Binary_Simulation_v2

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Generating covariates and finding coefficits for covariates in propensity model.

```r
covariate_coef <- function(desired_prop, n, cov_df) {


   alpha_0 = log(desired_prop/(1 - desired_prop))

   coef_L1 <- sample(cov_df$L1, 10000, replace = TRUE)

   coef_L2 <- sample(cov_df$L2, 10000, replace = TRUE)

   coef_L3 <- sample(cov_df$L3, 10000, replace = TRUE)

   A_logit <- vector(mode = "list",length = length(coef_L2))
   p_A <-  vector(mode = "numeric",length = length(coef_L2))

   u <- alpha_0 + coef_L1[1]*cov_df$L1 + coef_L2[1]*cov_df$L2 - coef_L3[1]*cov_df$L3

   p_A[1] <-  mean(exp(u)/(1 + exp(u)))

   tol <- 0.001

   i = 1

   while (abs(p_A[i] - 0.14) > tol) {

     i = i + 1

     A_logit[[i]] <-
       alpha_0 + coef_L1[i]*cov_df$L1 + coef_L2[i]*cov_df$L2 - coef_L3[i]*cov_df$L3

     p_A[i] <- mean(exp(A_logit[[i]])/(1 + exp(A_logit[[i]])))

     if (abs(p_A[i] - 0.14) < tol) {
       mean_treated_proportion <- p_A[i]
       desired_coef_L1 <- coef_L1[i]
       desired_coef_L2 <- coef_L2[i]
       desired_coef_L3 <- coef_L3[i]
     }
     if (i > length(coef_L2)) {
       stop("You need better coverage, mate.")
    }

   }

   return(tibble(alpha_0,  mean_treated_proportion,
            desired_coef_L1, desired_coef_L2, desired_coef_L3))
}
```

Generating 100 no boot samples

```
seed_vec <- rnorm(100000, mean = 0, sd = 100) %>% round(0) %>% unique()

generate_no_boot_data <- function(n, size = 5000, seeds = seed_vec) {

  df <- list()

  cov_df <- list()

  pb <- progress_bar$new(format = "generating data... [:bar]", total = n)

    for (i in 1:n) {
    pb$tick()
    set.seed(seeds[i])

    set.seed(seeds[i])
    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")

    cov_df[[i]] <- genData(5000, pre_data)

    cov_coef_df <- covariate_coef(0.14, 2, cov_df[[i]])

    L1_coef <- cov_coef_df$desired_coef_L1
    L2_coef <- cov_coef_df$desired_coef_L2
    L3_coef <- cov_coef_df$desired_coef_L3

    pre_data <- defData(pre_data, varname = "L1_coef", formula = L1_coef)
    pre_data <- defData(pre_data, varname = "L2_coef", formula = L2_coef)
    pre_data <- defData(pre_data, varname = "L3_coef", formula = L3_coef)

    pre_data <- defData(pre_data, varname = "A",
                        formula = "-1.815 + L1_coef*L1 + L2_coef*L2 + L3_coef*L3",
                    dist = "binary", link = "logit")
    pre_data <- defData(pre_data, varname = "Y",
                        formula = "0.437 + 0.767*A + 1.39*L2 -0.7*L3" ,
                    dist = "binary", link = "logit")

    df[[i]] <- genData(size, pre_data)
    df[[i]] <- df[[i]] %>% select(-L1_coef, -L2_coef, -L3_coef)
    }
  return(df)
}

no_boot_list <- generate_no_boot_data(100)
```

Implementing nearest-neighbor matching (NNM)

```
df <- no_boot_list

# could possible turn this into a function later.
matched_df <- list()

for (i in 1:length(df)) {

  matched <- matchit(A ~ L1 + L2 + L3,
                          data = df[[i]],
                          distance = "glm",
                          link = "logit",
                          method = "nearest",
                          ratio = 1) # perform NNM

  matched_df[[i]] <- match.data(matched, distance = "ps")
}
```

simple Bootstrap

```
# creating the tibble to apply map function
matched_tib <-
  tibble(data = matched_df)

# ### function to iterate glm over a list, to be used in purr:map ###
# returns tibble of parameter estimates and standard errors.

outcome_model_list <- function(list) {
  tib_coef <- tibble()
  pb3$tick()
  for (i in 1:length(list)) {
    mod <- glm(Y ~ A + ps,
               data = list[[i]],
               weights = weights,
               family = "binomial") %>% summary()
    coefs <- mod$coefficients[2,1:2]
    tib_coef <- bind_rows(tib_coef, tibble(estimate = coefs[1], se = coefs[2]))
  }
    return(tib_coef)
}

# ### input matched dataframe, output however many bootstrapped samples you want ###
# first, set seed vector for reproducibility


# now, define function

seed_vec_2 <- rnorm(100000, mean = 0, sd = 10000) %>% round(0) %>% unique()

simple_boot <- function(df, n, size = 500, seeds = seed_vec_2){
  boots <- list()
  pb2$tick()
  for (i in 1:n) {
  set.seed(seeds[i])
  boots[[i]] <-
    df %>%
    filter(subclass %in% sample(levels(subclass),
                                size,
                                replace =  TRUE))
  }
  return(boots)
}


# adding progress bars for sanity
pb2 <- progress_bar$new(format = "bootstrapping... [:bar]", total = nrow(matched_tib))
pb3 <- progress_bar$new(format = "performing glm... [:bar]", total = nrow(matched_tib))

# creating booted tibbles, applying functions through purr:map.
boot_tib <-
  matched_tib %>%
  mutate(
    boots = map(.x = data, ~simple_boot(.x, n = 100))
    ) %>%
  mutate(coef = map(.x = boots, ~outcome_model_list(.x)))
```

Unnesting bootstrap coefficients

```
boot_estimates <-
  boot_tib %>%
  mutate(seq = seq(1:nrow(boot_tib))) %>%
  select(coef, seq) %>% unnest(coef)
```

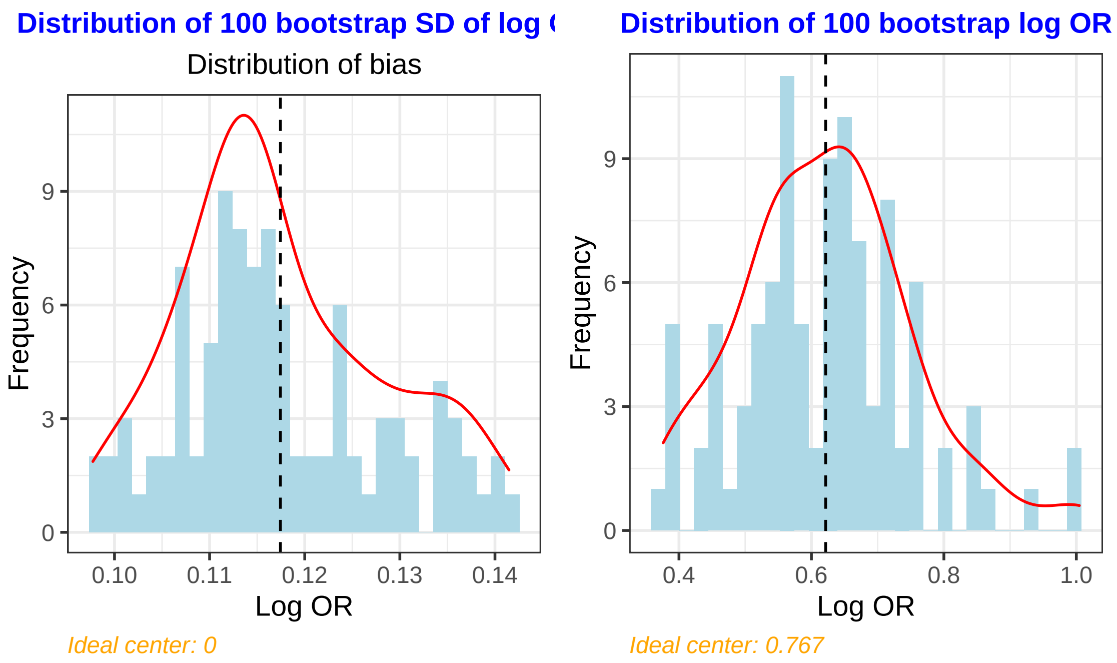
100 bootstrap summary

```
boot_result <-
  boot_estimates %>%
  group_by(seq) %>%
  summarize(mean_log_OR = mean(estimate), sd_log_OR = sd(estimate))

fig1 <-
  boot_result %>%
  ggplot(aes(x = sd_log_OR, color = sd_log_OR)) +
  geom_histogram(fill = "light blue",  bins = 30) +
  geom_density(aes(y = ..density..*0.25), colour = "red") +
  geom_vline(xintercept = mean(boot_result$sd_log_OR), linetype = "dashed") +
  labs(title = "Distribution of 100 bootstrap SD of log OR",
       subtitle = "Distribution of bias",
  caption = "Ideal center: 0", x = "Log OR", 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 = mean_log_OR)) +
  geom_histogram(fill = "light blue", bins = 30) +
  geom_density(aes(y = ..density..*3), colour = "red") +
  geom_vline(xintercept = mean(boot_result$mean_log_OR), linetype = "dashed") +
  labs(title = "Distribution of 100 bootstrap log OR",
       caption = "Ideal center: 0.767", x = "Log OR", 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)
```



100 Confidence Intervals Coverage Rate

```
CI_coverate_rate <- function(nboot){
  boot_CI_log_OR <- list()
  count_true <- list()

  for (i in 1:nboot) {
     boot_CI_log_OR[[i]] <-
       c(boot_result$mean_log_OR[i] - 1.96*boot_result$sd_log_OR,
         boot_result$mean_log_OR[i] + 1.96*boot_result$sd_log_OR)

      count_true[i] <-
        between(0.767, range(boot_CI_log_OR[[i]])[1], range(boot_CI_log_OR[[i]])[2])
  }

  result =
    as.vector(unlist(count_true)) %>%
    sum() %>% paste0("%")

  return(result)
}

CI_coverate_rate(100)
```

```
## [1] "86%"
```