Class 1 — iTV Experiments
Basic Statistical Inference for Causal Quantities

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0. Get ready to work. Today we will be working to deepen our understanding of potential outcomes and the link between counterfactual causal quantities (which, in this course, we define formally as functions of potential outcomes) and statistical inference.

1. In 2005 Costas Panagopoulos randomly assigned treatment with a non-partisan Get-out-the-vote newspaper advertisement in low-salience mayoral elections in two of these four cities ($Z \in \{0, 1\}$ is assignment to treatment with advertisements and Y is observed proportion of the city turning out to vote).

	Z	Y
1	0	16
2	1	22
3	0	14
4	1	7
5	0	23
6	1	27
7	0	58
8	1	61

   Assuming SUTVA, please write down the potential outcomes for a given unit i?

   If y is a potential outcome (lower case as a fixed quantity — i.e. not depending on random assignment and with no known sampling process or stochastic generating model), then under SUTVA we could write $y_{i,Z_i=1} \equiv y_{i,1}$ as the potential outcome of unit i when $Z_i = 1$ and $y_{i,Z_i=0} \equiv y_{i,0}$ as the potential outcome of unit i when $Z_i = 0$.

2. How would you write the sharp null hypothesis of no effects using your notation for potential outcomes?

   $H_0 : y_{i,1} = y_{i,0}$

3. Explain in words what the sharp null hypothesis of no effects means in terms of this particular research design.

   A hypothesis is a question or model. This question asks (or model posits) that all cities would have shown the same turnout regardless of treatment assignment.

4. Here is how the observed outcome relates to the potential outcomes for a unit i (using one notation scheme, yours may be different):

$$Y_i = Z_i y_{i,1} + (1 - Z_i) y_{i,0} \quad (1)$$

   Explain this equation in words.

   What we observe, Y_i, is one of the two potential outcomes. And the potential outcome that we get to observe is determined by the treatment assignment. The treatment assignment selects a potential outcome for us to observe (and one to hide from us — all under SUTVA).

5. How does Y_i (what we observe) relate to $y_{i,0}$ (the partially observed control potential outcomes) if we take $H_0 : y_{i,1} = y_{i,0}$ seriously? *Hint:* Try to get rid of $y_{i,1}$ from equation 1.

$$\begin{aligned} Y_i &= Z_i y_{i,1} + (1 - Z_i) y_{i,0} \\ &= Z_i y_{i,0} + (1 - Z_i) y_{i,0} \\ &= Z_i y_{i,0} + y_{i,0} - Z_i y_{i,0} \\ &= y_{i,0} \end{aligned}$$

   Under the sharp null hypothesis of no effects, what we observe is what we would observe in the control condition (because, there would be no effects).

6. How many elements does the set that Rosenbuam calls Ω have in this design? Write them out.

   This set, which is the set of all possible treatment assignments under this design, has 6 elements.

```
Om<-combn(4,2,FUN=function(x){ tmp<-rep(0,4); tmp[x]<-1; return(tmp)})
print(Om)
```

```
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    1    1    1    0    0    0
[2,]    1    0    0    1    1    0
[3,]    0    1    0    1    0    1
[4,]    0    0    1    0    1    1
```

```
## For lexicographic order
##Om.list<-list()
##for(i in 1:6){ Om.list[[i]]<-Om[,i] }
##my.ord<-function(...){order(...,decreasing=TRUE)}
##Om[do.call("my.ord",Om.list),]
```

7. What does Ω represent?

   The set of all possible treatment assignment vectors.

8. Say we summarized the relationship between treatment and outcomes using a difference of means (mean of those assigned to treatment minus mean of those assigned to control). And, say we repeated this experiment on these same cities (at the same moment in time, such that Y_i reveals the same y_i in each experiment) and calculated the difference of means each time:

```
Y<-c(23,27,58,61)
thedist<-apply(Om,2,function(z){ mean(Y[z==1])-mean(Y[z==0]) })
print(thedist)
```

```
[1] -34.5  -3.5  -0.5   0.5   3.5  34.5
```

```
table(thedist)/6
```

```
thedist
-34.5  -3.5  -0.5   0.5   3.5  34.5
0.167 0.167 0.167 0.167 0.167 0.167
```

   What does the variation in these means represent? What is this distribution called? What does this distribution represent?

   This is the variation that we would expect if the treatment had no relationship with the outcome. This is the randomization distribution or reference distribution of the sharp null hypothesis of no effects. It represents the variation we would expect in the test statistic in the absence of any treatment effect.

9. Use this distribution to calculate a one-sided upper-tailed p-value for H_0. *Hint:* You'll need to know the difference of means for the observed treatment assignment.

```
obsZ<-c(0,1,0,1)
```

```
obstz<-mean(Y[obsZ==1])-mean(Y[obsZ==0])
mean(thedist>=obstz)
```

```
[1] 0.333
```

10. What did we need to assume to make this p-value valid and meaningful?

    We needed to assume that we correctly represented the design of the study. Here, and specifically, we needed to say that each element of Ω could have been drawn with equal probability and independently of each other.

    To write down Y_i in terms of $y_{i,0}$ we had to assume no interference between units [although, see below about this assumption and whether it makes a big deal when testing the sharp null of no effects].

11. How, let us loosen one of those assumptions: Please write down the potential outcomes for a unit i when we do not make the SUTVA assumption.

```
cat("$$",paste(apply(Om,2,function(x){paste("y_{i,",paste(x,collapse=""),"}")}),collapse=','),"$$")
```

$$y_{i,1100}, y_{i,1010}, y_{i,1001}, y_{i,0110}, y_{i,0101}, y_{i,0011}$$

12. Challenge question: Write down a sharp null hypothesis of no effects without SUTVA. Test this hypothesis as we tested the sharp null of no effects under SUTVA above. A bit of code below generates Ω:

```
cat("$$ H_0:",paste(apply(Om,2,function(x){paste("y_{i,",paste(x,collapse=""),"}")}),collapse='='),"$$")
```

$$H_0 : y_{i,1100} = y_{i,1010} = y_{i,1001} = y_{i,0110} = y_{i,0101} = y_{i,0011}$$

That is one version of a sharp null hypothesis of no effects without assuming SUTVA (**?** calls it the sharp null hypothesis of "no primary effects" if you are interested to can see how he talks about "no effects" by using a new potential outcome called the "uniformity trial", $y_{i,000000}$.). See also**?** for a bit more on these kinds of hypotheses.

Notice that because all of the potential outcomes are equal, we can test the sharp null hypothesis of no effects under arbitrary interference with the same exact test that we used above: that is, a test of the sharp null of no effects assuming no interference between units is the same as the test of the sharp null of no effects allowing any kind of interference between units.

13. Use the built in methods of RItools to test this same hypothesis:

```
## This next in case you haven't done so already
install.packages("devtools")
library("devtools")
.libPaths(getwd()) # <- installs to the working directory rather than the system
install_github("RItools", user = "markmfredrickson", ref = "randomization-distribution")
```

```
library(parallel)
library("RItools",lib.loc=getwd())
```

Represent the design. We call them "samplers" because "random assigners" or "assigners" seemed strange:

```
paired.assignment.sampler<-simpleRandomSampler(z=news.df$z,
                                               b=news.df$s)
## test it
ten.experiments<-paired.assignment.sampler(10)
## Does it do the right thing?
## One test:
all(colSums(ten.experiments$samples)==4)
```

```
[1] TRUE
```

```
testH0<-RItest(y=news.df$r,
               z=news.df$z,
               test.stat=mean.difference,
               p.value=upper.p.value,
               sampler=paired.assignment.sampler,
               samples=100,
               include.distribution=T)
## The p-value
summary(testH0)
```

```
Call:  RItest(y = news.df$r, z = news.df$z, test.stat = mean.difference,
          p.value = upper.p.value, sampler = paired.assignment.sampler,
           samples = 100, include.distribution = T)
                        Value Pr(>x)
Observed Test Statistic   1.5   0.38
```

```
## The distribution of the test statistic
table(testH0@distribution)
```

```
  -5 -3.5   -3   -2 -1.5 -0.5    0  0.5  1.5    2    3  3.5    5
   1    1    1    1    2    1    2    1    2    1    1    1    1
```