

# Package ‘AIPW’

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**Title** Augmented Inverse Probability Weighting

**Version** 0.6.3.2

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**Description** The 'AIPW' package implements the augmented inverse probability weighting, a doubly robust estimator, for average causal effect estimation with user-defined stacked machine learning algorithms. To cite the 'AIPW' package, please use: ``Yongqi Zhong, Edward H. Kennedy, Lisa M. Bodnar, Ashley I. Naimi (2021, In Press). AIPW: An R Package for Augmented Inverse Probability Weighted Estimation of Average Causal Effects. American Journal of Epidemiology". Visit: <<https://yqzhong7.github.io/AIPW/>> for more information.

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**BugReports** <https://github.com/yqzhong7/AIPW/issues>

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AIPW	<i>Augmented Inverse Probability Weighting (AIPW)</i>
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**Description**

An R6Class of AIPW for estimating the average causal effects with users' inputs of exposure, outcome, covariates and related libraries for estimating the efficient influence function.

**Details**

An AIPW object is constructed by `new()` with users' inputs of data and causal structures, then it `fit()` the data using the libraries in `Q.SL.library` and `g.SL.library` with `k_split` cross-fitting, and provides results via the `summary()` method. After using `fit()` and/or `summary()` methods, propensity scores and inverse probability weights by exposure status can be examined with `plot.p_score()` and `plot.ip_weights()`, respectively.

If outcome is missing, analysis assumes missing at random (MAR) by estimating propensity scores of  $I(A=a, \text{observed}=1)$  with all covariates  $W$ . (`W.Q` and `W.g` are disabled.) Missing exposure is not supported.

See examples for illustration.

**Value**

AIPW object

**Constructor**

`AIPW$new(Y = NULL, A = NULL, W = NULL, W.Q = NULL, W.g = NULL, Q.SL.library = NULL, g.SL.library = NULL, k_split = 10, verbose = TRUE, save.sl.fit = FALSE)`

**Constructor Arguments:**

Argument	Type	Details
Y	Integer	A vector of outcome (binary (0, 1) or continuous)
A	Integer	A vector of binary exposure (0 or 1)
W	Data	Covariates for <b>both</b> exposure and outcome models.
W.Q	Data	Covariates for the <b>outcome</b> model (Q).
W.g	Data	Covariates for the <b>exposure</b> model (g).
Q.SL.library	SL.library	Algorithms used for the <b>outcome</b> model (Q).
g.SL.library	SL.library	Algorithms used for the <b>exposure</b> model (g).
k_split	Integer	Number of folds for splitting (Default = 10).
verbose	Logical	Whether to print the result (Default = TRUE)
save.sl.fit	Logical	Whether to save Q.fit and g.fit (Default = FALSE)

**Constructor Argument Details:**

W, W.Q & W.g It can be a vector, matrix or data.frame. If and only if W == NULL, W would be replaced by W.Q and W.g.

Q.SL.library & g.SL.library Machine learning algorithms from [SuperLearner](#) libraries

k\_split It ranges from 1 to number of observation-1. If k\_split=1, no cross-fitting; if k\_split>=2, cross-fitting is used (e.g., k\_split=10, use 9/10 of the data to estimate and the remaining 1/10 leftover to predict). **NOTE: it's recommended to use cross-fitting.**

save.sl.fit This option allows users to save the fitted sl object (libs\$Q.fit & libs\$g.fit) for debug use. **Warning: Saving the SuperLearner fitted object may cause a substantive storage/memory use.**

**Public Methods**

Methods	Details	Link
fit()	Fit the data to the <a href="#">AIPW</a> object	<a href="#">fit.AIPW</a>
stratified_fit()	Fit the data to the <a href="#">AIPW</a> object stratified by A	<a href="#">stratified_fit.AIPW</a>
summary()	Summary of the average treatment effects from AIPW	<a href="#">summary.AIPW_base</a>
plot.p_score()	Plot the propensity scores by exposure status	<a href="#">plot.p_score</a>
plot.ip_weights()	Plot the inverse probability weights using truncated propensity scores	<a href="#">plot.ip_weights</a>

**Public Variables**

Variable	Generated by	Return
n	Constructor	Number of observations
stratified_fitted	stratified_fit()	Fit the outcome model stratified by exposure status
obs_est	fit() & summary()	Components calculating average causal effects
estimates	summary()	A list of Risk difference, risk ratio, odds ratio
result	summary()	A matrix contains RD, ATT, ATC, RR and OR with their SE and 95%CI
g.plot	plot.p_score()	A density plot of propensity scores by exposure status

ip_weights.plot	plot.ip_weights()	A box plot of inverse probability weights
libs	fit()	<a href="#">SuperLearner</a> libraries and their fitted objects
sl.fit	Constructor	A wrapper function for fitting <a href="#">SuperLearner</a>
sl.predict	Constructor	A wrapper function using <code>sl.fit</code> to predict

### Public Variable Details:

`stratified_fit` An indicator for whether the outcome model is fitted stratified by exposure status in the `fit()` method. Only when using `stratified_fit()` to turn on `stratified_fit = TRUE`, summary outputs average treatment effects among the treated and the controls.

`obs_est` After using `fit()` and `summary()` methods, this list contains the propensity scores (`p_score`), counterfactual predictions (`mu`, `mu1` & `mu0`) and efficient influence functions (`aipw_eif1` & `aipw_eif0`) for later average treatment effect calculations.

`g.plot` This plot is generated by `ggplot2::geom_density`

`ip_weights.plot` This plot uses truncated propensity scores stratified by exposure status (`ggplot2::geom_boxplot`)

### References

Zhong Y, Kennedy EH, Bodnar LM, Naimi AI (2021, In Press). AIPW: An R Package for Augmented Inverse Probability Weighted Estimation of Average Causal Effects. *American Journal of Epidemiology*.

Robins JM, Rotnitzky A (1995). Semiparametric efficiency in multivariate regression models with missing data. *Journal of the American Statistical Association*.

Chernozhukov V, Chetverikov V, Demirer M, et al (2018). Double/debiased machine learning for treatment and structural parameters. *The Econometrics Journal*.

Kennedy EH, Sjolander A, Small DS (2015). Semiparametric causal inference in matched cohort studies. *Biometrika*.

### Examples

```
library(SuperLearner)
library(ggplot2)

#create an object
aipw_sl <- AIPW$new(Y=rbinom(100,1,0.5), A=rbinom(100,1,0.5),
                  W.Q=rbinom(100,1,0.5), W.g=rbinom(100,1,0.5),
                  Q.SL.library="SL.mean",g.SL.library="SL.mean",
                  k_split=1,verbose=FALSE)

#fit the object
aipw_sl$fit()
# or use `aipw_sl$stratified_fit()` to estimate ATE and ATT/ATC

#calculate the results
aipw_sl$summary(g.bound = 0.025)

#check the propensity scores by exposure status after truncation
aipw_sl$plot.p_score()
```

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AIPW_base	<i>Augmented Inverse Probability Weighting Base Class (AIPW_base)</i>
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**Description**

A base class for AIPW that implements the common methods, such as `summary()` and `plot.p_score()`, inherited by [AIPW](#) and [AIPW\\_tmle](#) class

**Format**

[R6Class](#) object.

**Value**

AIPW base object

**See Also**

[AIPW](#) and [AIPW\\_tmle](#)

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AIPW_nuis	<i>Augmented Inverse Probability Weighting (AIPW) uses tmle or tmle3 as inputs</i>
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**Description**

AIPW\_nuis class for users to manually input nuisance functions (estimates from the exposure and the outcome models)

**Details**

Create an AIPW\_nuis object that uses users' input nuisance functions from the exposure model  $P(A|W)$ , and the outcome models  $P(Y|do(A = 0), W)$  and  $P(Y|do(A = 1), W, Q)$ :

$$\psi(a) = E[I(A = a)/P(A = a|W)] * [Y - P(Y = 1|A, W)] + P(Y = 1|do(A = a), W)$$

Note: If outcome is missing, replace (A=a) with (A=a, observed=1) when estimating the propensity scores.

**Value**

AIPW\_nuis object

**Constructor**

`AIPW$new(Y = NULL, A = NULL, tmle_fit = NULL, verbose = TRUE)`

**Constructor Arguments:**

Argument	Type	Details
Y	Integer	A vector of outcome (binary (0, 1) or continuous)
A	Integer	A vector of binary exposure (0 or 1)
mu0	Numeric	User input of $P(Y = 1 do(A = 0), W_Q)$
mu1	Numeric	User input of $P(Y = 1 do(A = 1), W_Q)$
raw_p_score	Numeric	User input of $P(A = a W_g)$
verbose	Logical	Whether to print the result (Default = TRUE)
stratified_fitted	Logical	Whether mu0 & mu1 was estimated only using A=0 & A=1 (Default = FALSE)

## Public Methods

Methods	Details	Link
summary()	Summary of the average treatment effects from AIPW	<a href="#">summary.AIPW_base</a>
plot.p_score()	Plot the propensity scores by exposure status	<a href="#">plot.p_score</a>
plot.ip_weights()	Plot the inverse probability weights using truncated propensity scores	<a href="#">plot.ip_weights</a>

## Public Variables

Variable	Generated by	Return
n	Constructor	Number of observations
obs_est	Constructor	Components calculating average causal effects
estimates	summary()	A list of Risk difference, risk ratio, odds ratio
result	summary()	A matrix contains RD, ATT, ATC, RR and OR with their SE and 95%CI
g.plot	plot.p_score()	A density plot of propensity scores by exposure status
ip_weights.plot	plot.ip_weights()	A box plot of inverse probability weights

### Public Variable Details:

`stratified_fit` An indicator for whether the outcome model is fitted stratified by exposure status in the `fit()` method. Only when using `stratified_fit()` to turn on `stratified_fit = TRUE`, `summary` outputs average treatment effects among the treated and the controls.

`obs_est` This list includes propensity scores (`p_score`), counterfactual predictions (`mu`, `mu1` & `mu0`) and efficient influence functions (`aipw_eif1` & `aipw_eif0`)

`g.plot` This plot is generated by `ggplot2::geom_density`

`ip_weights.plot` This plot uses truncated propensity scores stratified by exposure status (`ggplot2::geom_boxplot`)

**Description**

AIPW\_tmle class uses a fitted tmle or tmle3 object as input

**Details**

Create an AIPW\_tmle object that uses the estimated efficient influence function from a fitted tmle or tmle3 object

**Value**

AIPW\_tmle object

**Constructor**

`AIPW$new(Y = NULL, A = NULL, tmle_fit = NULL, verbose = TRUE)`

**Constructor Arguments:**

Argument	Type	Details
Y	Integer	A vector of outcome (binary (0, 1) or continuous)
A	Integer	A vector of binary exposure (0 or 1)
tmle_fit	Object	A fitted tmle or tmle3 object
verbose	Logical	Whether to print the result (Default = TRUE)

**Public Methods**

Methods	Details	Link
<code>summary()</code>	Summary of the average treatment effects from AIPW	<a href="#">summary.AIPW_base</a>
<code>plot.p_score()</code>	Plot the propensity scores by exposure status	<a href="#">plot.p_score</a>
<code>plot.ip_weights()</code>	Plot the inverse probability weights using truncated propensity scores	<a href="#">plot.ip_weights</a>

**Public Variables**

Variable	Generated by	Return
n	Constructor	Number of observations
obs_est	Constructor	Components calculating average causal effects
estimates	<code>summary()</code>	A list of Risk difference, risk ratio, odds ratio
result	<code>summary()</code>	A matrix contains RD, ATT, ATC, RR and OR with their SE and 95%CI
g.plot	<code>plot.p_score()</code>	A density plot of propensity scores by exposure status
ip_weights.plot	<code>plot.ip_weights()</code>	A box plot of inverse probability weights

**Public Variable Details:**

`obs_est` This list extracts from the fitted tmle object. It includes propensity scores (`p_score`),

counterfactual predictions ( $\mu$ ,  $\mu_1$  &  $\mu_0$ ) and efficient influence functions (`aipw_eif1` & `aipw_eif0`)

`g.plot` This plot is generated by `ggplot2::geom_density`

`ip_weights.plot` This plot uses truncated propensity scores stratified by exposure status (`ggplot2::geom_boxplot`)

## Examples

```
vec <- function() sample(0:1,100,replace = TRUE)
df <- data.frame(replicate(4,vec()))
names(df) <- c("A","Y","W1","W2")

## From tmle
library(tmle)
library(SuperLearner)
tmle_fit <- tmle(Y=df$Y,A=df$A,W=subset(df,select=c("W1","W2")),
               Q.SL.library="SL.glm",
               g.SL.library="SL.glm",
               family="binomial")
AIPW_tmle$new(A=df$A,Y=df$Y,tmle_fit = tmle_fit,verbose = TRUE)$summary()
```

---

aipw\_wrapper

*AIPW wrapper function*

---

## Description

A wrapper function for `AIPW$new()$fit()$summary()`

## Usage

```
aipw_wrapper(
  Y,
  A,
  verbose = TRUE,
  W = NULL,
  W.Q = NULL,
  W.g = NULL,
  Q.SL.library,
  g.SL.library,
  k_split = 10,
  g_bound = 0.025,
  stratified_fit = FALSE
)
```

## Arguments

<code>Y</code>	Outcome (binary integer: 0 or 1)
<code>A</code>	Exposure (binary integer: 0 or 1)
<code>verbose</code>	Whether to print the result (logical; Default = FALSE)



W	covariates for both exposure and outcome models (vector, matrix or data.frame). If null, this function will seek for inputs from W.Q and W.g.
W.Q	Only valid when W is null, otherwise it would be replaced by W. Covariates for outcome model (vector, matrix or data.frame).
W.g	Only valid when W is null, otherwise it would be replaced by W. Covariates for exposure model (vector, matrix or data.frame)
Q.SL.library	SuperLearner libraries for outcome model
g.SL.library	SuperLearner libraries for exposure model
k_split	Number of splitting (integer; range: from 1 to number of observation-1): if k_split=1, no cross-fitting; if k_split>=2, cross-fitting is used (e.g., k_split=10, use 9/10 of the data to estimate and the remaining 1/10 leftover to predict). NOTE: it's recommended to use cross-fitting.
g_bound	Value between [0,1] at which the propensity score should be truncated. Defaults to 0.025.
stratified_fit	An indicator for whether the outcome model is fitted stratified by exposure status in the fit() method. Only when using stratified_fit() to turn on stratified_fit = TRUE, summary outputs average treatment effects among the treated and the controls.

**Value**

A fitted AIPW object with summarised results

**See Also**

[AIPW](#)

**Examples**

```
library(SuperLearner)
aipw_sl <- aipw_wrapper(Y=rbinom(100,1,0.5), A=rbinom(100,1,0.5),
  W.Q=rbinom(100,1,0.5), W.g=rbinom(100,1,0.5),
  Q.SL.library="SL.mean",g.SL.library="SL.mean",
  k_split=1,verbose=FALSE)
```

---

eager\_sim\_obs

*Simulated Observational Study*


---

**Description**

Datasets were simulated using baseline covariates (sampling with replacement) from the Effects of Aspirin in Gestation and Reproduction (EAGeR) study. Data generating mechanisms were described in our manuscript (Zhong et al. (inpreparation), Am. J. Epidemiol.). True marginal causal effects on risk difference, log risk ratio and log odds ratio scales were attached to the dataset attributes (true\_rd, true\_logrr,true\_logor).

**Usage**

```
data(eager_sim_obs)
```

**Format**

An object of class `data.frame` with 200 rows and 8 columns:

**sim\_Y** binary, simulated outcome which is condition on all other covariates in the dataset

**sim\_A** binary, simulated exposure which is condition on all other covariates except `sim_Y`.

**eligibility** binary, indicator of the eligibility stratum

**loss\_num** count, number of prior pregnancy losses

**age** continuous, age in years

**time\_try\_pregnant** count, months of conception attempts prior to randomization

**BMI** continuous, body mass index

**meanAP** continuous, mean arterial blood pressure

**References**

Schisterman, E.F., Silver, R.M., Leshner, L.L., Faraggi, D., Wactawski-Wende, J., Townsend, J.M., Lynch, A.M., Perkins, N.J., Mumford, S.L. and Galai, N., 2014. Preconception low-dose aspirin and pregnancy outcomes: results from the EAGeR randomised trial. *The Lancet*, 384(9937), pp.29-36.

Zhong, Y., Naimi, A.I., Kennedy, E.H., (In preparation). AIPW: An R package for Augmented Inverse Probability Weighted Estimation of Average Causal Effects. *American Journal of Epidemiology*

**See Also**

[eager\\_sim\\_rct](#)

---

eager\_sim\_rct

*Simulated Randomized Trial*

---

**Description**

Datasets were simulated using baseline covariates (sampling with replacement) from the Effects of Aspirin in Gestation and Reproduction (EAGeR) study.

**Usage**

```
data(eager_sim_rct)
```

**Format**

An object of class `data.frame` with 1228 rows and 8 columns:

**sim\_Y** binary, simulated outcome which is condition on all other covariates in the dataset

**sim\_T** binary, simulated treatment which is condition on eligibility only.

**eligibility** binary, indicator of the eligibility stratum

**loss\_num** count, number of prior pregnancy losses

**age** continuous, age in years

**time\_try\_pregnant** count, months of conception attempts prior to randomization

**BMI** continuous, body mass index

**meanAP** continuous, mean arterial blood pressure

**References**

Schisterman, E.F., Silver, R.M., Leshner, L.L., Faraggi, D., Wactawski-Wende, J., Townsend, J.M., Lynch, A.M., Perkins, N.J., Mumford, S.L. and Galai, N., 2014. Preconception low-dose aspirin and pregnancy outcomes: results from the EAGeR randomised trial. *The Lancet*, 384(9937), pp.29-36.

Zhong, Y., Naimi, A.I., Kennedy, E.H., (In preparation). AIPW: An R package for Augmented Inverse Probability Weighted Estimation of Average Causal Effects. *American Journal of Epidemiology*

**See Also**

[eager\\_sim\\_obs](#)

---

fit

*Fit the data to the [AIPW](#) object*

---

**Description**

Fitting the data into the [AIPW](#) object with/without cross-fitting to estimate the efficient influence functions

**Value**

A fitted [AIPW](#) object with `obs_est` and `libs` (public variables)

**R6 Usage**

`$fit()`

**See Also**

[AIPW](#)

---

plot.ip_weights	<i>Plot the inverse probability weights using truncated propensity scores by exposure status</i>
-----------------	--

---

**Description**

Plot and check the balance of propensity scores by exposure status

**Value**

ip\_weights.plot (public variable): A box plot of inverse probability weights using truncated propensity scores by exposure status (ggplot2::geom\_boxplot)

**R6 Usage**

```
$plot.ip_weights()
```

**See Also**

[AIPW](#) and [AIPW\\_tmle](#)

---

plot.p_score	<i>Plot the propensity scores by exposure status</i>
--------------	--

---

**Description**

Plot and check the balance of propensity scores by exposure status

**Value**

g.plot (public variable): A density plot of propensity scores by exposure status (ggplot2::geom\_density)

**R6 Usage**

```
$plot.p_plot()
```

**See Also**

[AIPW](#) and [AIPW\\_tmle](#)

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stratified_fit	<i>Fit the data to the <a href="#">AIPW</a> object stratified by A for the outcome model</i>
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**Description**

Fitting the data into the [AIPW](#) object with/without cross-fitting to estimate the efficient influence functions. Outcome model is fitted, stratified by exposure status A

**Value**

A fitted [AIPW](#) object with obs\_est and libs (public variables)

**R6 Usage**

```
$stratified_fit.AIPW()
```

**See Also**

[AIPW](#)

---

summary	<i>Summary of the average treatment effects from AIPW</i>
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---

**Description**

Calculate average causal effects in RD, RR and OR in the fitted [AIPW](#) or [AIPW\\_tmle](#) object using the estimated efficient influence functions

**Arguments**

g.bound	Value between [0,1] at which the propensity score should be truncated. Propensity score will be truncated to $[g.bound, 1 - g.bound]$ when one g.bound value is provided, or to $[\min(g.bound), \max(g.bound)]$ when two values are provided. <b>Defaults to 0.025.</b>
---------	--

**Value**

estimates and result (public variables): Risks, Average treatment effect in RD, RR and OR.

**R6 Usage**

```
$summary(g.bound = 0.025)
$summary(g.bound = c(0.025, 0.975))
```

**See Also**

[AIPW](#) and [AIPW\\_tmle](#)

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