

Package ‘WMAP’

November 7, 2024

Title Weighted Meta-Analysis with Pseudo-Populations

Version 1.0.0

Description Implementation of integrative weighting approaches for multiple observational studies and causal inferences. The package features three weighting approaches, each representing a special case of the unified weighting framework, introduced by Guha and Li (2024) <[doi:10.1093/biomtc/ujae070](https://doi.org/10.1093/biomtc/ujae070)>, which includes an extension of inverse probability weights for data integration settings.

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.2

LazyData true

Imports pkgcond, ggplot2, zeallot, caret, randomForest, forcats, utils, stats, grDevices

Depends R (>= 3.5.0)

NeedsCompilation no

Author Subharup Guha [aut, cre],
Mengqi Xu [aut],
Kashish Priyam [aut],
Yi Li [aut]

Maintainer Subharup Guha <s.guha@ufl.edu>

Repository CRAN

Date/Publication 2024-11-07 18:40:02 UTC

Contents

balancing.weights	2
causal.estimate	3
demo	5
plot.causal_estimates	5
summary.balancing_weights	6
summary.causal_estimates	7

Index	8
--------------	----------

balancing.weights *Compute balancing weights using FLEXOR or other methods*

Description

This function calculates balancing weights based on the specified pseudo-population method.

Usage

```
balancing.weights(
  S,
  Z,
  X,
  method,
  naturalGroupProp,
  num.random = 40,
  gammaMin = 0.001,
  gammaMax = (1 - 0.001),
  seed = NULL,
  verbose = TRUE
)
```

Arguments

S	Vector of factor levels representing the study memberships. Takes values in {1, ..., J}.
Z	Vector of factor levels representing the group memberships. Takes values in {1, ..., K}.
X	Covariate matrix of N rows and p columns.
method	Pseudo-population method, i.e., weighting method. Take values in FLEXOR, IC, or IGO.
naturalGroupProp	Relevant only for FLEXOR method: a fixed user-specified probability vector θ .
num.random	Relevant only for FLEXOR method: number of random starting points of γ in the two-step iterative procedure. Default is 40.
gammaMin	Relevant only for FLEXOR method: Lower bound for each γ_s in the two-step iterative procedure. Default is 0.001.
gammaMax	Relevant only for FLEXOR method: Upper bound for each γ_s in the two-step iterative procedure. Default is 0.999.
seed	Seed for random number generation. Default is NULL.
verbose	Logical; Relevant only for FLEXOR method: if TRUE (default), displays progress messages during computation to the console. Set to FALSE to suppress these messages.

Value

An S3 list object with the following components:

wt.v N empirically normalized sample weights.

percentESS Percentage sample effective sample size (ESS) for the pseudo-population.

Examples

```
data(demo)
balancing.weights(S, Z, X, method = "IC", naturalGroupProp)
```

causal.estimate	<i>Estimate causal effects using FLEXOR or other methods</i>
-----------------	--

Description

This function estimates causal effects based on the specified pseudo-population method. The FLEXOR method involves an iterative two-step procedure.

Usage

```
causal.estimate(
  S,
  Z,
  X,
  Y,
  B = 100,
  method,
  naturalGroupProp = NULL,
  num.random = 40,
  gammaMin = 0.001,
  gammaMax = (1 - 0.001),
  seed = NULL,
  verbose = TRUE
)
```

Arguments

S	Vector of factor levels representing the study memberships. Takes values in {1, ..., J}.
Z	Vector of factor levels representing the group memberships. Takes values in {1, ..., K}.
X	Covariate matrix of N rows and p columns.
Y	Matrix of L outcomes, with dimensions $N \times L$.
B	Number of bootstrap samples for variance estimation. Default is 100.

method	Pseudo-population method, i.e., weighting method. Take values in FLEXOR, IC, or IGO.
naturalGroupProp	Relevant only for FLEXOR method: a fixed user-specified probability vector θ .
num.random	Relevant only for FLEXOR method: number of random starting points of γ in the two-step iterative procedure. Default is 40.
gammaMin	Relevant only for FLEXOR method: Lower bound for each γ_s in the two-step iterative procedure. Default is 0.001.
gammaMax	Relevant only for FLEXOR method: Upper bound for each γ_s in the two-step iterative procedure. Default is 0.999.
seed	Seed for random number generation. Default is NULL.
verbose	Logical; if TRUE (default), displays progress messages during computation to the console. Set to FALSE to suppress these messages.

Value

An S3 list object with the following components:

percentESS Percentage sample effective sample size (ESS) of the pseudo-population.

moments.ar An array of dimension $3 \times K \times L$, containing:

- Estimated means, standard deviations (SDs), and medians (dimension 1),
- For K groups (dimension 2),
- And L counterfactual outcomes (dimension 3).

otherFeatures.v Estimated mean group differences for L outcomes.

collatedMoments.ar An array of dimension $3 \times K \times L \times B$, containing:

- `moments.ar` of the b th bootstrap sample (dimensions 1–3),
- For B bootstrap samples (dimension 4).

collatedOtherFeatures.mt A matrix of dimension $L \times B$ containing:

- `otherFeatures.v` of the b th bootstrap sample (dimension 1),
- For B bootstrap samples (dimension 2).

collatedESS A vector of length B containing percentage sample ESS for B bootstrap samples.

method Pseudo-population method, i.e., weighting method.

Examples

```
data(demo)
set.seed(1)
causal.estimate(S, Z, X, Y, B = 5, method = "IC", naturalGroupProp)
```

demo

Demo Dataset

Description

A dataset containing example data for demonstration purposes.

Usage

```
data(demo)
```

Format

An rda object, with 450 observations and the following variables:

S A vector of factor levels, representing the study memberships.

Z A vector of factor levels, representing the group memberships.

X A covariate matrix.

Y An outcome matrix.

naturalGroupProp The relative group prevalences of the larger natural population. Necessary only for FLEXOR weights; it should be skipped for IC and IGO weights.

groupNames Disease subtype names "IDC" or "ILC"

Details

Demo Dataset

Examples

```
data(demo)
```

`plot.causal_estimates` *Plot method for objects of class 'causal_estimates'*

Description

Plot method for objects of class 'causal_estimates'

Usage

```
## S3 method for class 'causal_estimates'  
plot(x, ...)
```

Arguments

`x` An object of class 'causal_estimates'.
`...` Additional arguments including:
y_limit The y-axis range. Default is `c(0, 50)`.
color The boxplot color. Default is "red".

Value

A boxplot of percent sample ESS for a specific weighting method (FLEXOR, IC, or IGO)

```
summary.balancing_weights
```

Summary method for objects of class 'balancing_weights'

Description

Summary method for objects of class 'balancing_weights'

Usage

```
## S3 method for class 'balancing_weights'
summary(object, ...)
```

Arguments

`object` An object of class 'balancing_weights'
`...` Additional arguments affecting the summary produced (so far no additional arguments are needed, so leave blank).

Value

Printed summary of the 'balancing_weights' object, including:

Weight length The total number of weights.

Weight distribution Statistical summary of weight values.

percentESS Percentage sample effective sample size (ESS) for the pseudo-population.

Examples

```
data(demo)
output1 <- balancing_weights(S, Z, X, method = "IC", naturalGroupProp)
summary(output1)
```

`summary.causal_estimates`*Summary method for objects of class 'causal_estimates'*

Description

Summary method for objects of class 'causal_estimates'

Usage

```
## S3 method for class 'causal_estimates'  
summary(object, ...)
```

Arguments

<code>object</code>	An object of class 'causal_estimates'
<code>...</code>	Additional arguments affecting the summary produced (so far no additional arguments are needed, so leave blank).

Value

Printed summary of the 'causal_estimates' object, including:

Percentage sample ESS Percentage sample effective sample size (ESS) for the pseudo-population.

Mean differences with 95% CI The mean differences between two groups with their corresponding 95% confidence intervals.

Sigma ratios with 95% CI The ratios of standard deviations between two groups with their corresponding 95% confidence intervals.

Examples

```
data(demo)  
set.seed(1)  
output2 <- causal.estimate(S, Z, X, Y, B = 5, method = "IC", naturalGroupProp)  
summary(output2)
```

Index

`balancing.weights`, [2](#)

`causal.estimate`, [3](#)

`demo`, [5](#)

`groupNames (demo)`, [5](#)

`naturalGroupProp (demo)`, [5](#)

`plot.causal_estimates`, [5](#)

`S (demo)`, [5](#)

`summary.balancing_weights`, [6](#)

`summary.causal_estimates`, [7](#)

`X (demo)`, [5](#)

`Y (demo)`, [5](#)

`Z (demo)`, [5](#)