STAT 461 Lab 6 - ANOVA in R

1. ANOVA Model and Important Hypotheses

Recall from lectures that the one-way ANOVA model with effects coding is written

$$Y_{it} = \mu + \tau_i + \epsilon_{it}, \quad i = 1, 2, \ldots, v \quad t = 1, 2, \ldots, r_i$$

$$\epsilon_{it} \overset{iid}{\sim} N(0, \sigma^2)$$

The v treatments are indexed by i and the number of replicates receiving the i-th treatment is r_i. The sample mean for the i-th treatment is

$$\bar{Y}_{i.} = \frac{1}{r_i} \sum_{t=1}^{r_i} Y_{it}$$

and the grand mean is

$$\bar{Y}_{..} = \frac{1}{n} \sum_{i=1}^{v} \sum_{t=1}^{r_i} Y_{it}$$

1.1 Testing for Equality of All Treatment Effects

The first hypothesis tested in an experiment is that there is any difference in mean response between the treatments. This is expressed as the null hypothesis:

$$H_0 : \tau_1 = \tau_2 = \ldots = \tau_v$$

1.2 Testing for Pairwise Differences Between Treatments

If a test of the above hypothesis shows that there are some differences in mean response between treatments, a common next step is to examine where those differences are. If the working hypothesis is that there is a difference between treatment means for treatment 1 and treatment 2, then we could test this by considering

$$H_0 : \tau_1 - \tau_2 = 0$$

We could similarly test all possible pairwise differences, one at a time:

$$H_0 : \tau_1 - \tau_3 = 0$$

$$H_0 : \tau_2 - \tau_3 = 0$$

and so on.

3 Example: Catching Flies

As an example of a hypothesis test, consider the following experiment. The aim was to test the maxim: "You can catch more flies with honey than with vinegar". The intended meaning of this statement is that being nice to others will benefit you more than being mean. We will not be testing the effects of being nice, but instead testing how attracted flies are to honey, vinegar, or water.

Eight bowls were laid out on a table in two rows. At random, each bowl was filled with either honey, vinegar, or water. The randomization was conducted so that three of the bowls were filled with honey, three with vinegar, and two with water. The bowls were watched for 10 minutes, and observers recorded each time a fly landed either on a bowl or the liquid in the bowl. At the end of 10 minutes, the total number of flies landing on each bowl was recorded:

Honey	Vinegar	Water
2	4	2
1	3	3
2	4	

We will denote the three treatments with the subscripts: H = Honey   V = Vinegar   W = Water

```
liquid<-c(rep("Honey", 3), rep("Vinegar", 3), rep("Water", 2))
numFlies<-c(2,1,3,5,4,5,1,3)
data<-data.frame(liquid=as.factor(liquid), numFlies=numFlies)
data
```

```
##     liquid numFlies
## 1    Honey        2
## 2    Honey        1
## 3    Honey        3
## 4  Vinegar        5
## 5  Vinegar        4
## 6  Vinegar        5
## 7    Water        1
## 8    Water        3
```

4 Testing for Significant Estimable Functions

If we reject the null hypothesis of no treatment effect, we typically want to understand which treatments are significantly greater than others. In general, we can test for the significance of any estimable function.

The most important estimable functions are **contrasts**, which can be written as

$$\sum_{i=1}^{v} c_i(\mu + \tau_i), \quad \text{with } \sum_{i=1}^{v} c_i = 0$$

Contrasts will allow us to test for pairwise differneces between means, and also for differences between groups of treatments when appropriate.

5.1 Testing All Pairwise Comparisons

We might be interested in testing the following pairwise comparisons

$$\tau_H - \tau_V = \text{The Mean Difference in Flies Between Honey and Vinegar}$$

$$\tau_H - \tau_W = \text{The Mean Difference in Flies Between Honey and Water}$$

$$\tau_W - \tau_V = \text{The Mean Difference in Flies Between Water and Vinegar}$$

with the null hypothesis being that the mean difference between the pair is zero, and the alternative hypothesis that the mean difference in treatment effects is different from zero. We can test all these pairwise contrasts by running the following code in R:

```r
model1<-aov(numFlies~liquid, data = data)
library(lsmeans)
```

```
## The 'lsmeans' package is being deprecated.
## Users are encouraged to switch to 'emmeans'.
## See help('transition') for more information, including how
## to convert 'lsmeans' objects and scripts to work with 'emmeans'.
```

```r
lsmLiquid=lsmeans(model1,  ~ liquid)
```

```r
summary(contrast(lsmLiquid, method="pairwise", adjust="tukey"),
infer=c(T,T), level=0.95, side="two-sided")
```

```
##  contrast            estimate        SE df   lower.CL      upper.CL t.ratio
##  Honey - Vinegar -2.666667e+00 0.7888106  5 -5.2333865 -0.09994684  -3.381
##  Honey - Water   -1.216188e-15 0.8819171  5 -2.8696800  2.86968000   0.000
##  Vinegar - Water  2.666667e+00 0.8819171  5 -0.2030133  5.53634667   3.024
##  p.value
##   0.0437
##   1.0000
##   0.0642
##
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 3 estimates
## P value adjustment: tukey method for comparing a family of 3 estimates
```

The adjust="tukey" option adjusts the p-values obtained in the tests of these three pairwise comparisons to account for the fact that we are making three tests at once. This adjustment becomes very important when we have many treatments. For example, if we had 10 treatments, then if we wanted to test all pairwise comparisons, we would conduct (10*9/2)=45 separate hypothesis tests. If we didn't adjust our p-values, we would likely find at least one significant result, even if there are no real differences between treatment means!

For nicer looking output use kable:

```r
library(knitr)
kable(summary(contrast(lsmLiquid, method="pairwise",
adjust="tukey"), infer=c(T,T), level=0.95, side="two-sided"))
```

contrast	estimate	SE	df	lower.CL	upper.CL	t.ratio	p.value
Honey - Vinegar	-2.666667	0.7888106	5	-5.2333865	-0.0999468	-3.380617	0.0437049
Honey - Water	0.000000	0.8819171	5	-2.8696800	2.8696800	0.000000	1.0000000
Vinegar - Water	2.666667	0.8819171	5	-0.2030133	5.5363467	3.023716	0.0641863

with each row corresponding to a test of a pairwise distance. The first row estimates $\tau_H - \tau_V$, the difference in mean number of flies on bowls with honey and vinegar. The "estimate" column contains the LS estimate $\hat{\tau_H} - \hat{\tau_V} = \bar{Y}_{H.} - \bar{Y}_{V.} = (5/3) - (11/3) = -2$. The adjusted p-value in the last column is the p-value for the

null hypothesis that there is no difference in means $H_0 : \tau_H - \tau_V = 0$.

Each additional row contains another pairwise comparison. We can interpret the results of these tests with the following statements:

1. The mean number of flies on a honey bowl is significantly less than the mean number of flies on a vinegar bowl.

2. The mean number of flies on a honey bowl is not significantly different from the mean number of flies on a water bowl.

3. The mean number of flies on a vinegar bowl is not significantly different from the mean number of flies on a water bowl.

Alternatively

```
TukeyHSD(model1, "liquid")
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = numFlies ~ liquid, data = data)
##
## $liquid
##                       diff         lwr       upr      p adj
## Vinegar-Honey  2.666667e+00  0.09994684 5.2333865 0.0437049
## Water-Honey    1.554312e-15 -2.86968000 2.8696800 1.0000000
## Water-Vinegar -2.666667e+00 -5.53634667 0.2030133 0.0641863
```

```
plot(TukeyHSD(model1))
```


4
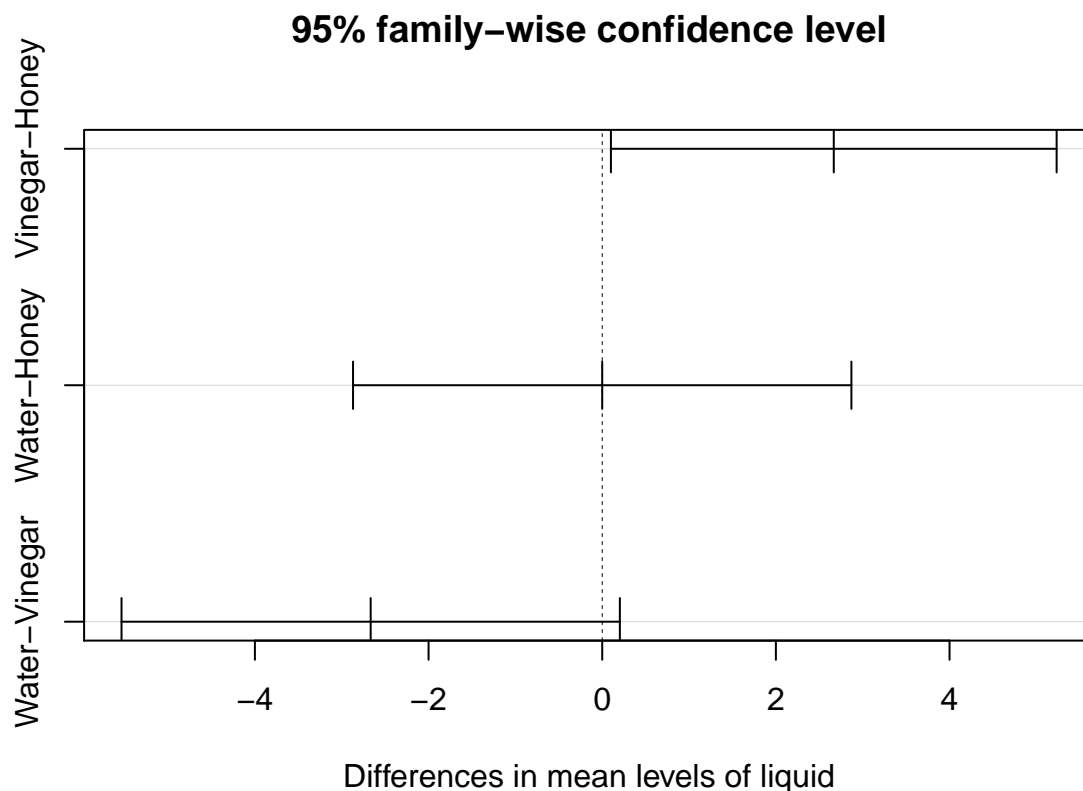
5.2 Calculate Tukey and Scheffe tests by programming the commands yourself

Tukey method for a pairwise test on Honey - Vinegar

```r
nu = 3; n = 8
MSerror = 0.9333
se = sqrt(MSerror*(1/3 + 1/3))
Dhat = mean(data$numFlies[which(data$liquid == "Honey")]) -
    mean(data$numFlies[which(data$liquid == "Vinegar")])

Tq = qtukey(1-0.05, nu, n-nu)/sqrt(2)

#CI
(lowerbound <- Dhat -Tq*se)
```

```
## [1] -5.233341
```

```r
(upperbound <- Dhat +Tq*se)
```

```
## [1] -0.09999268
```

Scheffe method

```r
Fvalue = qf(1-0.05, nu-1, n-nu)
S = sqrt((nu-1)*Fvalue)
#CI
(lowerbound <- Dhat -S*se)
```

```
## [1] -5.349998
```

```r
(upperbound <- Dhat +S*se)
```

```
## [1] 0.01666456
```

Homework Assignment

1. **Pedestrian light experiment** (Larry Lesher, 1985) Recall the pedestrian light experiment from Homework 4. This experiment questions whether pushing a certain pedestrian light button had an effect on the wait time before the pedestrian light showed walk. The treatment factor of interest was the number of pushes of the button, and 32 observations were taken with a mix of 0, 1, 2, and 3 pushes of the button. The waiting times for the walk sign are shown in the following table, with $r_0 = 7, r_1 = r_2 = 10, r_3 = 5$ (where the levels of the treatment factor are coded as 0, 1, 2, 3 for simplicity).

0	1	2	3
38.14	38.28	38.17	38.14
38.20	38.17	38.13	38.30
38.31	38.08	38.16	38.21
38.14	38.25	38.30	38.04
38.29	38.18	38.34	38.37
38.17	38.03	38.34	-
38.20	37.95	38.17	-
-	38.26	38.18	-
-	38.30	38.09	-
-	38.21	38.06	-

Answer the question: "Does pushing the button make the light change sooner?". Clearly state the null and alternative hypotheses, the model used, and all assumptions in the model. Obtain a test statistic (show all code and R output), and interpret the results of the test.

2. **Hot Dogs** A study was conducted to compare the calories and sodium in hot dogs made with different types of meat.

Type	Calories	Sodium
Beef	186	495
Beef	181	477
Beef	176	425
Beef	149	322
Beef	184	482
Beef	190	587
Beef	158	370
Beef	139	322
Beef	175	479
Beef	148	375
Beef	152	330
Beef	111	300
Beef	141	386
Beef	153	401
Beef	190	645
Beef	157	440
Beef	131	317
Beef	149	319
Beef	135	298
Beef	132	253
Pork	173	458
Pork	191	506

Type	Calories	Sodium
Pork	182	473
Pork	190	545
Pork	172	496
Pork	147	360
Pork	146	387
Pork	139	386
Pork	175	507
Pork	136	393
Pork	179	405
Pork	153	372
Pork	107	144
Pork	195	511
Pork	135	405
Pork	140	428
Pork	138	339
Chicken	129	430
Chicken	132	375
Chicken	102	396
Chicken	106	383
Chicken	94	387
Chicken	102	542
Chicken	87	359
Chicken	99	357
Chicken	107	528
Chicken	113	513
Chicken	135	426
Chicken	142	513
Chicken	86	358
Chicken	143	581
Chicken	152	588
Chicken	146	522
Chicken	144	545

(a) Read the data into R and plot calories as a response variable with the type of meat on the x-axis. Your plot could be either a boxplot or a plot with one dot for each hot dog.

(b) Answer the following question: "Are there differences in the average calories of hot dogs made with different kinds of meat?". To answer this question, write down a statistical model (clearly state the response variable, treatment levels, number of replicates, ...), express the above question as a testable null hypothesis, and report the p-value of the test statistic under the null hypothesis. Your answer should include all R code used, and the important R output.

(c) Are there significant differences in mean calories between Beef and Pork hot dogs? What about between Beef and Chicken hot dogs? What about between Pork and Chicken hot dogs?