

# Homework 3

MA 590 Special Topics: Causal Inference

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## Problem 1

Download the file “hintVSexp.csv” from ([https://drive.google.com/open?id=15yQCMUNszztQNzyp40pQpmLRNn4z1JV4&authuser=acsales%40umich.edu&usp=drive\\_fs](https://drive.google.com/open?id=15yQCMUNszztQNzyp40pQpmLRNn4z1JV4&authuser=acsales%40umich.edu&usp=drive_fs))[this link]. This is a group of 33 randomized experiments from the ASSISTments online learning platform in which users were randomized to be offered either a multi-step “hint” ( $Z = 1$ ) or an “explanation” as to how to do the problem. The outcome  $Y$  is a binary indicator of whether they got the next problem correct or not. Here, we will treat this as one large experiment with 33 blocks, corresponding with particular problems in ASSISTments.

```
#import estimatr package
library(estimatr)
#load data
data <- read.csv("hintVSexp.csv")
#convert Z to integer
data$Z <- as.integer(data$Z)
```

### A

Use Fisher’s method to estimate a p-value for the sharp null  $H_0^{\text{Fisher}} : y_i(1) = y_i(0)$  for all  $i$ , and a 95% confidence interval for a constant effect. (As I have mentioned in class, constant effects don’t make sense with binary outcomes. Let’s ignore that problem for now and estimate one anyway.) Use any (valid) test statistic you like.

### Solution

```
#define test statistics
diffMeans=function(Y,Z)
  mean(Y[Z==1])-mean(Y[Z==0])
ts=diffMeans(data$Y,data$Z)
#permutation test for each strata (block)
#overall test: T=replicate(5000,diffMeans(data$Y,sample(data$Z)))
T=replicate(1000,{
  #permutation test for each strata (block)
  Yperm=rep(NA,nrow(data))
  for (i in unique(data$block)){
    #subset data by block
    data_block <- subset(data,block==i)
    #permutation test
    Yperm[data_block$block==i]=sample(data_block$Y)
  }
  diffMeans(Yperm,data$Z)
```

```

})

#calculate p-value
p = 2*min(mean(T>=ts),mean(T<=ts))
p

## [1] 0.302

#calculate CI
CI = quantile(T,c(0.025,0.975))
CI

##          2.5%          97.5%
## -0.06725104  0.06229570

```

## B

Use Neyman's method to estimate a (possibly weighted) average treatment effect ( $\tau_w$ ), with a p-value for the null hypothesis  $H_0^{\text{Neyman}} : \tau_w = 0$  and a 95% confidence interval.

### Solution

```

trt <- subset(data,Z==1)
ctl <- subset(data,Z==0)

DM <- mean(trt$Y)-mean(ctl$Y)

Vhat <- var(trt$Y)/nrow(trt)+var(ctl$Y)/nrow(ctl)
SEhat <- sqrt(Vhat)

# CI:
c(DM-qnorm(.975)*SEhat,DM+qnorm(.975)*SEhat)

## [1] -0.03041221  0.09430146

# p-value:
Tneyman <- DM/SEhat
p=2*pnorm(-abs(Tneyman))
p

## [1] 0.3153473

# weighted average treatment effect
ATE <- 0
for (i in unique(data$block)){
  #subset data by block
  data_block <- subset(data,block==i)
  #calculate ATE
  ATE <- ATE + (mean(data_block$Y[data_block$Z==1])-
    mean(data_block$Y[data_block$Z==0]))*nrow(data_block)
}
ATE <- ATE/nrow(data)
ATE

## [1] 0.01241591

```

## Problem 2

When dealing with grouped data, in some cases it makes sense to “group-mean-center” the data, i.e. subtract each group’s mean observed outcome (pool treatment and control groups) from each of the group’s outcomes. In other words, conduct analysis on  $\hat{Y}_{ij} = Y_{ij} - \bar{Y}_j$ , rather than on  $Y_{ij}$ . In a stratified experiment, what effect will group-mean-centering the outcomes within strata have on the (Neyman-style) estimate and standard error? In a cluster-randomized experiment, what effect will group-mean-centering the outcomes within cluster have on the (Neyman-style) estimate and (cluster-robust) standard error?

### Solution

Consider the case of stratified experiment. Group-mean-centering the outcomes within strata will have no effect on the Neyman-style estimate as the shifting of the mean of each strata is the same for both treatment and control group. However, in the case of standard error, the variance of the Neyman-style in the stratified experiment would change as now the variance for each of them are estimated on the subset rather than the whole set where the correlation between the strata are not taken into account. Therefore, the standard error would be smaller than the original one.

In the cluster-randomized experiment, however, the Neyman-style estimate would not be the same due to the unbiasedness of the mean and the standard error would be larger than the original one as the Molton’s factor are strictly larger than 1.

## Problem 3

The “Fisherian”  $1 - \alpha$  confidence interval consists of all of the hypothetical constant effects  $\tau$  such that the  $p$ -value testing the null hypothesis  $H_\tau : y_i(1) - y_i(0) = \tau$  is greater than  $\alpha$ .

Show that this is a valid  $1 - \alpha$  confidence interval, i.e. that if there is a true  $\tau$ , the probability of estimating a CI that contains  $\tau$  is  $1 - \alpha$ . You may take for granted the fact that comparing fisherian  $p$ -values to  $\alpha$  gives a valid  $\alpha$ - level test, i.e. if you reject the null whenever  $p < \alpha$ , the probability of falsy rejecting a true null is  $\alpha$ . (Though I strongly recommend convincing yourself that this is true—you just needn’t write down your argument here.) Once you accept that Fisherian  $p$ -values give you valid  $\alpha$ -level hypothesis tests, the proof is very simple, like two or three lines. Don’t overthink it.

### Solution

One can invert the test to see that whether  $\tau$  is in the CI (i.e., find the acceptance region) is equivalent to whether  $p$  is greater than  $\alpha$  (i.e., find the rejection region). Thus, the probability of estimating a CI that contains  $\tau$  is  $1 - \alpha$  which then conclude that the CI is valid as the probability of not rejecting the null hypothesis is at least  $1 - \alpha$  is hold.