## Continuous Simulation

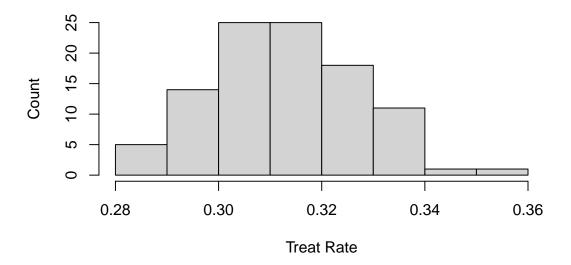
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#### Generating 100 Samples from Our Population

```
source("./shared_code/data_gen_continuous.R")
## -- Attaching packages ----- tidyverse 1.3.1 --
                  v purrr
## v ggplot2 3.3.5
                             0.3.4
## v tibble 3.1.6 v dplyr 1.0.7
## v tidyr 1.1.4 v stringr 1.4.0
## v readr
          2.1.1
                   v forcats 0.5.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                  masks stats::lag()
## Loading required package: ggpp
##
## Attaching package: 'ggpp'
## The following object is masked from 'package:ggplot2':
##
##
      annotate
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")
```

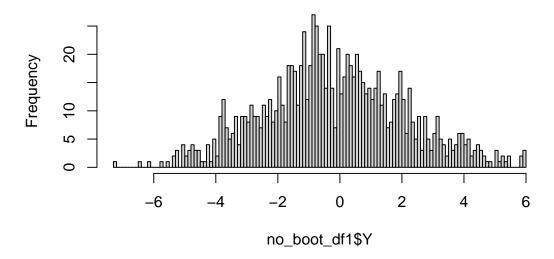
## **Hist of Treatment Dist**



```
no_boot_df1 <- no_boot_list[[1]]
sum(no_boot_df1$A) / nrow(no_boot_df1) # similar to desired_prop?
## [1] 0.313</pre>
```

hist(no\_boot\_df1\$Y, breaks = 100) # continuous distribution of outcome

# Histogram of no\_boot\_df1\$Y



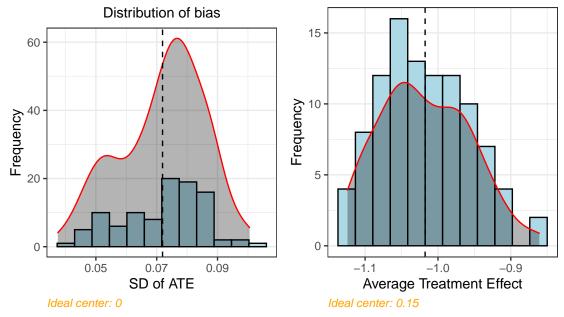
### The Simple Bootstrap

```
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))
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") +
  plot.title = element_text(color = "blue", size = 11, face = "bold"),
  plot.caption = element_text(color = "orange", face = "italic")
plot_grid(fig1, fig2)
```

#### f ATE from 1000 Bootstraps in 1000 Bubbletion 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 <-</pre>
  boot_result %>%
  mutate(ci_lower = ATE - 1.96*sd(ATE),
         ci_upper = ATE + 1.96*sd(ATE),
         covered = case_when(
           ci_lower <= beta1 & ci_upper >= beta1 ~ 1,
                                             TRUE ~ 0
         ),
         boot_type = c(0),
         scenario_id = c(6), # this needs to be updated each run
         empirical_mean = continuous_empirical_mean_se$empircal_mean,
         empirical_se = continuous_empirical_mean_se$empircal_se) %>%
  tibble()
cont complex df <-
 fin_estimate_df %>%
 mutate(ci_lower = ATE - 1.96*sd(ATE),
```