Package 'CORREP'

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Type Package

Title Multivariate Correlation Estimator and Statistical Inference
Procedures.

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Author Dongxiao Zhu and Youjuan Li

Maintainer Dongxiao Zhu <doz@stowers-institute.org>

Imports e1071, stats

Suggests cluster, MASS

Description Multivariate correlation estimation and statistical
inference. See package vignette.

License GPL (>= 2)

biocViews Microarray, Clustering, GraphAndNetwork

NeedsCompilation no

R topics documented:

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CORREP-package   *Multivariate Correlation Estimator from Replicated Data*

Description

This package implements multivariate correlation estimator for data with equivalent number of replicates as well as inequivalent number of replicates. For small sample data, this package provides permutation test for test if the true correlation vanishes, and for large sample data, this package provides Likelihood Ratio Test (LRT) to test if the true correlation vanishes. A function to calculate Bootstrap confidence interval was also included in the package.

Details

Package:	CORREP
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Version:	1.0
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License:	GPL 2.0 or newer

Author(s)

Dongxiao Zhu and Youjuan Li Maintainer: Dongxiao Zhu <doz@stowers-institute.org>

References

Zhu, D and Li Y. 2007. Multivariate Correlation Estimator for Inferring Functional Relationships from Replicated 'OMICS' data. Submitted.

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cor.balance   *Multivariate Correlation Estimator (Equal Number of Replicates)*

Description

cor.balance estimates correlation matrix from replicated data assuming equal number of replicates. The data must be formatted in the right format (rows correspond to replicates, columns correspond to conditions, see example below) and the variance of each row of the data MUST equal to 1 (see example below).

Usage

```
cor.balance(x, m, G)
```

Arguments

x	data matrix, column represents samples (conditions), and row represents variables (genes), see example below for format information
m	number of replicates for each variable (gene)
G	number of variables (genes)

Details

The multivariate correlation estimator assumes replicated omics data are iid samples from the multivariate normal distribution. It is derived by maximizing the likelihood function. Note that each off-diagonal element in the returned correlation matrix (G by G) is the average of off-diagonals of MLE of correlation matrix of a pair of variables (m by m).

Value

A correlation matrix estimated for G variables (genes)

Author(s)

Dongxiao Zhu and Youjuan Li

References

Zhu, D and Li Y. 2007. Multivariate Correlation Estimator for Inferring Functional Relationships from Replicated 'OMICS' data. Submitted.

See Also

[cor.balance](), [cor]()

Examples

```
library("CORREP")
d0 <- NULL
for(l in 1:10)
d0 <- rbind(d0, rnorm(100))
## The simulated data corresponds to the real-world data of 25 genes and 10 conditions, each gene expression
## profiles was replicated 4 times.
d0<- t(d0)
## This step is to make the standard deviation of each replicate equals to 1
## so that we can model the covariance matrix as correlation matrix.
d0.std <- apply(d0, 1, function(x) x/sd(x))
M <- cor.balance(t(d0.std), m=4, G=25)
```

---

cor.bootci   *Bootstrap Confidence Interval for Multivariate Correlation*

Description

This function calculates Bootstrap confidence interval for multivariate correlation. The procedure is very similar to those used to calculate Bootstrap CI's for other parameters, such as mean and correlation. See manuscript for detail.

Usage

```
cor.bootci(x, y = NULL, m, G, alpha)
```

Arguments

x	data matrix, column represents samples (conditions), and row represents variables (genes), see example below for format information
y	optional, used when x and y are vectors
m	number of replicates
G	number of genes
alpha	significant level

Details

See manuscript.

Value

upperCI	Upper bound of CI
lowerCI	Lower bound of CI

Author(s)

Dongxiao Zhu and Youjuan Li

References

Zhu, D and Li Y. 2007. Multivariate Correlation Estimator for Inferring Functional Relationships from Replicated 'OMICS' data. Submitted.

See Also

[cor.LRtest](), [cor.LRtest.std](), [cor.test](), [permutest]()

Examples

```
library("CORREP")
d0 <- NULL
## sample size is set to 5
for(l in 1:5)
d0 <- rbind(d0, rnorm(8))
## data must have row variance of 1
d0.std <- apply(d0, 2, function(x) x/sd(x))
M <- cor.balance(t(d0.std), m = 2, G= 4)
pv.bootci <- cor.bootci(t(d0.std), m = 2, G= 4, alpha = 0.05)
```

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cor.LRtest	*Maximum Likelihood Ratio Test for Multivariate Correlation Estimator (Positive Determinants)*

Description

Performs LRT to test if multivariate correlation vanishes. Note this code will return NaN's if the matrix determinant is negative (see below).

Usage

```
cor.LRtest(x, m1, m2)
```

Arguments

x	data matrix, column represents samples (conditions), and row represents variables (genes), see example below for format information
m1	number of replicates for gene X
m2	number of replicates for gene Y

Details

Under the multivaraite normal distribution assumption, the column vectors of the data are iid samples. We test the followiing hypothesis: H0: Z ~ N(mu, Sigma0), H1 ~ N(mu, Sigma1). Let M = Inverse(Sigma0)*Sigma1, the likelihood ratio test statistic G^2, is, n*[trace(M)-log(det(M))-(m1+m2)]. Under the H0, G^2 follows a chi-square distribution with $2m1*m2$ degree of freedom. In some case, the determinant of M is negative so that the log(det(M)) returns NaN. There are two ways to deal with this problem, one, those M's whose determinants are negative tend to consist of very small correlations that are biological irrelevant. Therefore, we can simply ignore those gene pairs that the determinants of correlation matrices M's are negative. Second, we can 'standardize' the M to make the determinant positive (implemented in function cor.LRtest.std). In most of cases, we recommend using function cor.LRtest. Use cor.LRtest.std only you know what you are doing.

Value

p.value	The p-value of the LRT

Author(s)

Youjuan Li and Dongxiao Zhu

References

Zhu, D and Li Y. 2007. Multivariate Correlation Estimator for Inferring Functional Relationships from Replicated 'OMICS' data. Submitted.

See Also

[cor.LRtest.std](#), [cor.test](#)

Examples

```
library("CORREP")
library("MASS")
Sigma <- matrix(c(1, 0.8, .5,.5, 0.8, 1,
0.5,0.5,0.5,0.5,1,0.6,0.5,0.5,0.6,1),4,4)
dat <- mvrnorm(50, mu=c(0,0,0,0), Sigma)
dat.std <- apply(dat,2,function(x) x/sd(x))
cor.LRtest(t(dat.std), m1=2, m2=2)
```

---

cor.LRtest.std   *Maximum Likehood Ratio Test for Multivariate Correlation Estimator*

Description

Performs LRT to test if multivariate correlation vanishes. Note this code 'standardizes' estimated correlation matrix to make sure its determinant is positive.

Usage

```
cor.LRtest.std(x, m1, m2)
```

Arguments

x	data matrix, column represents samples (conditions), and row represents variables (genes), see example below for format information
m1	number of replicates for gene X
m2	number of replicates for gene Y

Details

Under the multivaraite normal distribution assumption, the column vector of the data is iid sample. We test the followiing hypothesis: H0: Z ~ N(mu, Sigma0), H1 ~ N(mu, Sigma1). Let M = Inverse(Sigma0)*Sigma1, the likelihood ratio test statistic G^2, is, n[trace(M)-log(det(M))-(m1+m2)]. Under the H0, G^2 follows a chi-square distribution with $2m1*m2$ degree of freedom. In some case, the determinant of M is negative so that the log(det(M)) return NaN. There are two ways to deal with this problem, one, those M's whose determinant are negative tend to consist of very small correlations that are biological irrelevant. Therefore, we can simply ignore those gene pairs that the determinant correlation matrix M is negative. Second, we can 'standardize' the M to make the determinant positive (implemented in function cor.LRtest.std). In most of cases, we recommend using function cor.LRtest. Use cor.LRtest.std only you know what you are doing.

Value

p.value   The p-value of the LRT

Author(s)

Youjuan Li and Dongxiao Zhu

References

Zhu, D and Li Y. 2007. Multivariate Correlation Estimator for Inferring Functional Relationships from Replicated 'OMICS' data. Submitted.

See Also

[cor.LRtest](), [cor.test]()

Examples

```
library("CORREP")
library("MASS")
Sigma <- matrix(c(1, 0.8, .5,.5, 0.8, 1,
0.5,0.5,0.5,0.5,1,0.6,0.5,0.5,0.6,1),4,4)
dat <- mvrnorm(50, mu=c(0,0,0,0), Sigma)
dat.std <- apply(dat,2,function(x) x/sd(x))
cor.LRtest.std(t(dat.std), m1=2, m2=2)
```

---

cor.unbalance   *Multivariate Correlation Estimator (Unequal Number of Replicates)*

Description

cor.unbalance estimates correlation from replicated data of unequal number of replicates. different from [cor.balance](), [cor.unbalance]() takes a pair of variables at a time because of unequal number of replicates. the variance of each row of the data MUST equal to 1 (see example below)

Usage

```
cor.unbalance(x, m1, m2)
```

Arguments

x	data matrix, column represents samples (conditions), and row represents variables (genes), see example below for format information
m1	number of replicates for one variable (gene)
m2	number of replicates for another variable (gene)

Details

The multivariate correlation estimator assumes replicated omics data are iid samples from the multivariate normal distribution. It is derived by maximizing the likelihood function. Note that the off-diagonal elements in the returned correlation matrix (G by G) is the average of off-diagonals of MLE of correlation matrix of a pair of variables (m1+m2 by m1+m2).

Value

A correlation matrix containing only one distinct correlation coefficient for the pair of variables (genes)

Author(s)

Dongxiao Zhu and Youjuan Li

References

Zhu, D and Li Y. 2007. Multivariate Correlation Estimator for Inferring Functional Relationships from Replicated 'OMICS' data. Submitted.

See Also

[cor.unbalance](#), [cor](#)

Examples

```
library("CORREP")
d0 <- NULL
for(l in 1:10)
d0 <- rbind(d0, rnorm(8))
## The simulated data corresponds to the real-world data of 2 genes and 10 conditions, gene expression
## profiles were replicated 3 and 5 times.
## Note this function can only take calculate correlation matrix between two genes at a time.
d0<- t(d0)
## This step is to make the standard deviation of each replicate equal to 1
## so that we can model the covariance matrix as correlation matrix.
d0.std <- apply(d0, 1, function(x) x/sd(x))
M <- cor.unbalance(t(d0.std), m1=3, m2=5)
```

---

gal_all   *Galactose Metabolism Data*

Description

The data is compiled by Mario Medvedovic et al, 2003 based on the original full data reported in
Ideker et al, 2001. There are a total of 205 rows (genes), 20 experiments, and 4 repeated mea-
surements in the data. There are 4 classes (which correspond to functional categories). The data
contains approximately 8 of missing data. The missing values were filled by applying k-nearest
neighbor (k = 12) to impute all the missing values.

Usage

```
data(gal_all)
```

Format

A data frame with 205 variables on the following 80 replicated observations.

wtRG1 a numeric vector

wtRG2 a numeric vector

wtRG3 a numeric vector

wtRG4 a numeric vector

gal1RG1 a numeric vector

gal1RG2 a numeric vector

gal1RG3 a numeric vector

gal1RG4 a numeric vector

gal2RG1 a numeric vector

gal2RG2 a numeric vector

gal2RG3 a numeric vector

gal2RG4 a numeric vector

gal3RG1 a numeric vector

gal3RG2 a numeric vector

gal3RG3 a numeric vector

gal3RG4 a numeric vector

gal4RG1 a numeric vector

gal4RG2 a numeric vector

gal4RG3 a numeric vector

gal4RG4 a numeric vector

gal5RG1 a numeric vector

gal5RG2 a numeric vector

gal5RG3 a numeric vector

gal5RG4 a numeric vector

gal6RG1 a numeric vector

gal6RG2 a numeric vector

gal6RG3 a numeric vector

gal6RG4 a numeric vector

gal7RG1 a numeric vector

gal7RG2 a numeric vector

gal7RG3 a numeric vector

gal7RG4 a numeric vector

gal10RG1 a numeric vector

gal10RG2 a numeric vector

gal10RG3 a numeric vector

gal10RG4 a numeric vector

gal80RG1 a numeric vector

gal80RG2 a numeric vector

gal80RG3 a numeric vector

gal80RG4 a numeric vector

wtR1 a numeric vector

wtR2 a numeric vector

wtR3 a numeric vector

wtR4 a numeric vector

gal1R1 a numeric vector

gal1R2 a numeric vector

gal1R3 a numeric vector

gal1R4 a numeric vector

gal2R1 a numeric vector

gal2R2 a numeric vector

gal2R3 a numeric vector

gal2R4 a numeric vector

gal3R1 a numeric vector

gal3R2 a numeric vector

gal3R3 a numeric vector

gal3R4 a numeric vector

gal4R1 a numeric vector

gal4R2 a numeric vector

gal4R3 a numeric vector

gal4R4 a numeric vector

gal5R1 a numeric vector

gal5R2 a numeric vector

gal5R3 a numeric vector

gal5R4 a numeric vector

gal6R1 a numeric vector

gal6R2 a numeric vector

gal6R3 a numeric vector

gal6R4 a numeric vector

gal7R1 a numeric vector

gal7R2 a numeric vector

gal7R3 a numeric vector

gal7R4 a numeric vector

gal10R1 a numeric vector

gal10R2 a numeric vector

gal10R3 a numeric vector

gal10R4 a numeric vector

gal80R1 a numeric vector

gal80R2 a numeric vector

gal80R3 a numeric vector

gal80R4 a numeric vector

Details

The 205 genes have been classified into four functional classes based on their GO annotations. In the data examaple provided in the vignette, we assume the four classes as true memberships (external knowledge) and use it to evaluate the performances of different correlation measured based clustering methods.

Source

http://expression.microslu.washington.edu/expression/kayee/medvedovic2003/medvedovic_bioinf2003.html

References

Medvedovic M, Yeung KY and Bumgarner RE. 2004. Bayesian Mixture Model Based Clustering of Replicated Microarray Data. Bioinformatics, 22;20(8):1222-32. Ideker, T., Thorsson, V., Siegel, A. and Hood, L. Testing for Differentially-Expressed Genes by Maximum-Likelihood Analysis of DNA Microarray Data. Journal of Computational Biology 7: 805-817 (2000).

Examples

```
data(gal_all)
## maybe str(gal_all) ; plot(gal_all) ...
```

---

permutest *Permutation Test P-value for Multivaraite Correlation*

Description

This function calculates p-values of the multivariate correlation estimator by enumerating all permutations. We recommend using Likehood Ratio Test implemented in function cor.LRtest if your data has moderate to large sample size (>5) The procedure is same as those permutation tests for Pearson correlation coefficient or other parameters. Since the approximation of null distribution requires enumerating all permutations. The computational burden increases in n^2.

Usage

```
permutest(x, y=NULL, m, G)
```

Arguments

x	data matrix, column represents samples (conditions), and row represents variables (genes), see example below for format information
y	optional, used when x and y are vectors
m	number of replicates
G	number of genes

Details

See manuscript.

Value

PV	P-values of permutation tests

Author(s)

Dongxiao Zhu and Youjuan Li

References

Zhu, D and Li Y. 2007. Multivariate Correlation Estimator for Inferring Functional Relationships from Replicated 'OMICS' data. Submitted.

See Also

cor.LRtest, cor.LRtest.std, cor.test

Examples

```
library("CORREP")
library("e1071")
d0 <- NULL
## sample size is set to 5, it takes about a min to finish
for(l in 1:5)
d0 <- rbind(d0, rnorm(100))
## data must have row variance of 1
d0.std <- apply(d0, 2, function(x) x/sd(x))
M <- cor.balance(t(d0.std), m = 4, G= 25)
M.pv <- permutest(t(d0.std), m = 4, G= 25)
```

---

true.member	*The Pre-defined Class Memberships of 205 Genes According to GO Annotation*

Description

The four classes are: Biosynthesis; Energy pathways; Nucleobase and Transport It is used as true clusters (external knowledge) to compare performance of different clustering methods.

Usage

```
data(true.member)
```

Source

http://expression.microslu.washington.edu/expression/kayee/medvedovic2003/medvedovic_bioinf2003.html

References

Medvedovic M, Yeung KY and Bumgarner RE. 2004. Bayesian Mixture Model Based Clustering of Replicated Microarray Data. Bioinformatics, 22;20(8):1222-32.

Examples

```
data(true.member)
## maybe str(true.member) ; plot(true.member) ...
```

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