

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.

Men and Women Group Variable

```
>group #recall the group variable
[1] "Man" "Man" "Man" "Man" "Man" "Man" "Man" "Man" "Man" "Man"
"Man" "Man" "Man" "Man" "Man" "Man" "Man" "Man" "Woman" "Woman"
"Woman" "Woman" "Woman" "Woman" "Woman" "Woman" "Woman" "Woman"
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"Woman" "Woman" "Woman" "Woman" "Woman" "Woman" "Woman" "Woman"

>#on average groups are split evenly, but for any particular
randomization they often are not

>table(group, randomize())
group 0 1
Man 13 7
Woman 7 13

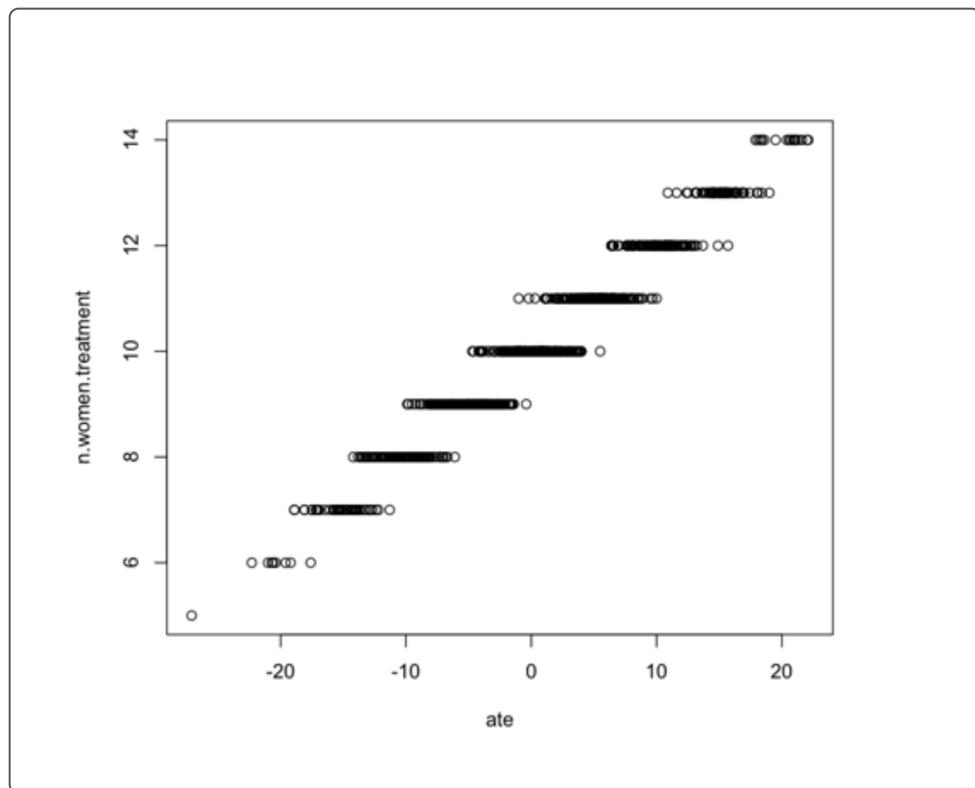
>table(group, randomize())
group 0 1
Man 9 11
Woman 11 9
```

Men and Women Group Variable (contd)

```
>randomize.blocked <- function() {  
+ c(  
+ sample(c(rep(0,10),rep(1,10))), #group A  
+ sample(c(rep(0,10),rep(1,10))) #group B  
+ )  
+ }  
  
>#now groups are always balanced  
  
>table(group, randomize.blocked())  
group 0 1  
Man 10 10  
Woman 10 10  
  
>table(group, randomize.blocked())  
group 0 1  
Man 10 10  
Woman 10 10
```

Simulate the Normal Study

```
>sim.normal.study <- function(){  
+ po.control <- c(seq(from = 1, to = 20), seq(from = 51, to = 70))  
+ po.treatment <- po.control  
+ treatment <- randomize()  
+ outcomes <- po.treatment * treatment + po.control * (1-treatment)  
+ ate <- est.ate(outcomes, treatment)  
+ n.women.treatment <- table(group, treatment)[2,2]  
+ return(list(ate = ate, n.women.treatment = n.women.treatment))  
+ }  
  
>results <- t(replicate(1000, sim.normal.study()))  
  
>plot(results)
```



Benefits of Blocking

DATASCI W241

Experiments and Causality

Benefits of Blocking

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>#results of the experiment with blocking
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>#results of the experiment with blocking  
>po.control <- c(seq(from = 1, to = 20), seq(from = 51, to = 70))  
>po.treatment <- po.control + 10 #simulate effect of 10
```

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```

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>outcomes.blocked <- po.treatment * treatment.blocked + po.control * (1-treatment.blocked)
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>outcomes.blocked <- po.treatment * treatment.blocked + po.control * (1-treatment.blocked)  
>ate <- est.ate(outcomes.blocked, treatment.blocked)  
>ate  
[1] 10
```

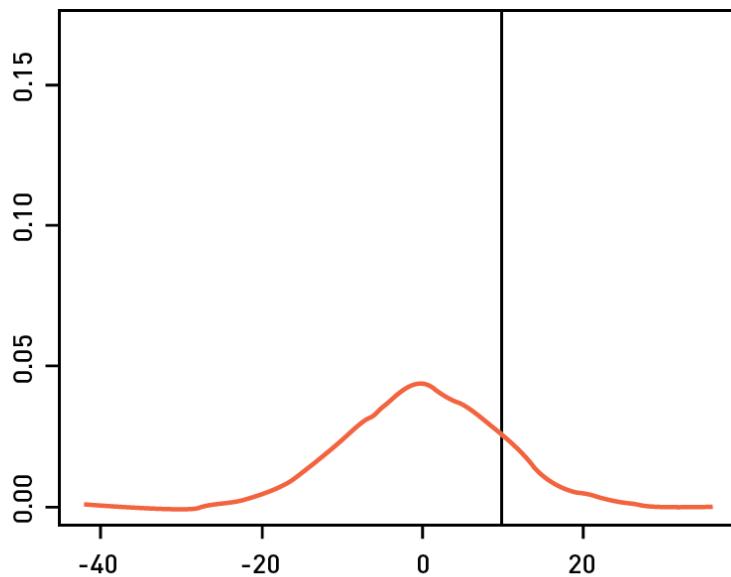
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>ate <- est.ate(outcomes.blocked, treatment.blocked)  
  
>ate  
[1] 10  
  
>plot(density(distribution.under.sharp.null), col="red", ylim=c(0,.17))  
#distribution without blocking  
  
>abline(v=ate)
```

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>plot(density(distribution.under.sharp.null), col="red", ylim=c(0,.17))  
#distribution without blocking  
  
>abline(v=ate)  
  
>mean(ate < distribution.under.sharp.null)  
[1] 0.1442
```

```
density.default(x = distribution.under.sharp.null)
```



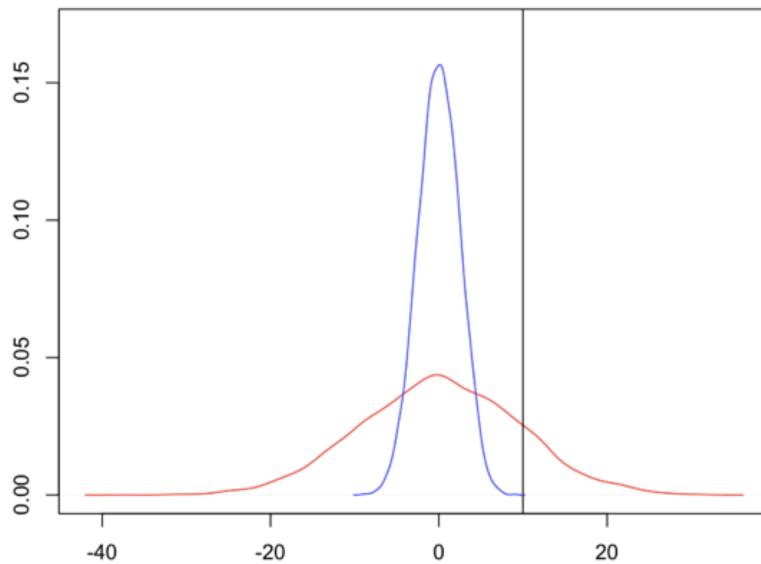
Benefits of Blocking (contd)

```
>distribution.under.sharp.null.blocked <- replicate(5000,  
est.ate(outcomes.blocked, randomize.blocked()))
```

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```
>distribution.under.sharp.null.blocked <- replicate(5000,  
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>lines(density(distribution.under.sharp.null.blocked), col="blue")  
#distribution with blocking  
  
>mean(ate < distribution.under.sharp.null.blocked)
```

density.default(x = distribution.under.sharp.null)



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#distribution with blocking  
  
>mean(ate < distribution.under.sharp.null.blocked)  
[1] 0
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#distribution with blocking  
  
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[1] 0
```

- Blocking allows more precision by not conducting randomizations where covariates (e.g., gender) are very imbalanced.

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>treatment <- randomize()  
>outcomes <- po.treatment * treatment + po.control * (1-treatment)  
>summary(lm(outcomes ~ treatment)) #without block indicator
```

[..]
Coefficients:

| | Estimate | Error | t value | Pr(> t) |
|-------------|----------|-------|---------|--------------|
| | Std. | | | |
| (Intercept) | 34.650 | 5.883 | 5.890 | 8.06e-07 *** |
| treatment | 11.700 | 8.319 | 1.406 | 0.168 |

Signif. Codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 26.31 on 38 degrees of freedom
Multiple R-squared: 0.04947, Adjusted R-squared: 0.02446
F-statistic: 1.978 on 1 and 38 DF, p-value: 0.1677

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Regression (contd)

```
>summary(lm(outcomes ~ treatment + factor(group))) #with block indicator
```

[...]
Coefficients:

| | Estimate Std. | Error | t value | Pr(> t) |
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| (Intercept) | 12.000 | 1.524 | 7.873 | 2.01e-097 *** |
| treatment | 6.667 | 1.825 | 3.653 | 0.000798 *** |
| factor (group)B | 50.333 | 1.825 | 27.580 | < 2e-16 *** |

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- Restricts randomizations and gains precision.

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- Standard deviation of outcome is often much smaller within groups of units identifiable ex-ante.
- Can also achieve this with regression.
- Use blockTools package in R with continuous variables.
- Use blocking for small samples for precision.

Overview

- Blocking: equally assigning units within values of a covariate to treatment and control.
- Sometimes units can be observed individually but must be assigned together.

Examples

- Lengthening hours in a school day
 - Cannot randomly assign treatment to each student.
 - Assignment is instead at the school level.
- TV advertisements to media markets
 - Cannot randomly assign individual advertisements.
 - Assignment is by geographic market.
- Stores to prices, with individual purchase data
 - Cannot randomly assign prices to individuals.

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- TV advertisements to media markets
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 - Assignment is by geographic market.
- Stores to prices, with individual purchase data
 - Cannot randomly assign prices to individuals.
 - But prices could be randomly assigned to stores, with each store being a "cluster."

Assignment

- Read FE pages 80–85.

Clustering Setup

- Randomly assigning teachers to different classrooms:

```
>n.classrooms <- 8
```

```
>n.students <- 16
```

- Consequences of clustering will be explored for the uncertainty in estimates.

- Cluster: the level or unit at which treatment is assigned.

Classroom Example

```
>all.classrooms <- unique(classroom.ids)
```

```
>all.classrooms  
[1] 1 2 3 4 5 6 7 8
```

- When treatment is assigned at a level higher than the individual, the uncertainty at that level must be taken into account.

```
>classroom.level.noise <- rnorm(length(all.classrooms))
```

```
>classroom.level.noise  
[1] -0.09677448 -0.92162355 -0.83917311 0.16667188 -1.55695401  
-0.48004472 0.18754375 1.27884390
```

Classroom Example (contd)

```
>student.outcomes.control <- rnorm(length(classroom.ids)) +
  classroom.level.noise[classroom.ids]

>student.outcomes.control
[1] -0.26668159 -1.06631660 -1.24747184 -0.32880261  0.63158035
-0.38429133 -0.35639291  0.80059169  1.13219006  0.33447677 [.....]

>student.outcomes.treat <- student.outcomes.control + 0.75
```

Random Assignments

```
>randomize.clustered <- function(){
+   treat.classroom.ids <- sample(all.classrooms, n.classrooms/2)
+   return(
+     as.numeric(classroom.ids %in% treat.classroom.ids)
+   )
+ }
```

- The vector must be made aware of the names of the cluster.

```
>sample(all.classrooms, n.classrooms/2)
[1] 6 8 7 2

>sample(all.classrooms, n.classrooms/2)
[1] 2 4 5 8

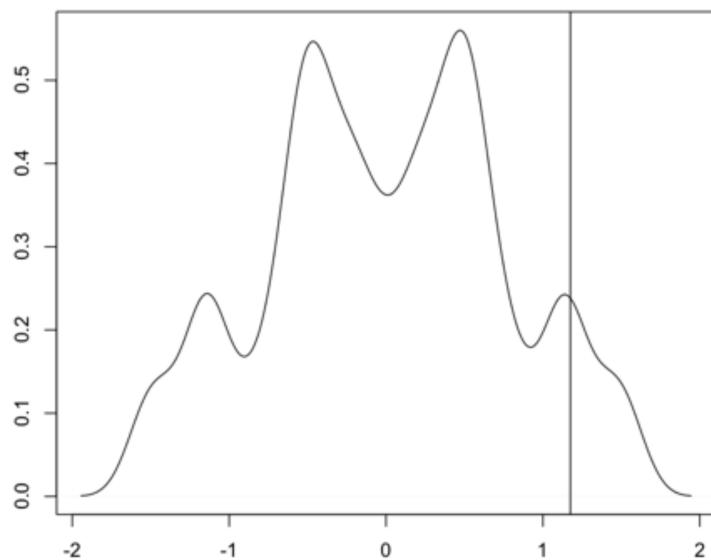
>sample(all.classrooms, n.classrooms/2)
[1] 7 3 5 8

>sample(all.classrooms, n.classrooms/2)
[1] 3 5 6 1
```

Random Assignments (contd)

Treatment Vector

```
density.default(x = distribution.under.sharp.null)
```



Distribution Under Sharp Null

```
>distribution.under.sharp.null <- replicate(5000, est.ate(outcomes,  
randomize.clustered()))  
  
>plot(density(distribution.under.sharp.null))  
  
>abline(v=ate) #pretty similar to one we'd get by chance  
  
>mean(ate <= distribution.under.sharp.null) #p-value  
[1] 0.0714
```

What If We Ignore Clustering?

- Analyzing results not taking into account data and treatment assigned at the cluster level

```
>randomize.ignoring.clustering <- function()  
sample(c(rep(0,n.classrooms*n.students/2),  
rep(1,n.classrooms*n.students/2)))  
  
>randomize.ignoring.clustering()  
[1] 0 1 0 1 0 1 0 1 1 0 0 0 0 1 1 0 0 0 1 1 0 0 0 0 0 0 0 0 0 1 0 0 1 1 1 0  
1 0 1 1 0 0 1 0 1 1 1 1 1 1 1 1 1 0 1 1 1 1 1 0 0 0 0 0 1 1 1 0 0 0 1 1 0 0 1  
0 0 1 0 0 0 1 1 1 0 0 1 1 0 1 0 1 1 1 1 0 1 0 0 0 0 0 1 0 0 1 1 1 1 0 0  
0 0 0 1 0 1 0 0 1 1 1 0 1 1 0 0 0 1 1 1 0
```

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

What If We Ignore Clustering? (contd)

```
>distribution.under.sharp.null.wrong <- replicate(5000,
est.ate(outcomes, randomize.ignoring.clustering()))
```

- Examines how large the differences will be between treatment and control by chance if there is no treatment effect for every unit

```
>plot(density(distribution.under.sharp.null), ylim=c(0,1.5))
>lines(density(distribution.under.sharp.null.wrong))
>abline(v=ate)
>mean(ate < distribution.under.sharp.null.wrong) #wrong p-value
[1] 0
```

Summary

- When units are assigned to treatment or control in groups, larger differences between T/C outcomes will happen by chance.
- To account for this uncertainty, assign units together in these clusters when simulating the distribution under the null.
- Statistical software like STATA can calculate correct clustered SEs in a regression.
- Use randomization inference when N clusters are small.
- Power worsens when:
 - Cluster-level noise is larger.
 - Number of clusters is smaller.
- Take into account the clustering process when estimating uncertainty, using randomization inference or regression.
- Cluster level noise: common shock that affects all individuals.