1. Hajek as a weighted least square estimator

The WLS residual can be written into matrix form

$$(X\beta - Y)^T W (X\beta - Y) \tag{1}$$

where W is the diagonal matrix with entries of weights

$$\hat{\beta} = \arg\min_{\beta} \left\{ (X\beta - Y)^T W (X\beta - Y) \right\} \tag{2}$$

F.O.C.

$$\nabla_{\hat{\beta}} \left\{ \beta^T X^T W X \beta - \beta^T X^T W Y - Y^T W X \beta + Y^T W Y \right\} = 0 \tag{3}$$

$$\begin{aligned} X^T W X \hat{\beta} &= X^T W Y \\ \hat{\beta} &= (X^T W X)^{-1} X^T W Y \end{aligned} \tag{4}$$

It's numerically identical to W times estimator of the OLS problem with transformed data $Y_i^* = Y_i w_i$, $X_i^* = X_i w_i$
Note that respectively,

$$w_i = \begin{cases} \frac{1}{\hat{e}(X_i)} & Z_i = 1 \\ \frac{1}{1-\hat{e}(X_i)} & Z_i = 0 \end{cases} \tag{5}$$

The OLS problem can be split into 2 parts,

$$\begin{cases} Y_i w_i = \alpha_i w_i & Z_i = 0 \\ Y_i w_i = \alpha_i w_i + \beta Z_i w_i & Z_i = 1 \end{cases} \tag{6}$$

Multiply w_i in both parts are subtract them (so as to get rid of α)

$$\hat{\beta} = \frac{\sum \frac{Z_i Y_i}{\hat{e}(X_i)}}{\sum \frac{Z_i}{e(X_i)}} - \frac{\sum \frac{(1-Z_i)Y_i}{1-\hat{e}(X_i)}}{\sum \frac{(1-Z_i)}{1-\hat{e}(X_i)}} = \tau^{hajek} \tag{7}$$

Problem 2

```
# A DIY function of Matching Estimator
# Some preparations: Distance Measure
Edistance <- function(X, Y)
{
  if (length(X) != length(Y)){print("Error: Length Not Matched")}
  else{return(sqrt(sum((X-Y)^2)))}
}
```

```
Mdistance <- function(X, Y, cov)
{
  if (length(X) != length(Y)){print("Error: Length Not Matched")}
  else{return(t(X - Y) %*% solve(cov) %*% (X-Y))}
}
kNN <- function(x0, x, y, numberOfMatch = 1, dis = "Euclidean", COV = 0)
{
  # x0 shall be a vector and x shall be a matrix, y shall be the corresponding vector
  # This function returns a numeric value if x0 is a number, and a vector if x0 is a v
  if (dis == "Euclidean")
  {
    rankDis = c()
    for (i in 1:nrow(x))
    {
      rankDis = c(rankDis, Edistance(x0, x[i,]))
    }
    rankDis = rank(rankDis)
    Y_hat = mean(y[which(rankDis<=numberOfMatch)])
    X_hat = x[which(rankDis<=numberOfMatch),]
    return(list("Y" = Y_hat, "X" = X_hat))
  }
  else if (dis == "M")
  {
    if (COV == 0){print("Error: covariance matrix not provided.")}
    else{
      rankDis = c()
      for (i in 1:nrow(x))
      {
        rankDis = c(rankDis, Mdistance(x0, x[i,], COV))
      }
      rankDis = rank(rankDis)
      Y_hat = mean(y[which(rankDis<=numberOfMatch)])
      X_hat = x[which(rankDis<=numberOfMatch),]
      return(list("Y" = Y_hat, "X" = X_hat))
    }
  }
}
MyMatching <- function(y, tr, x, numberOfMatch = 1, dis = "Euclidean", COV = 0)
{
  # First deal with the treatment group
  Y1_treat = y[tr == 1]
```

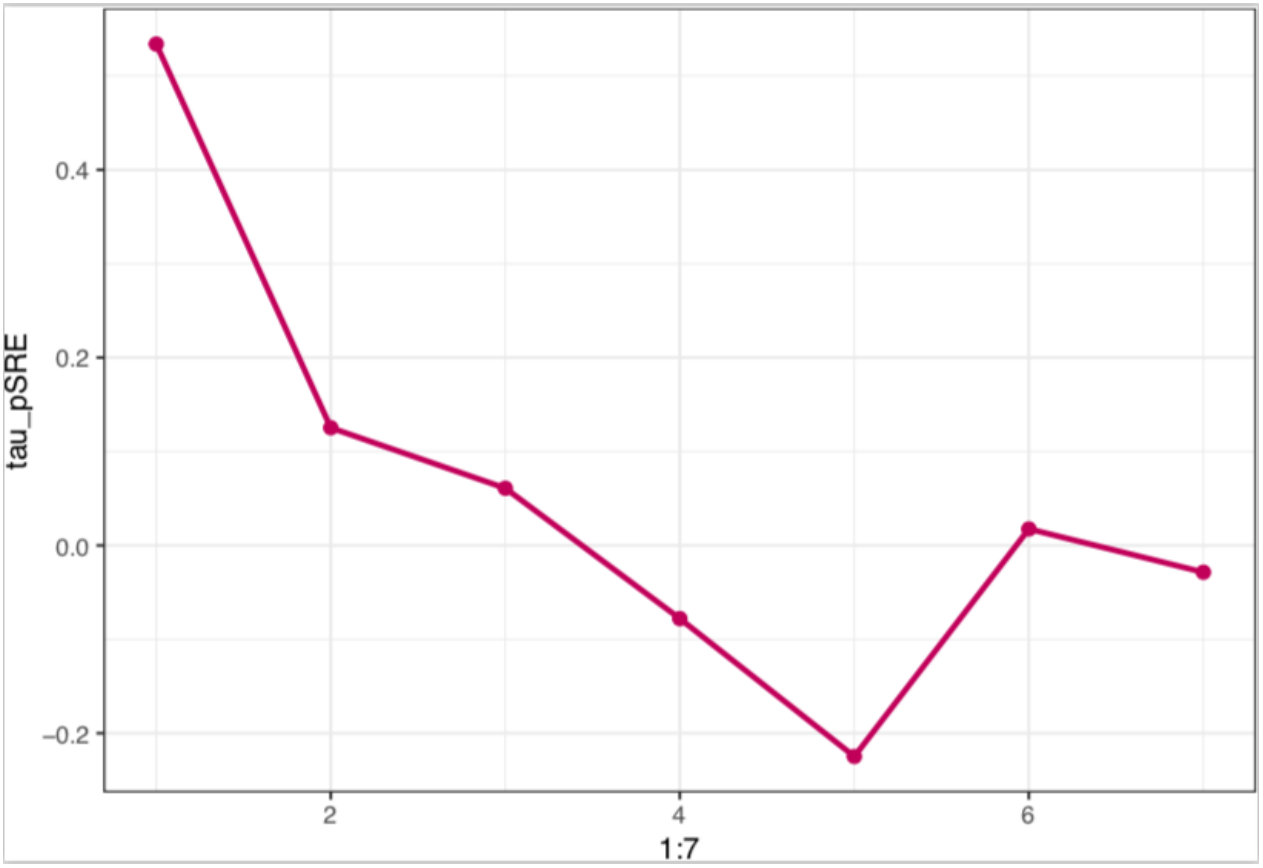
```
  Y0_treat = c()
  for (i in 1:length(y[tr == 1]))
  {
    Y0_treat = c(Y0_treat, kNN(x[i,], x[tr == 0,], y[tr == 0], numberOfMatch, dis, COV)$
  }
  # Then deal with the control group
  Y0_control = y[tr == 0]
  Y1_control = c()
  for (i in 1:length(y[tr == 0]))
  {
    Y1_control = c(Y1_control, kNN(x[i,], x[tr == 1,], y[tr == 1], numberOfMatch, dis, C
  }
  # Calculate the test statistics (matching estimator and bias-corrected matching esti
  tau_m = mean(c(Y1_treat, Y1_control) - c(Y0_treat, Y0_control))
    # Fit two models for Y0 and Y1, respectively
  model0 <- lm(Y1_treat~x[tr == 1,])$coef
  model1 <- lm(Y0_control~x[tr == 0,])$coef
  bias = 0
  for (i in 1:length(y[tr == 1]))
  {
    predx = c(1, x[i,]) %*% model0
    prednn = cbind(1, kNN(x[i,], x[tr == 0,], y[tr == 0], numberOfMatch, dis)$X) %*% mod
    bias = bias + mean(predx - prednn)
  }
  for (i in 1:length(y[tr == 0]))
  {
    predx = c(1, x[i,]) %*% model1
    prednn = cbind(1, kNN(x[i,], x[tr == 1,], y[tr == 1], numberOfMatch, dis)$X) %*% mod
    bias = bias + mean(prednn - predx)
  }
  bias = bias / length(y)
  tau_mbc = tau_m - bias
  return(list("tau_m" = tau_m, "tau_mbc" = tau_mbc))
}
```

```
data("nhanes_bmi")
z = nhanes_bmi$School_meal
y = nhanes_bmi$BMI
x = as.matrix(nhanes_bmi[, -c(1, 2)])
pscore = glm(z ~ x, family = binomial)$fitted.values

# Propensity Score Estimator
```

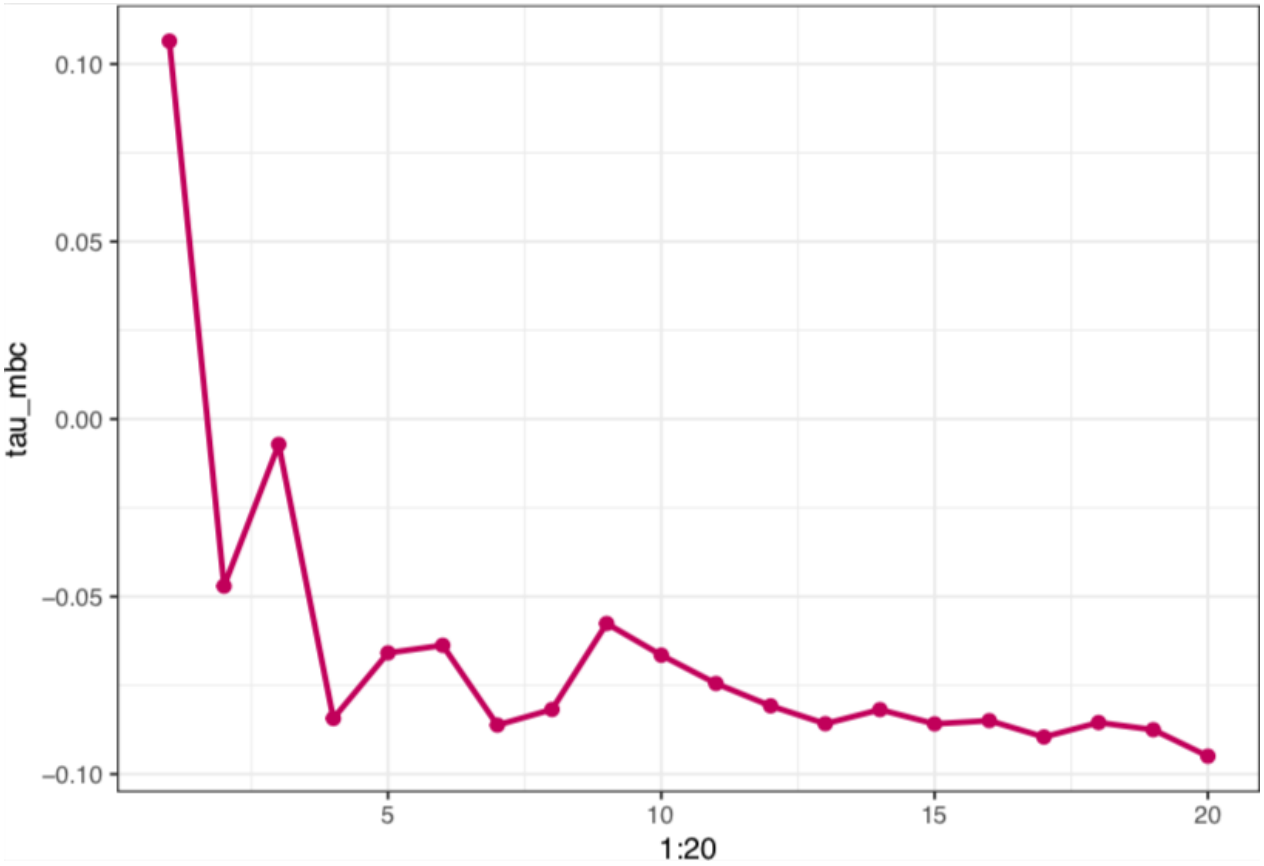
```
stat_SRE <- function(stratum, treatment, y){
  # Assume in our case that the stratum in arranged and indexed.
  # If not, then re-code it to an index.
  number = length(unique(stratum))
  tau = 0
  wil = 0
  r = 0
  # Calculate the three statistics as defined
  for (i in 1:number){
    tempy = y[stratum == i]
    tempt = treatment[stratum == i]
    n = length(tempy)
    pi = n/length(y)
    tau = tau + pi*(mean(tempy[tempt == 1] - mean(tempy[tempt == 0])))
    wil = wil + wilcox.test(tempy[tempt == 1], tempy[tempt == 0])$statistic / (n+1)
    tempy = tempy - mean(tempy)
  }
  y <- rank(y)
  for (i in 1:length(y)){
    if (treatment[i] == 1){
      r = r + y[i]
    }
  }
  return(c(taus = tau, wilcoxon = wil, alignedRank = r))
}
# Here we obtain the obs. values
tau_pSRE = c()
for (i in 1:7){
  stratum = floor(pscore*i) + 1
  obsValue <- stat_SRE(stratum, z, y)
  tau_pSRE = c(tau_pSRE, obsValue[1])
}
```

```
## Warning in wilcox.test.default(tempy[tempt == 1], tempy[tempt == 0]):
## cannot compute exact p-value with ties
```

```
ggplot()+
  theme_bw() +
  geom_point(aes(x = 1:7, y = tau_pSRE), color = 'maroon', size = 2) +
  geom_line(aes(x = 1:7, y = tau_pSRE), color = 'maroon', size = 1)
```

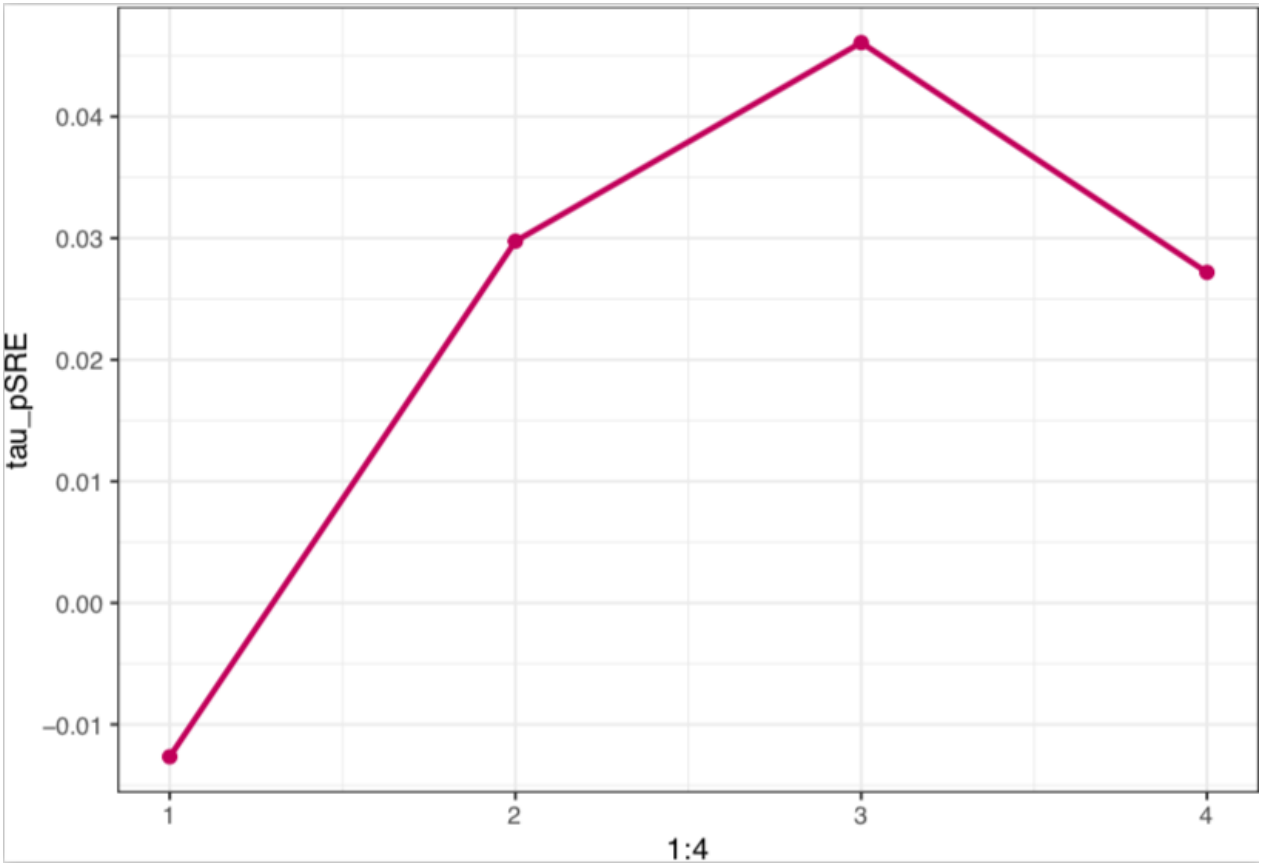



```
# Matching Estimator (Bias-Corrected)
tau_mbc = c()
se_tau = c()
for (i in 1:20)
{
  model = Match(y, z, x, estimand = "ATE", M = i, BiasAdjust = T)
  tau_mbc = c(tau_mbc, model$est)
  se_tau = c(se_tau, model$se)
}
ggplot()+
  theme_bw() +
  geom_point(aes(x = 1:20, y = tau_mbc), color = 'maroon', size = 2) +
  geom_line(aes(x = 1:20, y = tau_mbc), color = 'maroon', size = 1)
```

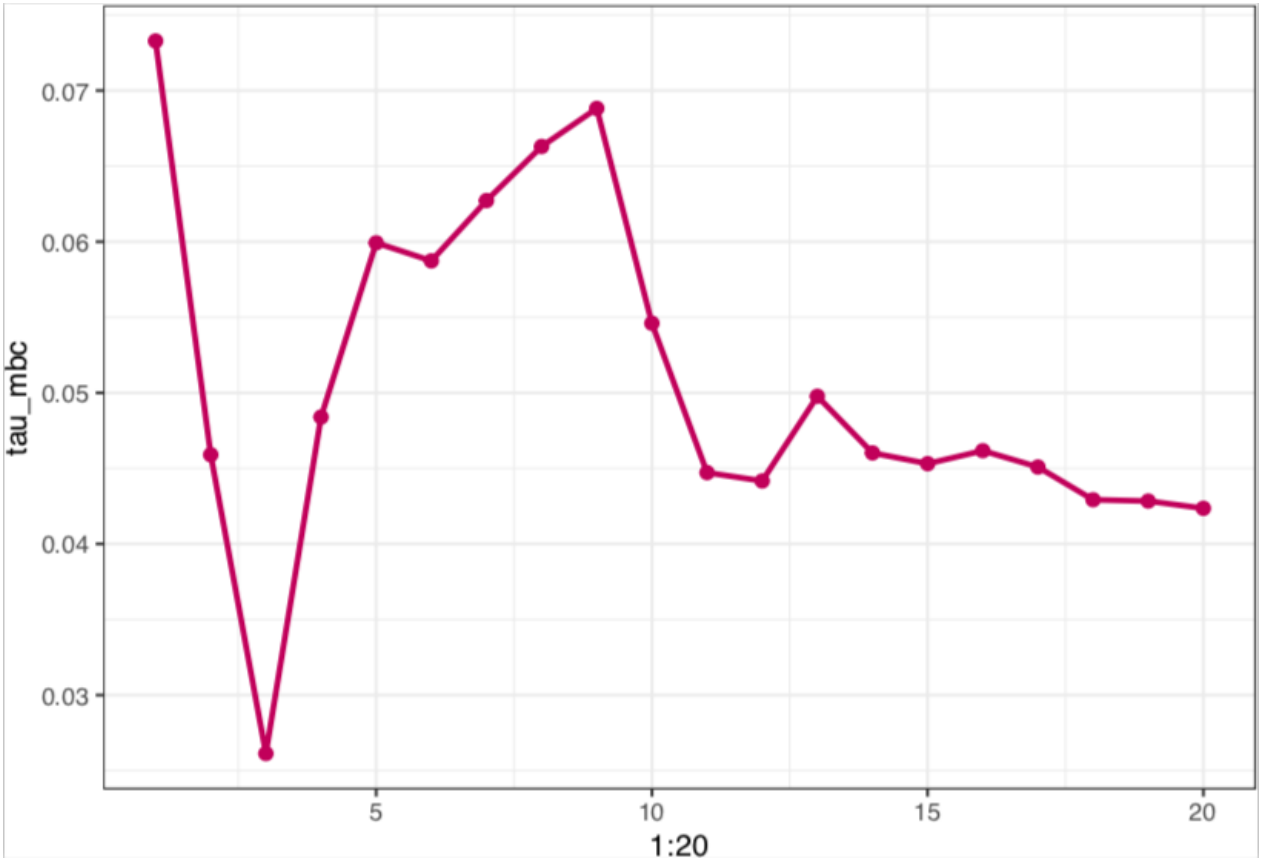



```
karolinska = read.table("karolinska.txt", header = TRUE)

z = karolinska$HighVolDiagHosp
y = 1 - (karolinska$YearsSurvivingAfterDiagnosis == 1)
x = as.matrix(karolinska[, c(3, 4, 5)])

pscore = glm(z ~ x, family = binomial)$fitted.values

# Propensity Score Estimator
stat_SRE <- function(stratum, treatment, y){
  # Assume in our case that the stratum in arranged and indexed.
  # If not, then re-code it to an index.
  number = length(unique(stratum))
  tau = 0
  wil = 0
  r = 0
  # Calculate the three statistics as defined
  for (i in 1:number){
    tempy = y[stratum == i]
```

```
    tempt = treatment[stratum == i]
    n = length(tempy)
    pi = n/length(y)
    tau = tau + pi*(mean(tempy[tempt == 1] - mean(tempy[tempt == 0])))
    tempy = tempy - mean(tempy)
  }
  y <- rank(y)
  for (i in 1:length(y)){
    if (treatment[i] == 1){
      r = r + y[i]
    }
  }
  return(c(taus = tau, alignedRank = r))
}
# Here we obtain the obs. values
tau_pSRE = c()
for (i in 1:4){
  stratum = floor(pscore*i) + 1
  obsValue <- stat_SRE(stratum, z, y)
  tau_pSRE = c(tau_pSRE, obsValue[1])
}
ggplot()+
  theme_bw() +
  geom_point(aes(x = 1:4, y = tau_pSRE), color = 'maroon', size = 2) +
  geom_line(aes(x = 1:4, y = tau_pSRE), color = 'maroon', size = 1)
```




```
# Matching Estimator (Bias-Corrected)
tau_mbc = c()
se_tau = c()
for (i in 1:20)
{
  model = Match(y, z, x, estimand = "ATE", M = i, BiasAdjust = T)
  tau_mbc = c(tau_mbc, model$est)
  se_tau = c(se_tau, model$se)
}
ggplot()+
  theme_bw() +
  geom_point(aes(x = 1:20, y = tau_mbc), color = 'maroon', size = 2) +
  geom_line(aes(x = 1:20, y = tau_mbc), color = 'maroon', size = 1)
```




```
library("car")
```

```
## Warning: package 'car' was built under R version 3.5.2
```

```
## Loading required package: carData
```

```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

```
## The following object is masked from 'package:purrr':
##
##     some
```

```
library("Matching")

## experimental data
lalonde = read.csv("cps1re74.csv", sep = " ")
```

```
y = lalonde$re78
z = lalonde$treat
x = as.matrix(lalonde[, c("age", "educ", "black",
                          "hispan", "married", "nodegree",
                          "re74", "re75")])

## analysis the randomized experiment via
# Lin's Estimator
xc = scale(x)
linols = lm(y ~ z + xc + z*xc)
tau_Lin = linols$coefficients[2]
round(summary(linols)$coef[2, ], 4)
```

```
##   Estimate Std. Error    t value   Pr(>|t|)
## -3689.8516  2457.3996    -1.5015     0.1332
```

```
sqrt(hccm(linols)[2, 2])
```

```
## [1] 3428.439
```

```
# Regression Imputation Shall return the same results as Lin
model1 = lm(y[z == 1]~x[z == 1,])
model0 = lm(y[z == 0]~x[z == 0,])
tau_reg = mean(cbind(1, x) %*% model1$coefficients - cbind(1, x) %*% model0$coefficients
tau_Lin - tau_reg
```

```
##             z
## 3.187779e-09
```

```
# Propensity score stratification
pscore = glm(z ~ x, family = binomial)$fitted.values
tau_pSRE = c()
for (i in 2:5){
  stratum = floor(pscore*i) + 1
  obsValue <- stat_SRE(stratum, z, y)
  tau_pSRE = c(tau_pSRE, obsValue[1])
}
tau_pSRE
```

```
##      taus      taus      taus      taus
## -8506.495 -7804.194 -7706.861 -7625.539
```

```
# IPW estimator
# With no truncation
```

```
truncpscore = c(0,1)
pscore = glm(z ~ x, family = binomial)$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_1 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
ipw_hajek_1 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 - z

# With certain truncation
truncpscore = c(0.1,0.9)
pscore = glm(z ~ x, family = binomial)$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_2 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
ipw_hajek_2 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 - z

# Doubly Robust Estimator
outcome1 = glm(y ~ x, weights = z, family = gaussian)$fitted.values
outcome0 = glm(y ~ x, weights = (1 - z), family = gaussian)$fitted.values
res1 = y - outcome1
res0 = y - outcome0
tau_dr = mean(outcome1 - outcome0) + mean(z*res1/pscore - (1 - z)*res0/(1 - pscore))

print(paste("Lin's estimator is ", tau_Lin, sep = ""))
```

```
## [1] "Lin's estimator is -3689.8515880728"
```

```
print(paste("Regression Imputation gives us an estimate same as Lin's ", tau_reg, sep =
```

```
## [1] "Regression Imputation gives us an estimate same as Lin's -3689.85158807599"
```

```
print(paste("pscore stratification's estimator is ", tau_pSRE, sep = ""))
```

```
## [1] "pscore stratification's estimator is -8506.49536105039"
## [2] "pscore stratification's estimator is -7804.1941784074"
## [3] "pscore stratification's estimator is -7706.8611458836"
## [4] "pscore stratification's estimator is -7625.53852433987"
```

```
print(paste("IPW estimator (hovic-thompson) without truncation is ",ipw_1, " and the haj
```

```
## [1] "IPW estimator (hovic-thompson) without truncation is -10452.7456142986 and the h
```

```
print(paste("IPW estimator (hovic-thompson) with truncation is ",ipw_2, " and the hajek
```

```
## [1] "IPW estimator (hovic-thompson) with truncation is -15955.5388374637 and the haje
```

```
print(paste("The doubly robust estimator is ", tau_dr))
```

```
## [1] "The doubly robust estimator is  -3688.65001081252"
```

```
# Propensity score stratification
pscore = glm(z ~ x, family = binomial(link = "probit"))$fitted.values
tau_pSRE = c()
for (i in 2:5){
  stratum = floor(pscore*i) + 1
  obsValue <- stat_SRE(stratum, z, y)
  tau_pSRE = c(tau_pSRE, obsValue[1])
}

# IPW estimator
# With no truncation
truncpscore = c(0,1)
pscore = glm(z ~ x, family = binomial(link = "probit"))$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_1 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
ipw_hajek_1 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 - z

# With certain truncation
truncpscore = c(0.1,0.9)
pscore = glm(z ~ x, family = binomial(link = "probit"))$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_2 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
ipw_hajek_2 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 - z

# Doubly Robust Estimator
outcome1 = glm(y ~ x, weights = z, family = gaussian)$fitted.values
outcome0 = glm(y ~ x, weights = (1 - z), family = gaussian)$fitted.values
res1 = y - outcome1
res0 = y - outcome0
tau_dr = mean(outcome1 - outcome0) + mean(z*res1/pscore - (1 - z)*res0/(1 - pscore))

print("If we fit e(x) by probit model,")
```

```
## [1] "If we fit e(x) by probit model,"
```

```
print(paste("Lin's estimator is ", tau_Lin, sep = ""))
```

```
## [1] "Lin's estimator is -3689.8515880728"
```

```
print(paste("Regression Imputation gives us an estimate same as Lin's ", tau_reg, sep =
```

```
## [1] "Regression Imputation gives us an estimate same as Lin's -3689.85158807599"
```

```
print(paste("pscore stratification's estimator is ", tau_pSRE, sep = ""))
```

```
## [1] "pscore stratification's estimator is -8506.49536105039"
## [2] "pscore stratification's estimator is -7826.07775869297"
## [3] "pscore stratification's estimator is -7199.12284967037"
## [4] "pscore stratification's estimator is -7185.93488163915"
```

```
print(paste("IPW estimator (hovic-thompson) without truncation is ",ipw_1, " and the haj
```

```
## [1] "IPW estimator (hovic-thompson) without truncation is -8738.13952518101 and the h
```

```
print(paste("IPW estimator (hovic-thompson) with truncation is ",ipw_2, " and the hajek
```

```
## [1] "IPW estimator (hovic-thompson) with truncation is -15953.1987455341 and the haje
```

```
print(paste("The doubly robust estimator is ", tau_dr))
```

```
## [1] "The doubly robust estimator is  -3686.27091355767"
```

```
print("The doubly robust estimator is the one closest to the golden rule estimation.")
```

```
## [1] "The doubly robust estimator is the one closest to the golden rule estimation."
```

```
library(MatchIt)
```

```
##
## Attaching package: 'MatchIt'
```

```
## The following object is masked _by_ '.GlobalEnv':
##
##     lalonde
```

```
data <- read.csv("FDA-Carpenter.csv")
# We perform similar data treatment
# The democrat is the senate is the treatment indicator, acttime is Y, and others are

## rescaling
data$hospdisc <- data$hospdisc/100000
data$natreg <- data$natreg/100
data$stafcder <- data$stafcder/100
data$prevgenx <- data$prevgenx/100
data$hhosleng <- data$hhosleng/10
data$condavg3 <- data$condavg3/10
data$orderent <- data$orderent/10
data$vandavg3 <- data$vandavg3/10
data$wpnoavg3 <- data$wpnoavg3/100
```

```
z <- data$demsnmaj
y <- data$acttime
x <- as.matrix(data %>%
  dplyr::select(-demsnmaj, -acttime))
## analysis the randomized experiment via
# Lin's Estimator
xc = scale(x)
linols = lm(y ~ z + xc + z*xc)
tau_Lin = linols$coefficients[2]
round(summary(linols)$coef[2, ], 4)
```

```
##   Estimate Std. Error    t value   Pr(>|t|)
##   -13.8625     4.4678    -3.1027     0.0021
```

```
sqrt(hccm(linols)[2, 2])
```

```
## [1] 4.389857
```

```
# Regression Imputation Shall return the same results as Lin
model1 = lm(y[z == 1]~x[z == 1,])
model0 = lm(y[z == 0]~x[z == 0,])
tau_reg = mean(cbind(1, x) %*% model1$coefficients - cbind(1, x) %*% model0$coefficients

# Propensity score stratification
pscore = glm(z ~ x, family = binomial)$fitted.values
tau_pSRE = c()
for (i in 2:5){
  stratum = floor(pscore*i) + 1
  obsValue <- stat_SRE(stratum, z, y)
  tau_pSRE = c(tau_pSRE, obsValue[1])
}
tau_pSRE
```

```
##      taus      taus      taus      taus
## -11.78213 -13.49131 -14.69429 -16.93254
```

```
# IPW estimator
# With no truncation
truncpscore = c(0,1)
pscore = glm(z ~ x, family = binomial)$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_1 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
ipw_hajek_1 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 -
```

```
# With certain truncation
truncpscore = c(0.1,0.9)
pscore = glm(z ~ x, family = binomial)$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_2 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
ipw_hajek_2 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 - z

# Doubly Robust Estimator
outcome1 = glm(y ~ x, weights = z, family = gaussian)$fitted.values
outcome0 = glm(y ~ x, weights = (1 - z), family = gaussian)$fitted.values
res1 = y - outcome1
res0 = y - outcome0
tau_dr = mean(outcome1 - outcome0) + mean(z*res1/pscore - (1 - z)*res0/(1 - pscore))

print(paste("Lin's estimator is ", tau_Lin, sep = ""))
```

```
## [1] "Lin's estimator is -13.8624685450355"
```

```
print(paste("Regression Imputation gives us an estimate same as Lin's ", tau_reg, sep =
```

```
## [1] "Regression Imputation gives us an estimate same as Lin's -13.8624685450355"
```

```
print(paste("pscore stratification's estimator is ", tau_pSRE, sep = ""))
```

```
## [1] "pscore stratification's estimator is -11.7821330501416"
## [2] "pscore stratification's estimator is -13.4913054500575"
## [3] "pscore stratification's estimator is -14.6942924219253"
## [4] "pscore stratification's estimator is -16.9325445893505"
```

```
print(paste("IPW estimator (hovic-thompson) without truncation is ",ipw_1, " and the haj
```

```
## [1] "IPW estimator (hovic-thompson) without truncation is -14.6313842730615 and the h
```

```
print(paste("IPW estimator (hovic-thompson) with truncation is ",ipw_2, " and the hajek
```

```
## [1] "IPW estimator (hovic-thompson) with truncation is -14.6646978648039 and the haje
```

```
print(paste("The doubly robust estimator is ", tau_dr))
```

```
## [1] "The doubly robust estimator is  -12.6943681855002"
```

```
data <- read.csv("Visibility-Koch.csv")
data <- subset(data, subset=c(repman==1 & voter==1))
data <- na.omit(data)
```

```
y = data$prcanid
z = 1 - data$rvisman
x = data %>%
  dplyr::select("repcan1", "goppty", "rideo", "rproj", "repft", "aware") %>%
  as.matrix

## analysis the randomized experiment via
# Lin's Estimator
xc = scale(x)
linols = lm(y ~ z + xc + z*xc)
tau_Lin = linols$coefficients[2]
round(summary(linols)$coef[2, ], 4)
```

```
##   Estimate Std. Error    t value   Pr(>|t|)
##    -0.0251     0.0602    -0.4168     0.6769
```

```
sqrt(hccm(linols)[2, 2])
```

```
## [1] 0.05782918
```

```
# Regression Imputation Shall return the same results as Lin
model1 = lm(y[z == 1]~x[z == 1,])
model0 = lm(y[z == 0]~x[z == 0,])
tau_reg = mean(cbind(1, x) %*% model1$coefficients - cbind(1, x) %*% model0$coefficients

# Propensity score stratification
pscore = glm(z ~ x, family = binomial)$fitted.values
tau_pSRE = c()
for (i in 2:5){
  stratum = floor(pscore*i) + 1
  obsValue <- stat_SRE(stratum, z, y)
  tau_pSRE = c(tau_pSRE, obsValue[1])
}
tau_pSRE
```

```
##         taus         taus         taus         taus
##  0.028850929  0.007541221          NaN -0.006391974
```

```
# IPW estimator
# With no truncation
truncpscore = c(0,1)
pscore = glm(z ~ x, family = binomial)$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_1 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
```

```
ipw_hajek_1 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 - z

# With certain truncation
truncpscore = c(0.1,0.9)
pscore = glm(z ~ x, family = binomial)$fitted.values
pscore = pmax(truncpscore[1], pmin(truncpscore[2], pscore))
ipw_2 = mean(z*y/pscore - (1 - z)*y/(1 - pscore))
ipw_hajek_2 = mean(z*y/pscore)/mean(z/pscore) - mean((1 - z)*y/(1 - pscore))/mean((1 - z

# Doubly Robust Estimator
outcome1 = glm(y ~ x, weights = z, family = gaussian)$fitted.values
outcome0 = glm(y ~ x, weights = (1 - z), family = gaussian)$fitted.values
res1 = y - outcome1
res0 = y - outcome0
tau_dr = mean(outcome1 - outcome0) + mean(z*res1/pscore - (1 - z)*res0/(1 - pscore))

print(paste("Lin's estimator is ", tau_Lin, sep = ""))
```

```
## [1] "Lin's estimator is -0.0250891102390644"
```

```
print(paste("Regression Imputation gives us an estimate same as Lin's ", tau_reg, sep =
```

```
## [1] "Regression Imputation gives us an estimate same as Lin's -0.025089110239063"
```

```
# Note that there could be Na values as stratums of pscores might not always include e
print(paste("pscore stratification's estimator is ", tau_pSRE, sep = ""))
```

```
## [1] "pscore stratification's estimator is 0.028850928914995"
## [2] "pscore stratification's estimator is 0.00754122081333689"
## [3] "pscore stratification's estimator is NaN"
## [4] "pscore stratification's estimator is -0.00639197365510275"
```

```
print(paste("IPW estimator (hovic-thompson) without truncation is ",ipw_1, " and the haj
```

```
## [1] "IPW estimator (hovic-thompson) without truncation is -0.142357535224816 and the
```

```
print(paste("IPW estimator (hovic-thompson) with truncation is ",ipw_2, " and the hajek
```

```
## [1] "IPW estimator (hovic-thompson) with truncation is -0.178563422656618 and the haj
```

```
print(paste("The doubly robust estimator is ", tau_dr))
```

```
## [1] "The doubly robust estimator is  -0.0394785911682918"
```

```
ATT.est = function(z, y, x, out.family = gaussian, Utruncpscore = 1)
{
```

```
  ## sample size
  nn  = length(z)
  nn1 = sum(z)

  ## fitted propensity score
  pscore   = glm(z ~ x, family = binomial)$fitted.values
  pscore   = pmin(Utruncpscore, pscore)
  odds.pscore = pscore/(1 - pscore)

  ## fitted potential outcomes
  outcome0 = glm(y ~ x, weights = (1 - z),
                 family = out.family)$fitted.values

  ## regression imputation estimator
  ace.reg0 = lm(y ~ z + x)$coef[2]
  ace.reg  = mean(y[z==1]) - mean(outcome0[z==1])
  ## propensity score weighting estimator
  ace.ipw0 = mean(y[z==1]) -
               mean(odds.pscore*(1 - z)*y)*nn/nn1
  ace.ipw  = mean(y[z==1]) -
               mean(odds.pscore*(1 - z)*y)/mean(odds.pscore*(1 - z))
  ## doubly robust estimator
  res0     = y - outcome0
  ace.dr   = ace.reg - mean(odds.pscore*(1 - z)*res0)*nn/nn1

  return(c(ace.reg0, ace.reg, ace.ipw0, ace.ipw, ace.dr))
}


ObsCausal.ATT = function(z, y, x, n.boot = 10^2,
                         out.family = gaussian, Utruncpscore = 1)
{
  point.est  = ATT.est(z, y, x, out.family, Utruncpscore)

  ## nonparametric bootstrap
  n.sample   = length(z)
  x          = as.matrix(x)
  boot.est   = replicate(n.boot,
                         {id.boot = sample(1:n.sample, n.sample, replace = TRUE)
                          ATT.est(z[id.boot], y[id.boot], x[id.boot, ],
                                  out.family, Utruncpscore)})
```

```
  boot.se    = apply(boot.est, 1, sd)

  res        = rbind(point.est, boot.se)
  rownames(res) = c("est", "se")
  colnames(res) = c("reg0", "reg", "HT", "Hajek", "DR")

  return(res)
}



n.sim   = 2000
ATT0    = rep(0, n.sim)
ATT     = matrix(0, 5, n.sim)
SEboot  = matrix(0, 5, n.sim)
n       = 200

## Baseline: simulation with correct models
## nonparallel y1 and y0
for(r in 1:n.sim)
{
  x       = matrix(rnorm(n*2), n, 2)
  x1      = cbind(1, x)
  beta.z  = c(0, 1, 1)
  pscore  = 1/(1 + exp(- as.vector(x1%*%beta.z)))
  z       = rbinom(n, 1, pscore)
  beta.y1 = c(1, 2, 1)
  beta.y0 = c(1, 1, 1)
  y1      = rnorm(n, x1%*%beta.y1)
  y0      = rnorm(n, x1%*%beta.y0)
  y       = z*y1 + (1 - z)*y0
  ATT0[r] = mean(y1[z==1]) - mean(y0[z==1])

  causaleffect = ObsCausal.ATT(z, y, x)
  ATT[, r]     = causaleffect[1, ]
  SEboot[, r]  = causaleffect[2, ]
}

apply(ATT, 1, mean) - mean(ATT0)
```

```
## [1] -0.359320852  0.004192477 -0.011764708  0.038584431  0.001900091
```

```
apply(ATT, 1, sd)
```

```
## [1] 0.1843905 0.2101216 0.7792105 0.3939605 0.2576940
```

```
apply(SEboot, 1, mean)
```

```
## [1] 0.1860617 0.2098427 0.5523045 0.3167784 0.2492950
```

```
## Case 1:
## Wrong Model for y1 and y0 but correct model for propensity score
for(r in 1:n.sim)
{
  x       = matrix(rnorm(n*2), n, 2)
  x1      = cbind(1, x)
  beta.z  = c(0, 1, 1)
  pscore  = 1/(1 + exp(- as.vector(x1%*%beta.z)))
  z       = rbinom(n, 1, pscore)
  beta.y1 = c(1, 2, 1)
  beta.y0 = c(1, 1, 1)
  realbeta.y1 = c(2, 3, 4)
  realbeta.y0 = c(100, 101, 102)
  y1      = rnorm(n, x1%*%realbeta.y1)
  y0      = rnorm(n, x1%*%realbeta.y0)
  y       = z*y1 + (1 - z)*y0
  ATT0[r] = mean(y1[z==1]) - mean(y0[z==1])

  causaleffect = ObsCausal.ATT(z, y, x)
  ATT[, r]     = causaleffect[1, ]
  SEboot[, r]  = causaleffect[2, ]
}

apply(ATT, 1, mean) - mean(ATT0)
```

```
## [1] 71.3687951608  0.0003030757  0.1103855378  4.1287009031 -0.0008410053
```

```
apply(ATT, 1, sd)
```

```
## [1] 12.00293 12.18383 66.10132 32.79879 12.18419
```

```
apply(SEboot, 1, mean)
```

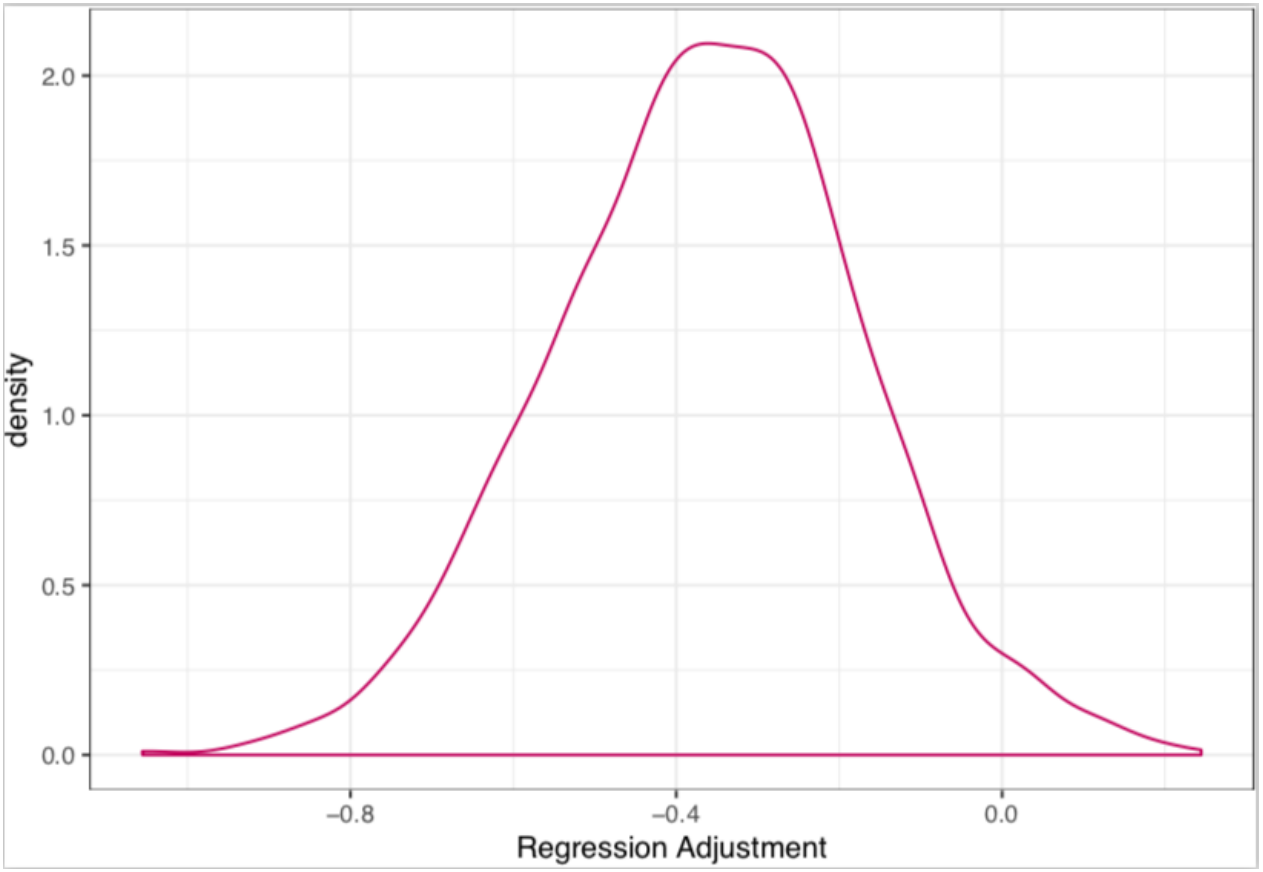
```
## [1] 11.93985 11.82235 48.30555 23.22371 11.82418
```

```
## Case 2:
## Correct Model for y1 and y0 but wrong model for propensity score
```

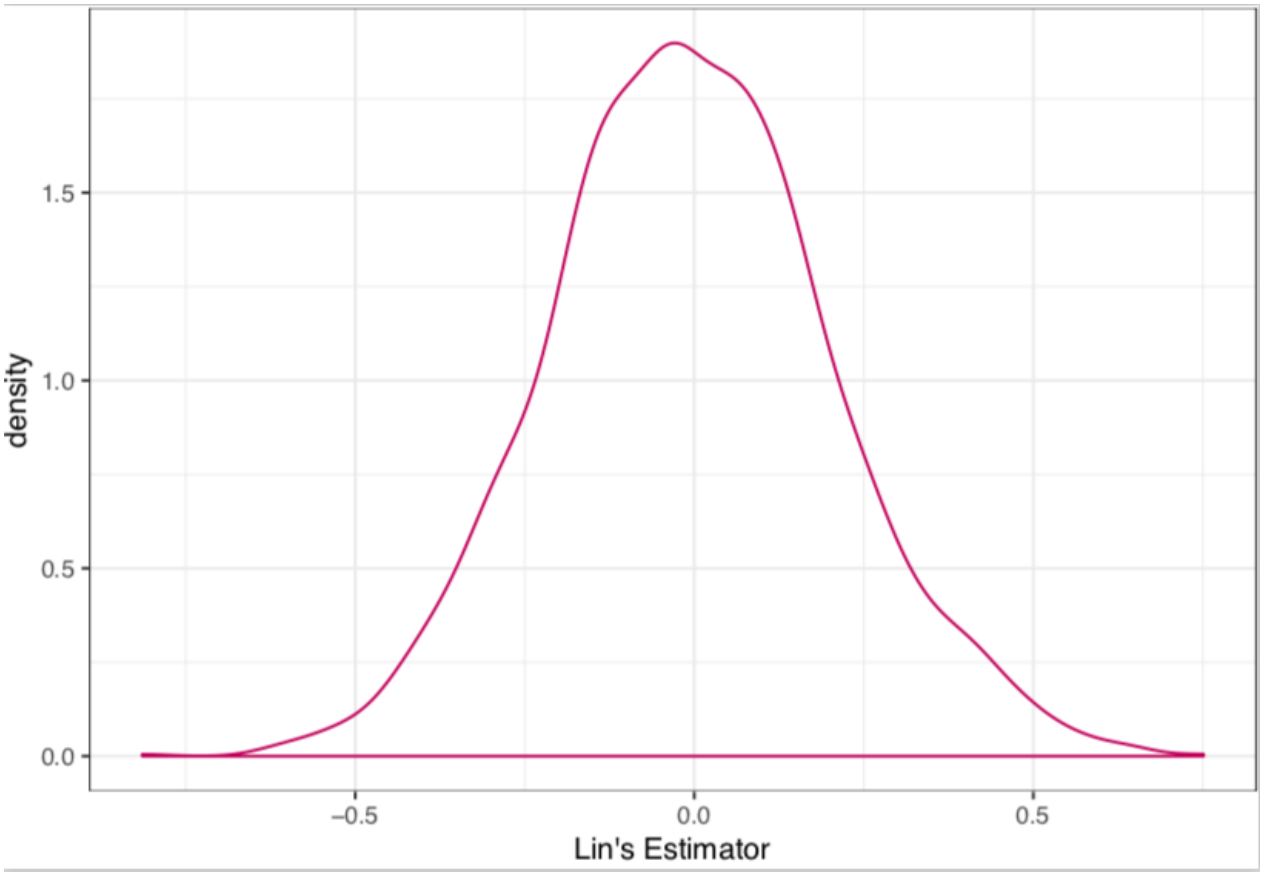
```
## Note that we're generating a uniform distribution of pscore. // z = rbinom(n, 1, psco
for(r in 1:n.sim)
{
  x       = matrix(rnorm(n*2), n, 2)
  x1      = cbind(1, x)
  beta.z  = c(0, 1, 1)
  pscore  = 1/(1 + exp(- as.vector(x1%*%beta.z)))
  realpscore = 1/(1 + exp(-as.vector(x1 %*% c(0,0,0))))
  z       = rbinom(n, 1, pscore)
  beta.y1 = c(1, 2, 1)
  beta.y0 = c(1, 1, 1)
  y1      = rnorm(n, x1%*%beta.y1)
  y0      = rnorm(n, x1%*%beta.y0)
  y       = z*y1 + (1 - z)*y0
  ATT0[r] = mean(y1[z==1]) - mean(y0[z==1])

  causaleffect = ObsCausal.ATT(z, y, x)
  ATT[, r]     = causaleffect[1, ]
  SEboot[, r]  = causaleffect[2, ]
}

apply(ATT, 1, mean) - mean(ATT0)
```

```
## [1] -0.363686898 -0.006544096  0.002204782  0.037634792 -0.010464628
```

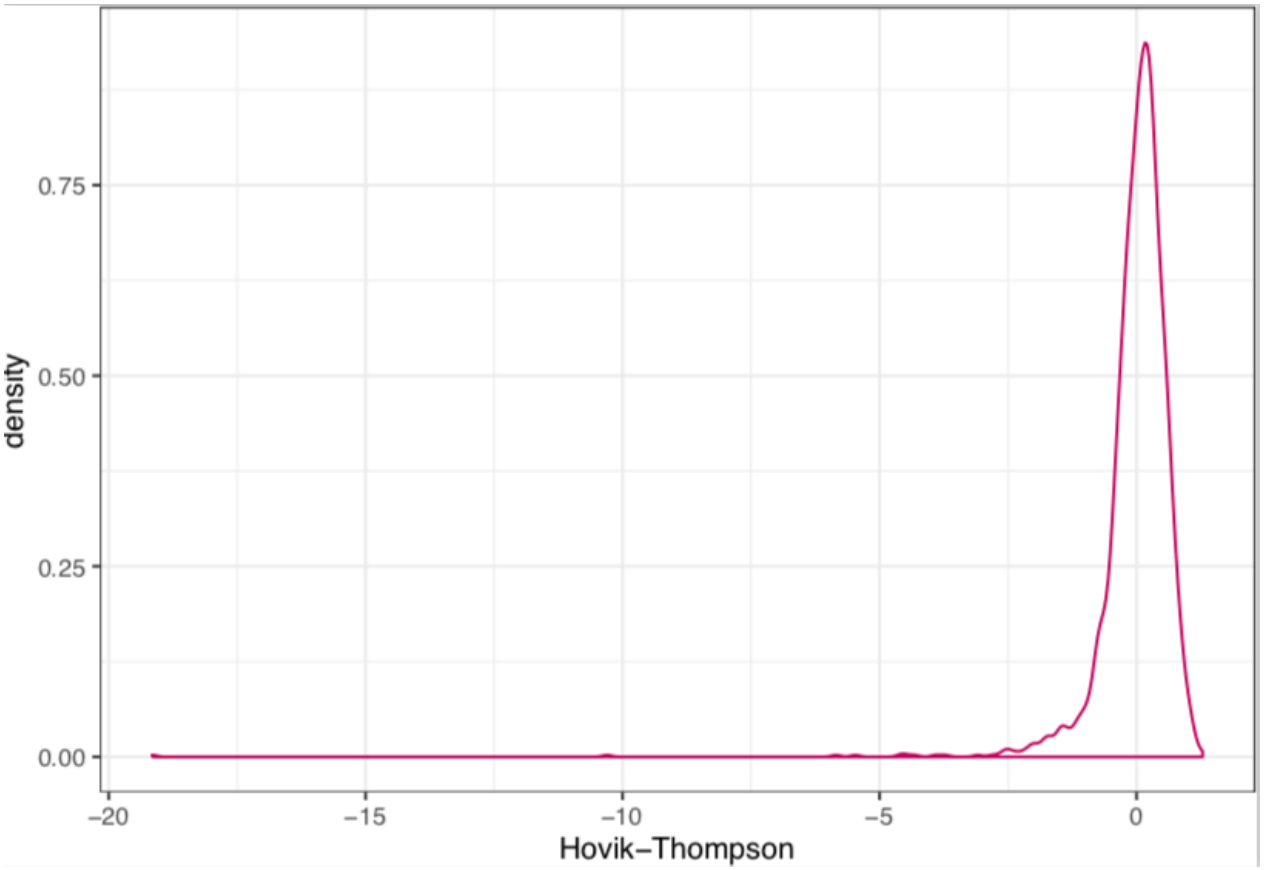
```
ggplot() + theme_bw() +
  geom_density(aes(x = ATT[1,] - mean(ATT0)), color = "maroon") + labs(x = "Regression A
```



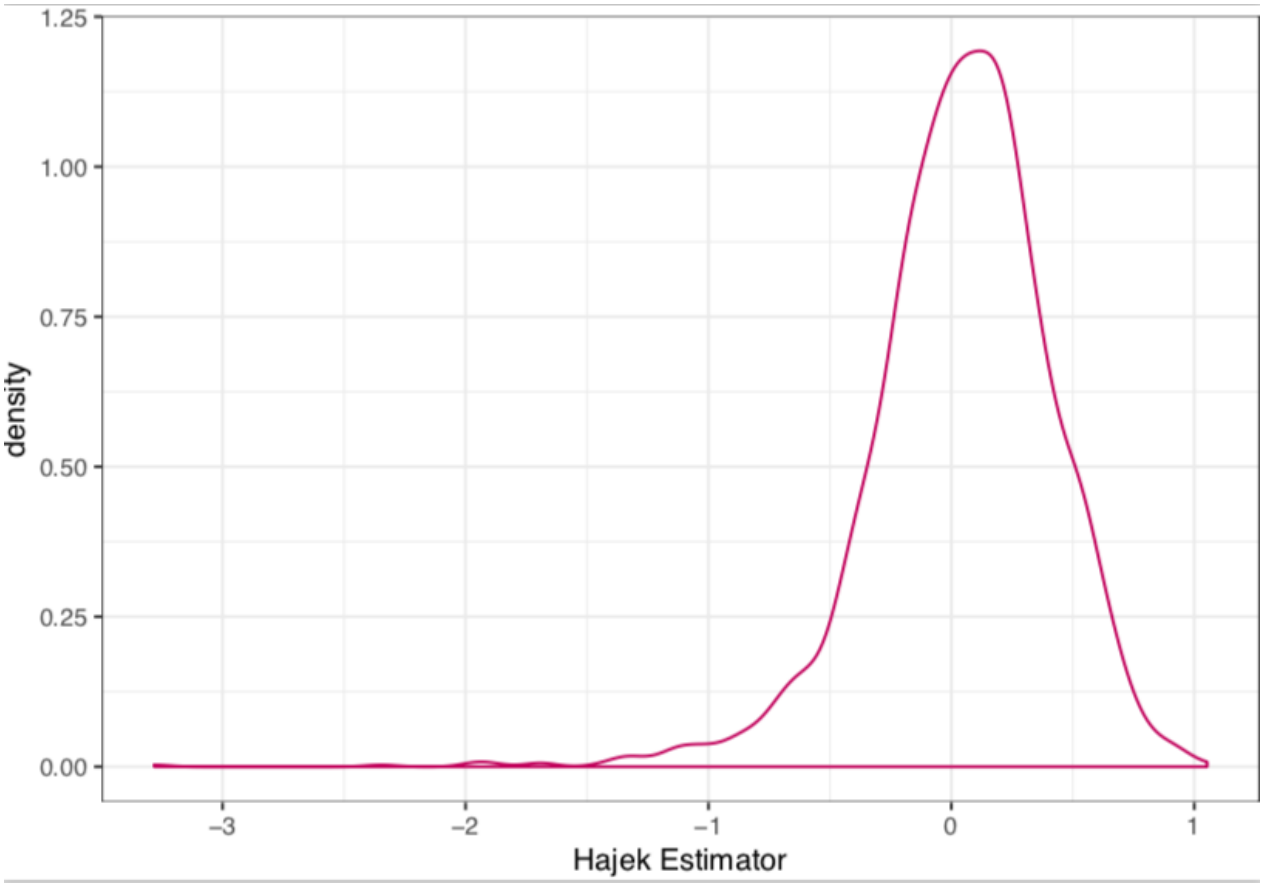

```
ggplot() + theme_bw() +
  geom_density(aes(x = ATT[2,] - mean(ATT0)), color = "maroon") + labs(x = "Lin's Estima
```



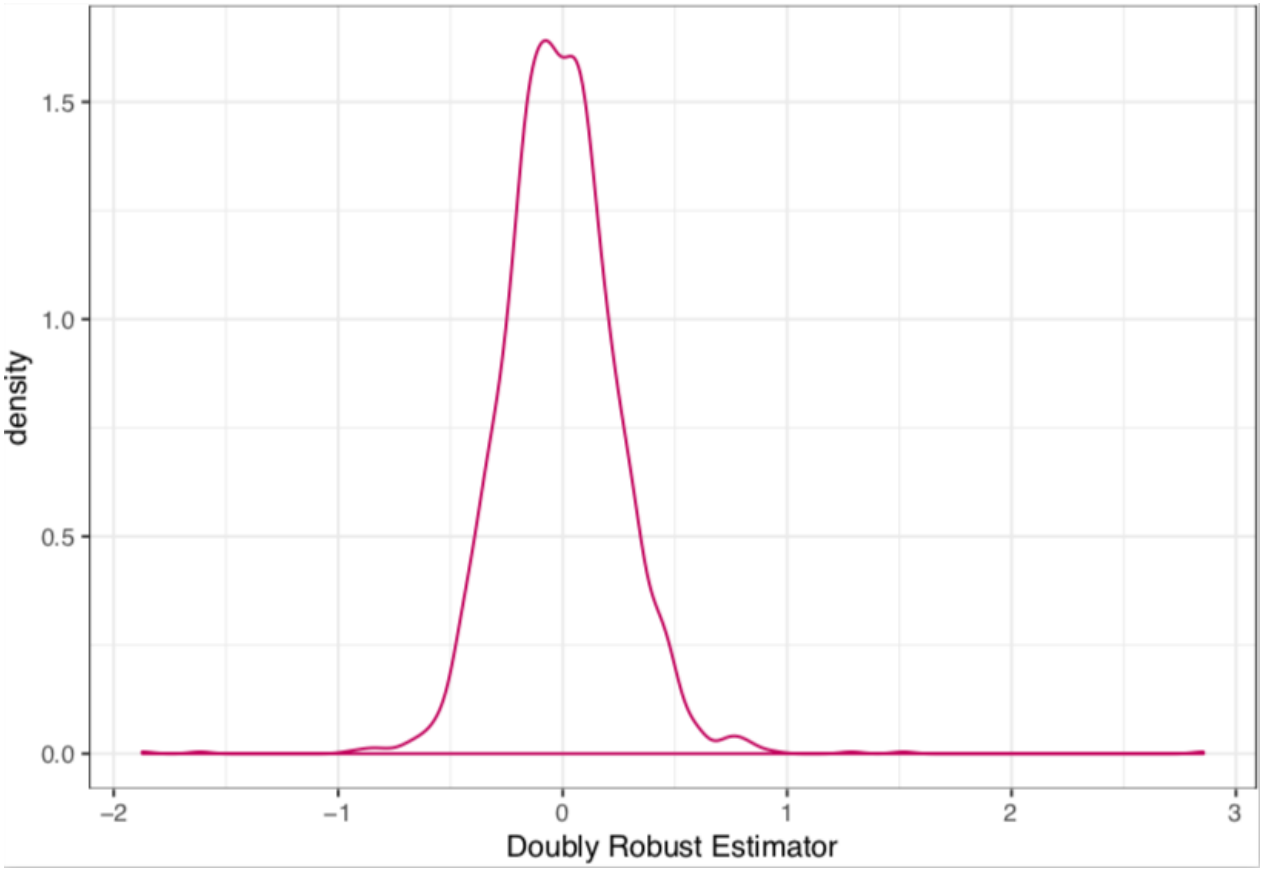

```
ggplot() + theme_bw() +
  geom_density(aes(x = ATT[3,] - mean(ATT0)), color = "maroon") + labs(x = "Hovik-Thomps
```




```
ggplot() + theme_bw() +
  geom_density(aes(x = ATT[4,] - mean(ATT0)), color = "maroon") + labs(x = "Hajek Estima
```




```
ggplot() + theme_bw() +
  geom_density(aes(x = ATT[5,] - mean(ATT0)), color = "maroon") + labs(x = "Doubly Robus
```




```
apply(ATT, 1, sd)
```

```
## [1] 0.1895128 0.2094865 0.7741395 0.3772193 0.2608904
```

```
apply(SEboot, 1, mean)
```

```
## [1] 0.1847593 0.2089299 0.5328994 0.3129829 0.2457885
```

```
apply(ATT, 1, mean) - mean(ATT0) - 1.96*apply(ATT, 1, sd)
```

```
## [1] -0.7351320 -0.4171376 -1.5151086 -0.7017150 -0.5218098
```

```
## Case 3:
## Wrong model for both y0/ y1 and pscore
for(r in 1:n.sim)
{
  x       = matrix(rnorm(n*2), n, 2)
  x1      = cbind(1, x)
  beta.z  = c(0, 1, 1)
  pscore  = 1/(1 + exp(- as.vector(x1%*%beta.z)))
  realpscore = 1/(1 + exp(-as.vector(x1 %*% c(0,0,0))))
```

```
  z       = rbinom(n, 1, pscore)
  beta.y1 = c(1, 2, 1)
  beta.y0 = c(1, 1, 1)
  realbeta.y1 = c(2, 3, 4)
  realbeta.y0 = c(100, 101, 102)
  y1      = rnorm(n, x1%*%realbeta.y1)
  y0      = rnorm(n, x1%*%realbeta.y0)
  y       = z*y1 + (1 - z)*y0
  ATT0[r] = mean(y1[z==1]) - mean(y0[z==1])

  causaleffect = ObsCausal.ATT(z, y, x)
  ATT[, r]     = causaleffect[1, ]
  SEboot[, r]  = causaleffect[2, ]
}

apply(ATT, 1, mean) - mean(ATT0)
```

```
## [1] 71.292947086 -0.004852229  3.120162985  5.626615117 -0.004806452
```

```
apply(ATT, 1, sd)
```

```
## [1] 12.08423 12.13165 61.82708 30.81661 12.13796
```

```
apply(SEboot, 1, mean)
```

```
## [1] 11.91909 11.84323 45.62230 22.54042 11.84496
```

Some Conclusions after 2000 simulations:
1. When the linear model is wrong but the propensity score model is correct, the simple regression model gives us an estimate that is far from truth. All other estimators (Lin, ht, hajek, dr) gives us a confidence interval containing zero. The non-parametric (naive) bootstrap is a good estimate for the regression estimators, but is significantly biased concerning the propensity score estimators.
2. When the pscore model is wrong but the linear model is correct, all the estimators (reg, Lin, ht, hajek, dr) gives us a confidence interval containing zero. It could be the case that the pscore generated is not so far from truth, it could also be the case that the pscore estimation itself is more stable. Still, the non-parametric (naive) bootstrap is a good estimate for the regression estimators, but is significantly biased concerning the propensity score estimators. In both cases, the doubly robust estimators are performing stably. 3. When both models are wrong, only Lin's estimator is providing us a reasonable result. Though all confidence intervals do contain zero, the variance is very high that the estimation is almost useless. The doubly robust estimation is almost always the best estimation of the ATE. 4. Concerning the normality of the estimation. Regression estimators are somehow more stable in terms of

less outliers. Hajek and Hovik-Th estimator are more prone to instablity of sampling. That's especially the case talking of HT estimators. (See the graphs above.)