w241: Experiments and Causality

Blocking and Clustering

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Blocking

- Hard to know if it was due to chance when there are large differences between treatment and control.
- Need to reduce the size of the differences that can arise by chance.
- Increase statistical power given an experiment with same sample and effect size.
- If some variables are related to the outcome, restrict ourselves to randomizations that keep treatment and control similar.

Make Data

```
d ← make_data(effect_size=0)
head(d)
```

```
##    Control Treatment group
## 1:       1         1   Man
## 2:       2         2   Man
## 3:       3         3   Man
## 4:       4         4   Man
## 5:       5         5   Man
## 6:       6         6   Man
```

Randomization

```
d[ , assignment := randomize(size=40)][ ,
  table('Sex' = group, 'Assignment' = assignment)]
```

```
##        Assignment
## Sex     Control Treatment
##   Man         9        11
##   Woman      11         9
```

```
d[ , assignment := randomize(size=40)][ ,
  table('Sex' = group, 'Assignment' = assignment)]
```

```
##        Assignment
## Sex     Control Treatment
##   Man         9        11
##   Woman      11         9
```

Block Randomization

```r
block_randomize ← function(size) {
  ## this function will be executed /within/ the  data.table that
  ## holds the data. It could be run outside, but the assignment
  ## in place that data.table provides make it clean inside.
  conditions ← c('Control', 'Treatment')

  if(size %% 2 == 0) {
    ## if there are an even number of units in each block this is easy
    urn ← rep(conditions, times = size/2)
  } else if(size %% 2 == 1) {
    ## if there are an odd number, then produce conditions to the
    ## nearest even number that is less than the number of units
    ## then add one more assignment condition, sampled at random
    urn ← c(rep(conditions, times = (size/2) - 0.5), sample(conditions, size = 1))
  }

  ## now, shuffle it up return the shuffled sequence
  assignment ← sample(urn)
  return(assignment)
}
```

Randomization

```
d[ , block_assignment := block_randomize(size=.N), by = group][ ,
  table('Sex' = group, 'Assignment' = block_assignment)]
```

```
##        Assignment
## Sex     Control Treatment
##   Man         10        10
##   Woman       10        10
```

```
d[ , block_assignment := block_randomize(size=.N), by = group][ ,
  table('Sex' = group, 'Assignment' = block_assignment)]
```

```
##        Assignment
## Sex     Control Treatment
##   Man         10        10
##   Woman       10        10
```

Conduct Experiment

```
conduct_experiment ← function(potential_control, potential_treatment, assignment) {
  outcomes ← potential_treatment * I(assignment == "Treatment") +
    potential_control * I(assignment == "Control")

  return(outcomes)
}

d[ , Y := conduct_experiment(Control, Treatment, block_assignment)]

head(d)
```

```
##    Control Treatment group assignment block_assignment Y
## 1:       1         1   Man  Treatment        Treatment 1
## 2:       2         2   Man    Control          Control 2
## 3:       3         3   Man  Treatment          Control 3
## 4:       4         4   Man  Treatment        Treatment 4
## 5:       5         5   Man  Treatment          Control 5
## 6:       6         6   Man  Treatment          Control 6
```

Estimate ATE

```
estimate_ate ← function(y_values, treatment, verbose=FALSE) {

  treatment_group_mean ← mean(y_values[treatment == 'Treatment'])
  control_group_mean   ← mean(y_values[treatment == 'Control'])

  ate ← treatment_group_mean - control_group_mean

  if(verbose) {
    return(
      list(
        "tg_mean" = treatment_group_mean,
        "cg_mean" = control_group_mean,
        "ate" = ate))
    } else {
      return("ate" = ate)
      }
}

ate ← d[ , estimate_ate(y_values = Y, treatment = block_assignment, verbose=TRUE)]
ate
```

```
##    tg_mean cg_mean ate
## 1:   36.15   34.85 1.3
```

Simulate A Normal Study

```
simulate_normal_study ← function(effect_size) {
  ## create world
  d ← make_data(effect_size=effect_size)

  ## randomly assign and count the number of women in treatment
  d[ , assignment := randomize()]

  women_in_treatment ← d[group == 'Woman' & assignment == 'Treatment', .N]

  ## measure outcomes
  d[ , Y := conduct_experiment(Control, Treatment, assignment)]

  ## estimate ate
  ate ← d[ , estimate_ate(y_values = Y, treatment = assignment)]

  ## return objects
  ##  - `ate` from the `estimate_ate` function.
  ##  - `women_in_treatment` as a count
  return(list('ate' = ate, 'women_in_treatment' = women_in_treatment))
}
```

Run One Normal Study

```
normal_study ← simulate_normal_study(effect_size = 0)
normal_study
```

```
## $ate
## [1] 14.1
##
## $women_in_treatment
## [1] 12
```

Simulate Many Normal Studies

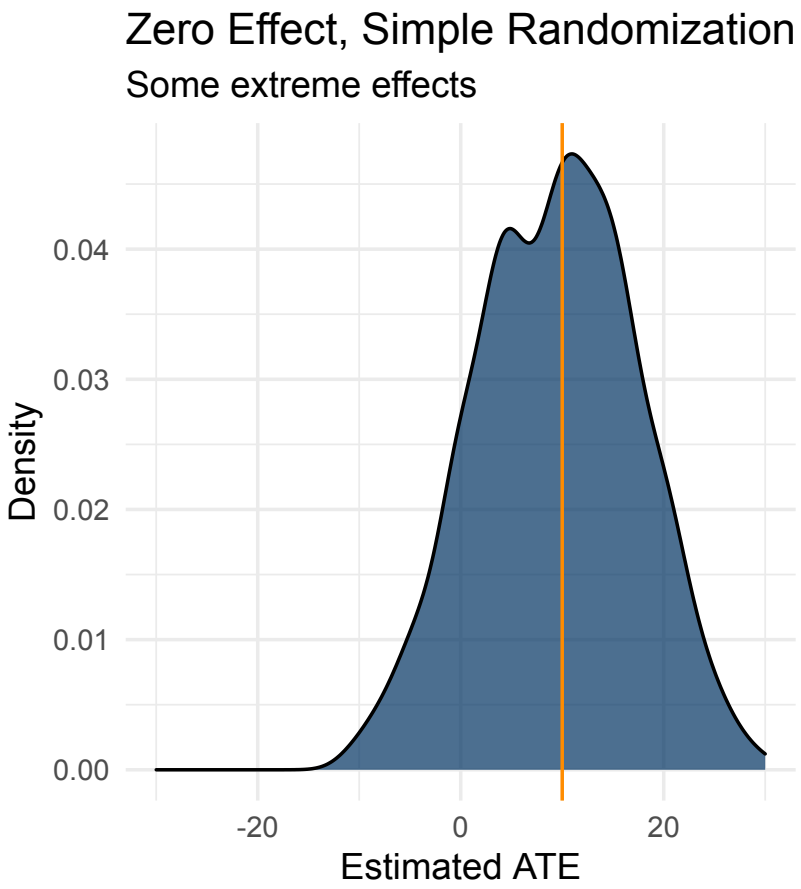
```
many_normal_studies ← replicate(
  n = 1000,
  expr = simulate_normal_study(effect_size = 10))

many_normal_studies ← t(many_normal_studies)
head(many_normal_studies)
```

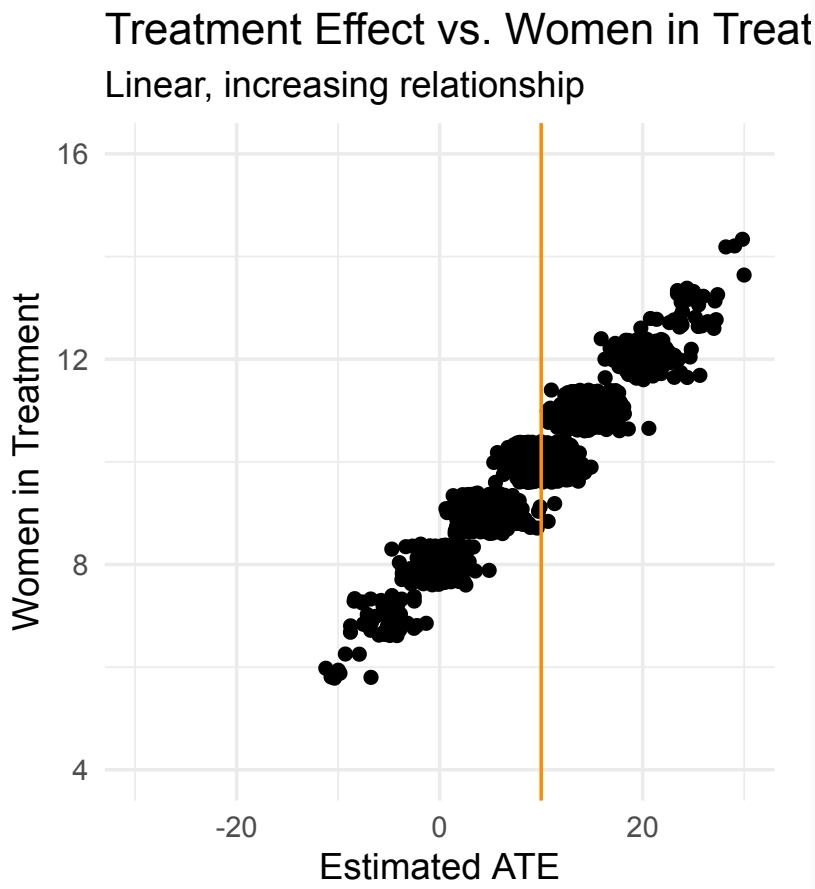
```
##      ate  women_in_treatment
## [1,] 1.9  8
## [2,] 3.2  9
## [3,] 18.5 12
## [4,] 10.9 11
## [5,] -5.5 7
## [6,] 4.2  9
```

Plot Normal ATE

```
## Warning: Removed 5 rows containing non-finite values (stat_density).
```

```
## Warning: Removed 5 rows containing missing values (geom_point).
```





Simulate a Block Randomized Study

```
simulate_blocked_study ← function(effect_size) {
  ## create world
  d ← make_data(effect_size=effect_size)

  ## randomly assign and count the number of women in treatment
  d[ , assignment := block_randomize(20), by = group]

  women_in_treatment ← d[group == 'Woman' & assignment == 'Treatment', .N]

  ## measure outcomes
  d[ , Y := conduct_experiment(Control, Treatment, assignment)]

  ## estimate ate
  ate ← d[ , estimate_ate(y_values = Y, treatment = assignment)]

  ## return objects
  ##  - `ate` from the `estimate_ate` function.
  ##  - `women_in_treatment` as a count
  return(list('ate' = ate, 'women_in_treatment' = women_in_treatment))
}
```

Simulate a Block Randomized Study

```
blocked_study ← simulate_blocked_study(effect_size = 10)
blocked_study
```

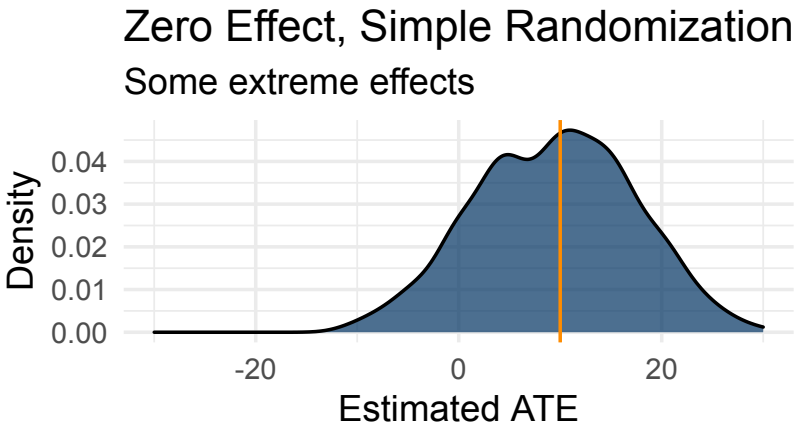
```
## $ate
## [1] 10.1
##
## $women_in_treatment
## [1] 10
```

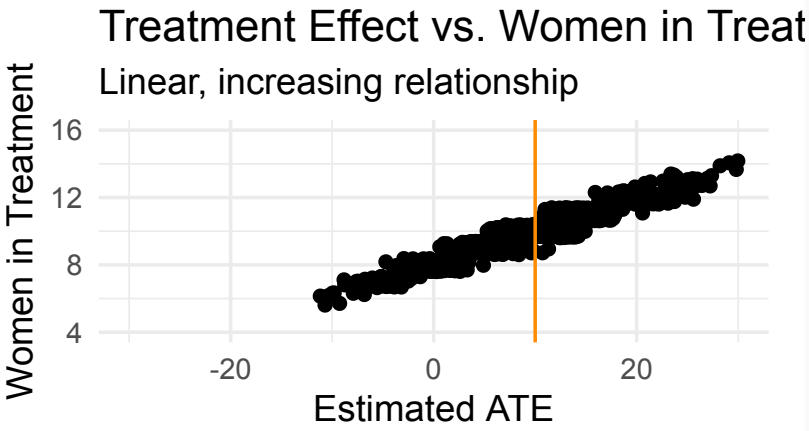
Simulate Many Block Randomized

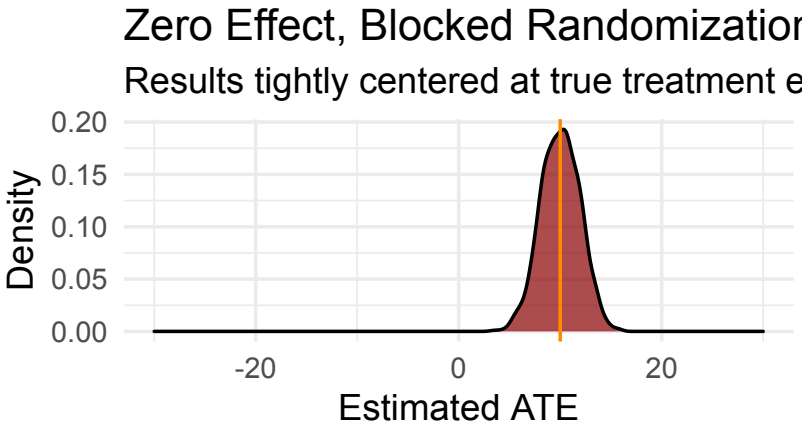
```
many_blocked_studies ← replicate(
  n = 1000,
  expr = simulate_blocked_study(effect_size = 10)
)

many_blocked_studies ← t(many_blocked_studies)
head(many_blocked_studies)
```

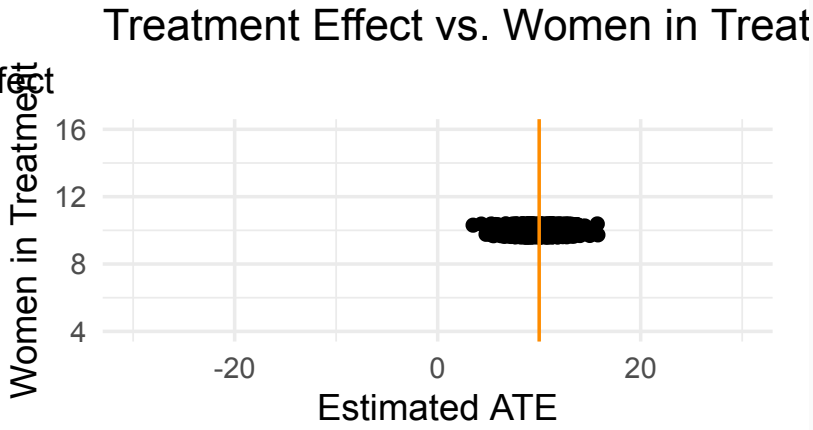
```
##      ate  women_in_treatment
## [1,] 11.5 10
## [2,] 9.1  10
## [3,] 4.8  10
## [4,] 9.9  10
## [5,] 6.3  10
## [6,] 10.3 10
```

Plot Blocked and Unblocked ATE









P-values of Blocked vs. Normal Study

- Blocking allows for more precision (efficiency) by not conducting randomization where covaraites (e.g. sex) are very imbalanced
- This means that your estimator will produce an estimate that is closer to the *true* causal effect
- This is an estimate that is closer to the orange lines on the last slide

Preview: Regression

```
d ← make_data(effect_size = 10)
d[ , assignment := randomize()]
d[ , Y := conduct_experiment(Control, Treatment, assignment)]

model_simple ← d[ , lm(Y ~ assignment)]
model_mf     ← d[ , lm(Y ~ assignment + group)]
```

Preview: Regression, Cont'd

```
##
## ================================================
##                          Dependent variable:
##                     ---------------------------
##                                  Y
##                         Unblocked       Blocked
##                           (1)             (2)
## ------------------------------------------------
## Assigned Treatment       1.200           11.250
##                     (-14.873, 17.273) (7.479, 15.021)
##                         p = 0.885      p = 0.00001***
##
## Group: Woman                              50.250
##                                       (46.479, 54.021)
##                                         p = 0.000***
##
## Intercept                39.900           9.750
##                     (28.535, 51.265)  (6.294, 13.206)
##                      p = 0.00000***    p = 0.00001***
##
## ------------------------------------------------
## Observations               40               40
## R2                        0.001            0.949
## Adjusted R2               -0.026           0.946
```

Summary of Blocking

Blocking

- Reduces the probability that a large Treatment vs. Control difference can occur by change by balancing the presence of similar units across Treatment and Control
- Can dramatically reduce the **standard error** of the estimator (i.e. the standard deviation of the sampling distribution)
- Is successful if the blocks predict the outcome
- Is unsuccessful if the blocks do **not** predict the outcome

Power

- Is affected by (a) sample size; and, (b) ratio of treatment effect to uncertainty about the estimate of treatment effect
- The standard deviation of the outcome is often much smaller within groups that are measurable before conducting the experiment

Clustering

Overview of Clustering

Clustering

- Often, units can be observed individually, but must be assigned to the same condition
- If there is covariance between group membership and outcomes (often there is) then this experiment does not do *as good a job* at breaking the relationship between treatment assignment and potential outcomes
- Alternatively, you might think of this experiment as producing less *information* about the treatment effect relative to the background noise of the world

Examples of Clustering

School Length

- Cannot randomly assign *at the student level* the length of the school day
- Instead, every student at the same school (or district, or state) has to receive the same length

Broadcast TV Advertisements

- In broadcast TV, it is not possible to assign advertisements (e.g. for Babbitt's Sports) to specific individuals
- Instead, whole markets receive the same ads

Retail Stores and Prices

- Retail stores cannot individually assign price discounts to shoppers
- However, prices can be manipulated at the store-level and purchases observed at the individual-level

Reading Assignment

- Please read *Field Experiments* pages 80-85.

Clustering Example

Setting up Data

Cluster: The level where treatment is assigned

- Notice that outcomes can be observed at more fine-grained levels
- There may be difference in *cluster-average* outcomes:
  - A teacher stubs their toe on the way to school
  - It is hot or cold in one classroom

```
classrooms_number ← 8
students_number   ← 16 # this is MIDS, not kindergarden

classroom_ids_vector ← rep(x = 1:8, each = 16)
classroom_ids_vector
```

```
##   [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3
##  [38] 3 3 3 3 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5
##  [75] 5 5 5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
## [112] 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
```

Classroom Example

```
classroom_noise_vector ← 1:8 + rnorm(n=8, mean=0, sd=.5)
```

```
potential_outcomes_data ← data.table(
  student_id      = 1:(8*16),
  classroom_id    = classroom_ids_vector,
  classroom_noise = rep(classroom_noise_vector, each = students_number)
)

setkey(potential_outcomes_data, 'classroom_id')

potential_outcomes_data[ ,
  student_outcomes_control := rnorm(n=.N, mean=10) + classroom_noise]
potential_outcomes_data[ ,
  student_outcomes_treat := student_outcomes_control + rnorm(n=.N, mean=1.5)]
```

Classroom Example, cont'd

```
urn ← rep(c('Control', 'Treatment'), each = classrooms_number/2)

cluster_assignment_table ← data.table(
  classroom_id         = potential_outcomes_data[ , unique(classroom_id)],
  classroom_assignment = sample(urn),
  key = 'classroom_id'
)

experiment_data ← merge(
  x = potential_outcomes_data,
  y = cluster_assignment_table,
  on = 'classroom_id')
```

Classroom Example, cont'd

```
head(experiment_data)
```

```
##    classroom_id student_id classroom_noise student_outcomes_control
## 1:            1          1      -0.1212204                 9.589522
## 2:            1          2      -0.1212204                11.055267
## 3:            1          3      -0.1212204                 8.996284
## 4:            1          4      -0.1212204                 8.761527
## 5:            1          5      -0.1212204                 8.727974
## 6:            1          6      -0.1212204                 8.938943
##    student_outcomes_treat classroom_assignment
## 1:               9.987568            Treatment
## 2:              11.737813            Treatment
## 3:               9.702525            Treatment
## 4:              10.537589            Treatment
## 5:              10.991949            Treatment
## 6:              11.529569            Treatment
```

Classroom Example, cont'd

```
experiment_data[ , classroom_assignment == 'Treatment']
```

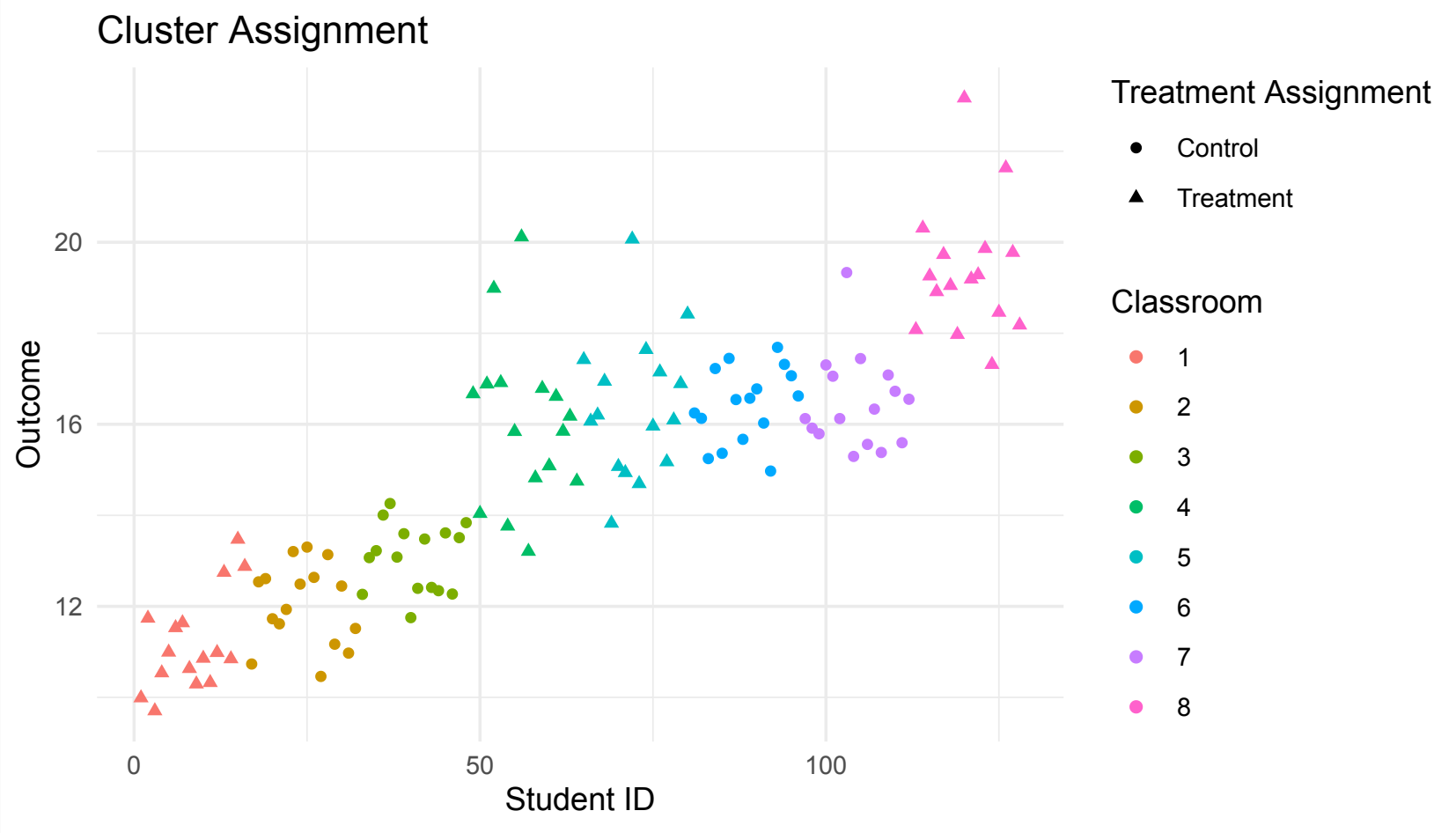
```
##   [1]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [13]  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [49]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [61]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [73]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE
##  [85] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
##  [97] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [109] FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
## [121]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
```

Classroom Example, cont'd

```
experiment_data[ , Y := conduct_experiment(
  potential_control   = student_outcomes_control,
  potential_treatment = student_outcomes_treat,
  assignment          = classroom_assignment )
  ]

cluster_ate ← experiment_data[ , estimate_ate(
  y_values  = Y,
  treatment =  classroom_assignment,
  verbose   = TRUE)
  ]

cluster_ate
```

```
##     tg_mean  cg_mean      ate
## 1: 15.75624 14.50215 1.254094
```

Notice ρ between classroom and Y



Classroom Example, Sharp Null

Repeat the reassignment process

- **Under the sharp null hypothesis** we assume that the potential outcomes to treatment that we *observe* for the units in the treatment group, $Y_i(1)|d_i = 1$, are equal to the potential outcomes to control that we *do not observe* for the units in the treatment group, $Y_i(0)|d_i = 1$.
- Similarly, **under the sharp null hypothesis** we assume that the potential outcomes to control that we *observe* for the people who are in the control group, $Y_i(0)|d_i = 0$ are equal to the potential outcomes to treatment that we *do not observe* for the units in the control group, $Y_i(1)|d_i = 0$

Take care

- Take care to notice how this statement of the sharp null hypothesis is different from the guarantees of apples-to-apples comparisions that are achieved through randomization

Classroom Example, Cluster RI Function

```
cluster_ri ← function(x_data, clustered) {
  if(clustered == TRUE) {
    urn ← rep(c('Control', 'Treatment'), each = x_data[ , length(unique(classroom_id)
    cluster_assignment_table ← data.table(
             classroom_id            = x_data[ , unique(classroom_id)],
             ri_classroom_assignment = sample(urn),
           key = 'classroom_id'
    )

    d ← merge(x_data, cluster_assignment_table, on = 'classroom_id')
    d[ , .(group_mean = mean(Y)),
       keyby = .(ri_classroom_assignment)
       ][ , diff(group_mean)]
  } else if(clustered == FALSE) {
    d ← x_data
    d[ , .(group_mean = mean(Y)),
       keyby = .(sample(classroom_assignment))
       ][ , diff(group_mean)]
  }
}
```

Classroom Example, Cluster RI Function

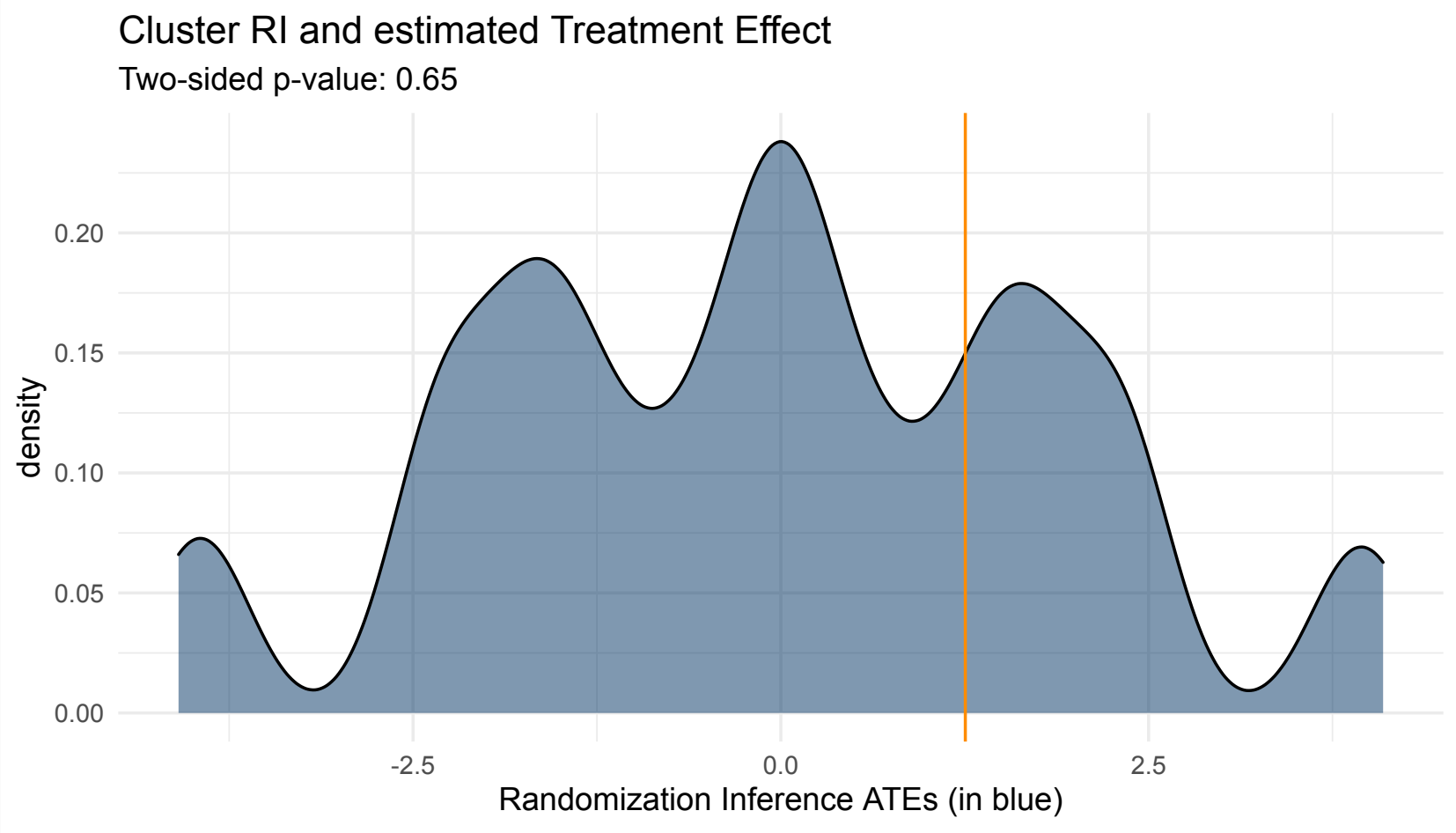
```
cluster_ri(x_data = experiment_data, clustered = TRUE)
```

```
## [1] 2.416797
```

Classroom Example, Conduct Cluster RI

```
cluster_ri_ates ← replicate(
  n = 5000,
  cluster_ri(x_data = experiment_data, clustered = TRUE)
)
```

Classroom Example, Plot Cluster RI



Perils of Ignoring Clustering

What if we ignore clustering?

What if we analyze results as though there wasn't clustering?

- Randomization happened at the classroom level, but our analysis ignores it?
- **Result**: p-values will be *too small* and false rejection rate will be larger than α that you're controlling for
- Potentially *much* larger depending on the correlation between classrooms and outcomes.

```
cluster_ri ← function(x_data, clustered) {
  if(clustered == TRUE) {
    ## ... we're going to use the second clause of
    ## `cluster_ri`, where we flag clustered==FALSE
  } else if(clustered == FALSE) {
    d ← x_data
    d[ , .(group_mean = mean(Y)),
       keyby = .(sample(classroom_assignment))
       ][ , diff(group_mean)]
  }
}
```

What if we ignore clustering?

- In the `clustered == FALSE` clause, randomization is handled by simply sampling the vector called `classroom_assignment`.
- Notice the individual-level randomization

```
experiment_data[ , sample(classroom_assignment)][1:40]
```

```
##  [1] "Control"   "Control"   "Treatment" "Control"   "Treatment" "Treatment"
##  [7] "Control"   "Treatment" "Control"   "Treatment" "Treatment" "Treatment"
## [13] "Control"   "Treatment" "Treatment" "Control"   "Treatment" "Treatment"
## [19] "Control"   "Control"   "Treatment" "Treatment" "Control"   "Treatment"
## [25] "Control"   "Treatment" "Control"   "Control"   "Control"   "Treatment"
## [31] "Treatment" "Control"   "Control"   "Treatment" "Treatment" "Control"
## [37] "Control"   "Control"   "Control"   "Control"
```

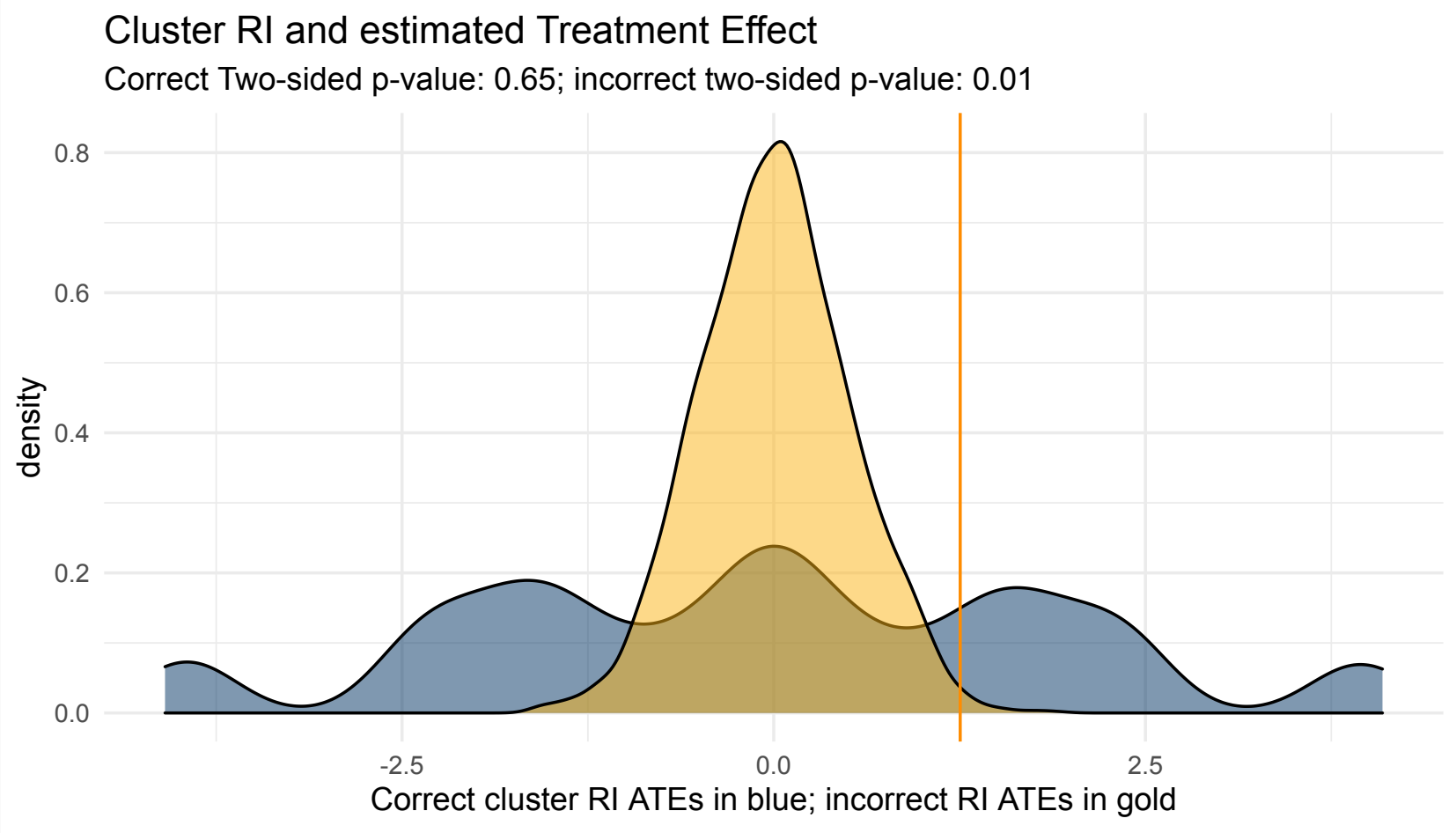
```
non_clustered_ates ← replicate(
  n = 5000,
  cluster_ri(x_data = experiment_data, clustered = FALSE)
)
```

Recall: Two-sample t-test

(Note: It isn't necessary to remember this formula from previous classes.)

$$t = \frac{\overline{X}_1 - \overline{X}_2}{\sqrt{\frac{s_1^2}{N_1} + \frac{s_2^2}{N_2}}}$$

What if we ignore clustering? (cont'd)



Summary

- When units are assigned to treatment or control in clusters, larger differences between `Treatment` and `Control` outcomes will happen by chance
- To account for this uncertainty, when conducting randomization inference, *match the experiment's assignment process*
  - If assignment happened at random, randomization inference needs to as well
  - If assignment happened with clusters, randomization inference needs to as well
  - If assignment happened with blocks, randomization inference needs to as well
- Stats software (e.g. `vcovCL` in R) can estimate correct clustered SEs in a regression framework

Summary

Power is relatively worse when

- Average between cluster differences are larger
- Within cluster differences are smaller
- The number of clusters is small

Power is relatively better when

- Average between cluster differences are smaller
- Within cluster differences are larger
- The number of clusters is large