Package ‘BalanceCheck’

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Title Balance Check for Multiple Covariates in Matched Observational Studies
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BalanceCheck

Balance Check for Multiple Covariates in Matched Observational Studies

Description

This package includes two tests for assessing whether multiple covariates in a treatment group and a matched control group are balanced in observational studies.

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References


See Also

CrossMST, CrossNN

CrossMST

Covariate balance checking through the minimum spanning tree

Description

This function tests whether covariates in a treatment group and a matched control group are balanced in observational studies through the minimum spanning tree constructed on the subjects.

Usage

CrossMST(distM, treated.index, perm=0, k=1, discrete.correction=TRUE)

Arguments

distM        The distance matrix for the pooled observations (pooled over the treated subjects and the matched controls). If there are n treated subjects and n matched controls, then this distance matrix is a 2n by 2n matrix with the [i,j] element the distance between observation i and observation j. What distance to use is decided by users. Some simple choices are the Euclidean distance, L1 distance, and mahalanobis distance.
treated.index The subject indices of the treated subjects. The subjects are ordered in the same way as for calculating the distance matrix, distM.
perm

The number of permutations performed to calculate the p-value of the test. The default value is 0, which means the permutation is not performed and only approximate p-value based on asymptotic theory is provided. Doing permutation could be time consuming, so be cautious if you want to set this value to be larger than 10,000.

k

Set as positive integer values, indicates k-MST is used.

discrete.correction

When this is set as TRUE (recommended), a continuation correction is done for computing the asymptotic p-value to account for the discrete nature of the statistic.

Value

test.stat.Z

The standardized test statistic (ZR in the reference paper.
pval.appr

The approximated p-value based on asymptotic theory.
pval.perm

The permutation p-value when argument ‘perm’ is positive.

References


See Also

crossnn

Examples

## A snippet of the smoking example in the reference paper.
## smoking.rda contains a 300 by 300 distance matrix, smokingDist.
## The indices of the treated subjects are 1:150.
data(smoking)
CrossMST(smokingDist, 1:150)

## Uncomment the following line to get permutation p-value with 1,000 permutations.
# CrossMST(smokingDist, 1:150, perm=1000)

CrossNN

Covariate balance checking through the nearest neighbor graph

Description

This function tests whether covariates in a treatment group and a matched control group are balanced in observational studies through the nearest neighbor graph constructed on the subjects.

Usage

CrossNN(distM, treated.index, perm=0, k=1, discrete.correction=TRUE)
Arguments

distM The distance matrix for the pooled observations (pooled over the treated subjects and the matched controls). If there are n treated subjects and n matched controls, then this distance matrix is a 2n by 2n matrix with the [i,j] element the distance between observation i and observation j. What distance to use is decided by users. Some simple choices are the Euclidean distance, L1 distance, and mahalanobis distance.

treated.index The subject indices of the treated subjects. The subjects are ordered in the same way as for calculating the distance matrix, distM.

perm The number of permutations performed to calculate the p-value of the test. The default value is 0, which means the permutation is not performed and only approximate p-value based on asymptotic theory is provided. Doing permutation could be time consuming, so be cautious if you want to set this value to be larger than 10,000.

k Set as positive integer values, indicates k-NN is used.

discrete.correction When this is set as TRUE (recommended), a continuation correction is done for computing the asymptotic p-value to account for the discrete nature of the statistic.

Value

test.stat.Z The standardized test statistic (ZD in the reference paper.
pval.appr The approximated p-value based on asymptotic theory.
pval.perm The permutation p-value when argument ‘perm’ is positive.

See Also

CrossMST

Examples

```r
# A snippet of the smoking example in the reference paper.
# smoking.rda contains a 300 by 300 distance matrix, smokingDist.
# The indices of the treated subjects are 1:150.
data(smoking)
CrossNN(smokingDist, 1:150)

# Uncomment the following line to get permutation p-value with 1,000 permutations.
# CrossNN(smokingDist, 1:150, perm=1000)
```
**getD**

*Get intermediate results for CrossNN*

**Description**

This function calculates D11 and D22 for the CrossNN test.

**Usage**

getD(distM, treated.index)

**Arguments**

- **distM**: The distance matrix for the pooled observations (pooled over the treated subjects and the matched controls). If there are n treated subjects and n matched controls, then this distance matrix is a 2n by 2n matrix with the [i,j] element the distance between observation i and observation j. What distance to use is decided by users. Some simple choices are the Euclidean distance, L1 distance, and mahalanobis distance.

- **treated.index**: The subject indices of the treated subjects. The subjects are ordered in the same way as for calculating the distance matrix, distM.

**See Also**

CrossNN

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**getDk**

*Get intermediate results for CrossNN under k-NN*

**Description**

This function calculates D11 and D22 for the CrossNN test when k-NN (k>1) is used.

**Usage**

getDk(distM, treated.index, k)

**Arguments**

- **distM**: The distance matrix for the pooled observations (pooled over the treated subjects and the matched controls). If there are n treated subjects and n matched controls, then this distance matrix is a 2n by 2n matrix with the [i,j] element the distance between observation i and observation j. What distance to use is decided by users. Some simple choices are the Euclidean distance, L1 distance, and mahalanobis distance.
treated.index  The subject indices of the treated subjects. The subjects are ordered in the same way as for calculating the distance matrix, distM.

k  An integer larger than 1.

See Also

CrossNN

getR1R2  Get intermediate results for CrossMST

Description

This function calculates R1 and R2 for the CrossMST test.

Usage

getR1R2(E,treated.index)

Arguments

E  A matrix with the number of rows the number of edges in the MST and 2 columns. Each row records the subject indices of the two ends of an edge in the MST.

treated.index  The subject indices of the treated subjects.

See Also

CrossMST

smokingDist  The distance matrix of the smoking data

Description

This is a 300 by 300 distance matrix with the indices of the treated subjects 1:150 and the indices of the matched controls 151:300. These treated subjects and matched controls are a subset of the original dataset used in the reference paper with 679 treated subjects and 679 matched controls.
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