(s)

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References

Tianxi Li, Xiwei Tang, and Ajay Chatrath. Compressed spectral screening for large-scale differential correlation analysis with application in selecting Glioblastoma gene modules. arXiv preprint arXiv:2111.03721, 2021.

See Also

[fast.SS](#)

Examples

```
X1 <- matrix(rnorm(200),10,20)
C1 <- cor(X1)
X2 <- matrix(rnorm(200),10,20)
C2 <- cor(X2)

D <- C1-C2

fit <- SS(D, 3, K.seq = FALSE, sv = FALSE)

fit$score
```

SS.boot

Bootstrapping function for spectral screening

Description

The function initialize a bootstrapping procedure for spectral score calculation, which can be used to determine a threshold for SS selection.

Usage

```
SS.boot(X1, X2, K, B, sv = FALSE, spearman = FALSE)
```

Arguments

X1	Matrix of the first group of observations. Each row is variable and each column is an observation. Note that this is different from the usual way of statistical data matrices, because usually number of variables is much larger than the number of observations in this case.
X2	Matrix of the second group of observations. Each row is variable and each column is an observation. Note that this is different from the usual way of statistical data matrices, because usually number of variables is much larger than the number of observations in this case.
K	Rank K in spectral screening
B	Number of bootstrap samples
sv	logical value. If TRUE, the square roots of singular values will be used in the score calculation.
spearman	logical value. If TRUE, Spearman's correlation is used. Otherwise (default), the calculation is based on Pearson's correlation.

Details

See the details in the reference paper.

Value

A matrix with B columns. Each column is a bootstrapped score for the p variables.

Author(s)

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References

Tianxi Li, Xiwei Tang, and Ajay Chatrath. Compressed spectral screening for large-scale differential correlation analysis with application in selecting Glioblastoma gene modules. arXiv preprint arXiv:2111.03721, 2021.

See Also

[SS](#)

Examples

```
X1 <- matrix(rnorm(200),10,20)
X2 <- matrix(rnorm(200),10,20)
```

```
bt <- SS.boot(X1,X2,3, 10)
```


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