

hw 6

2022-11-13

```
setwd("~/Documents/GitHub/stats100")
```

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr   0.3.5
## v tibble  3.1.8      v dplyr  1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

```
library(stats)
library(asbio)
```

```
## Loading required package: tcltk
```

```
## Warning in system2("/usr/bin/otool", c("-L", shQuote(DSO)), stdout = TRUE):
## running command ''/usr/bin/otool' -L '/Library/Frameworks/R.framework/Resources/
## library/tcltk/libs//tcltk.so'' had status 1
```

```
library(tcltk)
```

```
#1
```

```
iqq<- read.csv("IQ.csv")
iqq
```

```
##      group iq
## 1      A 44
## 2      A 40
## 3      A 44
## 4      A 39
## 5      A 25
## 6      A 37
## 7      A 31
## 8      A 40
## 9      A 22
## 10     A 34
## 11     A 39
```

```
## 12      A 20
## 13      A 39
## 14      A 42
## 15      A 41
## 16      B 36
## 17      B 40
## 18      B 37
## 19      B 35
## 20      B 39
## 21      B 40
## 22      B 36
## 23      B 38
## 24      B 24
## 25      B 27
## 26      B 29
## 27      B 24
## 28      B 45
## 29      B 44
## 30      B 44
## 31      C 52
## 32      C 50
## 33      C 51
## 34      C 52
## 35      C 45
## 36      C 49
## 37      C 47
## 38      C 46
## 39      C 47
## 40      C 47
## 41      C 46
## 42      C 45
## 43      C 50
## 44      C 47
## 45      C 49
```

On Canvas under Files you will find a dataset IQ.csv. It has two columns, the first of which denotes what major a student is from (A, B, or C). The second is the IQ measured by the Stanford–Binet Intelligence Scales. The goal is to determine if this IQ measure differs between majors. (a) Calculate the family-wise (simultaneous, Bonfer-roni) 95% confidence intervals for $(\mu_A - \mu_B)$, $(\mu_A - \mu_C)$, and $(\mu_B - \mu_C)$, assuming you will make $k = 3$ total confidence intervals.

```
summary(iqq)
```

```
##      group      iq
## Length:45      Min.   :20.00
## Class :character 1st Qu.:36.00
## Mode  :character Median  :40.00
##                      Mean   :39.96
##                      3rd Qu.:46.00
##                      Max.   :52.00
```

```
qt(1-0.05/(2*3), 45-3)
```

```
## [1] 2.493667
```

```
Ybar = aggregate(iq ~ group, data = iqq, mean)$iq
ni = aggregate(iq ~ group, data = iqq, length)$iq
```

```
the.model = lm(iq ~ group, data = iqq)
ANOVA.table = anova(the.model)
mse = ANOVA.table[2,3] #ms(within)
```

```
alpha = 0.05
I = 3 # number of groups
k = choose(I, 2)
n. = sum(ni) #total sample size

t_ag = qt(1- alpha/(2*k), df = n. - k) #t percentile
```

```
# 4. Construct the bonferroni CIs
```

```
BON12 = c(Ybar[1] - Ybar[2] - t_ag*sqrt(mse*(1/ni[1] + 1/ni[2])),
          Ybar[1] - Ybar[2] + t_ag*sqrt(mse*(1/ni[1] + 1/ni[2]))),
BON13 = c(Ybar[1] - Ybar[3] - t_ag*sqrt(mse*(1/ni[1] + 1/ni[3])),
          Ybar[1] - Ybar[3] + t_ag*sqrt(mse*(1/ni[1] + 1/ni[3]))),
BON23 = c(Ybar[2] - Ybar[3] - t_ag*sqrt(mse*(1/ni[2] + 1/ni[3])),
          Ybar[2] - Ybar[3] + t_ag*sqrt(mse*(1/ni[2] + 1/ni[3])))
```

```
# 5. We could calculate the two side p-value
```

```
pvalue12 = 2*pt(abs(Ybar[1] - Ybar[2])/sqrt(mse*(1/ni[1] + 1/ni[2])), df = n.-k, lower.tail = F)
pvalue13 = 2*pt(abs(Ybar[1] - Ybar[3])/sqrt(mse*(1/ni[1] + 1/ni[3])), df = n.-k, lower.tail = F)
pvalue23 = 2*pt(abs(Ybar[2] - Ybar[3])/sqrt(mse*(1/ni[2] + 1/ni[3])), df = n.-k, lower.tail = F)
allpvalues = c(pvalue12, pvalue13, pvalue23)
```

```
BON_all = rbind(BON12, BON13, BON23)
all.result = cbind(BON_all, allpvalues)
rownames(all.result) = c("A vs. B", "A vs. C", "B vs. C")
colnames(all.result) = c("Lower", "Upper", "P-value")
knitr::kable(all.result)
```

	Lower	Upper	P-value
A vs. B	-5.694712	5.561379	0.9765750
A vs. C	-18.028046	-6.771954	0.0000021
B vs. C	-17.961379	-6.705288	0.0000023

- (b) What is the largest significant difference in averages suggested by all of the confidence intervals? (This should be one number). A vs. C

```
18.028046-6.771954
```

```
## [1] 11.25609
```

- (c) What is the smallest significant difference in averages suggested by all of the confidence intervals? (This should be one number). B vs. C

```
17.961379-6.705288
```

```
## [1] 11.25609
```

- (d) What two majors were the most significantly different according to the confidence intervals? A and B

```
#2
```

```
beanz<- read.csv("beans.csv")
beanz
```

```
##      plant
## 1    Pinto
## 2    Pinto
## 3    Pinto
## 4    Pinto
## 5    Pinto
## 6    Pinto
## 7    Pinto
## 8    Pinto
## 9    Pinto
## 10   Pinto
## 11   Pinto
## 12   Pinto
## 13   Pinto
## 14   Pinto
## 15   Pinto
## 16   Pinto
## 17   Pinto
## 18   Pinto
## 19   Pinto
## 20   Pinto
## 21   Pinto
## 22   Pinto
## 23   Pinto
## 24   Pinto
## 25   Pinto
## 26   Pinto
## 27   Pinto
## 28   Pinto
## 29   Pinto
## 30   Pinto
## 31   Pinto
```

## 32	Pinto
## 33	Pinto
## 34	Pinto
## 35	Pinto
## 36	Pinto
## 37	Pinto
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## 39	Pinto
## 40	Pinto
## 41	Pinto
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## 43	Pinto
## 44	Pinto
## 45	Pinto
## 46	Pinto
## 47	Pinto
## 48	Pinto
## 49	Pinto
## 50	Pinto
## 51	Pinto
## 52	Pinto
## 53	Pinto
## 54	Pinto
## 55	Pinto
## 56	Pinto
## 57	Pinto
## 58	Pinto
## 59	Pinto
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## 61	Pinto
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## 117	Pinto
## 118	Pinto
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## 645 Northern
## 646 Northern
```

(a) Find the test statistic.

```
beantable<- table(beanz)
beantable
```

```
## plant
##   Cowpea   Navy Northern   Pinto
##      155      155      192      144
```

```
beantest<- chisq.test(beantable, correct = F)
beantest
```

```
##
## Chi-squared test for given probabilities
##
## data:  beantable
## X-squared = 8.1796, df = 3, p-value = 0.04244
```

Answer = 8.1796 (b) Find the p-value. Answer = 0.04244

(c) Did you reject or fail to reject the null if $\alpha = 0.05$? Answer $p < \alpha$ so we can reject

(d) Which bean plant(s) did the weevils prefer more than expected if the null was true?

```
beantable-beantest$expected
```

```
## plant
##   Cowpea   Navy Northern   Pinto
##      -6.5      -6.5      30.5      -17.5
```


Answer = Northern (e) What category contributed most to the value of the test-statistic?

```
beantest$residuals^2
```

```
## plant
## Cowpea Navy Northern Pinto
## 0.2616099 0.2616099 5.7600619 1.8962848
```

Answer = Northern #3

```
blood<- read_csv("blood.csv")
```

```
## Rows: 100 Columns: 2
## -- Column specification -----
## Delimiter: ","
## chr (2): Type, Disease
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
blood
```

```
## # A tibble: 100 x 2
##   Type Disease
##   <chr> <chr>
## 1 0 yes
## 2 0 yes
## 3 0 yes
## 4 0 yes
## 5 0 yes
## 6 0 yes
## 7 0 yes
## 8 0 yes
## 9 0 yes
## 10 0 yes
## # ... with 90 more rows
```

- (a) State the appropriate null for testing if having this particular disease is independent of blood type and alternative hypothesis for testing if having this particular disease is independent of blood type.

Null:Disease is not independent from blood type Alt: Disease is independent from blood type

- (b) Find the test-statistic.

```
bloodtable<- table(blood$Type, blood$Disease)
bloodtable
```

```
##
##      no yes
## A  12  15
## AB   7   2
## B   8  17
## 0   9  30
```

```
bloodtest<- chisq.test(bloodtable, correct = F)
```

```
## Warning in chisq.test(bloodtable, correct = F): Chi-squared approximation may be
## incorrect
```

```
bloodtest
```

```
##
## Pearson's Chi-squared test
##
## data: bloodtable
## X-squared = 10.654, df = 3, p-value = 0.01375
```

Answer = 10.654 (c) Find the p-value. Answer = 0.01375

(d) State your conclusion in terms of the problem, assuming $\alpha = 0.01$.

$p > \alpha$ so we cannot reject. We cannot say for sure that they are independent

(e) Were blood type A individuals more or less likely to have the disease than what we expected if the null was true?

```
bloodtest$observed - bloodtest$expected
```

```
##
##      no    yes
##  A  2.28 -2.28
##  AB  3.76 -3.76
##  B  -1.00  1.00
##  O  -5.04  5.04
```

Answer = Less likely

(f) Were blood type O individuals more or less likely to have the disease than what we expected if the null was true?

Answer = More likely

(g) Which group contributed most to the value of the test-statistic?

```
bloodtest$residuals^2
```

```
##
##      no      yes
##  A 0.5348148 0.3008333
##  AB 4.3634568 2.4544444
##  B 0.1111111 0.0625000
##  O 1.8092308 1.0176923
```

Answer = AB