

Appendix:

Targeted Maximum Likelihood Estimation for a Binary Treatment: A Tutorial

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APPENDIX

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1. TMLE with R: code for the illustration

```
#####  
# Miguel Angel Luque Fernandez, Michael Schomaker, Bernard Rachet, Mireille Schnitzer  
# Targeted Maximum Likelihood Estimation for a Binary treatment: A tutorial  
# R-syntax included in the boxes of the manuscript  
#####  
  
# Function to generate data (DGP)  
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=0)  
  w4 <- round(runif(n, min=0, max=5), digits=0)  
  A <- rbinom(n, size=1, prob= plogis(-5 + 0.05*w2 + 0.25*w3 + 0.6*w4 + 0.4*w2*w4))  
  # counterfactual  
  Y.1 <- rbinom(n, size=1, prob= plogis(-1 + 1 -0.1*w1 + 0.35*w2 + 0.25*w3 + 0.20*w4 + 0.15*w2*w4))  
  Y.0 <- rbinom(n, size=1, prob= plogis(-1 + 0 -0.1*w1 + 0.35*w2 + 0.25*w3 + 0.20*w4 + 0.15*w2*w4))  
  # Observed outcome  
  Y <- Y.1*A + Y.0*(1 - A)  
  # return data.frame  
  data.frame(w1, w2, w3, w4, A, Y, Y.1, Y.0)  
}  
# True ATE in the population  
set.seed(7777)  
ObsDataTrueATE <- generateData(n = 5000000)  
True_EY.1 <- mean(ObsDataTrueATE$Y.1)  
True_EY.0 <- mean(ObsDataTrueATE$Y.0)  
True_ATE <- True_EY.1-True_EY.0 ;True_ATE  
True_MOR <- (True_EY.1*(1-True_EY.0))/((1-True_EY.1)*True_EY.0);True_MOR  
  
cat("\n True_ATE:", abs(True_ATE))  
  
# Data for analysis  
set.seed(7722)  
ObsData <- generateData(n = 10000)  
write.csv(ObsData, "ObsData.csv")  
  
# Naive approach: conditional odds ratio  
naive <- glm(data = ObsData, Y ~ A + w1 + w2 + w3 + w4, family = binomial)  
summary(naive)  
exp(naive$coef[2])  
exp(confint(naive))
```

TMLE implementation by hand

Step 1 estimation and prediction of the model for the outcome (G-computation)

```
gm <- glm(Y ~ A + w1 + w2 + w3 + w4, family = binomial, data = ObsData)
# Prediction for A, A = 1 and, A = 0
QAW_0 <- predict(gm, type = "response")
Q1W_0 = predict(gm, newdata=data.frame(A = 1, ObsData[,c("w1", "w2", "w3", "w4")]), type = "response")
Q0W_0 = predict(gm, newdata=data.frame(A = 0, ObsData[,c("w1", "w2", "w3", "w4")]), type = "response")
# Estimated mortality risk difference
mean(Q1W_0 - Q0W_0)
# Estimated MOR
mean(Q1W_0)*(1-mean(Q0W_0))/((1-mean(Q1W_0))*mean(Q0W_0))
```

Step 2 estimation and prediction of the propensity score (ps)

```
psm <- glm(A ~ w1 + w2 + w3 + w4, family = binomial, data = ObsData)
gW = predict(psm, type = "response")
summary(gW)
```

Step 3 computation of H (clever covariates) and estimation of epsilon

```
H1W = ObsData$A / gW
H0W = (1-ObsData$A) / (1 - gW)
epsilon <- coef(glm(ObsData$Y ~ -1 + H0W + H1W + offset(qlogis(QAW_0)), family = binomial))
```

Step 4 Targeted estimate of the ATE and Marginal Odds Ratio

```
Q1W_1 <- plogis(qlogis(Q1W_0) + epsilon[2] / gW)
Q0W_1 <- plogis(qlogis(Q0W_0) + epsilon[1] / (1-gW))
```

ATE

```
ATEtmle1 <- mean(Q1W_1 - Q0W_1); ATEtmle1
cat("\n ATEtmle1_bias:", abs(True_ATE - ATEtmle1))
cat("\n ATEtmle1_rel_bias:",abs(True_ATE - ATEtmle1)/True_ATE,"%")
```

Marginal OR

```
tmle1.MOR <- mean(Q1W_1) * (1 - mean(Q0W_1)) / ((1 - mean(Q1W_1)) * mean(Q0W_1)); tmle1.MOR
```

Table to visualize the data

```
psi <- Q1W_1 - Q0W_1
library(DT)
df <- round(cbind(Q1W_0, Q0W_0, gW, eps1=epsilon[1], eps2=epsilon[2], psi), digits = 4)
datatable(head(df, n = nrow(df)), options = list(pageLength = 5, digits = 3))
```

Step 5 statistical inference (efficient influence curve)

Efficient influence curve ATE

```
EY1tmle <- mean(Q1W_1)
EY0tmle <- mean(Q0W_1)
d1 <- ((ObsData$A) * (ObsData$Y - Q1W_1)/gW) + Q1W_1 - EY1tmle
d0 <- ((1 - ObsData$A) * (ObsData$Y - Q0W_1))/(1 - gW) + Q0W_1 - EY0tmle
IC <- d1 - d0
n <- nrow(ObsData)
varHat.IC <- var(IC) / n
ATEtmle1CI <- c(ATEtmle1 - 1.96 * sqrt(varHat.IC), ATEtmle1 + 1.96 * sqrt(varHat.IC)); ATEtmle1;
ATEtmle1CI
```

```

# Efficient influence curve MOR
ICmor_tmle <- (1 - EY0tmle) / EY0tmle / (1 - EY1tmle)^2 * d1 - EY1tmle / (1 - EY1tmle) / EY0tmle^2 *
d0
varHat2.IC <- var(ICmor_tmle) / n
tmle1_ORCI <- tmle1.MOR + c(-1.96,1.96)*sqrt(varHat2.IC); tmle1.MOR; tmle1_ORCI

# Augmented inverse probability treatment weighting (AIPTW) estimator
EY1aiptw <- mean((ObsData$A) * (ObsData$Y - Q1W_0) / gW + Q1W_0)
EY0aiptw <- mean((1 - ObsData$A) * (ObsData$Y - Q0W_0) / (1 - gW) + Q0W_0)

AIPTW_ATE <- EY1aiptw - EY0aiptw; AIPTW_ATE
cat("\n AIPTW_bias:", abs(True_ATE - AIPTW_ATE))
cat("\n AIPTW_rel_bias:",abs(True_ATE - AIPTW_ATE) / True_ATE,"%")

D1 <- (ObsData$A) * (ObsData$Y - Q1W_0) / gW + Q1W_0 - EY1aiptw
D0 <- (1 - ObsData$A) * (ObsData$Y - Q0W_0) / (1 - gW) + Q0W_0 - EY0aiptw
varHat_AIPTW <- var(D1 - D0) / n

# AIPTW ATE 95%CI
ATEaiptw_CI <- c(AIPTW_ATE - 1.96 * sqrt(varHat_AIPTW), AIPTW_ATE + 1.96 *
sqrt(varHat_AIPTW)); AIPTW_ATE; ATEaiptw_CI

# AIPTW MOR 95%CI
AIPTW_MOR <- (EY1aiptw * (1 - EY0aiptw))/((1 - EY1aiptw) * EY0aiptw);AIPTW_MOR
ICmor_aiptw <- (1 - EY0aiptw) / EY0aiptw / (1 - EY1aiptw)^2 * D1 - EY1aiptw / (1 - EY1aiptw) /
EY0aiptw^2 * D0
varHat_AIPTW2 <- var(ICmor_aiptw) / n
MORaiptw_CI <-c(AIPTW_MOR - 1.96*sqrt(varHat_AIPTW2), AIPTW_MOR +
1.96*sqrt(varHat_AIPTW2)); AIPTW_MOR; MORaiptw_CI

# R-package tmle (base implementation includes SL.step, SL.glm and SL.glm.interaction)
library(tmle)
library(SuperLearner)
TMLE2 <- tmle(Y = ObsData$Y, A = ObsData$A, W = ObsData[,c("w1", "w2", "w3", "w4")], family =
"binomial")

#NOTE:
#Note that the tmle function default bounds the probabilities in the clever covariate denominators at 0.025.
#You can remove this bound by specifying gbound=0

ATEmtle2 <- TMLE2$estimates$ATE$psi;ATEmtle2
TMLE2$estimates$ATE$CI
MORMtle2 <- TMLE2$estimates$OR$psi;MORMtle2
TMLE2$estimates$OR$CI

cat("\n ATEmtle2_bias:", abs(True_ATE - ATEmtle2))
cat("\n ATEmtle2_Rel_bias:",abs(True_ATE - ATEmtle2) / True_ATE,"%")

```

R-package tmle with user-selected Super learner libraries

```
library(tmle)
```

```
library(SuperLearner)
```

```
SL.library <- c("SL.glm", "SL.step", "SL.step.interaction", "SL.glm.interaction", "SL.gam",  
              "SL.randomForest", "SL.rpart")
```

```
TMLE3 <- tmle(Y = ObsData$Y, A = ObsData$A, W = ObsData[, c("w1", "w2", "w3", "w4")],  
            family = "binomial", Q.SL.library = SL.library, g.SL.library = SL.library)
```

```
ATEtmle3 <- TMLE3$estimates$ATE$psi; ATEtmle3
```

```
TMLE3$estimates$ATE$CI
```

```
MORtmle3 <- TMLE3$estimates$OR$psi; MORtmle3
```

```
TMLE3$estimates$OR$CI
```

```
cat("\n ATEtmle3_bias:", abs(True_ATE - ATEtmle3))
```

```
cat("\n ATEtmle3_rel_bias:", abs(True_ATE - ATEtmle3) / True_ATE, "%")
```

Readers interested in simulating more complex dependence structures among the covariates W1-W4 could potentially use the R-package **simcausal** (Sofrygin O, van der Laan MJ, Neugebauer R (2015). *simcausal: Simulating Longitudinal Data with Causal Inference Applications*. R package version 0.5).

See the example here below:

```
library(simcausal)
```

```
M <- DAG.empty()
```

```
M <- M +
```

```
  node("w1", # age (0/1); 1 -> high age
```

```
    distr = "rbern",
```

```
    prob = .5) +
```

```
  node("w2", # ses (1/2/3/4/5); higher age, higher probability of belonging to upper class
```

```
    distr = "rcat.b1",
```

```
    probs = {
```

```
      plogis(-3.1 + 0.05*w1); # upper middle class, 4%
```

```
      plogis(-1.25 + 0.04*w1); # middle class, 22%
```

```
      plogis(-0.05 + 0.03*w1); # lower middle 49%
```

```
      plogis(-1.65 + 0.02*w1); # working class 16%
```

```
      plogis(-2.3 + 0.01*w1)}) +
```

```
  node("w3", #comorbidities (1/2/3/4/5);
```

```
    distr = "rcat.b1",
```

```
    probs = {
```

```
      plogis(-0.8 + 0.005*w1 + 0.1*w2);
```

```
      plogis(-0.1 + 0.010*w1 + 0.12*w2);
```

```
      plogis(-1.2 + 0.015*w1 + 0.15*w2);
```

```
      plogis(-1.6 + 0.020*w1 + 0.2*w2);
```

```
      plogis(-2.5 + 0.025*w1 + 0.25*w2)}) +
```

```
  node("w4", # stage (1/2/3/4); # the higher the worse
```

```
    distr = "rcat.b1",
```

```
    probs = {
```

```
      plogis(-1 + 0.01*w1 - 0.04*w2);
```

```
      plogis(-0.2 + 0.02*w1 - 0.05*w2);
```

```
      plogis(-0.8 + 0.03*w1 - 0.055*w2);
```

```
      plogis(-2 + 0.04*w1 - 0.1*w2)}) +
```

```
  node("a", # a = 0 mono therapy; a = 1 dualtherapy
```

```
    distr = "rbern",
```

```

    prob = plogis(-1.4 + 0.05*w1 + 0.25*w3 + 0.1*exp(w4))) +
node("y", #y = 0 -> death; y = 1 -> alive
    distr = "rbern",
    prob = plogis(-3.4 + 0.75*a - 0.1*w1 + 0.35*w2 + 0.25*w3 + 0.20*sqrt(1/w4) - 0.9*a*w2 + 1.1*a*w3))
Mset <- set.DAG(M)

# simulate observed data
Odat <- simcausal::sim(DAG = Mset, n = 10000, rndseed = 7693)

# specify the two interventions
a1 <- node("a", distr = "rbern", prob = 1)
Mset <- Mset + action("a1", nodes = a1)
a0 <- node("a", distr = "rbern", prob = 0)
Mset <- Mset + action("a0", nodes = a0)

# counterfactual data
dat <- simcausal::sim(DAG = Mset, actions = c("a1", "a0"), n = 1000000, rndseed = 7693)
head(dat[["a1"]]); head(dat[["a0"]])

# E(y) under a=1 (chemo)
Mset <- set.targetE(Mset, outcome = "y", param = "a1")
eval.target(Mset, data = dat)$res

# E(y) unter a=0 (chemo and radio)
Mset <- set.targetE(Mset, outcome = "y", param = "a0")
eval.target(Mset, data = dat)$res

# ATE (additive scale)
Mset <- set.targetE(Mset, outcome = "y", param = "a1-a0")
eval.target(Mset, data = dat)$res

# multiplicative scale
Mset <- set.targetE(Mset, outcome = "y", param = "a1/a0")
eval.target(Mset, data = dat)$res

#DAG
plotDAG(Mset, xjitter = 0.3, yjitter = 0.04, edge_attrs = list(width = 0.5, arrow.width = 0.2, arrow.size = 0.3),
vertex_attrs = list(size = 12, label.cex = 0.8))

```

2. STATA code for manual TMLE estimation of the ATE

```

cd "your path to the data"
import delimited ObsData.csv, clear
set more off

* Step 1: prediction model for the outcome Q0 (g-computation)
glm y a w1 w2 w3 w4, fam(binomial)
predict double QAW_0, mu
gen aa=a
replace a = 0
predict double Q0W_0, mu
replace a = 1
predict double Q1W_0, mu
replace a = aa
drop aa

```

*** Q to logit scale**

```
gen logQAW = log(QAW / (1 - QAW))
gen logQ1W = log(Q1W / (1 - Q1W))
gen logQ0W = log(Q0W / (1 - Q0W))
```

*** Step 2: prediction model for the treatment g0 (IPTW)**

```
glm a w1 w2 w3 w4, fam(binomial)
predict gw, mu
gen double H1W = a / gw
gen double H0W = (1 - a) / (1 - gw)
```

*** Step 3: Computing the clever covariate H(A,W) and estimating the parameter (epsilon) (MLE)**

```
glm y H1W H0W, fam(binomial) offset(logQAW) noconstant
mat a = e(b)
gen eps1 = a[1,1]
gen eps2 = a[1,2]
```

*** Step 4: update from Q0 to Q1**

```
gen double Q1W_1 = exp(eps1 / gw + logQ1W) / (1 + exp(eps1 / gw + logQ1W))
gen double Q0W_1 = exp(eps2 / (1 - gw) + logQ0W) / (1 + exp(eps2 / (1 - gw) + logQ0W))
```

*** Step 5: Targeted estimate of the ATE**

```
gen ATE = (Q1W_1 - Q0W_1)
summ ATE
global ATE = r(mean)
```

*** Step 6: Statistical inference (efficient influence curve)**

```
qui sum(Q1W_1)
gen EY1tmle = r(mean)
qui sum(Q0W_1)
gen EY0tmle = r(mean)

gen d1 = ((a * (y - Q1W_1)/gw)) + Q1W_1 - EY1tmle
gen d0 = ((1 - a) * (y - Q0W_1)/(1 - gw)) + Q0W_1 - EY0tmle

gen IC = d1 - d0
qui sum IC
gen varIC = r(Var) / r(N)

global LCI = $ATE - 1.96*sqrt(varIC)
global UCI = $ATE + 1.96*sqrt(varIC)
display "ATE:" %05.4f $ATE _col(15) "95%CI: " %05.4f $LCI "," %05.4f $UCI
```

Alternatively, one may consider exporting the data from Stata ("export delimited using "your path/yourdata.csv", replace") and then reading the data into R (read.csv("your path/yourdata.csv")) and follow the steps explained in the main manuscript.

3. Link to our GitHub repository for the implementation of TMLE in Stata:

The following link provides access to a developmental free testing version of TMLE implemented in Stata software.

More details and instructions for installation are provided at the following links:

<https://github.com/migariane/meltmlle>
<https://github.com/migariane/weltmlle>

Example

```
*****
* eltmle Y X Z [if] [,tmle tmlebgam]
*****
use http://www.stata-press.com/data/r14/cattaneo2.dta
describe
gen lbw = cond(bweight<2500,1,0.)
lab var lbw "Low birthweight, <2500 g"
save "your path/cattaneo2.dta", replace
cd "your path"
```

```
eltmle lbw mbsmoke mage medu prenatal mmarried, tmle
```

To replicate the results in the **box 9** from the tutorial you can type:

```
cd "your path to the data"
import delimited ObsData.csv, clear
set more off
```

```
eltmle y a w1 w2 w3 w4, tmle
```

4. R code for simulations (Table 2)

```
# Super Learner libraries
SL.library <- c("SL.glm", "SL.step", "SL.step.interaction", "SL.glm.interaction",
               "SL.gam", "SL.randomForest", "SL.glmnet")

# Data generation A: dual misspecification for the model of the outcome and treatment
set.seed(7777)
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=0)
  w4 <- round(runif(n, min=0, max=5), digits=0)
  A <- rbinom(n, size=1, prob= plogis(-5 + 0.5*w2 + 0.25*w3 + 0.6*w4 + 0.4*w2*w4))
  # counterfactuals
  Y.1 <- rbinom(n, size=1, prob= plogis(-1 + 1 -0.1*w1 + 0.35*w2 + 0.25*w3 + 0.20*w4 + 0.15*w2*w4))
  Y.0 <- rbinom(n, size=1, prob= plogis(-1 + 0 -0.1*w1 + 0.35*w2 + 0.25*w3 + 0.20*w4 + 0.15*w2*w4))
  # Observed outcome
  Y <- Y.1*A + Y.0*(1 - A)
  # return data.frame
  data.frame(w1, w2, w3, w4, A, Y, Y.1, Y.0)
}

# Data generation B: misspecification for the model of the outcome
set.seed(7777)
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=0)
  # w4 <- round(runif(n, min=0, max=5), digits=0)
  # A <- rbinom(n, size=1, prob= plogis(-5 + 0.7*w1 + 0.5*w2 + 0.25*w3 + 0.6*w4))
  # counterfactuals
  # Y.1 <- rbinom(n, size=1, prob= plogis(-1 + 1 -0.1*w1 + 0.35*w2 + 0.25*w3 + 0.15*w2*w4))
  # Y.0 <- rbinom(n, size=1, prob= plogis(-1 + 0 -0.1*w1 + 0.35*w2 + 0.25*w3 + 0.15*w2*w4))
  # Observed outcome
  # Y <- Y.1*A + Y.0*(1 - A)
  # return data.frame
  # data.frame(w1, w2, w3, w4, A, Y, Y.1, Y.0)
#}
```



```

# True ATE
ObsDataTrueATE <- generateData(n=5000000)
True_ATE <- mean(ObsDataTrueATE$Y.1 - ObsDataTrueATE$Y.0);True_ATE
True_EY.1 <- mean(ObsDataTrueATE$Y.1)
True_EY.0 <- mean(ObsDataTrueATE$Y.0)
True_MOR <- (True_EY.1 * (1-True_EY.0)) / ((1-True_EY.1) * True_EY.0);True_MOR

#Simulations
library(tmlle)
library(SuperLearner)
R <- 1000
#Empty vectors
naive_OR <- rep(NA,R)
ATEtmlle1 <- rep(NA,R)
MORtmlle1 <- rep(NA,R)
AIPTW <- rep(NA,R)
MOR_AIPTW <- rep(NA,R)
ATEtmlle2 <- rep(NA,R)
MORtmlle2 <- rep(NA,R)
ATEtmlle3 <- rep(NA,R)
MORtmlle3 <- rep(NA,R)

for(r in 1:R){
print(paste("This is simulation run number",r))
CancerData <- generateData(n=1000)

# ATE naive approach
naive_OR[r] <- exp(glm(data = CancerData, Y ~ A + w1 + w2 + w3 + w4, family = "binomial")$coef[2])

# TMLE implementation by hand
# Step 1
gm <- glm(Y ~ A + w1 + w2 + w3 + w4, family="binomial", data=CancerData)

# Prediction for A, A=1 and, A=0
QAW <- predict(gm)
Q1W = predict(gm, newdata=data.frame(A = 1, CancerData[,c("w1","w2","w3","w4")]))
Q0W = predict(gm, newdata=data.frame(A = 0, CancerData[,c("w1","w2","w3","w4")]))

# Step 2 estimation of the propensity score (ps)
psm <- glm(A ~ w1 + w2 + w3 + w4, family = binomial, data=CancerData)
gW = predict(psm, type = "response")
g1W = (1 / gW)
g0W = (-1 / (1-gW))

# Step 3 computation of H and estimation of epsilon
HAW <- (CancerData$A / gW - (1-CancerData$A) / (1 - gW))
H1W = (1/gW)
H0W = (-1 / (1 - gW))
epsilon <- coef(glm(CancerData$Y ~ -1 + HAW + offset(QAW), family = "binomial"))

# Step 4 updated ATE
ATEtmlle1[r] <- mean(plogis(Q1W + epsilon * H1W) - plogis(Q0W + epsilon * H0W))

# Step 5 updated MOR
T1.EY1 <- mean(plogis(Q1W + epsilon * H1W))
T1.EY0 <- mean(plogis(Q0W + epsilon * H0W))
MORtmlle1[r] <- (T1.EY1 * (1-T1.EY0)) / ((1-T1.EY1) * T1.EY0)

```

```

# Augmented inverse probability treatment weight (AIPTW) estimator
AIPTW[r] <- mean((HAW*(CancerData$Y - plogis(QAW)) + (plogis(Q1W)-plogis(Q0W))))
AIPTW1 <- mean(CancerData$A * (CancerData$Y - plogis(Q1W)) / gW + plogis(Q1W) )
AIPTW0 <- mean((1- CancerData$A) * (CancerData$Y - plogis(Q0W)) / (1-gW) + plogis(Q0W))
MOR_AIPTW[r] <- (AIPTW1 * (1- AIPTW0)) / ((1- AIPTW1) * AIPTW0)

# R-package tmle (base implementation includes SL.step, SL.glm and SL.glm.interaction)
ATE2 <- tmle(Y=CancerData$Y, A=CancerData$A,
W=CancerData[,c("w1","w2","w3","w4")], family="binomial")
ATEtmle2[r] <- ATE2$estimates$ATE$psi
CORtmle2[r] <- ATE2$estimates$OR$psi

# Improved Super learner
ATE3 <- tmle(Y = CancerData$Y, A=CancerData$A, W=CancerData[,c("w1","w2","w3","w4")],
family="binomial", Q.SL.library=SL.library, g.SL.library=SL.library)
ATEtmle3[r] <- ATE3$estimates$ATE$psi
MORTmle3[r] <- ATE3$estimates$OR$psi
}

# Mean naive
mean(naive_OR)
# Mean AIPTW
mean(AIPTW)
mean(MOR_AIPTW)
# Estimate of TMLE
mean(ATEtmle1)
mean(MORTmle1)
# Estimate of TMLE + SL
mean(ATEtmle2)
mean(MORTmle2)
# Estimate of TMLE + SL2
mean(ATEtmle3)
mean(MORTmle3)
save.image("your path\\results.RData")

```

5. Super Learner, cross-validation and ensemble learning

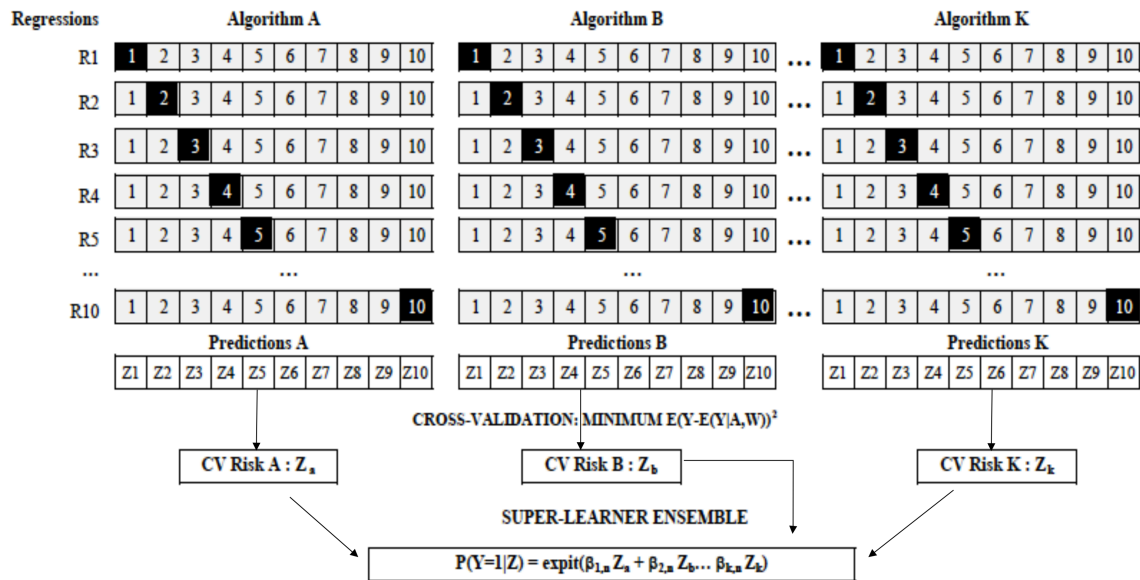
With TMLE we can call the R-package Super-Learner (SL). The SL combines cross-validation and ensemble learning techniques to improve model prediction and performance.¹ The SL algorithm provides a system based on V-fold cross-validation²⁻⁴ (e.g. 10-fold) to combine multiple algorithms into an improved algorithm and returns a function that can be used for prediction in new datasets. The principal interest in calling the Super-Learner is to obtain the less-biased prediction estimates of $\bar{Q}^0(A, \mathbf{W})$ and $g(A, \mathbf{W})$.

Briefly, the SL algorithm can be described in four steps:

- 1) First split the data into blocks of equal size (i.e. ten blocks of 100 observations for a sample size of 1,000 units and 10-fold cross-validation) and fit each of the selected algorithms on the training set (i.e. the 9 grey blocks in Supplementary Figure 2).
- 2) Then, predict the estimated probabilities of the outcome (Y) using the validation set (i.e. the black blocks in Supplementary Figure 2) for each algorithm, based on the corresponding training set;

- 3) Repeat steps 1 and 2 for each of the ten blocks (R2-R10 in Supplementary Figure 1).
 - 4) Afterwards, the SL estimates the cross-validation risk for each algorithm, e.g. the sum of the squared differences between the predicted and actual values of Y.
 - 5) Finally, the SL chooses the weighted combination of algorithms that minimises the cross-validated risk (e.g. mean squared error). The selection of the weighted combination is based on the stacking regressions method, which forms a linear combination of different predictors to give improved prediction accuracy.^{1,3}
- For a binary outcome, this relates to fitting a logistic regression model where the ensemble of cross-validated predictions, for each algorithm (Z) are used as independent variables to predict the outcome (Y).

Supplementary Figure 1.



References

1. Breiman L. Stacked regressions. *Machine learning*. 1996;24(1):49--64.
2. Efron B, Efron B. *The jackknife, the bootstrap and other resampling plans*. Vol 38: SIAM; 1982.
3. van der Laan MJ, Polley EC, Hubbard AE. Super learner. *Stat Appl Genet Mol Biol*. 2007;6:Article25.
4. Gruber S, van der Laan M. tml: An R Package for Targeted Maximum Likelihood Estimation. *U.C. Berkeley Division of Biostatistics Working Paper Series*. 2011.