# Day 08: Mediation and Moderation

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#### Moderators

- Motivate treatment effect heterogeneity
- Preliminary tests
- Structured tests
- Discuss caution needed
- A note on factorial experiments
- Labs
  - » reinforce HTE tests
  - » a note on power
- Discussion of your designs

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  - » So far, we've talked about average treatment effects
  - » Looking at the average effects ignores variability
    - (A feature not a bug of looking at the average)
- We might, however, be interested in this variability
  - » For whom are there big effects?
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Part 1 - is there heterogeneity?

- Is  $Var(\tau_i) > 0$ ?
- Imagine a test of null  $Var(\tau_i) = 0$ 
  - » In other words...  $\tau_i = \tau \ \forall i$
  - » Reject null ightarrow evidence of heterogeneity
- But, not possible to estimate  $\mathit{Var}( au_i)$ ! Why?

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$$Var(\tau_i) = Var(Y_i(1) - Y_i(0)) = Var(Y_i(1)) + Var(Y_i(0)) - 2Cov(Y_i(1), Y_i(0))$$

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## Preliminary investigations

To answer is  $Var(\tau_i) > 0$ ? we want to say something about null of  $Var(\tau_i) = 0$ .

- 1. Estimating bounds of  $Var(\tau_i)$
- 2. Testing whether  $Var(\tau_i) = 0$

```
1. Bounding Var(\tau_i) (GG pg 292-293)
    Y \leftarrow c(1,2,3,4,5,6)
    Z \leftarrow c(0,0,0,1,1,1)
```

8

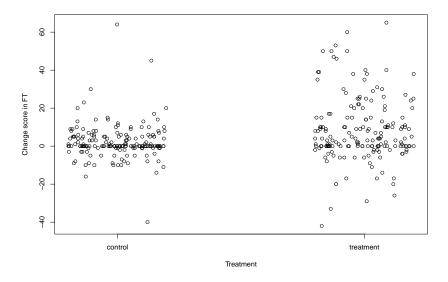
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    Y \leftarrow c(1,2,3,4,5,6)
    Z \leftarrow c(0,0,0,1,1,1)
    # Pair in ascending order
    sort(Y[Z==0])
    ## [1] 1 2 3
    sort(Y[Z==1])
    ## [1] 4 5 6
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    var(sort(Y[Z==1]) - sort(Y[Z==0]))
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→ Lower bound >> greater than 0 suggests TE beterogeneit

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    # Upper bound -- ests of tau_i when Cov is as large as possible
   var(sort(Y[Z==1], decreasing = T) - sort(Y[Z==0]))
   ## [1] 4
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 $\rightarrow$  Lower bound >> greater than 0 suggests TE heterogeneity



```
## [1] 630.2649
```

- → suggests there's heterogeneity
  - effect of outparty conversation varies from conversation to conversation
  - not surprising, right

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#### Testing null that $Var(\tau_i) = 0$

- We  $\mathit{can}$  estimate  $\mathit{Var}(\mathit{Y_i}(1))$  and  $\mathit{Var}(\mathit{Y_i}(0))$
- So, test of null that distributions of potential outcomes are identical except for a constant shift  $\boldsymbol{\tau}$ 
  - » Test null that  $Var(Y_i(1)) = Var(Y_i(0))$
- Why do we get to do this instead? Board

- 1. R
- 2. Regression

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# Example GG pg 295

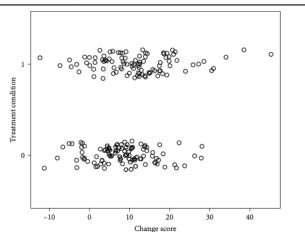
- Elementary schools
- Teachers in treated schools given bonuses (Z) according to standardized test scores
- Y = scores year 2 scores year 1
- Find that ATE is 11.7 big and significant

### Visual inspection

Is treatment group variation in Y larger/smaller/same as control?

FIGURE 9.1

Distribution of outcomes for treatment and control groups in the teacher incentives experiment



Source: Muralidharan and Sundararaman 2011. The plotted circles have been jittered to make it easier to see each observation.

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```

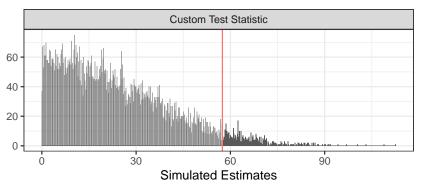
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out <- ri2::conduct_ri(test_function = var_fun,</pre>
    declaration = declaration,
    assignment = "Z",
    sharp_hypothesis = ate_obs,
    data = df,
    p = "upper",
    sims = 10000)
out
```

```
## term estimate upper_p_value
## 1 Custom Test Statistic 57.44728 0.0476
```

plot(out)

#### Randomization Inference



Estimate

Observed Value

- Reject the null hypothesis that ATE = 5.2 for all schools
- Evidence to suggest effects vary from school to school

#### What can and can't these preliminary tests do for us?

- Methods are for continuous outcomes
  - » Special methods needed for binary outcomes
- Good when we lack theoretical guidance about subgroups that may have different treatment effects
- Tests of equal variances tend to lack power
  - » First step in more structured assessment of HTE
    - Especially if evidence suggests heterogeneity

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Part 2 – treatment by covariate interactions

- Partition units by some covariate (i.e., religion, age)
- Look at ATE within the subgroup
  - » A new estimand!
  - » CATE is conditional average treatment effect
  - » e.g., CATE<sub>catholic</sub> is ATE among Catholics

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- Interact treatment with covariate  $(X \cdot Z)$ 
  - » Interaction is change/difference in treatment effect
  - » CATE<sub>catholic</sub> CATE<sub>noncatholic</sub>
    - Board
  - » As long at treatment randomly assigned, we get an unbiased estimate of the difference between two CATEs
- Common examples

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## Examples in print

Strength of partisanship, pages 31 and 32 (expressive partisanship)

PID, page 12 (opting out)

Strength of friendship, Figure 2c (61 million person experiment)

- "To measure a per-friend treatment effect, we compared behaviour in the friends connected to a user who received the social message to behaviour in the friends connected to a user in the control group"
- "For validated vote (Fig. 2c), the observed treatment effect is near zero for weak ties, but it spikes upwards and falls outside the null distribution for the top two deciles."

Null hypothesis is that CATEs in both groups are equal

$$CATE_{catholic} = CATE_{noncatholic}$$

Null model has just one common ATE

$$Y_i = a + bZ_i + cX_i + u_i$$

Alternative model has two CATEs (board)

$$Y_i = a + bZ_i + cX_i + dZ_iX_i + u_i$$

Note these are nested models (null equals alternative when...?)

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Null hypothesis is that CATEs in both groups are equal

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Note these are nested models (null equals alternative when...?)

- Recall: smaller SSR  $\rightarrow$  better fitting model
- F stat: compares SSR from two nested models

$$F = \frac{\frac{\text{SSR under null hyp - SSR under alt hyp}}{\text{No. params in null mod - No. of params in alt mod}} \\ \frac{\frac{\text{SSR under alt hyp}}{\text{N - No.of params in alt mod}}$$

- Calculate p value of observing F-stat as large or larger given null hypothesis (of no interaction) is true
  - » if different ATEs for different subgroups reduces SSR, numerator is positive, F stat is bigger
    - in the tails? unlikely given null; evidence supportive of interaction
  - » what if allowing for different ATEs does nothing to fit?

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### Example

```
null_mod <- lm(outparty_change ~ Z + pid2, data = results[results$full_cluster,])
summary(null_mod)</pre>
```

```
##
## Call:
## lm(formula = outparty_change ~ Z + pid2, data = results[results$full_cluster,
     1)
##
##
## Residuals:
##
      Min
              10 Median
                             30
                                    Max
## -51.604 -7.600 -1.255 3.748 62.748
##
## Coefficients:
##
             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.2553
                        0.9763 2.310 0.0212 *
## 7.
              7.3485 1.1209 6.556 1.23e-10 ***
## pid2R
              -1.0035 1.1207 -0.895 0.3710
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 13.47 on 575 degrees of freedom
## Multiple R-squared: 0.07075, Adjusted R-squared: 0.06752
## F-statistic: 21.89 on 2 and 575 DF, p-value: 6.88e-10
```

### Example

```
alt_mod <- lm(outparty_change ~ Z*pid2, data = results[results$full cluster.])
summary(alt mod)
##
## Call:
## lm(formula = outparty change ~ Z * pid2, data = results[results$full cluster.
##
     1)
##
## Residuals:
##
      Min
              10 Median
                             30
                                    Max
## -52.238 -7.908 -1.599 3.966 62.092
##
## Coefficients:
##
             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.5986 1.1302 1.414
                                          0.158
              8.6395 1.5847 5.452 7.42e-08 ***
## Z
## pid2R
              0.3099 1.5984 0.194 0.846
## Z:pid2R
              -2.5820 2.2412 -1.152 0.250
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 13.47 on 574 degrees of freedom
## Multiple R-squared: 0.0729, Adjusted R-squared: 0.06805
## F-statistic: 15.04 on 3 and 574 DF, p-value: 1.942e-09
```

## Example

```
anova(null_mod, alt_mod)

## Analysis of Variance Table

##

## Model 1: outparty_change ~ Z + pid2

## Model 2: outparty_change ~ Z * pid2

## Res.Df RSS Df Sum of Sq F Pr(>F)

## 1 575 104362

## 2 574 104121 1 240.76 1.3272 0.2498
```

#### Side note

P-values are the same because of the relationship between the t and F distributions

$$Y_i = a + bZ_i + cX_i + dZ_iX_i + u_i$$

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- -b+d is CATER
- d is interaction effect, or difference in CATEs

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- more on this later in the semester
- evaluate enough hypothesis, and one is likely to be significant at .05 level even though no effect
- reject a true null; false positive!
- 2. Pre-register a specific set of subgroup analyses
- without PAP, book advises to "regard hypothesis tests with skepticism pending replication by another study"
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- Moderator not randomly assigned
- Republican/Democrat is a marker of many things...
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- Therefore, think of this as either descriptive or exploratory

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#### Investigating treatment effect heterogeneity is challenging

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- » plan in the PAP!
- Without (or with) a PAP
  - » start with prelim tests to shed light on the question
  - » if you find a tentative yes, use theory to guide testable interaction effects
- Ideally, build additional factors into the design
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## Labs