Package ‘maicChecks’

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Type Package

Title Assessing the Numerical Feasibility for Conducting a
Matching-Adjusted Indirect Comparison (MAIC)

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Description A collection of easy-to-implement tools for checking whether a MAIC can be conducted. An alternative way of calculating weights is also included. These methods are introduced in Glimm & Yau (2021) <arXiv:2108.01896>.

Depends R (>= 3.5.0)

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eAD

Example AD data

Description
Example AD data

Usage

data("eAD")

Format
A data frame with 3 observations on the following 3 variables.

- **scen** corresponds to scenarios A, B, and C in the reference manuscript (Glimm & Yau (2021)).
  - Scenario A is very close to IPD center (see data(ipd)) and is within the IPD convex hull;
  - scenario B is further away from IPD center but otherwise still inside the IPD convex hull;
  - scenario C is outside IPD convex hull.

- **y1** a numeric vector
- **y2** a numeric vector

References

Examples

print(eAD)

eIPD

Example ipd set

Description
Example ipd data

Usage

data("eIPD")
maicLP

Format
A data frame with 42 observations on the following 2 variables. The illustrative example used in the reference manuscript (Glimm & Yau (2021)).

y1 a numeric vector
y2 a numeric vector

References


Examples

head(eIPD)

________________________________________________________________________

maicLP Checks if AD is within the convex hull of IPD using lp-solve

Description

Checks if AD is within the convex hull of IPD using lp-solve

Usage

maicLP(ipd, ad)

Arguments

ipd a dataframe with n row and p coln, where n is number of subjects and p is the number of variables used in matching.
ad a dataframe with 1 row and p coln. The matching variables should be in the same order as that in ipd. The function does not check this.

Value

lp.check 0 = AD is inside IPD, and MAIC can be conducted; 2 = otherwise

Author(s)

Lillian Yau

References

Examples

```r
## eAD[1,] is the scenario A in the reference paper, i.e. when AD is within IPD convex hull
maicLP(eIPD, eAD[1,2:3])

## eAD[3,] is the scenario C in the reference paper, i.e. when AD is outside IPD convex hull
maicLP(eIPD, eAD[3,2:3])
```

**maicMD**  
Checks if AD is within the convex hull of IPD using Mahalanobis distance

**Description**

Should only be used when all matching variables are normally distributed

**Usage**

```r
maicMD(ipd, ad, n.ad = Inf)
```

**Arguments**

- `ipd`: a dataframe with n row and p coln, where n is number of subjects and p is the number of variables used in matching.
- `ad`: a dataframe with 1 row and p coln. The matching variables should be in the same order as that in ipd. The function does not check this.
- `n.ad`: default is NULL assuming ad is a fixed (known) quantity with infinit accuracy. In most MAIC applications ad is only the sample statistics and n.ad is known.

**Details**

When AD does not have the largest Mahalanobis distance, in the original scale AD can still be outside of the IPD convex hull. On the other hand, when AD does have the largest Mahalanobis distance, in the original scale, AD is for sure outside the IPD convex hull.

**Value**

Prints a message whether AD is furthest away from 0, i.e. IPD center in terms of Mahalanobis distance. Also returns ggplot object for plotting.

- `md.dplot`: dot-plot of AD and IPD in Mahalanobis distance
- `md.check`: 0 = AD has the largest Mahalanobis distance to the IPD center; 2 = otherwise

**Author(s)**

Lillian Yau
References


Examples

```
## eAD[,1] is the scenario A in the reference paper, 
## i.e. when AD is perfectly within IPD
md <- maicMD(eIPD, eAD[,2:3])
md ## a dot-plot of IPD Mahalanobis distances along with AD in the same metric.
```

```
maicPCA

Checks whether AD is outside IPD in PC coordinates

Description

Checks whether AD is outside IPD in principal component (PC) coordinates

Usage

maicPCA(ipd, ad)

Arguments

  ipd          a dataframe with n row and p coln, where n is number of subjects in IPD set and p is the number of variables used in matching.
  ad           a dataframe with 1 row and p coln. The matching variables should be in the same order as that in ipd. The function does not check this.

Details

When AD is within the IPD PC ranges, AD can still be outside the IPD convex hull in the original scale. On the other hand, if AD is outside the IPD PC ranges, in the original scale AD is for sure outside the IPD convex hull.

Value

Prints a message whether AD is inside or outside IPD PC coordinates. Also returns a ggplot object to be plotted.

  pc.dplot     dot-plot of AD and IPD both in IPD’s PC coordinates
  pca.check    0 = AD within the ranges of IPD’s PC coordinates; 2 = otherwise

Author(s)

Lillian Yau
References


Examples

```r
## eAD[1,] is the scenario A in the reference paper,
## i.e. when AD is perfectly within IPD
a1 <- maicPCA(eIPD, eAD[1,2:3])
a1 ## the dot plots of PC's for IPD and AD

## eAD[3,] is the scenario C in the reference paper,
## i.e. when AD is outside IPD
a3 <- maicPCA(eIPD, eAD[3,2:3])
a3 ## the dot plots of PC's for IPD and AD
```

---

### `maicT2Test`

*Hotelling’s T-square test to check whether maic is needed*

**Description**

Conducts Hotelling’s T-square test

**Usage**

```r
maicT2Test(ipd, ad, n.ad = Inf)
```

**Arguments**

- `ipd`: a dataframe with `n` row and `p` coln, where `n` is number of subjects and `p` is the number of variables used in matching.
- `ad`: a dataframe with 1 row and `p` coln. The matching variables should be in the same order as that in `ipd`. The function does not check this.
- `n.ad`: default is Inf assuming `ad` is a fixed (known) quantity with infinit accuracy. In most MAIC applications `ad` is the sample statistics and `n.ad` is known.

**Details**

When `n.ad` is not Inf, the covariance matrix is adjusted by the factor `n.ad/(n.ipd + n.ad)`, where `n.ipd` is `nrow(ipd)`, the sample size of `ipd`.

**Value**

- `T_sq.f`: the value of the $T^2$ test statistic
- `p.val`: the p-value corresponding to the test statistic. When the p-value is small, matching is necessary.
Author(s)
Lillian Yau & Ekkehard Glimm

References

Examples
```r
## eAD[1,] is the scenario A in the reference paper,
## i.e. when AD is perfectly within IPD
maicT2Test(eIPD, eAD[1:2:3])
```

---

**maicWt**  
Estimates the MAIC weights

### Description
Estimates the MAIC weights for each individual in the IPD. Should only be used after it is ascertained that AD is indeed within the convex hull of IPD.

### Usage
```r
maicWt(ipd, ad, max.it = 25)
```

### Arguments
- **ipd**: a dataframe with n row and p coln, where n is number of subjects and p is the number of variables used in matching.
- **ad**: a dataframe with 1 row and p coln. The matching variables should be in the same order as that in ipd. The function does not check this.
- **max.it**: maximum iteration passed to optim(). if ad is within ipd convex hull, then the default 25 iterations of optim() should be enough.

### Details
The main code are taken from Philippo (2016). It returns the following:

### Value
- **optim.out**: results of optim()
- **maic.wt**: MAIC un-scaled weights for each subject in the IPD set
- **maic.wt.rs**: re-scaled weights which add up to the original total sample size, i.e. nrow(ipd)
- **ipd.ess**: effective sample size
- **ipd.wtsumm**: weighted summary statistics of the matching variables after matching. they should be identical to the input AD when AD is within the IPD convex hull.
maxessWt

Description

Estimates an alternative set of weights which maximizes effective sample size (ESS) for a given set of variates used in the matching. Should only be used after it is ascertained that AD is indeed within the convex hull of IPD.

Usage

maxessWt(ipd, ad)

Arguments

ipd a dataframe with n row and p coln, where n is number of subjects and p is the number of variables used in matching.
ad a dataframe with 1 row and p coln. The matching variables should be in the same order as that in ipd. The function does not check this.

Details

The weights maximize the ESS subject to the set of baseline covariates used in the matching.

Value

maxess.wt maximum ESS weights. Scaled to sum up to the total IPD sample size, i.e. nrow(ipd)
ipd.ess effective sample size. It is no smaller than the ESS given by the MAIC weights.
ipd.wtsumm weighted summary statistics of the matching variables after matching. they should be identical to the input AD when AD is within the IPD convex hull.

Author(s)

Lillian Yau
References


Examples

```r
## eAD[1,] is scenario A in the reference manuscript
m0 <- maxessWt(eIPD, eAD[1,2:3])
```
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