PS Bootstrap Binary Standardization

Hun

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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 = "0.5*A + 0.8*L2 + -0.1*L3",
                dist = "binary", link = "logit")

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

expit <- function(beta) {
    return(exp(beta)/(1 + exp(beta)))
}

ATE <- expit(sum(0.5 + 0.8*df$L2 - 0.1*df$L3)) - expit(sum(0.8*df$L2 - 0.1*df$L3))
# this is not true ATE

# True log odds ratio: 0.5
```

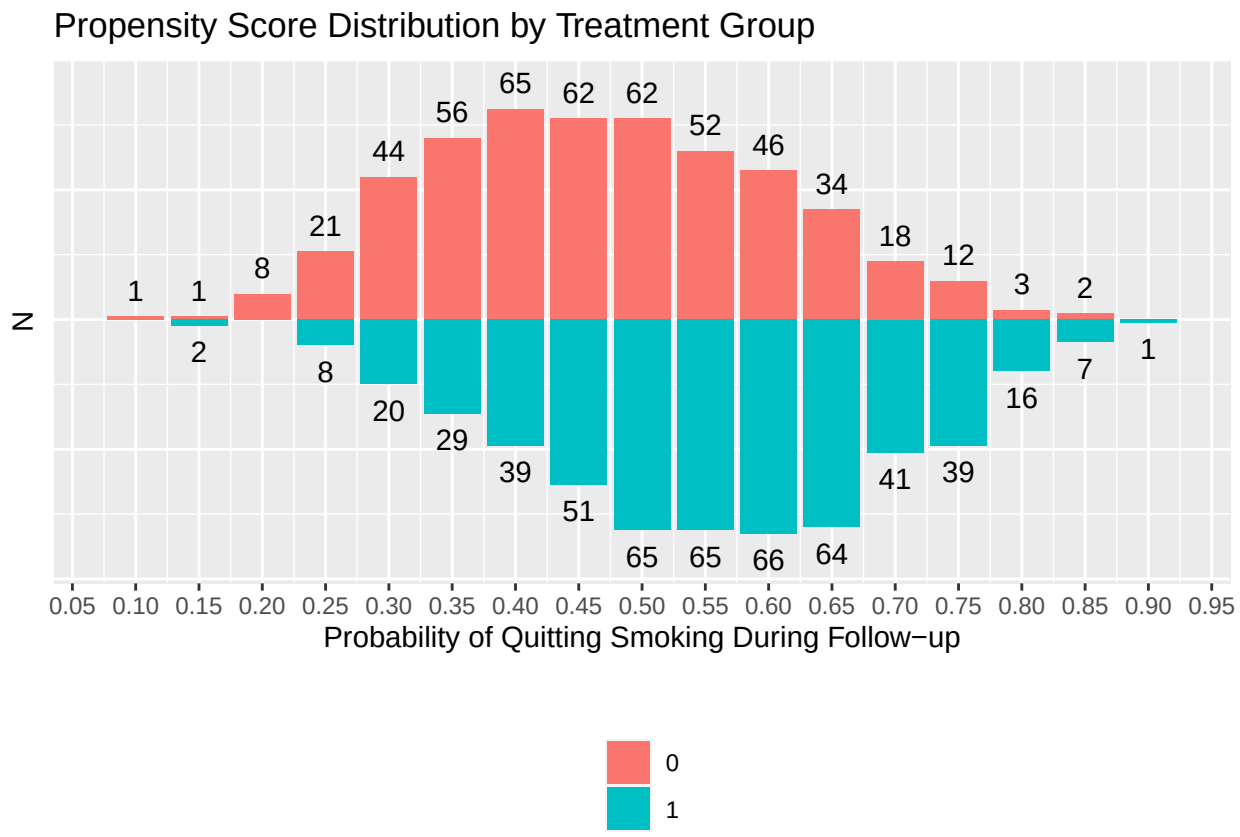
Propensity Score Model

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.
```



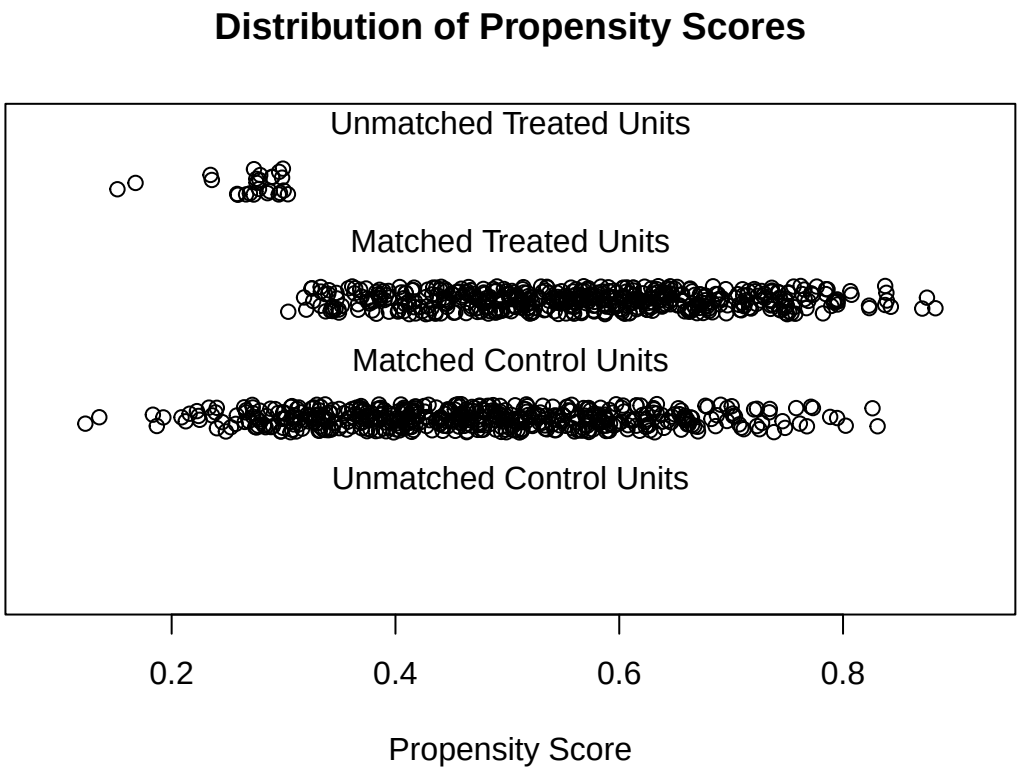
Nearest neighbor propensity score matching

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

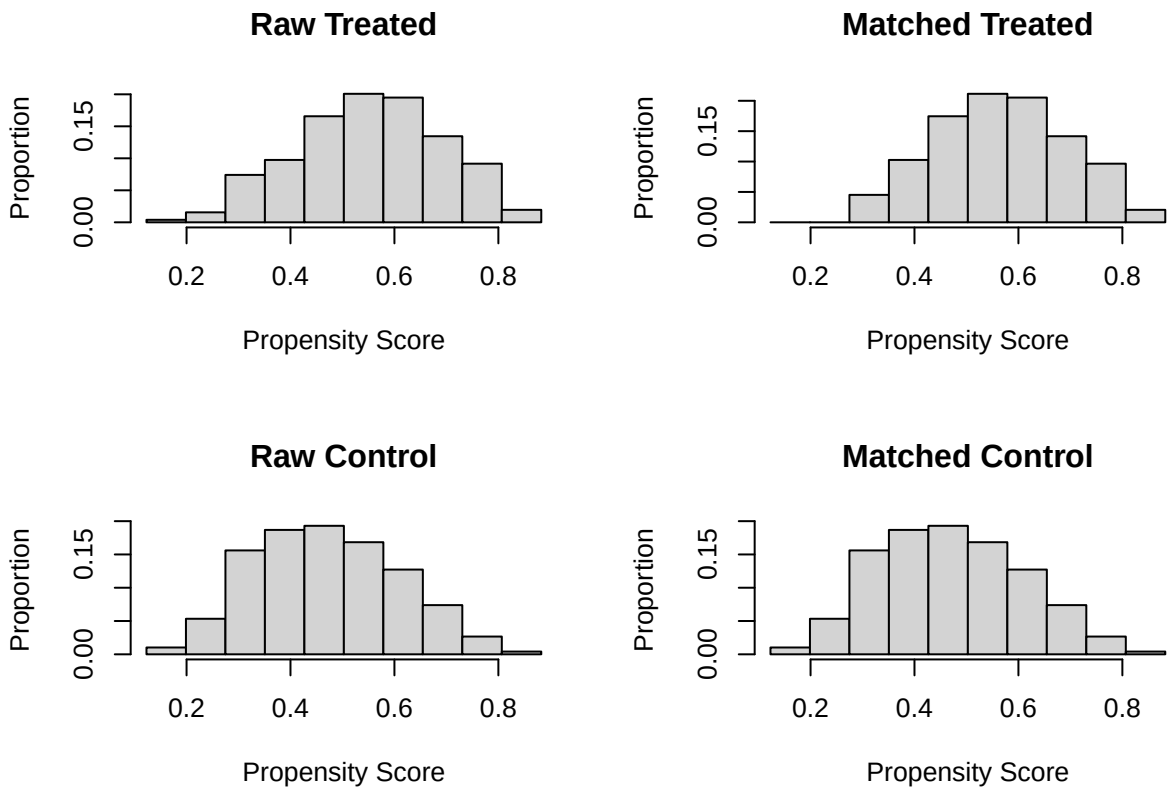
```
summary(matched)[2]
```

```
## $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)
```




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



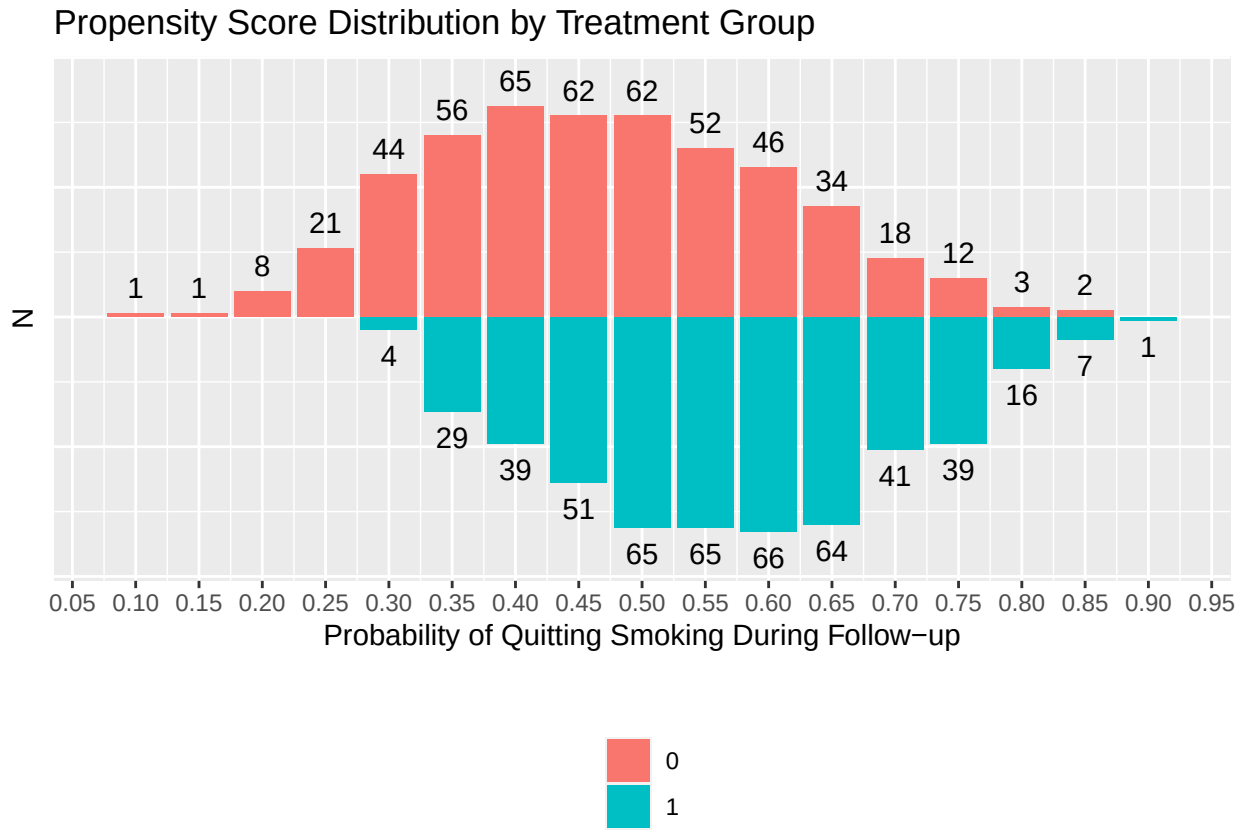

```
matched_df <-
  match.data(matched)
```

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.
```



simple bootstrap

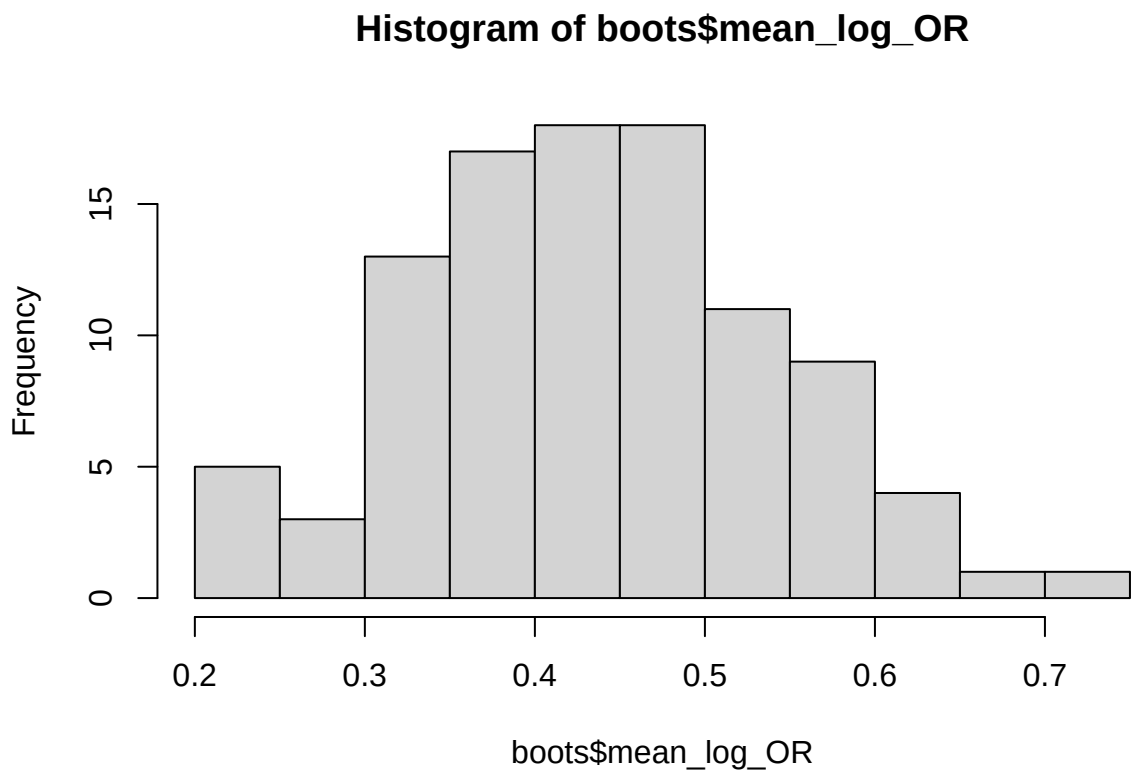
```
nboot <- 100
# set up a matrix to store results
boots <- data.frame(i = 1:nboot,
                    se_OR = NA,
                    mean_log_OR = NA,
                    mean1 = NA,
                    mean0 = NA,
                    difference = NA
                    )
# loop to perform the bootstrapping

for(i in 1:nboot) {
  # sample with replacement
  sampl <- matched_df %>% filter(subclass %in% sample(levels(subclass),500, replace =  TRUE))

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

  # 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, type = "response")

sampl.untreated$pred.y <-
  predict(bootmod, sampl.untreated, type = "response")

 # output results

boots[i, "mean_log_OR"] <- summary(bootmod)$coeff[2,1]

boots[i, "se_OR"] <- summary(bootmod)$coeff[2,2]

boots[i, "mean1"] <- mean(sampl.treated$pred.y)
boots[i, "mean0"] <- mean(sampl.untreated$pred.y)
boots[i, "difference"] <- boots[i, "mean1"] - boots[i, "mean0"]

se_ATE <- sd(boots$difference)

ATE <- mean(boots$difference)

# 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("log OR:")
  cat(mean(boots$mean_log_OR))
  cat("\n")
  cat("\n")
  cat("se_OR:")
  cat(mean(boots$se_OR))
  cat("\n")
  cat("\n")
  cat("95% CI for log odds ratio:")
  cat(mean(boots$mean_log_OR) - 1.96*mean(boots$se_OR),
      ",",
```

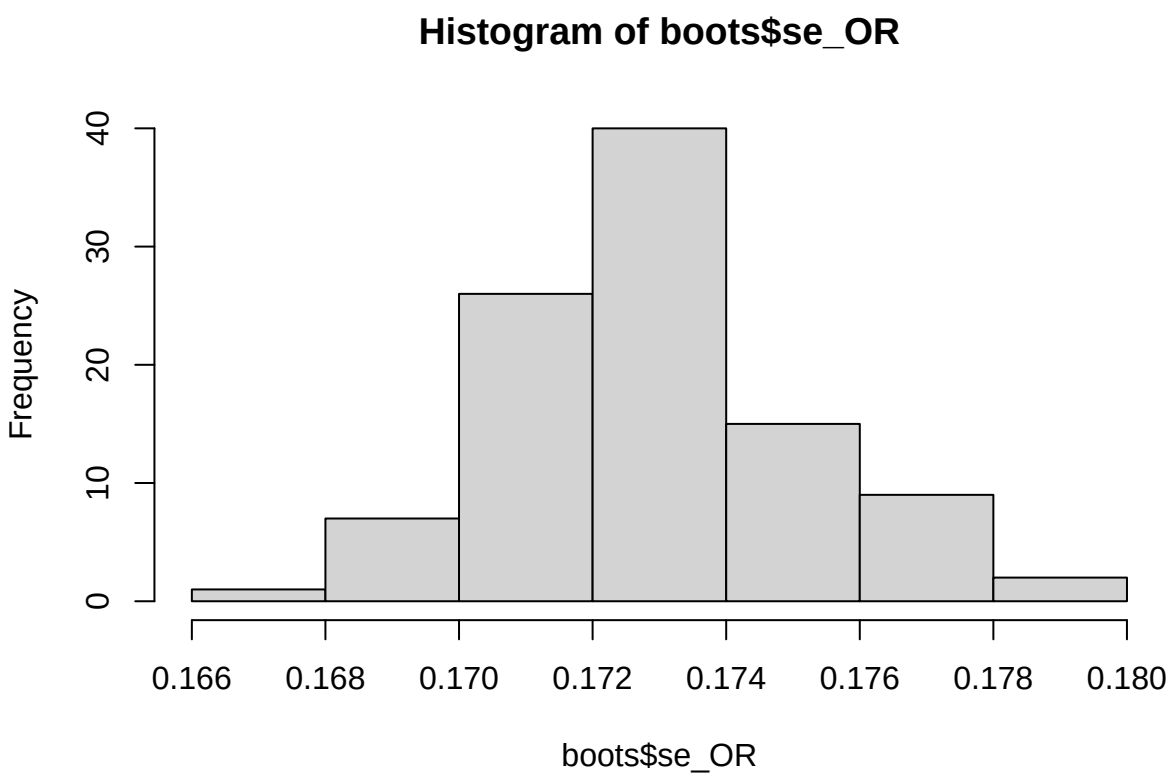
```
        mean(boots$mean_log_OR) + 1.96*mean(boots$se_OR))
  }
}
```

```
## ATE:0.1068614
##
## se_ATE:0.025629
##
## 95% CI for ATE:0.05662853 , 0.1570942
##
## log OR:0.4353995
##
## se_OR:0.172854
##
## 95% CI for log odds ratio:0.09660568 , 0.7741934
```

```
hist(boots$mean_log_OR)
```




```
hist(boots$se_OR)
```


Histogram of boots$se_OR
Frequency
0
10
20
30
40
0.166
0.168
0.170
0.172
0.174
0.176
0.178
0.180
boots$se_OR