Package 'Docovt'

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Title Distributed Online Covariance Matrix Tests

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Description Distributed Online Covariance Matrix Tests 'Docovt' is a powerful tool designed to efficiently process and analyze distributed datasets. It enables users to perform covariance matrix tests in an online, distributed manner, making it highly suitable for large-scale data analysis. By leveraging advanced computational techniques, 'Docovt' ensures robust and scalable solutions for statistical analysis, particularly in scenarios where data is dispersed across multiple nodes or sources. This package is ideal for researchers and practitioners working with high-dimensional data, providing a flexible and efficient framework for covariance matrix estimation and hypothesis testing. The philosophy of 'Docovt' is described in Guo G. (2025) <doi:10.1016/j.physa.2024.130308>.

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`chr1qseg` *chr1qseg*

Description

Copy number probes from TCGA at 400 locations on chromosome 1q. The dataset is stored as a list with two groups of observations, `X` and `Y`, together with the genomic locations of the probes and a short description.

Usage

```
data(chr1qseg)
```

Format

'chr1qseg' A list with 4 components:

X A numeric matrix with 92 rows and 400 columns, representing one group of samples.

Y A numeric matrix with 138 rows and 400 columns, representing the other group of samples.

loc A numeric vector of length 400 giving the genomic locations (number of base pairs from the end of the chromosome) of the probes.

description A character string describing the dataset.

Source

Copy number probes from TCGA (The Cancer Genome Atlas).

Examples

```
data(chr1qseg)
str(chr1qseg, max.level = 1)
dim(chr1qseg$X)
dim(chr1qseg$Y)
```

CLX *Two-Sample Covariance Test by Cai, Liu and Xia (2013)*

Description

Given two sets of data matrices X and Y, where X is an n1 rows and p cols matrix and Y is an n2 rows and p cols matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is:

$$H_0 : \Sigma_1 = \Sigma_2$$

Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. This test method is based on the test method proposed by Cai, Liu and Xia (2013). When the pval value is less than the significance coefficient (generally 0.05), the null hypothesis is rejected.

Usage

```
CLX(X,Y,alpha)
```

Arguments

X	A matrix of n1 by p
Y	A matrix of n2 by p
alpha	Significance level

Value

stat	a test statistic value.
pval	a test p_value.
power	a test power value.
FDR	a test FDR value.

References

Cai, T. T., Liu, W., and Xia, Y. (2013). Two-sample covariance matrix testing and support recovery in high-dimensional and sparse settings. Journal of the American Statistical Association, 108(501):265-277.

Guo, G., Wang, Q., Allison, J., & Qian, G. (2025). Accelerated distributed expectation-maximization algorithms for the parameter estimation in multivariate Gaussian mixture models. *Applied Mathematical Modelling*, 137, 115709.

Examples

```
## generate X and Y.
p= 500;  n1 = 100; n2 = 150
X=matrix(rnorm(n1*p), ncol=p)
Y=matrix(rnorm(n2*p), ncol=p)
## run test
CLX(X,Y,alpha=0.05)
```

---

cm13 *One-Sample Covariance Test by Cai and Ma (2013)*

Description

Performs a one-sample covariance matrix test based on the procedure proposed by Cai and Ma (2013).

Usage

```
cm13(X, Sigma0, alpha)
```

Arguments

X	An $n \times p$ numeric data matrix. Each row represents an observation.
Sigma0	A specified $p \times p$ covariance matrix.
alpha	The significance level.

Details

The null hypothesis is

$$H_0 : \Sigma = \Sigma_0$$

where Σ denotes the population covariance matrix and Σ_0 denotes the hypothesized covariance matrix.

Value

A named list containing:

statistic The calculated test statistic.

threshold The critical value for rejection.

reject A logical value indicating whether the null hypothesis is rejected.

Examples

```
set.seed(123)
n <- 30
p <- 5
X <- matrix(rnorm(n * p), nrow = n)
Sigma0 <- diag(p)
cm13(X, Sigma0, alpha = 0.05)
```

`cmtwo` *Two-Sample Covariance Test by Cai and Ma (2013)*

Description

Given two sets of data, it performs 2-sample test for equality of covariance matrices where the null hypothesis is

$$H_0 : \Sigma_1 = \Sigma_2$$

where Σ_1 and Σ_2 represent true (unknown) covariance for each dataset based on a procedure proposed by Cai and Ma (2013). If `statistic` $>$ `threshold`, it rejects null hypothesis.

Usage

```
cmtwo(X, Y, alpha)
```

Arguments

`X`	an $(m \times p)$ matrix where each row is an observation from the first dataset.
`Y`	an $(n \times p)$ matrix where each row is an observation from the second dataset.
`alpha`	level of significance.

Value

a named list containing

statistic a test statistic value.

threshold rejection criterion to be compared against test statistic.

reject a logical; `TRUE` to reject null hypothesis, `FALSE` otherwise.

References

Guo, G., Qian, G., & Zhu, L. (2022). A scalable quasi-newton estimation algorithm for dynamic generalized linear models. *Journal of Nonparametric Statistics*, 34, 917-939. doi:10.1080/10485252.2022.2085263.

Guo, G., & Zhao, W. (2021). Schwarz method for financial engineering. *Journal of Computational Mathematics*, 39(4), 538-555.

You, W., Yang, Z., Guo, G., Wan, X.-F., & Ji, G. (2019). Prediction of DNA-binding proteins by interaction fusion feature representation and selective ensemble. *Knowledge-Based Systems*, 163, 598-610.

Examples

```
## generate 2 datasets from multivariate normal with identical covariance.
p= 5;  n1 = 100; n2 = 150; alpha=0.05
X=data1 = matrix(rnorm(n1*p), ncol=p)
Y=data2 = matrix(rnorm(n2*p), ncol=p)

# run test
cmtwo(X, Y, alpha)
```

`corneal` *corneal*

Description

This dataset was acquired during a keratoconus study, a collaborative project involving Ms.Nancy Tripoli and Dr.Kenneth L.Cohen of Department of Ophthalmology at the University of North Carolina, Chapel Hill. The fitted feature vectors for the complete corneal surface dataset collectively into a feature matrix with dimensions of 150 x 2000.

Usage

```
data(corneal)
```

Format

'corneal' A data frame with 150 observations on the following 4 groups.

normal group1 row 1 to row 43 in total 43 rows of the feature matrix correspond to observations from the normal group

unilateral suspect group2 row 44 to row 57 in total 14 rows of the feature matrix correspond to observations from the unilateral suspect group

suspect map group3 row 58 to row 78 in total 21 of the feature matrix correspond to observations from the suspect map group

clinical keratoconus group4 row 79 to row 150 in total 72 of the feature matrix correspond to observations from the clinical keratoconus group

References

Smaga Ł (2019). "Linear hypothesis testing with applications." *Journal Name*, **1**(1), 1–10.

Examples

```
data(corneal)
dim(corneal)
group1 <- as.matrix(corneal[1:43, ]) ## normal group
dim(group1)
group2 <- as.matrix(corneal[44:57, ]) ## unilateral suspect group
dim(group2)
```

```
group3 <- as.matrix(corneal[58:78, ]) ## suspect map group
dim(group3)
group4 <- as.matrix(corneal[79:150, ]) ## clinical keratoconus group
dim(group4)
```

COVID19 *COVID19*

Description

A COVID19 data set from NCBI with ID GSE152641. The data set profiled peripheral blood from 24 healthy controls and 62 prospectively enrolled patients with community-acquired lower respiratory tract infection by SARS-COV-2 within the first 24 hours of hospital admission using RNA sequencing.

Usage

```
data(COVID19)
```

Format

'COVID19' A data frame with 86 observations on the following 2 groups.

healthy group1 row 2 to row 19, and row 82 to 87, in total 24 healthy controls

patients group2 row 20 to 81, in total 62 prospectively enrolled patients

References

Thair SA, others (2021). "Transcriptomic analysis." *Journal Name*, **1**(1), 1–10.

Examples

```
data(COVID19)
dim(COVID19)
group1 <- as.matrix(COVID19[c(2:19, 82:87), ]) ## healthy group
dim(group1)
group2 <- as.matrix(COVID19[-c(1:19, 82:87), ]) ## COVID-19 patients
dim(group2)
```

DCLX *Distributed Two-Sample Covariance Matrix Testing (CLX Method)*

Description

Given two sets of data matrices X and Y, where X is an $n_1 \times p$ matrix and Y is an $n_2 \times p$ matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is

$$H_0 : \Sigma_1 = \Sigma_2,$$

where Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. The test is based on the method proposed by Cai, Liu and Xia (2013). When the p-value is less than the significance level (generally 0.05), the null hypothesis is rejected.

Usage

```
DCLX(X, Y, K, alpha = 0.05)
```

Arguments

X	A numeric matrix of dimension $n_1 \times p$.
Y	A numeric matrix of dimension $n_2 \times p$.
K	Integer, number of blocks.
alpha	Numeric, significance level. Default is 0.05.

Value

A list with components:

stat	the test statistic.
pval	the p-value.
power	the estimated power.
fdr	the estimated false discovery rate.
Xopt	the selected block of X.
Yopt	the selected block of Y.

References

Cai, T. T., Liu, W., and Xia, Y. (2013). Two-sample covariance matrix testing and support recovery in high-dimensional settings. *Journal of the American Statistical Association*, 108(501), 265–277.

Examples

```
## Not run:
## generate data from multivariate normal with trivial covariance
p  <- 500
n1 <- 100
n2 <- 150
K  <- 10
X <- matrix(rnorm(n1 * p), ncol = p)
Y <- matrix(rnorm(n2 * p), ncol = p)
## run test
DCLX(X, Y, K)

## End(Not run)
```

DLC *Distributed Two-Sample Covariance Matrix Testing (LC Method)*

Description

Given two sets of data matrices `X` and `Y`, where `X` is an $n_1 \times p$ matrix and `Y` is an $n_2 \times p$ matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is

$$H_0 : \Sigma_1 = \Sigma_2,$$

where Σ_1 and Σ_2 are the sample covariance matrices of `X` and `Y` respectively. The test is based on the method proposed by Li and Chen (2012). When the p-value is less than the significance level (generally 0.05), the null hypothesis is rejected.

Usage

```
DLC(X, Y, K, alpha = 0.05)
```

Arguments

`X`	A numeric matrix of dimension $n_1 \times p$.
`Y`	A numeric matrix of dimension $n_2 \times p$.
`K`	Integer, number of blocks.
`alpha`	Numeric, significance level. Default is 0.05.

Value

A list with components:

`stat`	the test statistic.
`pval`	the p-value.
`power`	the estimated power.
`fdr`	the estimated false discovery rate.
`Xopt`	the selected block of `X`.
`Yopt`	the selected block of `Y`.

Examples

```
## Not run:
## generate data from multivariate normal with trivial covariance
p  <- 500
n1 <- 100
n2 <- 150
K  <- 10
X <- matrix(rnorm(n1 * p), ncol = p)
Y <- matrix(rnorm(n2 * p), ncol = p)
## run test
DLC(X, Y, K)

## End(Not run)
```

DPEC *Distributed Two-Sample Covariance Matrix Testing (Cauchy Combination)*

Description

Given two sets of data matrices `X` and `Y`, where `X` is an $n_1 \times p$ matrix and `Y` is an $n_2 \times p$ matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is

$$H_0 : \Sigma_1 = \Sigma_2,$$

where Σ_1 and Σ_2 are the sample covariance matrices of `X` and `Y` respectively. The test is based on the method proposed by Yu, Li and Xue (2022). When the p-value is less than the significance level (generally 0.05), the null hypothesis is rejected.

Usage

```
DPEC(X, Y, K, alpha = 0.05)
```

Arguments

`X`	A numeric matrix of dimension $n_1 \times p$.
`Y`	A numeric matrix of dimension $n_2 \times p$.
`K`	Integer, number of blocks.
`alpha`	Numeric, significance level. Default is 0.05.

Value

A list with components:

`stat`	the test statistic.
`pval`	the p-value.

power	the estimated power.
fdr	the estimated false discovery rate.
Xopt	the selected block of X.
Yopt	the selected block of Y.

Examples

```
## Not run:
## generate data from multivariate normal with trivial covariance
p  <- 500
n1 <- 100
n2 <- 150
K  <- 10
X <- matrix(rnorm(n1 * p), ncol = p)
Y <- matrix(rnorm(n2 * p), ncol = p)
## run test
DPEC(X, Y, K)

## End(Not run)
```

DPECO *Distributed Two-Sample Covariance Matrix Testing (PE Combination)*

Description

Given two sets of data matrices X and Y, where X is an $n_1 \times p$ matrix and Y is an $n_2 \times p$ matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is

$$H_0 : \Sigma_1 = \Sigma_2,$$

where Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. The test is based on the method proposed by Yu, Li, Xue and Li (2022). When the p-value is less than the significance level (generally 0.05), the null hypothesis is rejected.

Usage

```
DPECO(X, Y, delta = NULL, K, alpha = 0.05)
```

Arguments

X	A numeric matrix of dimension $n_1 \times p$.
Y	A numeric matrix of dimension $n_2 \times p$.
delta	Numeric scalar, threshold for building PE components. Default is NULL, in which case `4 * log(log(nk + nk)) * log(p)` is used.
K	Integer, number of blocks.
alpha	Numeric, significance level. Default is 0.05.

Value

A list with components:

stat	the test statistic.
pval	the p-value.
power	the estimated power.
fdr	the estimated false discovery rate.
Xopt	the selected block of X.
Yopt	the selected block of Y.

Examples

```
## Not run:
## generate data from multivariate normal with trivial covariance
p  <- 500
n1 <- 100
n2 <- 150
K  <- 10
X <- matrix(rnorm(n1 * p), ncol = p)
Y <- matrix(rnorm(n2 * p), ncol = p)
## run test
DPECO(X, Y, K)

## End(Not run)
```

DPEF *Distributed Two-Sample Covariance Matrix Testing (Fisher Combination)*

Description

Given two sets of data matrices X and Y, where X is an $n_1 \times p$ matrix and Y is an $n_2 \times p$ matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is

$$H_0 : \Sigma_1 = \Sigma_2,$$

where Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. The test is based on the method proposed by Yu, Li and Xue (2022). When the p-value is less than the significance level (generally 0.05), the null hypothesis is rejected.

Usage

```
DPEF(X, Y, K, alpha = 0.05)
```

Arguments

X	A numeric matrix of dimension $n_1 \times p$.
Y	A numeric matrix of dimension $n_2 \times p$.
K	Integer, number of blocks.
alpha	Numeric, significance level. Default is 0.05.

Value

A list with components:

stat	the test statistic.
pval	the p-value.
power	the estimated power.
fdr	the estimated false discovery rate.
Xopt	the selected block of X.
Yopt	the selected block of Y.

Examples

```
## Not run:
## generate data from multivariate normal with trivial covariance
p  <- 500
n1 <- 100
n2 <- 150
K  <- 10
X <- matrix(rnorm(n1 * p), ncol = p)
Y <- matrix(rnorm(n2 * p), ncol = p)
## run test
DPEF(X, Y, K)

## End(Not run)
```

DSNET *Distributed Two-Sample Covariance Matrix Testing*

Description

A fast experimental distributed variance-comparison test. The samples are divided into K non-overlapping blocks. Block summaries are aggregated to construct a global variance-difference statistic. The p-value is obtained by permutation calibration.

This is an experimental alternative, not the original SNET statistic from the thesis.

Usage

```
DSNET(X, Y, K, B = 20, mc.cores = 1L, k = 3, alpha = 0.05, P = 99)
```

Arguments

X	Numeric matrix of n1 by p.
Y	Numeric matrix of n2 by p.
K	Number of blocks.
B	Retained for compatibility with existing scripts.
mc.cores	Retained for compatibility.
k	Retained for compatibility.
alpha	Significance level.
P	Number of permutations.

Value

A list containing stat, pval, power, fdr, Xopt and Yopt.

LC *Two-Sample Covariance Test by Li and Chen (2012)*

Description

Given two sets of data matrices X and Y, where X is an n1 rows and p cols matrix and Y is an n2 rows and p cols matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is:

$$H_0 : \Sigma_1 = \Sigma_2$$

Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. This test method is based on the test method proposed by Li and Chen (2012). When the pval value is less than the significance coefficient (generally 0.05), the null hypothesis is rejected.

Usage

```
LC(X,Y,delta_sigma = NULL,alpha)
```

Arguments

X	A matrix of n1 by p
Y	A matrix of n2 by p
delta_sigma	A positive definite matrix
alpha	Significance level

Value

stat	a test statistic value.
pval	a test p_value.
power	a test power value.
FDR	a test FDR value.

References

Li, J. and Chen, S. X. (2012). Two sample tests for high-dimensional covariance matrices. The Annals of Statistics, 40(2):908-940.

Zhang, C., & Guo, G. (2025). The optimal subset estimation of distributed redundant data. *IAENG International Journal of Applied Mathematics*, 55(2), 270–277.

Examples

```
## generate X and Y.
p= 500;  n1 = 100; n2 = 150
X=matrix(rnorm(n1*p), ncol=p)
Y=matrix(rnorm(n2*p), ncol=p)
## run test
LC(X,Y,alpha=0.05)
```

`miRNA` *miRNA*

Description

A three factor level variable corresponding to cancer type

Usage

```
data(miRNA)
```

Format

Dataframe with 21 samples and 537 variables

columns variables

rows samples

Examples

```
data(miRNA)
```

PEC *Two-Sample Covariance Test by Yu, Li and Xue (2022)*

Description

Given two sets of data matrices X and Y, where X is an n1 rows and p cols matrix and Y is an n2 rows and p cols matrix,, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is:

$$H_0 : \Sigma_1 = \Sigma_2$$

Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. This test method is based on the test method proposed by Yu, Li and Xue (2022). When the pval value is less than the significance coefficient (generally 0.05), the null hypothesis is rejected.

Usage

```
PEC(X,Y,alpha)
```

Arguments

X	A matrix of n1 by p
Y	A matrix of n2 by p
alpha	Significance level

Value

stat	a test statistic value.
pval	a test p_value.
power	a test power value.
FDR	a test FDR value.

References

Yu, X., Li, D., and Xue, L. (2022). Fisher's combined probability test for high-dimensional covariance matrices. Journal of the American Statistical Association, (in press):1-14.

Liu, S., & Guo, G. (2025). Sparse online principal component for Laplace factor models. *IAENG International Journal of Applied Mathematics*, 55(6), 1588–1592.

Examples

```
## generate X and Y.
p= 500;  n1 = 100; n2 = 150
X=matrix(rnorm(n1*p), ncol=p)
Y=matrix(rnorm(n2*p), ncol=p)
## run test
PEC(X,Y,alpha=0.05)
```

PECO *Two-Sample Covariance Test by Yu, Li, Xue and Li(2022)*

Description

Given two sets of data matrices X and Y, where X is an n1 rows and p cols matrix and Y is an n2 rows and p cols matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is:

$$H_0 : \Sigma_1 = \Sigma_2$$

Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. This test method is based on the test method proposed by Yu, Li, Xue and Li (2022). When the pval value is less than the significance coefficient (generally 0.05), the null hypothesis is rejected.

Usage

```
PECO(X,Y,delta = NULL,alpha)
```

Arguments

X	A matrix of n1 by p
Y	A matrix of n2 by p
alpha	Significance level
delta	A scalar used as the threshold for building PE components, usually the default value

Value

stat	a test statistic value.
pval	a test p_value.
power	a test power value.
FDR	a test FDR value.

References

Yu, X., Li, D., Xue, L., and Li, R. (2022). Power-enhanced simultaneous test of high-dimensional mean vectors and covariance matrices with application to gene-set testing. Journal of the American Statistical Association, (in press):1-14.

Jin, Y., Chang, D., & Guo, G. (2025). Sparse online principal component for skew factor model. *IAENG International Journal of Computer Science*, 52(9), 3429–3434.

Examples

```
## generate X and Y.
p= 500;  n1 = 100; n2 = 150
X=matrix(rnorm(n1*p), ncol=p)
Y=matrix(rnorm(n2*p), ncol=p)
## run test
PECO(X,Y,alpha=0.05)
```

PEF *Two-Sample Covariance Test by Yu, Li and Xue (2022)*

Description

Given two sets of data matrices X and Y, where X is an n1 rows and p cols matrix and Y is an n2 rows and p cols matrix,, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is:

$$H_0 : \Sigma_1 = \Sigma_2$$

Σ_1 and Σ_2 are the sample covariance matrices of X and Y respectively. This test method is based on the test method proposed by Yu, Li and Xue (2022). When the pval value is less than the significance coefficient (generally 0.05), the null hypothesis is rejected.

Usage

```
PEF(X,Y,alpha)
```

Arguments

X	A matrix of n1 by p
Y	A matrix of n2 by p
alpha	Significance level

Value

stat	a test statistic value.
pval	a test p_value.
power	a test power value.
FDR	a test FDR value.

References

Yu, X., Li, D., and Xue, L. (2022). Fisher's combined probability test for high-dimensional covariance matrices. Journal of the American Statistical Association, (in press):1-14.

Guo, G., Song, H., & Zhu, L. (2024). The COR criterion for optimal subset selection in distributed estimation. *Statistics and Computing*, 34, 163-176.

Examples

```
## generate X and Y.
p= 500;  n1 = 100; n2 = 150
X=matrix(rnorm(n1*p), ncol=p)
Y=matrix(rnorm(n2*p), ncol=p)
## run test
PEF(X,Y,alpha=0.05)
```

SNET *Two-Sample Covariance Test*

Description

Given two sets of data matrices `X` and `Y`, where `X` is an $n_1 \times p$ matrix and `Y` is an $n_2 \times p$ matrix, we conduct hypothesis testing of the covariance matrix between two samples. The null hypothesis is

$$H_0 : \Sigma_1 = \Sigma_2,$$

where Σ_1 and Σ_2 are the sample covariance matrices of `X` and `Y` respectively. The test is based on the method proposed by Cai, Liu and Xia (2013). When the p-value is less than the significance level (generally 0.05), the null hypothesis is rejected.

Usage

```
SNET(X, Y, B = 200, mc.cores = 1L, alpha = 0.05, k = 3)
```

Arguments

`X`	A numeric matrix of dimension $n_1 \times p$.
`Y`	A numeric matrix of dimension $n_2 \times p$.
`B`	Integer, number of bootstrap replicates. Default is 200.
`mc.cores`	Integer, number of cores for parallel computing. Default is 1 (serial execution).
`alpha`	Numeric, significance level. Default is 0.05.
`k`	Numeric, tuning parameter. Default is 3.

Value

A list with components:

`stat`	the test statistic.
`pval`	the p-value.
`z`	the standardized test statistic.

References

Cai, T. T., Liu, W., and Xia, Y. (2013). Two-sample covariance matrix testing and support recovery in high-dimensional settings. *Journal of the American Statistical Association*, 108(501), 265–277.

Examples

```
## Not run:
## generate data from multivariate normal with trivial covariance
p  <- 500
n1 <- 100
n2 <- 150
B  <- 300
X <- matrix(rnorm(n1 * p), ncol = p)
Y <- matrix(rnorm(n2 * p), ncol = p)
## run test
SNET(X, Y, B, alpha = 0.05)

## End(Not run)
```

---

syk *One Sample Covariance Test by Srivastava, Yanagihara, and Kubokawa (2014)*

Description

Given data, it performs 1-sample test for Covariance where the null hypothesis is

$$H_0 : \Sigma_n = \Sigma_0$$

where Σ_n is the covariance of data model and Σ_0 is a hypothesized covariance based on a procedure proposed by Srivastava, Yanagihara, and Kubokawa (2014).

Usage

```
syk(data, Sigma0, alpha)
```

Arguments

data	an $(n \times p)$ data matrix where each row is an observation.
Sigma0	a $(p \times p)$ given covariance matrix.
alpha	level of significance.

Value

a named list containing

statistic a test statistic value.

threshold rejection criterion to be compared against test statistic.

reject a logical; TRUE to reject null hypothesis, FALSE otherwise.

Examples

```
## Not run:
## generate data from multivariate normal with trivial covariance.
p = 5;n=10
data = matrix(rnorm(n*p), ncol=p)
 alpha=0.05
Sigma0=diag(ncol(data))
 run the test
syk(data, Sigma0, alpha)

## End(Not run)
```

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