

Taregeted Maximum Likelihood Estimation for a Binary Outcome: Tutorial and Guided Implementation

Code ▼

By: Miguel Angel Luque Fernandez

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1 Introduction

During the last 30 years, the modern epidemiology has been able to identify significant limitations of classic epidemiologic methods when the focus is to explain the main effect of a risk factor on a disease or outcome.

Causal Inference based on the **Neyma-Rubin Potential Outcomes Framework** (Rubin, 2011), first introduced in Social Science by Donal Rubin (Rubin, 1974) and later in Epidemiology and Biostatistics by James Robins (Greenland and Robins, 1986), has provided the theory and statistical methods needed to overcome recurrent problems in observational epidemiologic research, such as:

1. non-collapsibility of the odds and hazard ratios,
2. impact of paradoxical effects due to conditioning on colliders,
3. selection bias related with the vague understanding of the effect of time on exposure and outcome and,
4. effect of time-dependent confounding and mediators,
5. etc.

Classical epidemiologic methods to control for confounding require making the assumption that the effect measure is constant across levels of confounders included in the model.

Alternatively, James Robins in 1986 demonstrated that using standardisation, implemented through the use of the **G-formula**, allows obtaining a unconfounded marginal estimation of the causal average treatment effect (ATE) under causal untestable assumptions (Greenland and Robins, 1986), (Robins *et al.*, 2000). The most commonly used estimator for a binary treatment effect is the risk difference or $ATE = \psi(P_0)$.

2 The G-Formula

$$\psi(P_0) = \sum_w \left[\sum_y P(Y = y | A = 1, W = w) - \sum_y P(Y = y | A = 0, W = w) \right] P(W = w)$$

where,

$$P(Y = y | A = a, W = w) = \frac{P(W = w, A = a, Y = y)}{\sum_y P(W = w, A = a, Y = y)}$$

is the conditional probability distribution of $Y = y$, given $A = a$, $W = w$ and,

$$P(W = w) = \sum_{y,a} P(W = w, A = a, Y = y)$$

- Classical epidemiologic methods require making the assumption that the effect measure is constant across levels of confounders included in the model. However, **Standardisation** allows us to obtain an unconfounded summary effect measure without requiring this assumption. The **G-formula** is a *generalisation of standardisation* (Greenland and Robins, 1986).
- The ATE can be estimated **non-parametrically** using the G-formula. However, the curse of dimensionality in observational studies limits its estimation.
- Hence, the estimation of the ATE using the G-formula relies mostly on **parametric modelling** assumptions and maximum likelihood estimation. The **correct model specification** in parametric modelling is crucial to obtain unbiased estimates of the true ATE (Rubin, 2011).

However, Mark van der Laan and collaborators have developed a double-robust estimation procedure **to reduce bias against misspecification**. The targeted maximum likelihood estimation (TMLE) is a semiparametric, efficient substitution estimator (Laan and Rose, 2011).

3 TMLE

TMLE allows for data-adaptive estimation while obtaining valid statistical inference based on the targeted minimum loss-based estimation and machine learning algorithms to minimise the risk of model misspecification (Laan and Rose, 2011). The main characteristics of **TMLE** are:

1. **TMLE** is a general algorithm for the construction of double-robust, semiparametric, efficient substitution estimators. **TMLE** allows for data-adaptive estimation while obtaining valid statistical inference.
2. **TMLE** implementation uses the G-computation estimand (G-formula). Briefly, the **TMLE** algorithm uses information in the estimated exposure mechanism $P(A|W)$ to update the initial estimator of the conditional expectation of the outcome given the treatment and the set of covariates W , $E_0(Y|A,W)$.
3. The targeted estimates are then substituted into the parameter mapping Ψ . The updating step achieves a targeted bias reduction for the parameter of interest $\psi(P_0)$ (the true target parameter) and serves to solve the efficient score equation, namely the Influence Curve (IC). As a result, **TMLE** is a double robust estimator.
4. **TMLE** it will be consistent for $\psi(P_0)$ if either the conditional expectation $E_0(Y|A,W)$ or the exposure mechanism $P_0(A|W)$ are estimated consistently.
5. **TMLE** will be efficient if the previous two functions are consistently estimated achieving the lowest asymptotic variance among a large class of estimators. These asymptotic properties typically translate into lower bias and variance in finite samples (Bühlmann *et al.*, 2016).
6. The general formula to estimate the ATE using the TMLE method:

$$\psi^{TMLE, n} = \Psi(Q_n^*) = \frac{1}{n} \sum_{i=1}^n \bar{Q}_n^1(1, W_i) - \bar{Q}_n^1(0, W_i). \quad (1)$$

7. The efficient influence curve (IC) based on Hampel seminal paper (Hampel, 1974) is applied for statistical inference using TMLE:

$$IC_n(O_i) = \left(\frac{I(A_i = 1)}{g_n(1|W_i)} - \frac{I(A_i = 0)}{g_n(0|W_i)} \right) \left[Y_i - \bar{Q}_n^1(A_i, W_i) \right] + \bar{Q}_n^1(1, W_i) - \bar{Q}_n^1(0, W_i) - \psi^{TMLE, n}. \quad (2)$$

where the variance of the ATE:

$$\sigma(\psi_0) = \sqrt{\frac{\text{Var}(IC_n)}{n}}. \quad (3)$$

8. The procedure is available with standard software such as the **tmle** package in R (Gruber and Laan, 2011).

4 Structural causal framework

4.1 Direct Acyclic Graph (DAG)

Back-door criterion

Minimal sufficient sets for estimating the total effect of A on Y:
 $A \perp\!\!\!\perp Y \mid W3, W4$

Under conditional exchangeability: $A \perp\!\!\!\perp Y_1, Y_0 \mid W$
 $\Psi(P_0) \text{ (ATE)} = E[E(Y \mid A = 1; W) - E(Y \mid A = 0; W)]$

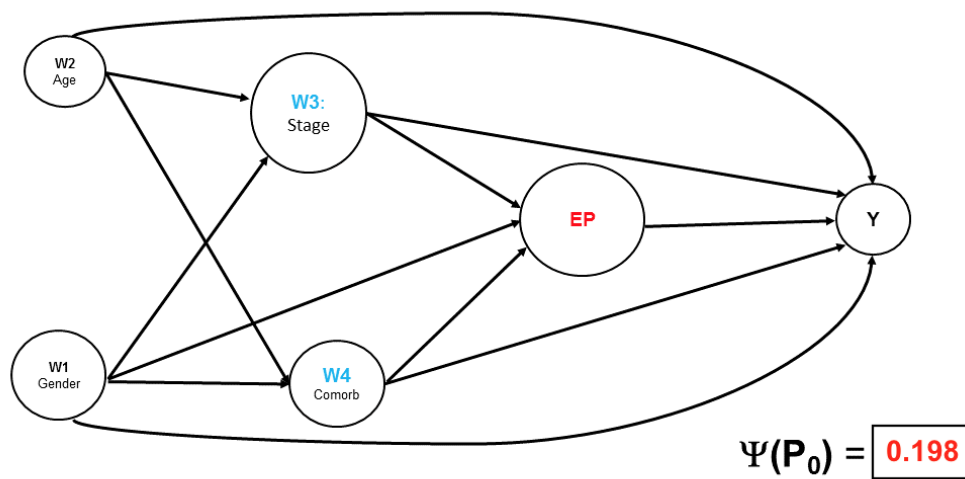


Figure 1. Direct Acyclic Graph

Source: Miguel Angel Luque-Fernandez

4.2 DAG interpretation

The ATE is interpreted as the population risk difference in one-year mortality for lung cancer patients diagnosed via emergency presentations versus non-emergency presentations. Under causal assumptions, and compared with non-emergency presentations of lung cancer, the risk difference of one-year mortality for emergency presentations increases by approximately 20%.

5 Causal assumptions

Under the counterfactual framework the following assumptions have to be considered to estimate the $\psi(P_0)$ (ATE) with a model for P_0 augmented with additional nontestable causal assumptions (Rubin, 2011), (Laan and Rose, 2011):

5.1 CMI or Randomization

$(Y_0, Y_1 \perp A | W)$ of the binary treatment effect (A) on the outcome (Y) given the set of observed covariates (W), where $W = (W_1, W_2, W_3, \dots, W_k)$.

5.2 Positivity

$a \in A: P(A=a | W) > 0$

$P(A=1|W=w) > 0$ and $P(A=0| W = w) > 0$ for each possible w.

5.3 Consistency or SUTVA:

The observed outcome value, under the observed treatment, is equal to the counterfactual outcome corresponding to the observed treatment for identical independent distributed (i.i.d.) variables.

6 TMLE flow chart

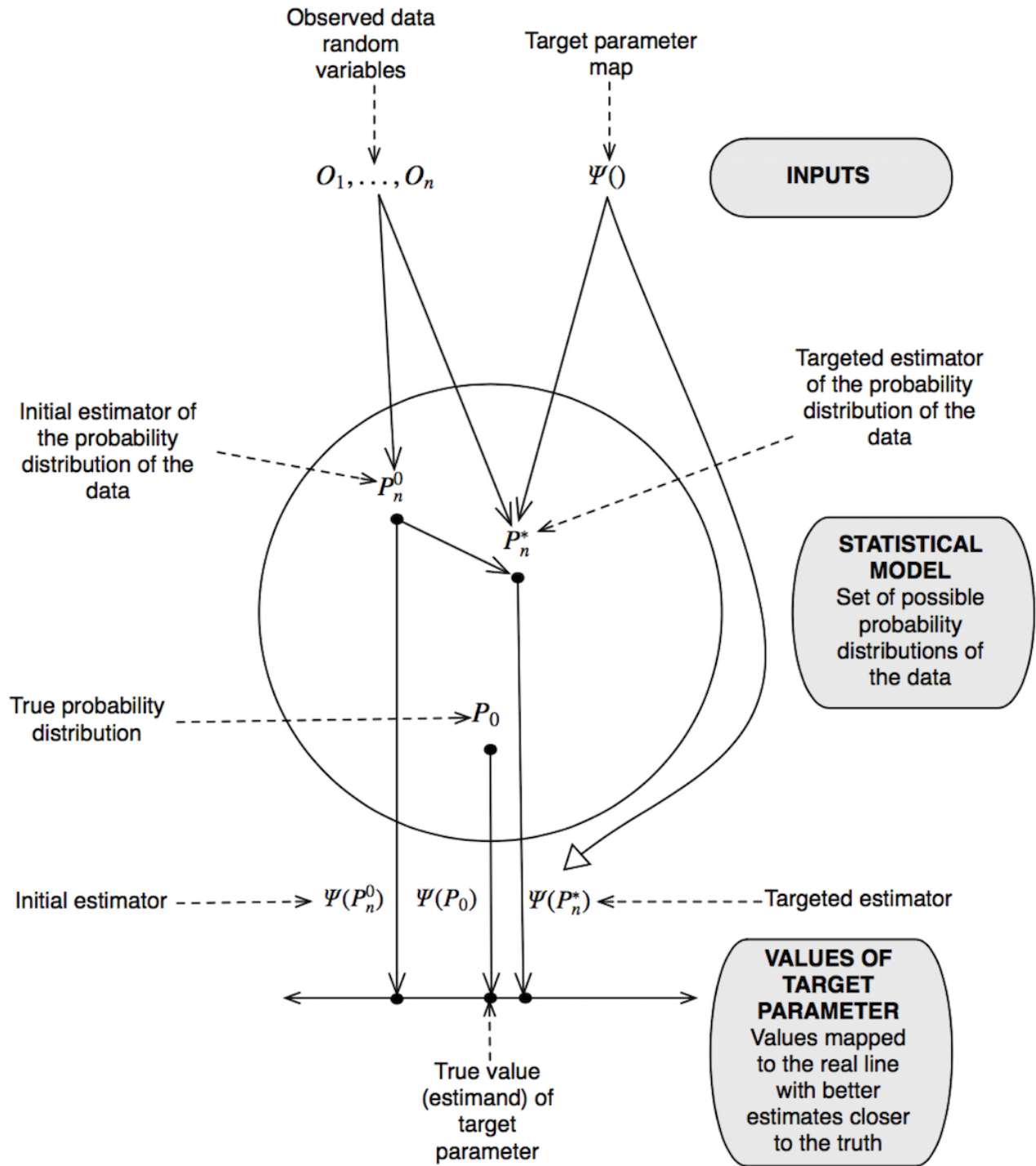


Figure 2. TMLE flow chart (Road map)

Source: Mark van der Laan and Sherri Rose. Targeted learning: causal inference for observational and experimental data Springer Series in Statistics, 2011.

7 Data generation

7.1 Simulation

In R we create a function to generate the data. The function will have as input **number of draws** and as output the generated **observed data** (ObsData) including the counterfactuals (Y1, Y0).

The simulated data replicationg the DAG in Figure 1:

1. Y: mortality binary indicator (1 death, 0 alive)
2. A: binary treatment for emergency presentation at cancer diagnosis (1 EP, 0 NonEP)
3. W1: Gender (1 male; 0 female)
4. W2: Age at diagnosis (0 <65; 1 >=65)
5. W3: Cancer TNM classification (scale from 1 to 4)
6. W4: Comorbidities (scale from 1 to 5)

[Hide](#)

```
options(digits=4)
generateData <- function(n){
  w1 <- rbinom(n, size=1, prob=0.5)
  w2 <- rbinom(n, size=1, prob=0.65)
  w3 <- round(runif(n, min=0, max=4), digits=3)
  w4 <- round(runif(n, min=0, max=5), digits=3)
  A <- rbinom(n, size=1, prob= plogis(-0.4 + 0.2*w2 + 0.15*w3 + 0.2*w4 + 0.15*w2*w4))
  Y <- rbinom(n, size=1, prob= plogis(-1 + A -0.1*w1 + 0.3*w2 + 0.25*w3 + 0.2*w4 + 0.15
*w2*w4))

  # counterfactual
  Y.1 <- rbinom(n, size=1, prob= plogis(-1 + 1 -0.1*w1 + 0.3*w2 + 0.25*w3 + 0.2*w4 + 0.1
5*w2*w4))
  Y.0 <- rbinom(n, size=1, prob= plogis(-1 + 0 -0.1*w1 + 0.3*w2 + 0.25*w3 + 0.2*w4 + 0.1
5*w2*w4))

  # return data.frame
  data.frame(w1, w2, w3, w4, A, Y, Y.1, Y.0)
}
set.seed(7777)
ObsData <- generateData(n=10000)
True_Psi <- mean(ObsData$Y.1-ObsData$Y.0);
cat(" True_Psi:", True_Psi)
```

True_Psi: 0.198

[Hide](#)

```
Bias_Psi <- lm(data=ObsData, Y~ A)
cat("\n")
```

[Hide](#)

```
cat("\n Naive_Biased_Psi:",summary(Bias_Psi)$coef[2, 1])
```

```
Naive_Biased_Psi: 0.2631
```

Hide

```
Naive_Bias <- ((summary(Bias_Psi)$coef[2, 1])-True_Psi); cat("\n Naives bias:", Naive_Bias)
```

```
Naives bias: 0.06509
```

Hide

```
Naive_Relative_Bias <- (((summary(Bias_Psi)$coef[2, 1])-True_Psi)/True_Psi)*100; cat("\n Relative Naives bias:", Naive_Relative_Bias,"%")
```

```
Relative Naives bias: 32.88 %
```

7.2 Data visualization

Hide

```
# DT table = interactive
# install.packages("DT") # install DT first
library(DT)
datatable(head(ObsData, n = nrow(ObsData)), options = list(pageLength = 5, digits = 2))
```

Show

5

 entries

Search:

	w1	w2	w3	w4	A	Y	Y.1	Y.o
1	0	1	3.282	3.541	1	1	0	0
2	1	0	0.047	1.425	1	1	0	0
3	1	0	3.354	4.158	1	1	1	0
4	1	1	2.085	1.737	1	1	0	0
5	0	1	2.487	0.419	1	1	0	1

Showing 1 to 5 of 10,000 entries

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8 TMLE simple implementation

8.1 Step 1: $Q_0(A, W)$

Estimation of the initial probability of the outcome (Y) given the treatment (A) and the set of covariates (W), denoted as $Q_0(A, W)$. To estimate $Q_0(A, W)$ we can use a standard logistic regression model:

$$\text{logit}[P(Y = 1|A, W)] = \beta_0 + \beta_1 A + \beta_2^T W.$$

Therefore, we can estimate the initial probability as follows:

$$\bar{Q}^0(A, W) = \text{expit}(\hat{\beta}_0 + \hat{\beta}_1 A + \hat{\beta}_2^T W).$$

The predicted probability can be estimated using the Super-Learner library implemented in the R package “Super-Learner” (Van der Laan *et al.*, 2007) to include any terms that are functions of A or W (e.g., polynomial terms of A and W, as well as the interaction terms of A and W, can be considered).

Consequently, for each subject, the predicted probabilities for both potential outcomes $\bar{Q}^0(0, W)$ and $\bar{Q}^0(1, W)$ can be estimated by setting A = 0 and A = 1 for everyone respectively:

$$\bar{Q}^0(0, W) = \text{expit}(\hat{\beta}_0 + \hat{\beta}_2^T W),$$

and,

$$\bar{Q}^0(1, W) = \text{expit}(\hat{\beta}_0 + \hat{\beta}_1 A + \hat{\beta}_2^T W).$$

Note: see appendix one for a short introduction to the Super-Learner and ensemble learning techniques.

[Hide](#)

```
ObsData <-subset(ObsData, select=c(w1,w2,w3,w4,A,Y))
Y <- ObsData$Y
A <- ObsData$A
w1 <- ObsData$w1
w2 <- ObsData$w2
w3 <- ObsData$w3
w4 <- ObsData$w4
m <- glm(Y ~ A + w1 + w2 + w3 + w4, family=binomial, data=ObsData)
Q <- cbind(QAW = predict(m),
           Q1W = predict(m, newdata=data.frame(A = 1, w1, w2, w3, w4)),
           Q0W = predict(m, newdata=data.frame(A = 0, w1, w2, w3, w4)))
Q0 <- as.data.frame(Q)
Y1<-Q0$Q1W
Y0<-Q0$Q0W
#Inverse logit (probability scale)
psi <- (exp(Y1)/(1+exp(Y1)) - exp(Y0)/(1+exp(Y0)))
Psi <- mean(exp(Y1)/(1+exp(Y1)) - exp(Y0)/(1+exp(Y0))); cat("\n Q0:", Psi)
```

Q0: 0.1992

[Hide](#)


```
df <- round(cbind(Q0,psi), digits= 3)
```

Visualizing the first step:

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```
datatable(head(df, n = nrow(df)), options = list(pageLength = 5, digits = 3))
```

Show entries

Search:

	QAW	Q1W	QoW	psi
1	2.368	2.368	1.341	0.122
2	0.045	0.045	-0.981	0.239
3	1.824	1.824	0.798	0.172
4	1.346	1.346	0.32	0.214
5	1.15	1.15	0.123	0.229

Showing 1 to 5 of 10,000 entries

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8.2 Step 2: $g_0(A, W)$

Estimation of the probability of the treatment (A) given the set of covariates (W), denoted as $g_0(A, W)$. We can use again a logistic regression model and to improve the prediction algorithm we can use the Super-Learner library or any other machine learning strategy:

$$\text{logit}[P(A = 1|W)] = \beta_0 + \beta_1^T W.$$

Then, we estimate the predicted probability of $P(A|W) = \hat{g}(1, W)$ using:

$$\hat{g}(1, W) = \text{expit}(\hat{\beta}_0 + \hat{\beta}_2^T W).$$

Hide

```
g <- glm(A ~ w2 + w3 + w4, family = binomial)
glW = predict(g, type = "response");cat("\n Propensity score = glW", "\n");summary(glW)
```

```
Propensity score = glW
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.358   0.594   0.681   0.671   0.759   0.875
```

8.3 Step 3: HAW and ϵ

This step aims to find a better prediction model targeted at minimising the mean squared error (MSE) for the potential outcomes. For the ATE on step convergence is guaranteed given \bar{Q}^0 and $\hat{g}(1, W)$.

The fluctuation parameters ($\hat{\epsilon}_0, \hat{\epsilon}_1$) are estimated using maximum likelihood procedures by setting $\text{logit}(\bar{Q}^0(A, W))$ as an offset in a intercept-free logistic regression with H_0 and H_1 as independent variables:

$$\bar{Q}^1(A, W) = \text{expit} \left[\text{logit} \left(\bar{Q}^0(A, W) \right) + \hat{\epsilon}_0 H_0(A, W) + \hat{\epsilon}_1 H_1(A, W) \right] \quad (5)$$

$$\bar{Q}^1(0, W) = \text{expit} \left[\text{logit} \left(\bar{Q}^0(A, W) \right) + \hat{\epsilon}_0 H_0(0, W) \right]$$

$$\bar{Q}^1(1, W) = \text{expit} \left[\text{logit} \left(\bar{Q}^0(A, W) \right) + \hat{\epsilon}_1 H_1(1, W) \right]$$

Where,

$$H_0(A, W) = \frac{I(A=0)}{\hat{g}(0|W)} \text{ and } H_1(A, W) = \frac{I(A=1)}{\hat{g}(1|W)}$$

are the stabilized inverse probability treatment (A) weights (IPTW), called the clever covariates and I defines an indicator function (note that $\hat{g}(A|W)$ is estimated from step 2).

Hide

```
#Model 5: Clever covariate and fluctuating/substitution paramteres
h <- cbind(gAW=(A/g1w -(1-A)/(1-g1w)), g1W=(1/g1w), g0W=(-1/(1-g1w)))
epsilon <- coef(glm(Y ~ -1 + h[,1] + offset(Q[, "QAW"]), family = binomial));cat("\n Epsilon:",epsilon)
```

Epsilon: 0.001189

Hide

```
df <- round(cbind(Q0,PS=(g1w),H=(h),epsilon), digits= 4)
```

Visualizing the 3rd step (PS = propensity score; H = IPTW or clever covarites):

Hide

```
datatable(head(df, n = nrow(df)), options = list(pageLength = 5, digits = 3))
```

Show entries

Search:

	QAW	Q1W	QoW	PS	H.gAW	H.g1W	H.goW	epsilon
1	2.3678	2.3678	1.3413	0.8065	1.2399	1.2399	-5.1681	0.0012
2	0.0452	0.0452	-0.9812	0.4596	2.1759	2.1759	-1.8504	0.0012
3	1.8244	1.8244	0.7979	0.7595	1.3166	1.3166	-4.1582	0.0012
4	1.3463	1.3463	0.3199	0.6705	1.4914	1.4914	-3.0351	0.0012

	QAW	Q1W	QoW	PS	H.gAW			H.g1W			H.goW		epsilon
5	1.1499	1.1499	0.1234	0.5939	1.6839			1.6839			-2.4622		0.0012
Showing 1 to 5 of 10,000 entries				Previous	1	2	3	4	5	...	2000	Next	

8.4 Step 4 \bar{Q}_n^* : from \bar{Q}_0^0 to \bar{Q}_1^1

Afterwards, the estimated probability of the potential outcomes is updated by the substitution parameters $(\hat{\epsilon}_0, \hat{\epsilon}_1)$. The substitution update is performed by setting $A = 0$ and $A = 1$ for each subject in the initial estimate probability of the potential outcomes $\bar{Q}^1(0, W)$, $\bar{Q}^1(1, W)$, as well as in the clever covariates $H_0(0, W)$ and $H_1(1, W)$.

For the $\Psi(\bar{Q}_n^*)$, the updated estimate of the potential outcomes only needs one iteration from $\bar{Q}^0(A, W) \Rightarrow \bar{Q}^1(A, W)$. Therefore, model (5) targets $E[\hat{Y}_{A=0}]$ and $E[\hat{Y}_{A=1}]$ simultaneously by including both $H_0(A, W)$ and $H_1(A, W)$ in the model. Hence ψ is finally estimated as follows:

$$\psi_{TMLE, n} = \Psi(\bar{Q}_n^*) = \frac{1}{n} \sum_{i=1}^n \bar{Q}_n^1(1, W_i) - \bar{Q}_n^1(0, W_i). \quad (1)$$

Hide

```
Qstar <- plogis(Q + epsilon*h)
psi <- (Qstar[, "Q1W"] - Qstar[, "Q0W"])
Psi <- mean(Qstar[, "Q1W"] - Qstar[, "Q0W"]);
cat("TMLE_Psi:", Psi)
```

```
TMLE_Psi: 0.2004
```

Hide

```
cat("\n TMLE.SI_bias:", abs(True_Psi-Psi))
```

```
TMLE.SI_bias: 0.002383
```

Hide

```
cat("\n Relative_TMLE.SI_bias:", abs(True_Psi-Psi)/True_Psi*100, "%")
```

```
Relative_TMLE.SI_bias: 1.204 %
```

Visualizing the 4th step (H = IPTW or clever covarites):

Hide

```
df <- round(cbind(Q0=(Q0),H=(h),epsilon,psi), digits= 4)
datatable(head(df, n = nrow(df)), options = list(pageLength = 5, digits = 3))
```

Show

5

 entries

Search:

	Qo.QAW	Qo.Q1W	Qo.QoW	H.gAW	H.g1W	H.goW	epsilon	psi
1	2.3678	2.3678	1.3413	1.2399	1.2399	-5.1681	0.0012	0.1228
2	0.0452	0.0452	-0.9812	2.1759	2.1759	-1.8504	0.0012	0.2397
3	1.8244	1.8244	0.7979	1.3166	1.3166	-4.1582	0.0012	0.1728
4	1.3463	1.3463	0.3199	1.4914	1.4914	-3.0351	0.0012	0.2154
5	1.1499	1.1499	0.1234	1.6839	1.6839	-2.4622	0.0012	0.2298

Showing 1 to 5 of 10,000 entries

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Hide

```
cat("\n Psi first row:", plogis((0.001189*1.2399)+(2.3678))-(plogis((0.001189*-5.1681)+(1.3413))))
```

Psi first row: 0.1228

Hide

```
cat("\n TMLE_Psi:", Psi)
```

TMLE_Psi: 0.2004

8.5 Step 5: Inference

TMLE uses the efficient influence curve (IC) for inference (i.e., to obtain standard errors for ψ).

$$IC_n(O_i) = \left(\frac{I(A_i = 1)}{g_n(1|W_i)} - \frac{I(A_i = 0)}{g_n(0|W_i)} \right) \left[Y_i - \bar{Q}_n^1(A_i, W_i) \right] + \bar{Q}_n^1(1, W_i) - \bar{Q}_n^1(0, W_i) - \psi^{TMLE, n}. \tag{2}$$

where the standard deviation for ψ is estimated as follows:

$$\sigma(\psi_0) = \sqrt{\frac{Var(IC_n)}{n}}. \tag{3}$$

Note: see appendix two for a short introduction to the theory of the Influence Curve.

Hide

```
Q <- as.data.frame(Q)
IC <- h[,1]*(Y-Q$QAW) + Q$Q1W - Q$Q0W - Psi;summary(IC)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-2.950  -0.855  -0.200  -0.006   0.570   14.300
```

Hide

```
n <- nrow(ObsData)
varHat.IC <- var(IC)/n; varHat.IC
```

```
[1] 0.0002024
```

Hide

```
#Psi and 95%CI for Psi
cat("\n TMLE_Psi:", Psi)
```

```
TMLE_Psi: 0.2004
```

Hide

```
cat("\n 95%CI:", c(Psi-1.96*sqrt(varHat.IC), Psi+1.96*sqrt(varHat.IC)))
```

```
95%CI: 0.1725 0.2283
```

Hide

```
cat("\n TMLE.SI_bias:", abs(True_Psi-Psi))
```

```
TMLE.SI_bias: 0.002383
```

Hide

```
cat("\n Relative_TMLE.SI_bias:",abs(True_Psi-Psi)/True_Psi*100,"%")
```

```
Relative_TMLE.SI_bias: 1.204 %
```

9 TMLE vs. AIPTW

1. The advantages of **TMLE** have repeatedly been demonstrated in both simulation studies and applied analyses (Laan and Rose, 2011).

- Evidence shows that **TMLE** provides the less unbiased ATE estimate compared with other double-robust estimators (Neugebauer and Laan, 2005), (Laan and Rose, 2011) such as the combination of regression adjustment with inverse probability of treatment weighting (IPTW-RA) and the augmented inverse probability of treatment weighting (AIPTW). The **AIPTW** estimation is a two-step procedure with two equations (propensity score equation and, mean outcome equation).
- To estimate the ATE using the **AIPTW** estimator one can set the estimation equation (EE) (4) equal to zero and use bootstrap to derive 95% confidence intervals (CI). However, solving the EE using the generalised method of moments (GMM), stacking both equations (propensity score and outcome), reduces the estimation and inference steps to only one. However, given that the propensity score in equation (4) can easily fall outside the range [0, 1] (if for some observations $g_n(1|W_i)$ is close to 1 or 0) the **AIPTW** estimation can be unstable (near violation of the positivity assumption). AIPTW instability under near violation of the positivity assumption represents the price of not being a substitution estimator as **TMLE**.

$$\psi_0^{AIPTW-ATE} = \frac{1}{n} \sum_{i=1}^n \left(\frac{I(A_i = 1)}{g_n(1|W_i)} - \frac{I(A_i = 0)}{g_n(0|W_i)} \right) [Y_i - \bar{Q}_n^0(A_i, W_i)] + \frac{1}{n} \sum_{i=1}^n \bar{Q}_n^0(1, W_i) - \bar{Q}_n^0(0, W_i). \quad (4)$$

Hide

```
AIPTW <- mean( (h[,1]*(Y-Q$QAW))+(Q$Q1W-Q$Q0W)); AIPTW
```

```
[1] 0.1948
```

Hide

```
cat("\n AIPTW_bias:", abs(True_Psi-AIPTW))
```

```
AIPTW_bias: 0.003211
```

Hide

```
cat("\n Relative_AIPTW_bias:",abs(True_Psi-AIPTW)/True_Psi*100,"%")
```

```
Relative_AIPTW_bias: 1.622 %
```

Compared with AIPTW, TMLE showed smaller relative bias.

10 TMLE using the Super-Learner

With TMLE we can call the Super-Learner (SL). The SL is a R-package using V-fold cross-validation and ensemble learning (prediction using the all the predictions of multiple stacked learning algorithms) techniques to improve model prediction performance (Breiman, 1996).

The basic implementation of TMLE in the R-package **tmle** uses by default three algorithms:

- SL libraries SL.glm (main terms logistic regression of A and W),
- SL.step (stepwise forward and backward model selection using AIC criterion, restricted to second order polynomials) and,

3. `SL.glm.interaction` (a `glm` variant that includes second order polynomials and two by two interactions of the main terms included in the model).

The principal interest of calling the Super-Learner is to obtain the less-unbiased estimated for $\bar{Q}_n^0(A, W)$ and $g_0(A, W)$. It is achieved by obtaining the smallest expected loss function for Y or A (binary outcomes), respectively. For instance, the negative logarithmic loss function for Y is computed as the minimizer of the expected squared error loss:

$$\bar{Q}_0 = \arg \min_{\bar{Q}} E_0 L(O, \bar{Q}),$$

where $L(O, \bar{Q})$ is:

$$(Y - \bar{Q}(A, W))^2$$

Note: see appendix one for a short introduction to the Super-Learner and ensemble learning techniques.

1. Step One: $\bar{Q}_n^0(A, W)$ prediction

[Hide](#)

```
#Q0
library(SuperLearner)
#Specify SuperLearner libraries
SL.library <- c("SL.glm", "SL.step", "SL.glm.interaction")
#Data frame with X with baseline covariates and exposure
X <- subset(ObsData, select=c(A, w1, w2, w3, w4))
n <- nrow(ObsData)
#Create data frames with A=1 and A=0
X1<-X0<-X
X1$A <-1
X0$A <-0
#Create new data by stacking
newdata <- rbind(X,X1,X0)
#Call superlearner
Qinit <- SuperLearner(Y=ObsData$Y, X=X, newX=newdata, SL.library=SL.library, family="binomial")
Qinit
```

```
Call:
SuperLearner(Y = ObsData$Y, X = X, newX = newdata, family = "binomial",
  SL.library = SL.library)

              Risk    Coef
SL.glm_All      0.1766 0.6002
SL.step_All      0.1766 0.0000
SL.glm.interaction_All 0.1767 0.3998
```

[Hide](#)

```

#Predictions
#Pred prob of survival given A, W
QbarAW <- Qinit$SL.predict[1:n]
#Pred prob of surv for each subject given A=1 and w
Qbar1W <- Qinit$SL.predict[(n+1):(2*n)]
#Pred prob of surv for each subject given A=0 and w
Qbar0W <- Qinit$SL.predict[(2*n+1):(3*n)]
#Simple substitution estimator Psi(Q0)
PsiHat.SS <- mean(Qbar1W-Qbar0W);PsiHat.SS

```

```
[1] 0.199
```

2. Step two: $g_0(A, W)$ prediction

[Hide](#)

```

#Step 2  $g_0(A/W)$  with SuperLearner
w <- subset(ObsData, select=c(w1,w2,w3,w4))
gHatSL <- SuperLearner(Y=ObsData$A, X=w, SL.library=SL.library, family = binomial)
gHatSL;mean(gHatSL)

```

```

Call:
SuperLearner(Y = ObsData$A, X = w, family = binomial, SL.library = SL.library)

```

	Risk	Coef
SL.glm_All	0.2093	0.0000
SL.step_All	0.2092	0.4876
SL.glm.interaction_All	0.2092	0.5124

```

[1] NA

```

[Hide](#)

```

#Generate the pred prob of A=1 and, A=0 given covariates
gHat1W <- gHatSL$SL.predict
gHat0W <- 1-gHat1W
#Step 3: Clever covariate
HAW <- as.numeric(ObsData$A==1)/gHat1W - as.numeric(ObsData$A==0)/gHat0W;summary(HAW)

```

```

      V1
Min.   :-8.641
1st Qu.: -2.230
Median :  1.292
Mean    :  0.004
3rd Qu.:  1.525
Max.    :  2.598

```

[Hide](#)


```
H1W <- 1/gHat1W
H0W <- -1/gHat0W
```

3. Steps 3 and 4: fluctuation step and substitution estimation for for $\bar{Q}_n^0(A, W)$ to $\bar{Q}_n^1(A, W)$

Hide

```
#Step 4: Substitution estimaiton Q* of the ATE.
logitUpdate <- glm(ObsData$Y ~ -1 + offset(qlogis(QbarAW))+HAW, family='binomial')
eps <- logitUpdate$coef;eps
```

```
HAW
0.0005187
```

Hide

```
#Calculating the predicted values for each subject under each txt
QbarAW.star <- plogis(qlogis(QbarAW)+eps*HAW)
Qbar1W.star <- plogis(qlogis(Qbar1W)+eps*H1W)
Qbar0W.star <- plogis(qlogis(Qbar0W)+eps*H0W)
PsiHat.TMLE.SL <- mean(Qbar1W.star) - mean(Qbar0W.star)
cat("PsiHat.TMLE.SL:", PsiHat.TMLE.SL)
```

```
PsiHat.TMLE.SL: 0.1995
```

Hide

```
cat("\n PsiHat.TMLE.SL_bias:", abs(True_Psi-PsiHat.TMLE.SL))
```

```
PsiHat.TMLE.SL_bias: 0.001525
```

Hide

```
cat("\n Relative_PsiHat.TMLE.SL_bias:",abs(True_Psi-PsiHat.TMLE.SL)/True_Psi*100,"%")
```

```
Relative_PsiHat.TMLE.SL_bias: 0.7703 %
```

11 R-TMLE

Using the R-package **tmle**.

The basic implementation of TMLE in the R-package **tmle** uses by default three algorithms:

1. SL libraries SL.glm (main terms logistic regression of A and W),
2. SL.step (stepwise forward and backward model selection using AIC criterion, restricted to second order polynomials) and,

3. SL.glm.interaction (a glm variant that includes second order polynomials and two by two interactions of the main terms included in the model).

Hide

```
library(tmle)
w <- subset(ObsData, select=c(w1,w2,w3,w4))
tmle <- tmle(Y, A, W=w)
cat("TMLER_Psi:", tmle$estimates[[2]][[1]],";","95%CI(", tmle$estimates[[2]][[3]],",")"
```

```
TMLER_Psi: 0.1994 ; 95%CI( 0.18 0.2189 )
```

Hide

```
cat("\n TMLE_bias:", abs(True_Psi-tmle$estimates[[2]][[1]]))
```

```
TMLE_bias: 0.00143
```

Hide

```
cat("\n Relative_TMLE_bias:",abs(True_Psi-tmle$estimates[[2]][[1]])/True_Psi*100,"%")
```

```
Relative_TMLE_bias: 0.7221 %
```

12 R-TMLE improving prediction

In addition to the default algorithms implemented in the R-tmle package, we can improve our estimation calling more efficient machine learning algorithms, such as generalized additive models, the Random Forest and, Recursive Partitioning and Regression Trees:

Hide

```
SL.TMLER.Psi <- tmle(Y=Y, A=A, W=w, family="binomial",
  Q.SL.library = c("SL.glm", "SL.step", "SL.glm.interaction", "SL.gam", "SL.randomFore
st", "SL.rpart"),
  g.SL.library = c("SL.glm", "SL.step", "SL.glm.interaction", "SL.gam", "SL.randomFore
st", "SL.rpart"))
cat("SL.TMLER.Psi:", SL.TMLER.Psi$estimates[[2]][[1]],";","95%CI(", SL.TMLER.Psi$estimat
es[[2]][[3]],",")"
```

```
SL.TMLER.Psi: 0.1993 ; 95%CI( 0.1799 0.2188 )
```

Hide

```
cat("\n SL.TMLER.Psi_bias:", abs(True_Psi-SL.TMLER.Psi$estimates[[2]][[1]]))
```

```
SL.TMLER.Psi_bias: 0.001317
```

[Hide](#)

```
cat("\n Relative_SL.TMLER.Psi_bias:",abs(True_Psi-SL.TMLER.Psi$estimates[[2]][[1]])/True_Psi*100,"%")
```

```
Relative_SL.TMLER.Psi_bias: 0.6649 %
```

We have demonstrated:

1. **TMLE excels** the AIPTW estimator and,
2. TMLE **best performance** is obtained when calling more advanced **Super-Learner** algorithms.

13 Appendix One

Efron in 1982 showed that the empirical **Influence Curve** estimate of standar error is the same as the one obtained using the **infinitesimal jackknife** and the **nonparametric deltha method** (Efron and Efron, 1982).

1. The Delat Method uses the first order of the Taylor series expansion:

$$f(x) \approx f(\mu) + (x - \mu)f'(\mu);$$

where $f'(\mu)$ is the derivative of the function with respect to X evaluated at the mean of X. Therefore, squaring both terms, the variance is approximately estimate as follwos:

$$E[f(x) - f(\mu)]^2 \approx E(x - \mu)^2 \times [f'(\mu)]^2;$$

The left-hand side of the above equation is approximately the variance of $f(x)$ and applied to the empirical distribution of X, the sample estimate of variance for X replaces:

$$E(x_i - \mu)^2.$$

The infinitesimal jackknife estimate of the standard error is defined as follows:

$$SD_{ij}(\theta_e) = \left(\frac{\sum_{i=1}^n U_i^2}{n^2} \right)^{1/2};$$

where θ_e is the estimate of the parameter θ and U_i is a **directional derivative** in the direction of the i th coordinate centered at the mean of the empirical distribution function.

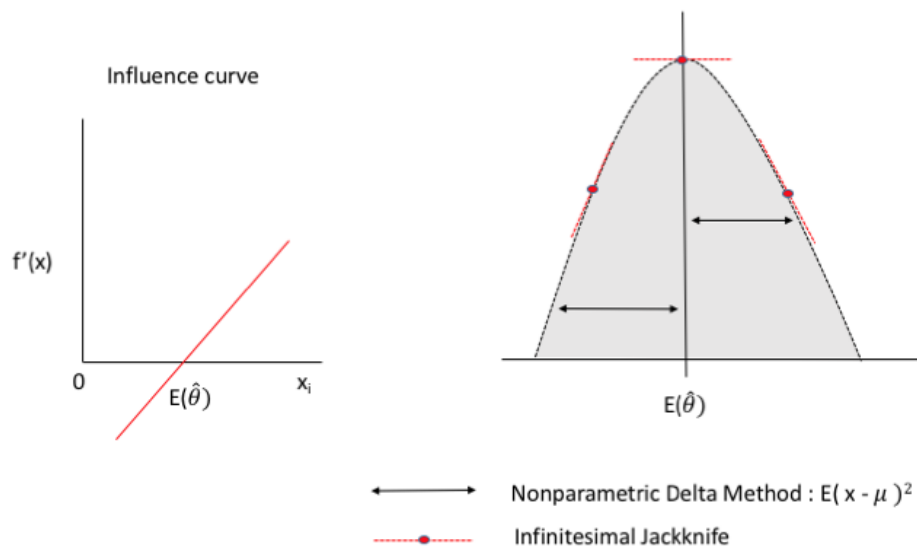


Figure 3. Estimate of the ψ Standard Error using the efficient Influence Curve.
Image credit: Miguel Angel Luque-Fernandez.

14 Appendix Two

With TMLE we can call the R-package **Super-Learner (SL)**. The *SL* uses **cross-validation** and **ensembled learning** (using all the predictions of multiple stacked learning algorithms) techniques to improve model prediction performance (Breiman, 1996).

The **SL** algorithm provides a system based on V-fold cross-validation (Efron and Gong, 1983) (10-folds) to combine adaptively multiple algorithms into an improved estimator, and returns a function that can be used for prediction in new datasets.

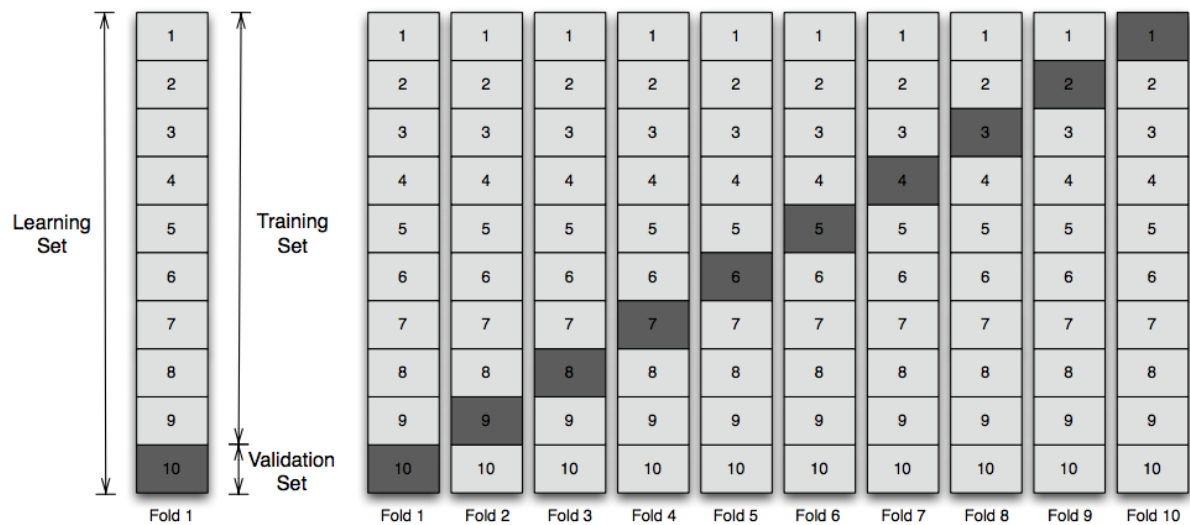


Figure 4: 10-fold cross-validation algorithm.

Source: Sherri Rose in Esembles in Public Health and Healt Policy. May 4, 2016.

The basic implementation of TMLE in the R-package **tmle** uses by default three algorithms: 1. SL libraries SL.glm (main terms logistic regression of A and W),

2. SL.step (stepwise forward and backward model selection using AIC criterion, restricted to second order polynomials) and, 3. SL.glm.interaction (a glm variant that includes second order polynomials and two by two interactions of the main terms included in the model).

The principal interest of calling the Super-Learner is to obtain the less-unbiased estimated for $\bar{Q}_n^0(A, W)$ and $g_0(A, W)$. It is achieved by obtaining the smallest expected loss function for Y or A (binary outcomes), respectively. For instance, the negative logarithmic loss function for Y is computed as the minimizer of the expected squared error loss:

$$\bar{Q}_0 = \arg \min_{\bar{Q}} E_0 L(O, \bar{Q}),$$

where $L(O, \bar{Q})$ is:

$$(Y - \bar{Q}(A, W))^2$$

The **SL** algorithm first split the data into ten blocks and fits each of the selected algorithms on the training set (non-shaded blocks), then predicts the estimated probabilities of the outcome (Y) using the validation set (shaded block) for each algorithm, based on the corresponding training set. Afterwards, the **SL** estimates the cross-validating risk for each algorithm averaging the risks across validation sets resulting in one estimated cross-validated risk for each algorithm. Finally, the **SL** selects the combination of Z that minimises the cross-validation risk, defined as the minimum mean square error for each of the selected algorithms using Y and Z. A weighted combination of the algorithms (ensemble learning) in Z is then used to predict the outcome (Y) (see Figure 5).

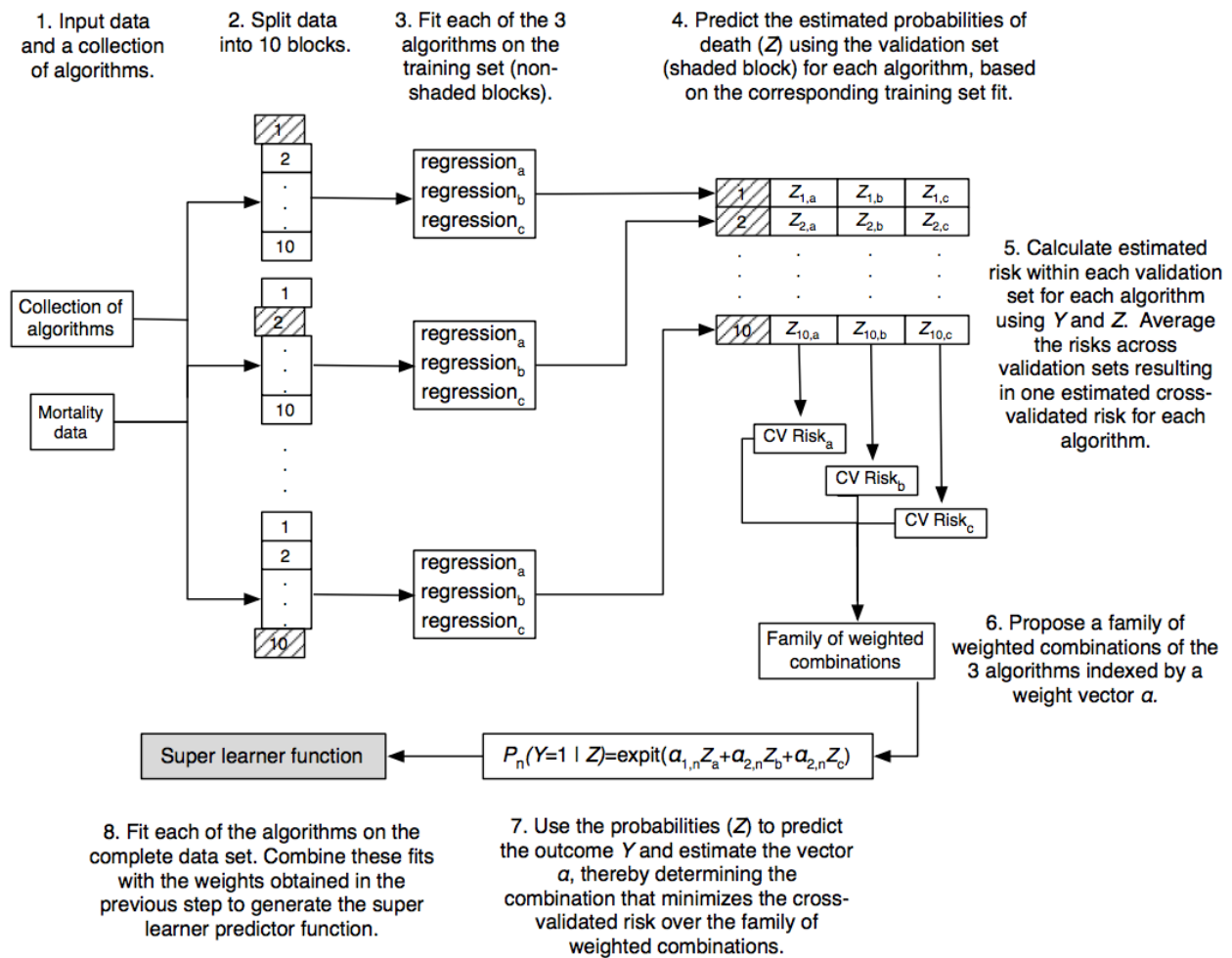


Figure 5: Flow Diagram for the Super-Learner algorithm.

Source: Mark van der Laan and Sherri Rose. Targeted learning: causal inference for observational and experimental data Springer Series in Statistics, 2011.

15 Session Info

Hide

```
devtools::session_info()
```

16 Thank you

Thank you for participating in this tutorial.

If you have updates or changes that you would like to make, please send me (<https://github.com/migariane/MALF>) a pull request. Alternatively, if you have any questions, please e-mail me. You can cite this repository as: Luque-Fernandez MA, (2016). Taregeted Maximum Likelihood Estimation for a Binary Outcome: Tutorial and Guided Implementation. GitHub repository, <http://migariane.github.io/TMLE.nb.html> (<http://migariane.github.io/TMLE.nb.html>).

Miguel Angel Luque Fernandez

E-mail: [miguel-angel.luque at lshtm.ac.uk](mailto:miguel-angel.luque@lshtm.ac.uk)

Twitter @WATZILEI

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