

# Package ‘WMAP’

June 17, 2025

**Title** Weighted Meta-Analysis with Pseudo-Populations

**Version** 1.2.0

**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](mailto:s.guha@ufl.edu)>

**Repository** CRAN

**Date/Publication** 2025-06-17 04:20:06 UTC

## Contents

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

|              |          |
|--------------|----------|
| <b>Index</b> | <b>8</b> |
|--------------|----------|

---

|                   |  |
|-------------------|--|
| balancing.weights | <i>Compute balancing weights using FLEXOR or other methods</i> |
|-------------------|--|

---

## 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 $\theta$ .   |
| num.random       | Relevant only for FLEXOR method: number of random starting points of $\gamma$ in the two-step iterative procedure. Default is 40.                                   |
| gammaMin         | Relevant only for FLEXOR method: Lower bound for each $\gamma_s$ in the two-step iterative procedure. Default is 0.001.   |
| gammaMax         | Relevant only for FLEXOR method: Upper bound for each $\gamma_s$ 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 $\{1, \dots, J\}$ . |
| Z | Vector of factor levels representing the group memberships. Takes values in $\{1, \dots, K\}$ . |
| 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.                            |

|                               |  |
|-------------------------------|--|
| <code>method</code>           | Pseudo-population method, i.e., weighting method. Take values in FLEXOR, IC, or IGO.   |
| <code>naturalGroupProp</code> | Relevant only for FLEXOR method: a fixed user-specified probability vector $\theta$ .  |
| <code>num.random</code>       | Relevant only for FLEXOR method: number of random starting points of $\gamma$ in the two-step iterative procedure. Default is 40.  |
| <code>gammaMin</code>         | Relevant only for FLEXOR method: Lower bound for each $\gamma_s$ in the two-step iterative procedure. Default is 0.001.            |
| <code>gammaMax</code>         | Relevant only for FLEXOR method: Upper bound for each $\gamma_s$ in the two-step iterative procedure. Default is 0.999.            |
| <code>seed</code>             | Seed for random number generation. Default is NULL.  |
| <code>verbose</code>          | 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](#)