Quant 2, Lab 2

Bootstrapping & Cluster Analysis

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Outline

- Tip of the week: Pacman

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- Bootstrapping

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- Clustered analysis

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- Bootstrapping
- Clustered analysis
- Bootstrapping x Clustered analysis
- Intro to git (if we have time)

Pacman

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- R Package for package management
- `pacman::p_load`: loads or installs automatically
- `pacman::p_install_version`: installs a specific version

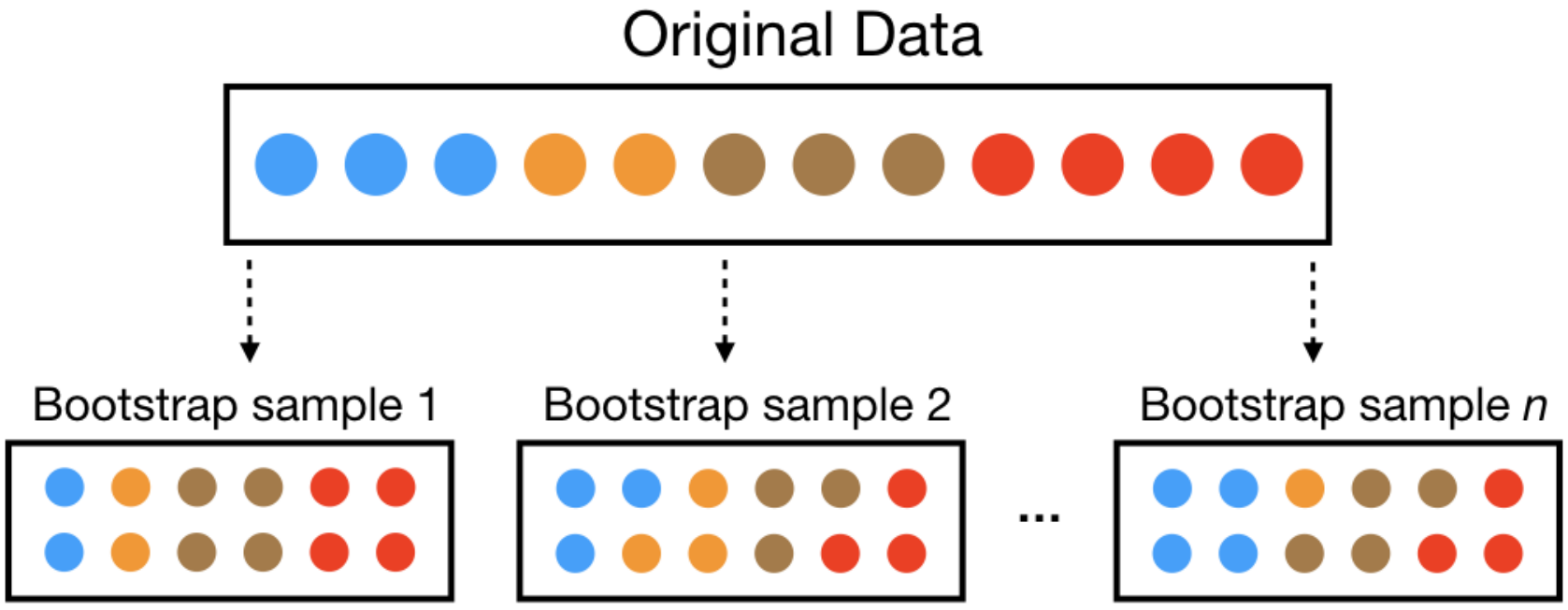
Bootstrapping

- I heard you like samples

Bootstrapping

- I heard you like samples
- So I made a sample of samples from a sample

Bootstrapping



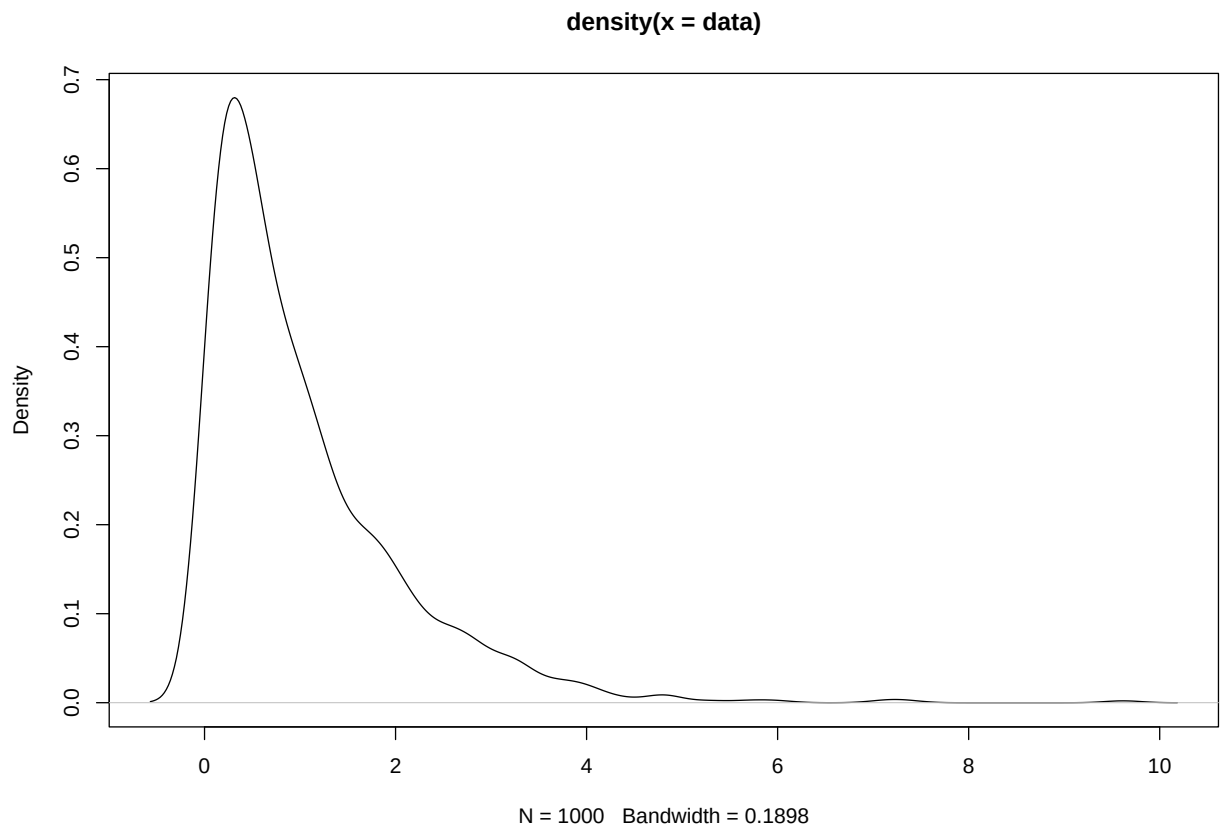
Bootstrapping

- Get confidence intervals for estimators we can't (or don't want to) derive variances for

Bootstrap Example: Quantile CIs

- Let's say we are interested in estimating the 90th percentile value

```
N <- 1000
data <- mysterious_dgp(N)
density(data) %>% plot()
```



Bootstrap Example: Quantile CIs

- We can estimate the sample 90th quantile...

```
quantile(data, 0.9)
```

```
##      90%
## 2.395541
```

Bootstrap Example: Quantile CIs

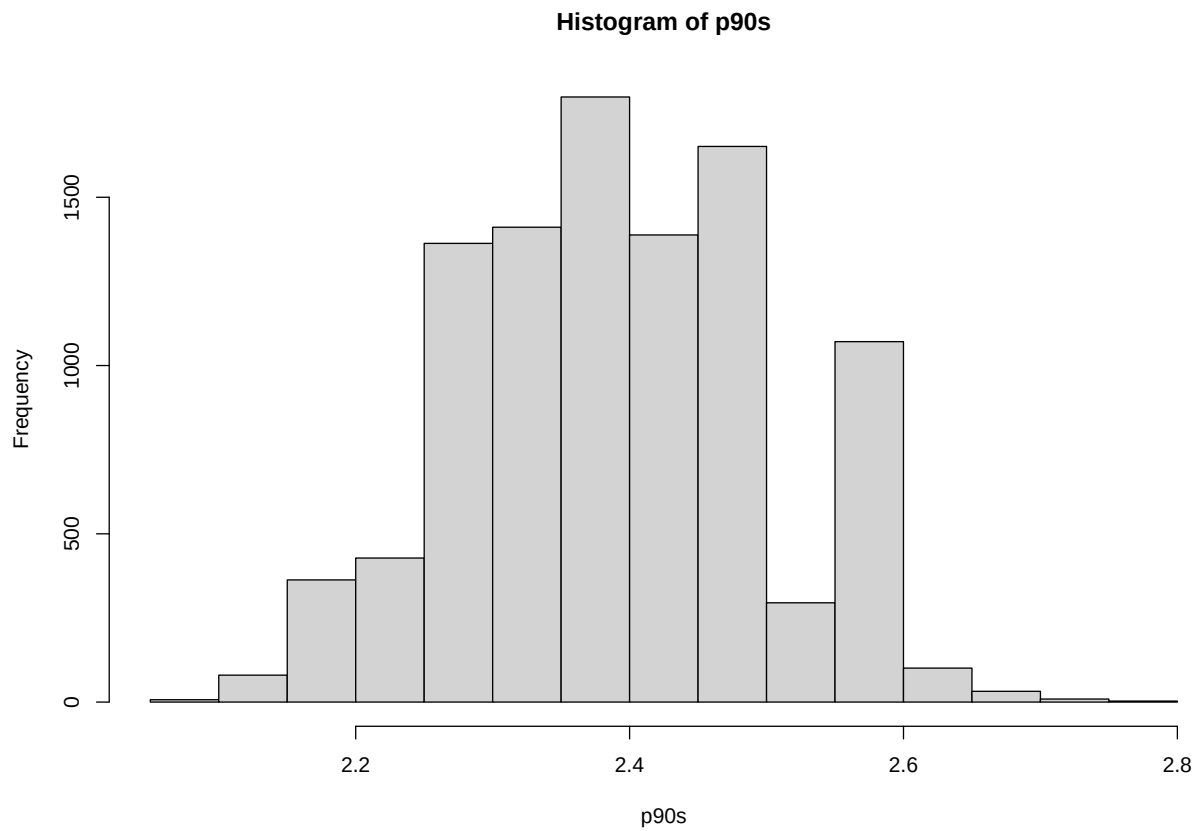
- We can estimate the sample 90th quantile...
- But how would we calculate the confidence interval on this estimate?

```
quantile(data, 0.9)
```

```
##      90%
## 2.395541
```

Bootstrap Example: Quantile CIs

```
N.bs <- 10000
# Draw 10K samples from our data with replacement
sample.of.samples <- map(1:N.bs, \(x) sample(data, N, replace = T))

# Calculate the p90 for each sample
p90s <- map(sample.of.samples, \(x) quantile(x, 0.9)) %>% unlist()
hist(p90s)
```



Bootstrap Example: Quantile CIs

- Estimate the CI with the bootstrap sample statistics

```
quantile(p90s, c(0.025, 0.975))
```

```
##     2.5%    97.5%
## 2.164831 2.584656
```

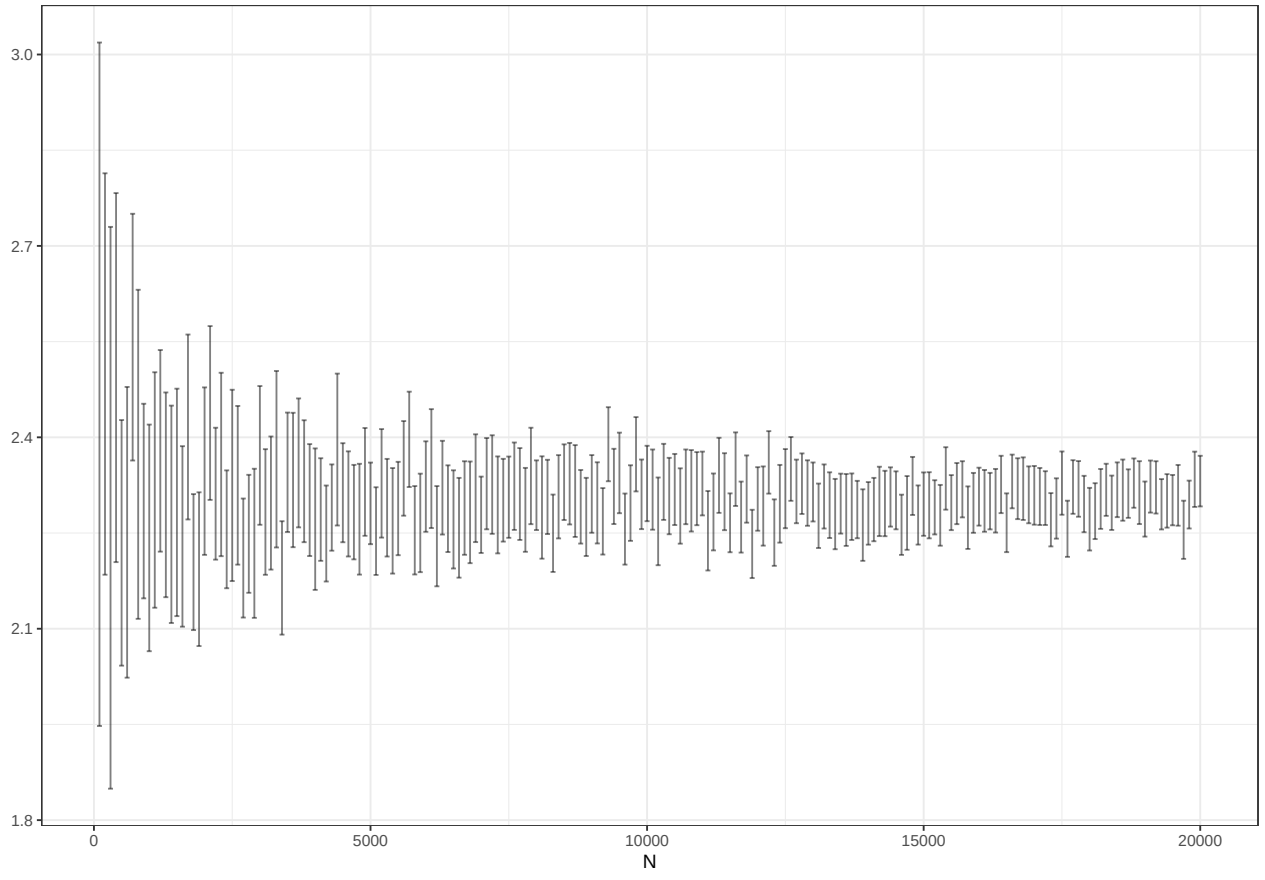
Just for comparison...

```
samples <- map(1:N.bs, \(x) mysterious_dgp(N))

true.p90s <- map(samples, \(x) quantile(x, 0.9)) %>% unlist()

quantile(true.p90s, c(0.025, 0.975))
```

```
##     2.5%    97.5%
## 2.120499 2.490750
```

- Bias corrected and/or studentized bootstrapping are also options

Bootstrap validity is also asymptotic



Cluster Analysis

- Data and treatments often **clustered**

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- State wide minimum wage policy change

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- Classroom wide distribution of technology

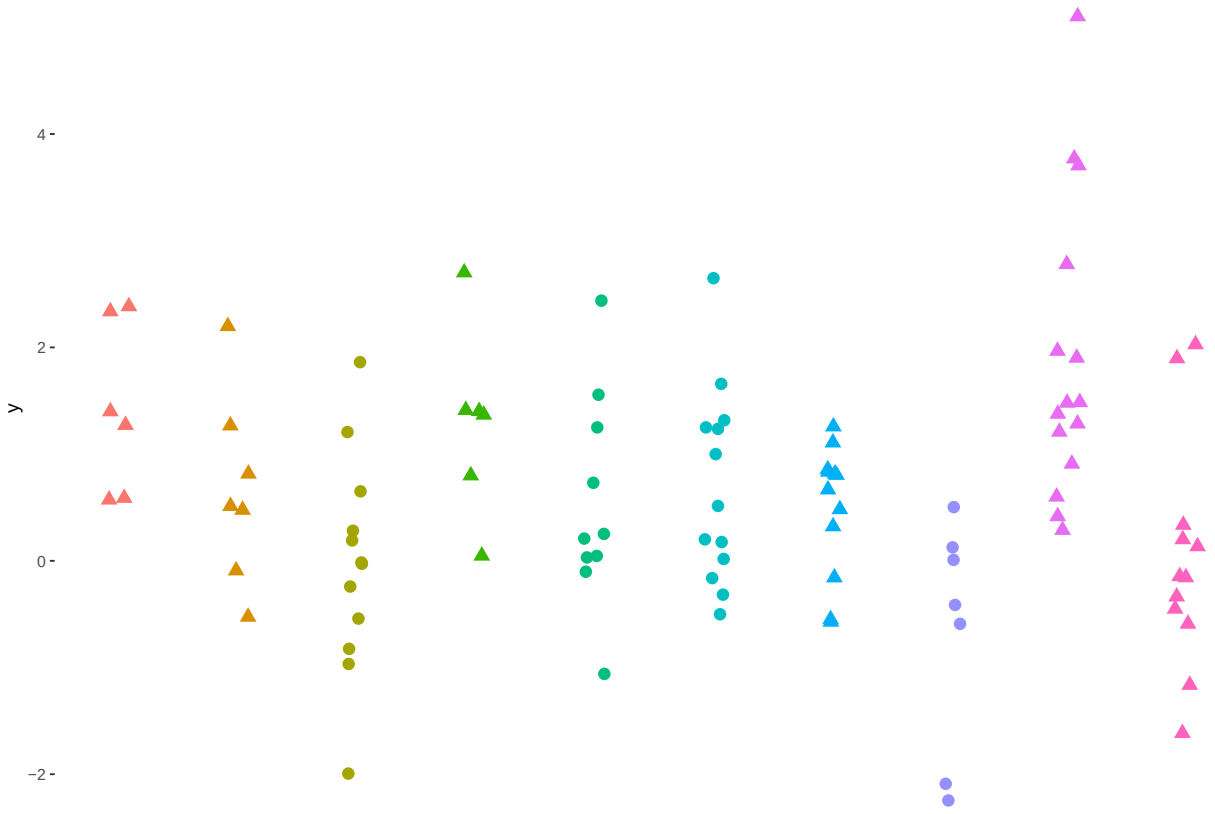
Cluster Analysis

- Data and treatments often **clustered**
- State wide minimum wage policy change
- Classroom wide distribution of technology
- Etc.

Cluster simulation

```r
make_clustered_data <- function(G, N) {
    g <- sample(1:G, size = N, replace = T)
    treat.g <- sample(c(0, 1), size = G, replace = T)
    while (is.na(sd(treat.g))) {
        treat.g <- sample(c(0, 1), size = G, replace = T)
    }
    treat.i <- sapply(g, \(x) treat.g[x])
    effect.g <- rnorm(1:G)
    g.i <- sapply(g, \(x) effect.g[x])
    y <- rnorm(N) + g.i + 0.5 * treat.i
    data.frame(
        g = g,
        treat = treat.i,
        y = y
    )
}
```

Cluster simulation



Cluster simulation

```
model <- lm(y ~ treat, data = df)
summary(model) %>% tidy()
```

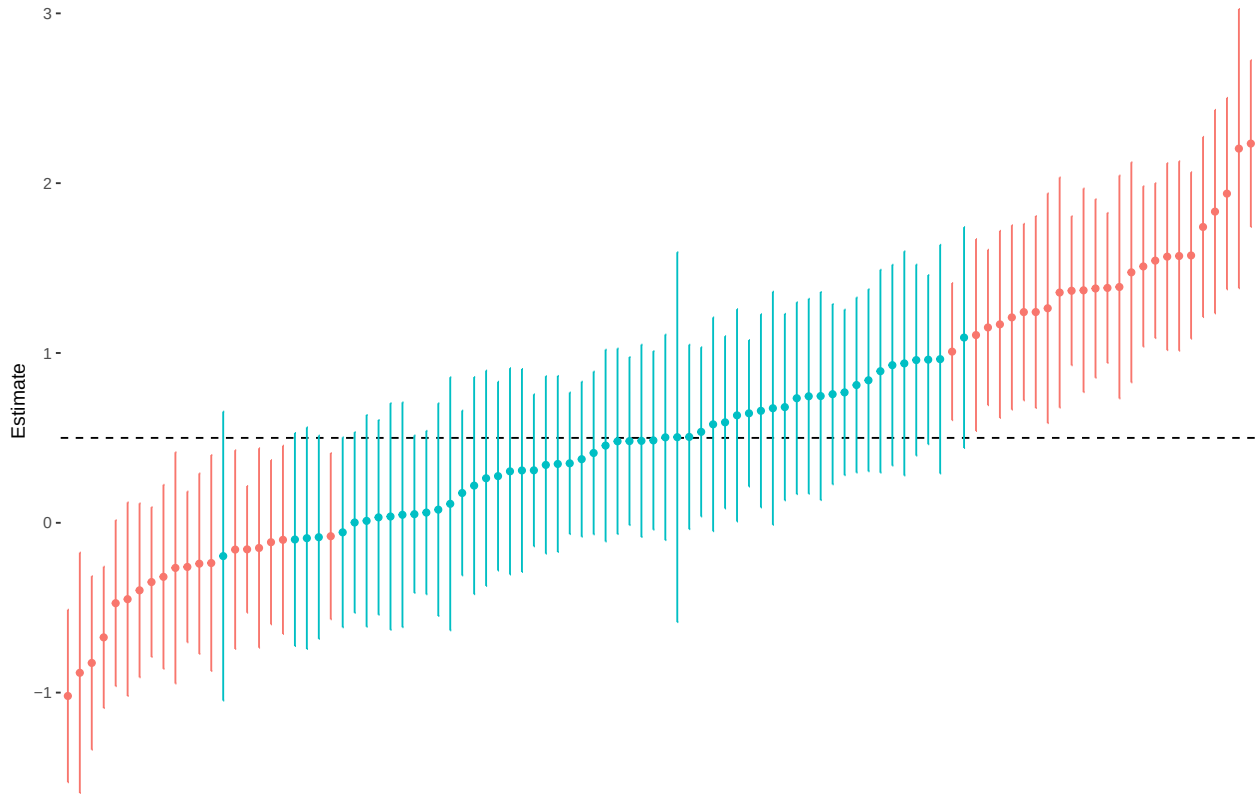
```
## # A tibble: 2 x 5
##   term        estimate std.error statistic p.value
##   <chr>          <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Intercept)    0.221     0.179      1.23 0.220
## 2 treat          0.731     0.235      3.12 0.00241
```

Cluster simulation

```r
make_sim <- function(x) {
    df <- make_clustered_data(G = 10, N = 100)
    model <- summary(lm(y ~ treat, data = df))$coefficients["treat", ]
    model
}
res <- map(1:100, make_sim) %>%
    bind_rows() %>%
    mutate(
        lo = Estimate - 1.96 * `Std. Error`,
        hi = Estimate + 1.96 * `Std. Error`,
        cover = lo < 0.5 & hi > 0.5,
        i = 1:100
    )
```

Cluster simulation

- Only 56% cover the true value



Cluster Bootstrapping: Vanilla

- Let's try to bootstrap SEs for β_{treat}

```
vanilla_bootstrap <- function(a) {
    resampled.data <- df %>% sample_frac(1, replace = T)
    tidy(lm(y ~ treat, data = resampled.data)) %>% filter(term == "trea
}
vb.results <- map(1:1000, vanilla_bootstrap) %>%
    bind_rows()
sd(vb.results$estimate)
```

```
## [1] 0.2306454
```

Cluster Bootstrapping: Block / Pair

- Bootstrap procedure with clustered data needs to reflect the clustered structure

```
get_block_bs_sample <- function(df) {
    sample(size = n_clusters, df$g, replace = T) %>%
        map(\(x) filter(df, g == x)) %>%
        bind_rows()
}
```

Cluster Bootstrapping: Block / Pair

- Bootstrap procedure with clustered data needs to reflect the clustered structure
- Block/Pair bootstrapping ressamples at the **cluster** level

```
get_block_bs_sample <- function(df) {
    sample(size = n_clusters, df$g, replace = T) %>%
        map(\(x) filter(df, g == x)) %>%
        bind_rows()
}
```

Cluster Bootstrapping: Block / Pair

```
bb.estimates <- map(1:1001, \(a) {
    resampled.data <- get_block_bs_sample(df)
    tidy(lm(y ~ treat, data = resampled.data)) %>% filter(term == "trea
}) %>%
    bind_rows() %>%
    .$estimate
```

Cluster Bootstrapping: Block / Pair

```
sd(bb.estimates)
```

```
## [1] NA
```

Cluster Bootstrapping: Block / Pair

```
table(get_block_bs_sample(df)$treat)
```

```
##
##  0  1
## 74 37
```

```
table(get_block_bs_sample(df)$treat)
```

```
##
##  0  1
## 14 94
```

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- Then, construct `y_star = y_pred + randomized_residual` and estimate `y_star ~ treat`

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- Let's not draw conventional bootstrap samples
- Instead, **randomize the sign of the residual** at the **cluster level**
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- Do this `N_boot` times

Cluster Bootstrapping: Wild

- Let's not draw conventional bootstrap samples
- Instead, **randomize the sign of the residual** at the **cluster level**
- Then, construct `y_star = y_pred + randomized_residual` and estimate `y_star ~ treat`
- Do this `N_boot` times
- Lab activity: implement in pairs using `wild_bs.R` as a starting template

Cluster Bootstrapping: Wild

```r
model <- lm(y ~ treat, df)
df$y_pred <- predict(model, df)
df$residuals <- df$y - df$y_pred
wild_bootstrap_3 <- function(a) {
    flip <- sample(c(-1, 1), n_clusters, replace = T)
    bs.resid.sign <- sapply(df$g, \(x) flip[x])
    df$y_star <- df$y_pred + df$residuals * bs.resid.sign

    tidy(lm(y_star ~ treat, data = df)) %>% filter(term == "treat")
}
wb3.estimates <- lapply(1:2000, wild_bootstrap_3) %>% bind_rows()
```

Cluster Bootstrapping: Wild

```
sd(wb3.estimates$estimate)
```

```
## [1] 0.4036346
```

Wild Cluster via Sandwich

- `fwildclusterboot` seems to have a broken dependency

```
vcv.wild <- sandwich::vcovBS(
    model,
    type = "wild-rademacher", cluster = ~g, R = 1000
)
coeftest(model, vcv.wild)
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.22076    0.23435  0.9420  0.34851
## treat        0.73145    0.40175  1.8207  0.07171 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cluster Robust SEs with fixest, estimatr

```
fixest::feols(y ~ treat, data = df, cluster = ~g)
```

```
## OLS estimation, Dep. Var.: y
## Observations: 100
## Standard-errors: Clustered (g)
##             Estimate Std. Error  t value Pr(>|t|)
## (Intercept) 0.220756   0.247647 0.891414  0.39591
## treat       0.731449   0.429948 1.701252  0.12311
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## RMSE: 1.14716   Adj. R2: 0.080828
```

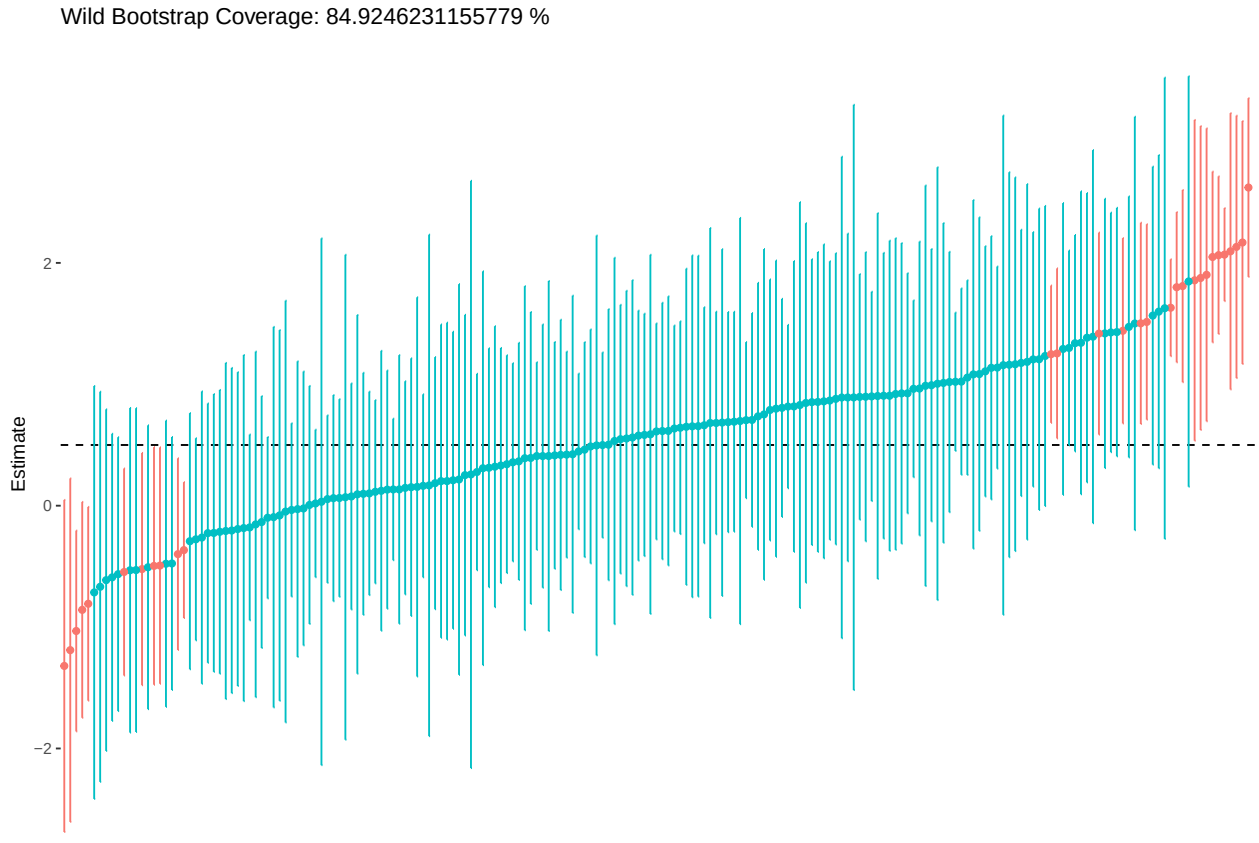
```
estimatr::lm_robust(y ~ treat, data = df, cluster = g)
```

```
##              Estimate Std. Error  t value  Pr(>|t|)   CI Lower CI Up
## (Intercept) 0.2207557  0.2694841 0.819179 0.4759311 -0.6663693 1.107
## treat       0.7314494  0.4645722 1.574458 0.1643331 -0.3935894 1.856
##                    DF
## (Intercept) 2.832031
## treat       6.269208
```

Coverage test: wild

```
conduct_sims(wild_sim, "Wild Bootstrap", 200)
```

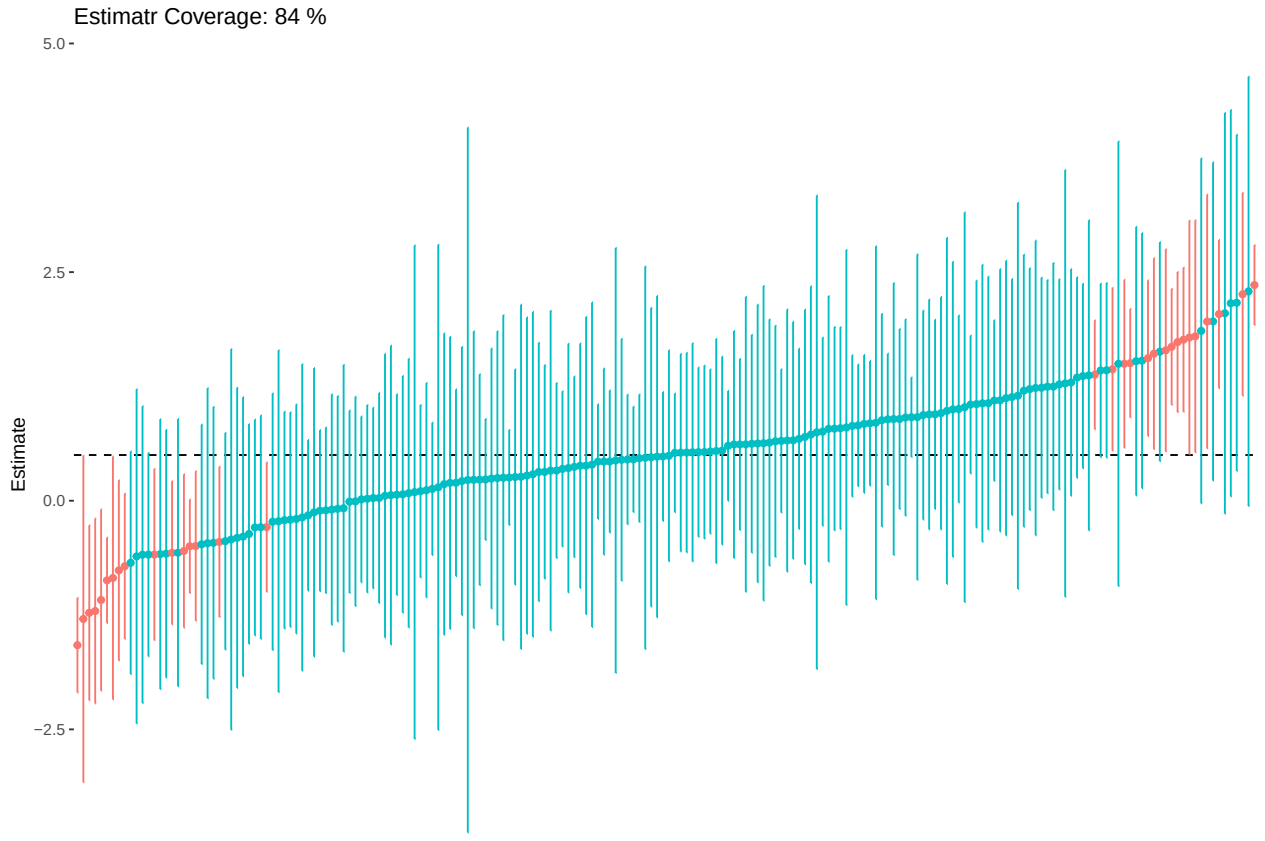
```
## Warning: Removed 1 row containing missing values or values outside t
## (`geom_point()`).
```



Coverage test: estimatr

```
conduct_sims(estimatr_sim, "Estimatr", 200)
```

```
## Warning in sqrt(diag(vcov_fit$Vcov_hat)): NaNs produced
```



Git intro

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- `git add` and `git commit` stage and commit changes
- `git stash` undo non-commited changes