Package: maicChecks (via r-universe)

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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)

Imports data.table, tidyr, ggplot2, lpSolve, quadprog

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Contents

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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

Glimm & Yau (2021). Geometric approaches to assessing the numerical feasibility for conducting matching-adjusted indirect comparisons. arXiv 2108.01896.

Examples

```
print(eAD)
```

eIPD *Example ipd set*

Description

Example ipd data

Usage

```
data("eIPD")
```

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

Glimm & Yau (2021). Geometric approaches to assessing the numerical feasibility for conducting matching-adjusted indirect comparisons. arXiv 2108.01896.

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

Glimm & Yau (2021). Geometric approaches to assessing the numerical feasibility for conducting matching-adjusted indirect comparisons. arXiv 2108.01896.

Examples

```
## 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

```
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

Glimm & Yau (2021). Geometric approaches to assessing the numerical feasibility for conducting matching-adjusted indirect comparisons. arXiv 2108.01896.

Examples

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

Glimm & Yau (2021). Geometric approaches to assessing the numerical feasibility for conducting matching-adjusted indirect comparisons. arXiv 2108.01896.

Examples

```
## 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

```
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

Glimm & Yau (2021). Geometric approaches to assessing the numerical feasibility for conducting matching-adjusted indirect comparisons. arXiv 2108.01896.

Examples

```
## 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

```
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.

Author(s)

Lillian Yau

References

Phillippo DM, Ades AE, Dias S, et al. (2016). Methods for population-adjusted indirect comparisons in submissions to NICE. NICE Decision Support Unit Technical Support Document 18.

Examples

```
## eAD[1,] is scenario A in the reference manuscript
m1 <- maicWt(eIPD, eAD[1,2:3])
```

---

maxessWt *Maximum ESS Weights*

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

Glimm & Yau (2021). Geometric approaches to assessing the numerical feasibility for conducting matching-adjusted indirect comparisons. arXiv 2108.01896.

Examples

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

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