

Continuous Simulation

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```
source("./shared_code/setup.R")

## -- Attaching packages ----- tidyverse 1.3.1 --
## v ggplot2 3.3.5      v purrr 0.3.4
## v tibble 3.1.6       v dplyr 1.0.7
## v tidyr 1.1.3        v stringr 1.4.0
## v readr 2.0.1        v forcats 0.5.1

## Warning: package 'tibble' was built under R version 4.1.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

## Warning: package 'simstudy' was built under R version 4.1.2
## Warning: package 'MatchIt' was built under R version 4.1.2
## Warning: package 'ggpmisc' was built under R version 4.1.2
## Loading required package: ggpp
## Warning: package 'ggpp' was built under R version 4.1.2
##
## Attaching package: 'ggpp'
## The following object is masked from 'package:ggplot2':
##
##     annotate
## Warning: package 'cowplot' was built under R version 4.1.2
## Warning: package 'beepr' was built under R version 4.1.2
scenario_id = 6
```

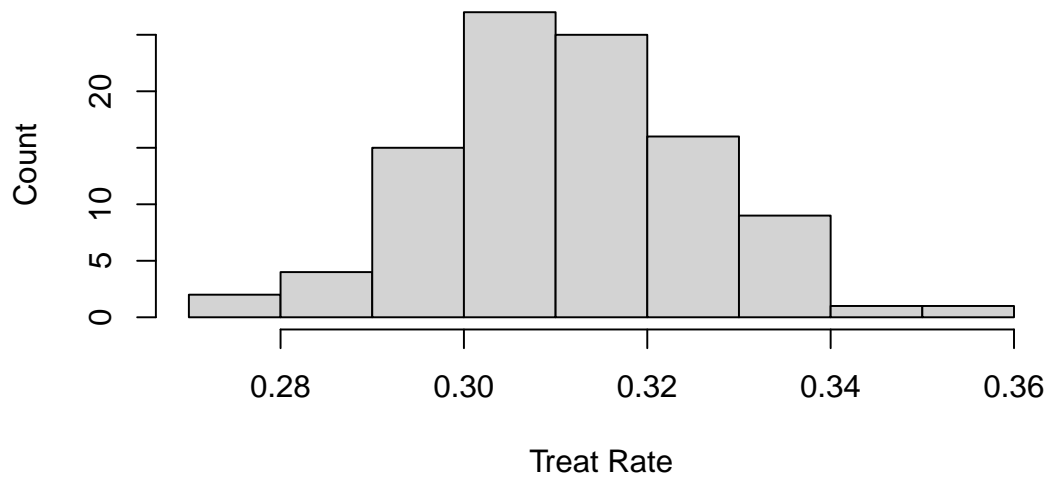
Generating 100 Samples from Our Population

```
source("./shared_code/data_gen_continuous_updated.R")
```

Let's take a look at one of our "no-boot" aka sub-population data sets.

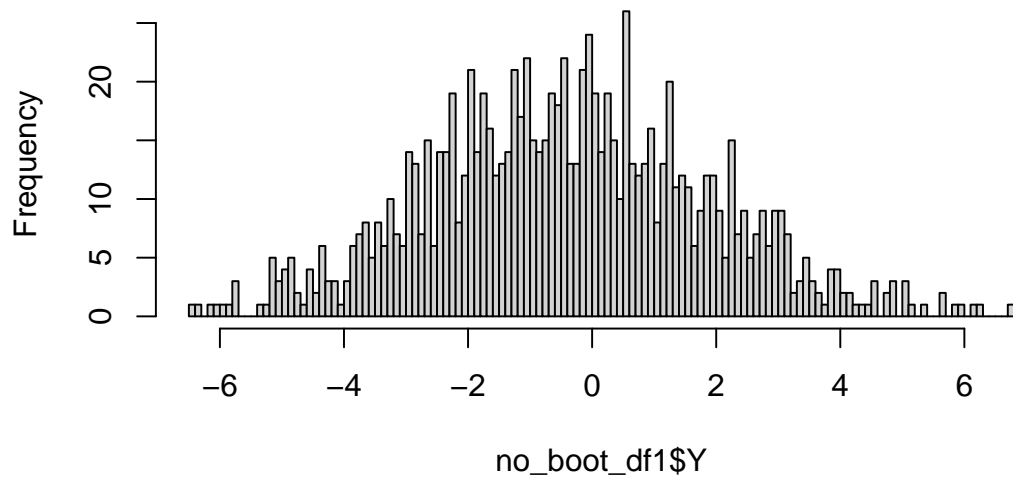
```
hist(map_dbl(1:length(no_boot_list), function(i) mean(no_boot_list[[i]]$A)),
     main = "Hist of Treatment Dist",
     xlab = "Treat Rate",
     ylab = "Count")
```

Hist of Treatment Dist



```
no_boot_df1 <- no_boot_list[[1]]  
  
sum(no_boot_df1$A) / nrow(no_boot_df1) # similar to desired_prop?  
  
## [1] 0.319  
  
hist(no_boot_df1$Y, breaks = 100) # continuous distribution of outcome
```

Histogram of no_boot_df1\$Y



The Simple Bootstrap

```
source("./shared_code/boot_cont_simple.R")
```

Summary of 1000 Simple Bootstraps in 100 Sub-Populations

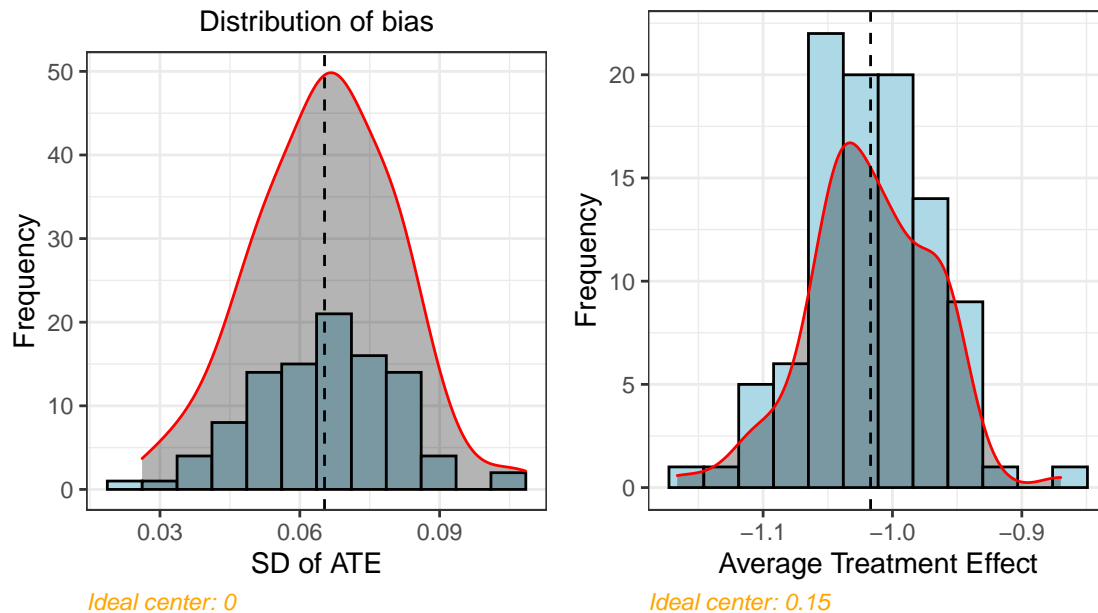
```
boot_result <-
  boot_estimates %>%
  group_by(seq) %>%
  summarize(ATE = mean(estimate),
            sd_ATE = sd(estimate),
            simp_perc_25 = quantile(estimate, probs = 0.025),
            simp_perc_975 = quantile(estimate, probs = 0.975))

fig1 <-
  boot_result %>%
  ggplot(aes(x = sd_ATE, color = sd_ATE)) +
  geom_histogram(fill = "light blue", bins = 12, color = "black") +
  geom_density(aes(y = ..density..*2), colour = "red",
              fill = "black", alpha = 0.3) +
  geom_vline(xintercept = mean(boot_result$sd_ATE), linetype = "dashed") +
  labs(title = "SD of ATE from 1000 Bootstraps in 100 Sub-Populations",
       subtitle = "Distribution of bias",
       caption = "Ideal center: 0", x = "SD of ATE", y = "Frequency") +
  theme(
    plot.title = element_text(color = "blue", size = 11, face = "bold"),
    plot.subtitle = element_text(color = "black"),
    plot.caption = element_text(color = "orange", face = "italic")
  )

fig2 <-
  boot_result %>%
  ggplot(aes(x = ATE)) +
  geom_histogram(fill = "light blue", bins = 12, color = "black") +
  geom_density(aes(y = ..density..*2), colour = "red",
              fill = "black", alpha = 0.3) +
  geom_vline(xintercept = mean(boot_result$ATE), linetype = "dashed") +
  labs(title = "Distribution of ATE in 1000 Bootstraps of 100 Sub-Populations",
       caption = "Ideal center: 0.15", x = "Average Treatment Effect", y = "Frequency") +
  theme(
    plot.title = element_text(color = "blue", size = 11, face = "bold"),
    plot.caption = element_text(color = "orange", face = "italic")
  )

plot_grid(fig1, fig2)
```

Distribution of ATE in 1000 Bootstraps of 100 Sub



```
rm(boot_estimates, boot_tib, df, matched, matched_df, matched_tib)
```

Running Complex Bootstraps

```
source("./shared_code/boot_cont_complex.R")
```

Confidence Intervals Coverage Rates

Generating Output

```
cont_simple_df <-
  boot_result %>%
  mutate(ci_lower = ATE - qnorm(0.975)*sd_ATE,
         ci_upper = ATE + qnorm(0.975)*sd_ATE,
         covered = case_when(
           ci_lower <= beta1 & ci_upper >= beta1 ~ 1,
           TRUE ~ 0
         ),
         boot_type = c(0),
         scenario_id = c(scenario_id),
         empirical_mean = continuous_empirical_mean_se$empirical_mean,
         empirical_se = continuous_empirical_mean_se$empirical_se) %>%
  relocate(-simp_perc_25, - simp_perc_975) %>%
  tibble()

cont_complex_df <-
  fin_estimate_df %>%
  mutate(ci_lower = ATE - qnorm(0.975)*sd_ATE,
         ci_upper = ATE + qnorm(0.975)*sd_ATE,
         covered = case_when(
           ci_lower <= beta1 & ci_upper >= beta1 ~ 1,
```

```

TRUE ~ 0

),
boot_type = c(1),
scenario_id = c(scenario_id),
empirical_mean = continuous_empirical_mean_se$empircal_mean,
empirical_se = continuous_empirical_mean_se$empircal_se) %>%
relocate(-comp_perc_975, -comp_perc_25) %>%
tibble() %>%
relocate(seq)

to_combine_df <- bind_rows(cont_simple_df, cont_complex_df)

dataset_name <- paste0("cont_df_scen_", scenario_id)

save_command <- paste0('save(', dataset_name, ", file = './new_output_data/", dataset_name, ".RData')")

eval(parse(text = paste(dataset_name, "to_combine_df", sep = " <- ")), envir = .GlobalEnv)

eval(parse(text = save_command))

beep()
#save(cont_df_scen_7, file = "./output_data/continuous_scen_7.RData") # change object name and file nam

```