# 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=15yQCMUNszztQNzyp40pQpm LRNn4z1JV4&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)
```

```
})
hist(T, main="Histogram of test statistics on permuted data")
```

## Histogram of test statistics on permuted data
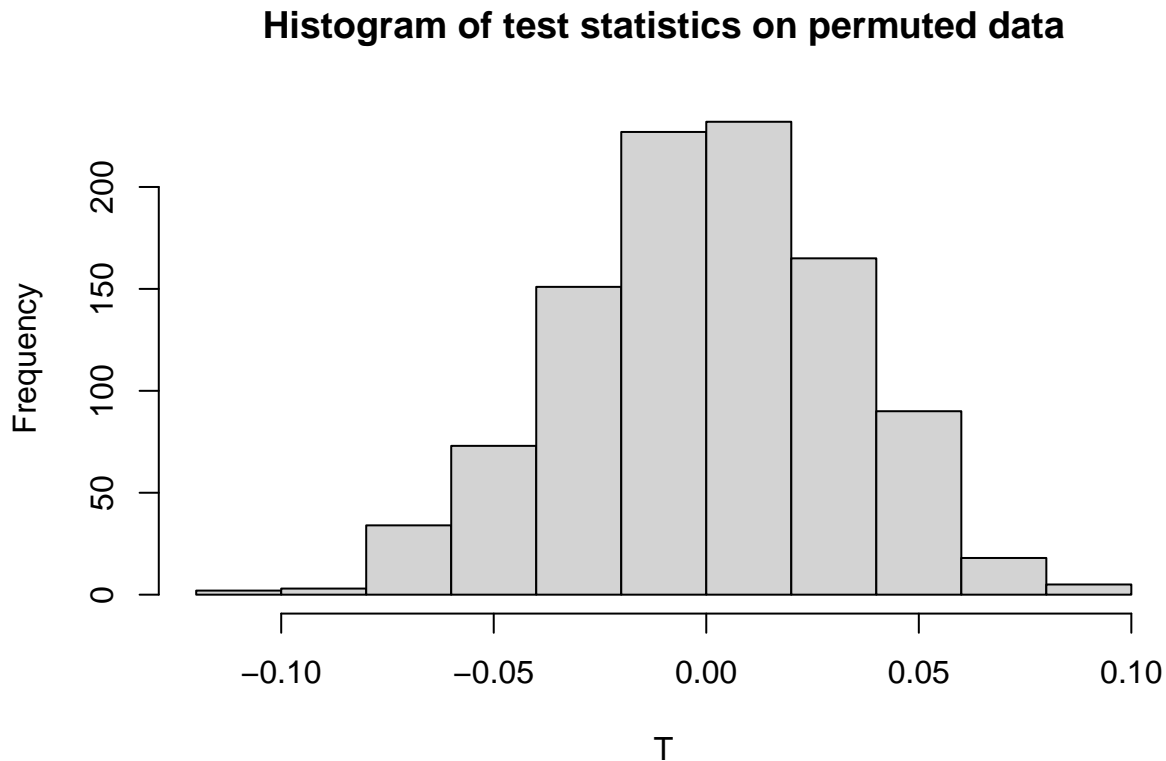


```
#calculate p-value
p = 2*min(mean(T>=ts),mean(T<=ts))
p
```

```
## [1] 0.324
```

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

```
##        2.5%        97.5%
## -0.06714991   0.05825052
```

## B

Use Neyman's method to estimate a (possibly weighted) average treatment effect $(\tau_w)$, with a p-value for the null hypothesis $H_0^{\mathrm{Neyman}} : \tau_w = 0$ 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)
```

```
# 95\%
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 $\tilde{Y}_{ij} = Y_{ij} - \bar{Y}_j$, 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**

# 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.