

# PS Bootstrap Continuous Outcome

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```
## Warning: package 'tidyr' was built under R version 4.1.2
```

```
## Warning: package 'readr' was built under R version 4.1.2
```

```
## Warning: package 'simstudy' was built under R version 4.1.2
```

```
## Warning: package 'MatchIt' was built under R version 4.1.2
```

## Generating data with true log odds ratio and its standard deviation

```
pre_data <- defData(varname = "L1", formula = "0", variance = 1,
                    dist = "normal")
pre_data <- defData(pre_data, varname = "L2", formula = "0", variance = 1,
                    dist = "normal")
pre_data <- defData(pre_data, varname = "L3", formula = "0", variance = 1,
                    dist = "normal")
pre_data <- defData(pre_data, varname = "A",
                    formula = " 0.5*L1 + 0.27*L2 -0.17*L3",
                    dist = "binary", link = "logit")
pre_data <- defData(pre_data, varname = "Y",
                    formula = "2 + 1.5*A + 0.8*L2 + -0.1*L3",
                    dist = "nonrandom")

set.seed(7777)
df <- genData(1000, pre_data)

# TRUE ATE: 1.5
```

## Propensity Score Model

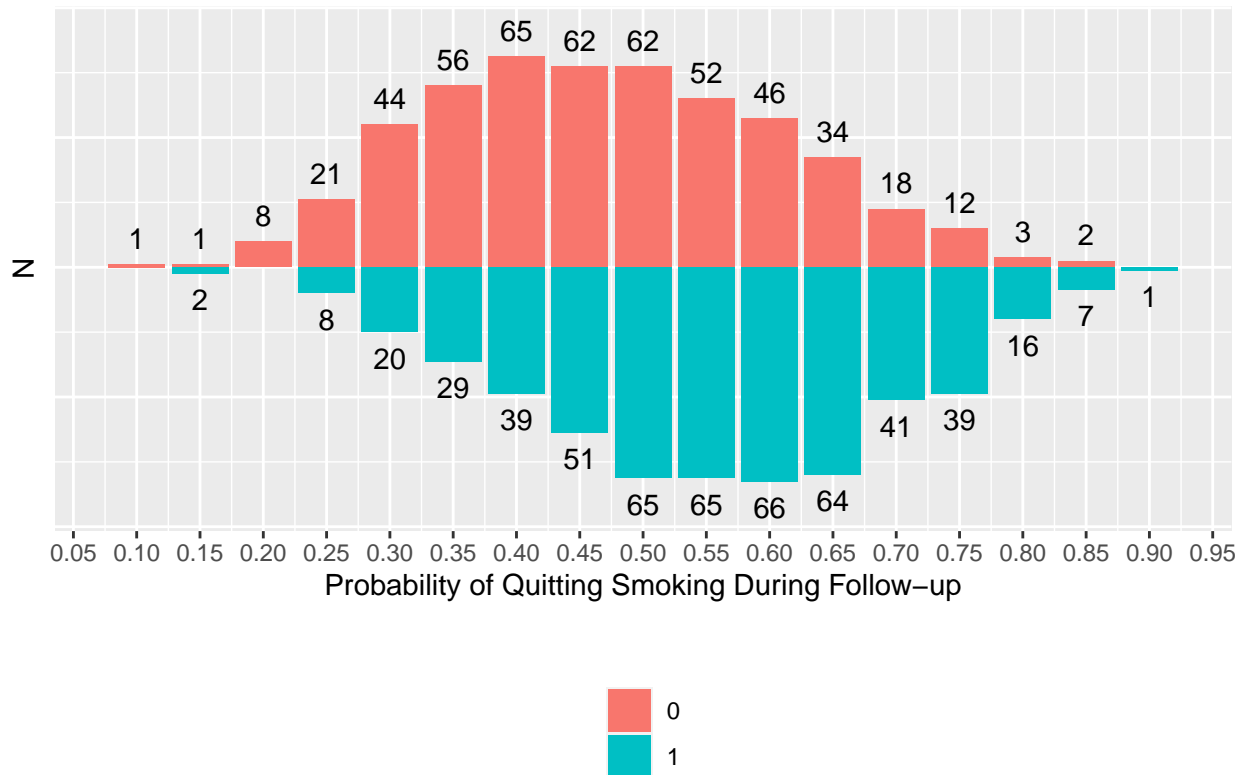
### 500 pairs Propensity Score distribution

```
df %>%
  mutate(ps.grp = round(ps/0.05) * 0.05) %>%
  group_by(A, ps.grp) %>%
  summarize(n = n()) %>%
  ungroup() %>%
```

```
mutate(n2 = ifelse(A == 0, yes = n, no = -1*n)) %>%
  ggplot(aes(x = ps.grp, y = n2, fill = as.factor(A))) +
  geom_bar(stat = 'identity', position = 'identity') +
  geom_text(aes(label = n, x = ps.grp, y = n2 + ifelse(A == 0, 8, -8))) +
  xlab('Probability of Quitting Smoking During Follow-up') +
  ylab('N') +
  ggtitle('Propensity Score Distribution by Treatment Group') +
  scale_fill_discrete('') +
  scale_x_continuous(breaks = seq(0, 1, 0.05)) +
  theme(legend.position = 'bottom', legend.direction = 'vertical',
        axis.ticks.y = element_blank(),
        axis.text.y = element_blank())
```

## 'summarise()' has grouped output by 'A'. You can override using the '.groups' argument.

### Propensity Score Distribution by Treatment Group



### Nearest neighbor propensity score matching

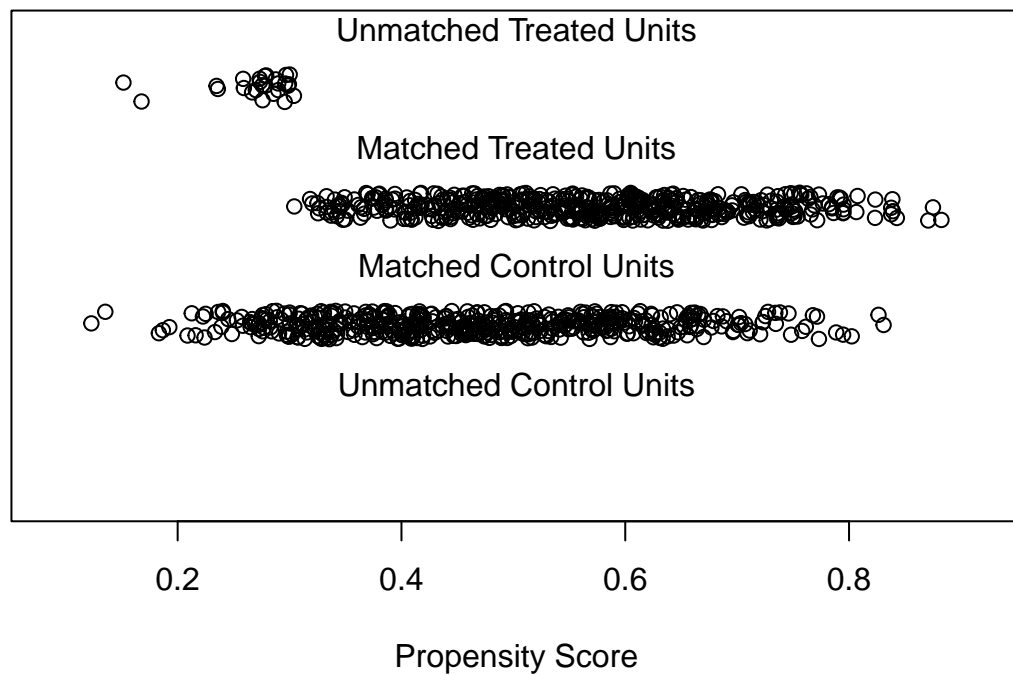
```
matched <- matchit(A ~ L1 + L2 + L3, data = df,
  distance = "glm", link = "logit",
  method = "nearest", ratio = 1)
```

```
summary(matched)[2]
```

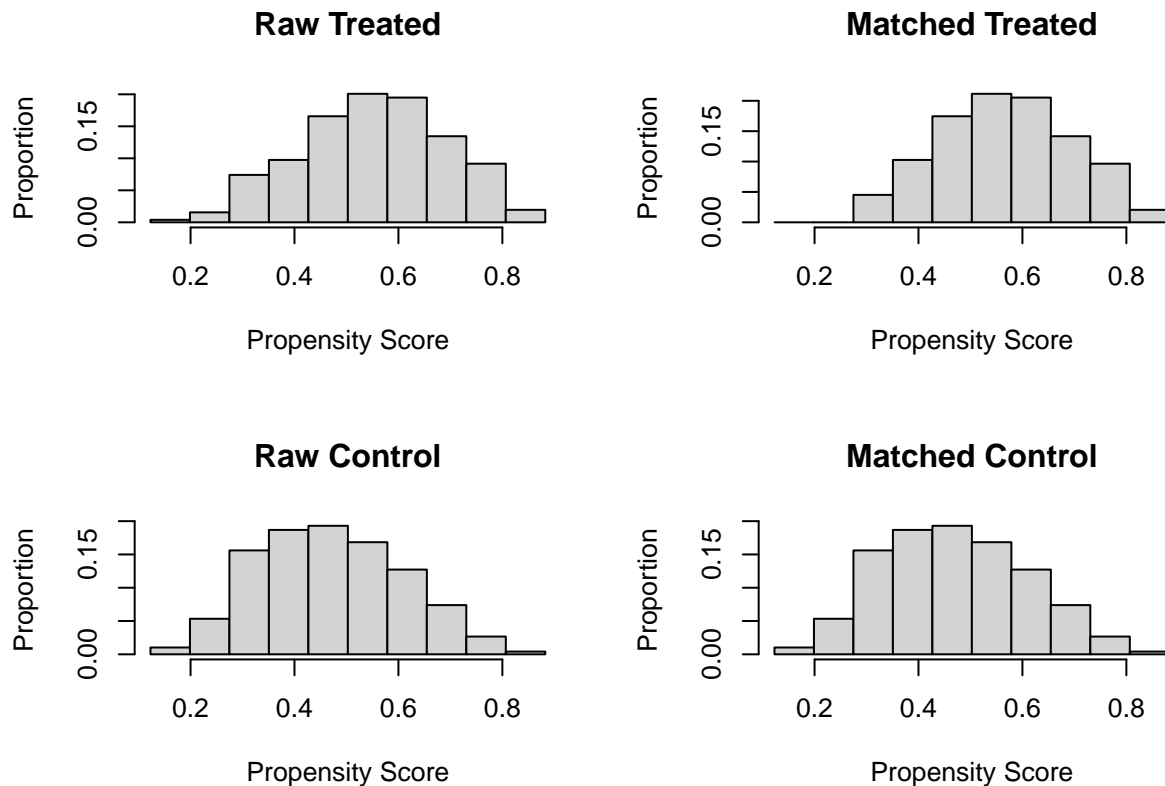
```
## $nn
##           Control Treated
## All (ESS)      487      513
## All            487      513
## Matched (ESS)  487      487
## Matched        487      487
## Unmatched       0       26
## Discarded      0        0
```

```
plot(matched, type = "jitter", interactive = FALSE)
```

## Distribution of Propensity Scores



```
plot(matched, type = "histogram")
```



```
matched_df <-  
  match.data(matched)
```

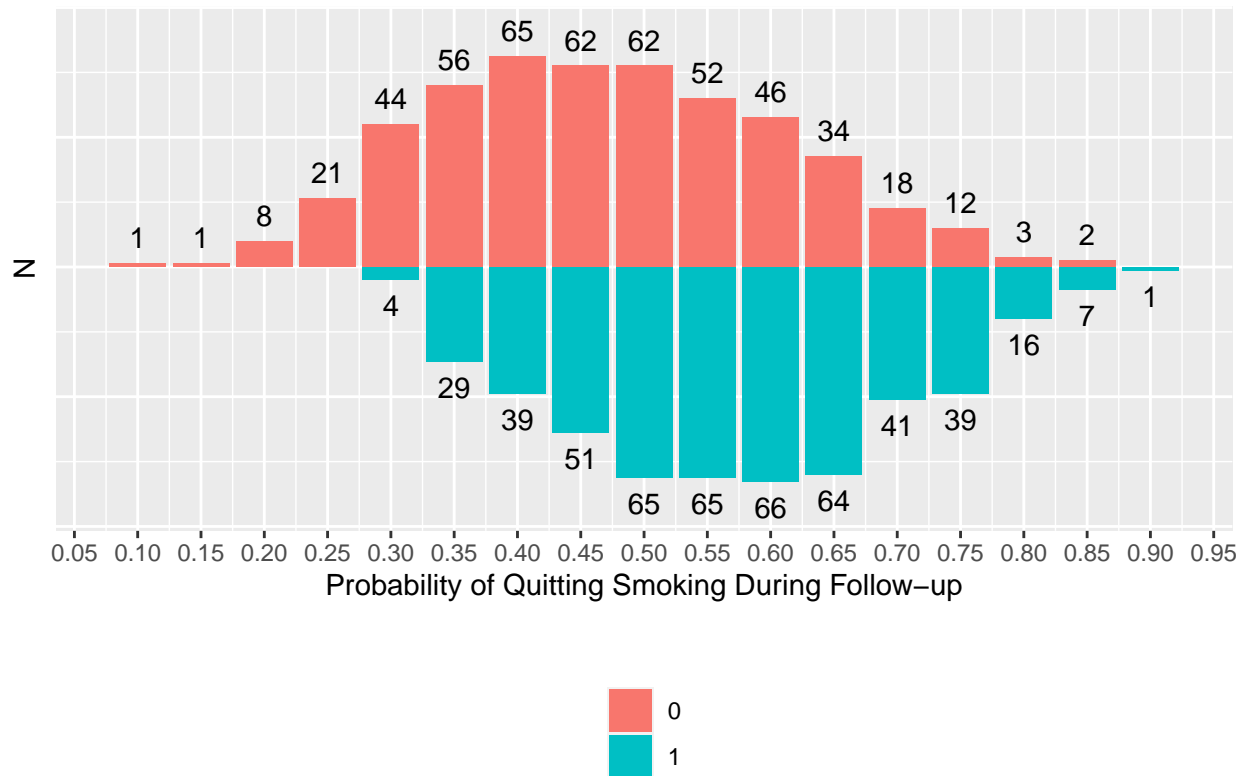
## 495 pairs propensity score distribution

```
matched_df %>%  
  mutate(ps.grp = round(ps/0.05) * 0.05) %>%  
  group_by(A, ps.grp) %>%  
  summarize(n = n()) %>%  
  ungroup() %>%  
  mutate(n2 = ifelse(A == 0, yes = n, no = -1*n)) %>%  
  ggplot(aes(x = ps.grp, y = n2, fill = as.factor(A))) +  
  geom_bar(stat = 'identity', position = 'identity') +  
  geom_text(aes(label = n, x = ps.grp, y = n2 + ifelse(A == 0, 8, -8))) +  
  xlab('Probability of Quitting Smoking During Follow-up') +  
  ylab('N') +  
  ggtitle('Propensity Score Distribution by Treatment Group') +  
  scale_fill_discrete('') +  
  scale_x_continuous(breaks = seq(0, 1, 0.05)) +  
  theme(legend.position = 'bottom', legend.direction = 'vertical',  
        axis.ticks.y = element_blank(),  
        axis.text.y = element_blank())
```

## 'summarise()' has grouped output by 'A'. You can override using the '.groups'

```
## argument.
```

Propensity Score Distribution by Treatment Group



## simple bootstrap

```
nboot <- 100
# set up a matrix to store results
boots <- data.frame(i = 1:nboot,
                    se = NA,
                    mean1 = NA,
                    mean0 = NA,
                    beta1 = NA,
                    ATE = NA
                    )
# loop to perform the bootstrapping

for(i in 1:nboot) {
  # sample with replacement
  sampl <- matched_df %>% filter(subclass %in% sample(levels(subclass),487, replace = TRUE))

  bootmod <- glm(Y ~ A + ps, data = sampl,
                weights = weights)

  # create new data sets
  sampl.treated <- sampl %>%
```

```

mutate(A = 1)

sampl.untreated <- sampl %>%
  mutate(A = 0)

# predict values
sampl.treated$pred.y <-
  predict(bootmod, sampl.treated)

sampl.untreated$pred.y <-
  predict(bootmod, sampl.untreated)

# output results

boots[i, "beta1"] <- summary(bootmod)$coeff[2,1]
boots[i, "mean1"] <- mean(sampl.treated$pred.y)
boots[i, "mean0"] <- mean(sampl.untreated$pred.y)
boots[i, "ATE"] <- boots[i, "mean1"] - boots[i, "mean0"]

se_ATE <- sd(boots$ATE)

ATE <- mean(boots$ATE)

# once loop is done, print the results
if (i == nboot){
  cat("ATE:")
  cat(ATE)
  cat("\n")
  cat("\n")
  cat("se_ATE:")
  cat(se_ATE)
  cat("\n")
  cat("\n")
  cat("95% CI for ATE:")
  cat(ATE - 1.96*se_ATE,
      ", ",
      ATE + 1.96*se_ATE)
  cat("\n")
  cat("\n")
  cat("ATE from beta:") #checking if our computation is correct
  cat(mean(boots$beta1))
}
}

```

```

## ATE:1.491826
##
## se_ATE:0.03750028
##
## 95% CI for ATE:1.418326 , 1.565327
##
## ATE from beta:1.491826

```

```
hist(boots$ATE)
```

