Tukey HSD in R Tutorial

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Contents

1. Introduction

This document illustrates how to conduct ANOVA and a Tukey HSD test in R.

2. ANOVA

GOAL: Perform ANOVA on *chickwts*.

Important functions: *setnames()*, *aggregate()*, *merge()*, *aov()*, *summary()*, *plotmeans()*, *TukeyHSD()*

First, we need to load the *gplots* library into R. Loading all the libraries that we may use at the beginning is good practice, as sometimes we need libraries earlier than we initially expect.

```
library(gplots) # if not already installed, type install.packages('gplots')
```

Next, we need to load the data. The easiest way is with *data()*, which imports datasets pre-loaded into R.

```
data(chickwts)
```

2a. Summary Statistics

We nead the number of occurences; mean of the weights; and standard deviations for each supplement ("feed"). We know that *NROW()* counts the number of rows; *mean()* calculates the average; and *sd()* estimates the standard deviation. To execute these functions by groups (in this case, by feed), we can use *aggregate()*.

```
sum_stats <- aggregate(weight ~ feed, chickwts,
                       function(x) c(obs = NROW(x), mean = mean(x), sd = sd(x)))

sum_stats
```

```
##        feed weight.obs weight.mean weight.sd
## 1    casein   12.00000   323.58333  64.43384
## 2 horsebean   10.00000   160.20000  38.62584
## 3   linseed   12.00000   218.75000  52.23570
## 4  meatmeal   11.00000   276.90909  64.90062
## 5   soybean   14.00000   246.42857  54.12907
## 6 sunflower   12.00000   328.91667  48.83638
```

The function *aggregate()* computes a specific function on a dataset–in this particular example, we use *NROW*, *mean*, and *sd* to calculate the number of observations, mena, and standard deviation, respectively, of the chick weights by type of feed. The formula *weight* ~ *feed* is interpreted as "compute a function on weight BY feed."

2b. ANOVA

To estimate ANOVA, we need *aov()*.

```
chickwts_anova <- aov(data = chickwts, formula = weight ~ feed)
summary(chickwts_anova)
```

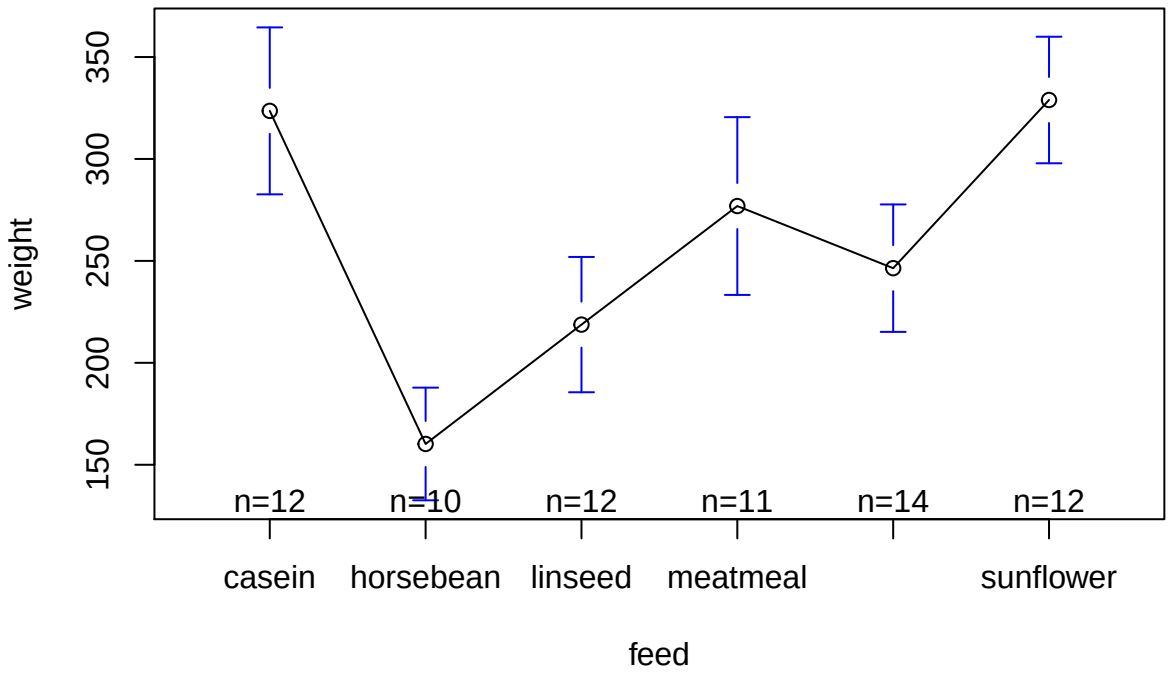
```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## feed         5 231129   46226   15.37 5.94e-10 ***
## Residuals   65 195556    3009
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

What does the p-value signify? Can we reject the null hypothesis that the feed type is irrelevant in determining a chick's weight? The p-value signifies the probability of comitting a Type I Error (i.e., a false positive). Because $p < 0.05$ (a conventional rule), we can reject the null hypothesis: the type of feed matters in influencing weight.

2c. Confidence Intervals

We need the *gplots* library, which we already loaded into R earlier, and *plotmeans()*.

```
with(chickwts, plotmeans(weight ~ feed))
```



```
  # with() allows us to specify a dataset we want to work with.
  #   In this way, we don't have to type "chickwts$" repeatedly.
```

Which groups overlap? Based on the plot, *horsebean* overlaps with *linseed*; *meatmeal* overlaps with all groups except *horsebean*; *linseed* overlaps with *soybean* and *horsebean*; and *sunflower* overlaps with *casein* and *meatmeal*.

2d. Tukey HSD

We need *TukeyHSD()*, which we apply over our ANOVA results.

```
TukeyHSD(chickwts_anova)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = weight ~ feed, data = chickwts)
##
## $feed
##                           diff         lwr       upr     p adj
## horsebean-casein    -163.383333 -232.346876 -94.41979 0.0000000
## linseed-casein      -104.833333 -170.587491 -39.07918 0.0002100
## meatmeal-casein      -46.674242 -113.906207  20.55772 0.3324584
## soybean-casein       -77.154762 -140.517054 -13.79247 0.0083653
## sunflower-casein       5.333333  -60.420825  71.08749 0.9998902
## linseed-horsebean     58.550000  -10.413543 127.51354 0.1413329
## meatmeal-horsebean   116.709091   46.335105 187.08308 0.0001062
## soybean-horsebean     86.228571   19.541684 152.91546 0.0042167
## sunflower-horsebean  168.716667   99.753124 237.68021 0.0000000
## meatmeal-linseed      58.159091   -9.072873 125.39106 0.1276965
## soybean-linseed       27.678571  -35.683721  91.04086 0.7932853
## sunflower-linseed    110.166667   44.412509 175.92082 0.0000884
## soybean-meatmeal     -30.480519  -95.375109  34.41407 0.7391356
## sunflower-meatmeal    52.007576  -15.224388 119.23954 0.2206962
## sunflower-soybean     82.488095   19.125803 145.85039 0.0038845
```

Recall that each of the contrasts is a t-test. Which groups had statistically significant differences? How do you know? What can we say from these results?

3. Two-way ANOVA

GOAL: Perform Two-way ANOVA on *CO2*.

METHOD:
1. *uptake* is the response variable.
2. **Treatment * Type** are the factors.
3. *aov()*, *TukeyHSD()*, and *interaction.plot()* are to be used (as stated in the assignment).

Important functions: *table()*, *aov()*, *summary()*, *plotmeans()*, *interaction.plot()*

Load the following dataset:

```
data(CO2)
```

3a. Treatment vs. Type

Let's generate a table comparing *Treatment* against *Type* (column against row). We thus need *with()* to sepecify our working dataset and *table()* for the actual table.

```
with(CO2, table(Type, Treatment)) # we need Type as the row and Treatment as the column.
```

```
##              Treatment
## Type          nonchilled chilled
##   Quebec              21      21
##   Mississippi         21      21
```

Is the design balanced or unbalanced? Why?

3b. Main and Interaction Effects

We need a Two-way ANOVA with factors.

```
CO2_anova <- aov(uptake ~ Treatment*Type, data = CO2)
summary(CO2_anova)
```

```
##                Df Sum Sq Mean Sq F value   Pr(>F)
## Treatment       1    988     988  15.416 0.000182 ***
## Type            1   3366    3366  52.509 2.38e-10 ***
## Treatment:Type  1    226     226   3.522 0.064213 .
## Residuals      80   5128      64
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

What are the statistically significant results? Based on what significance level?

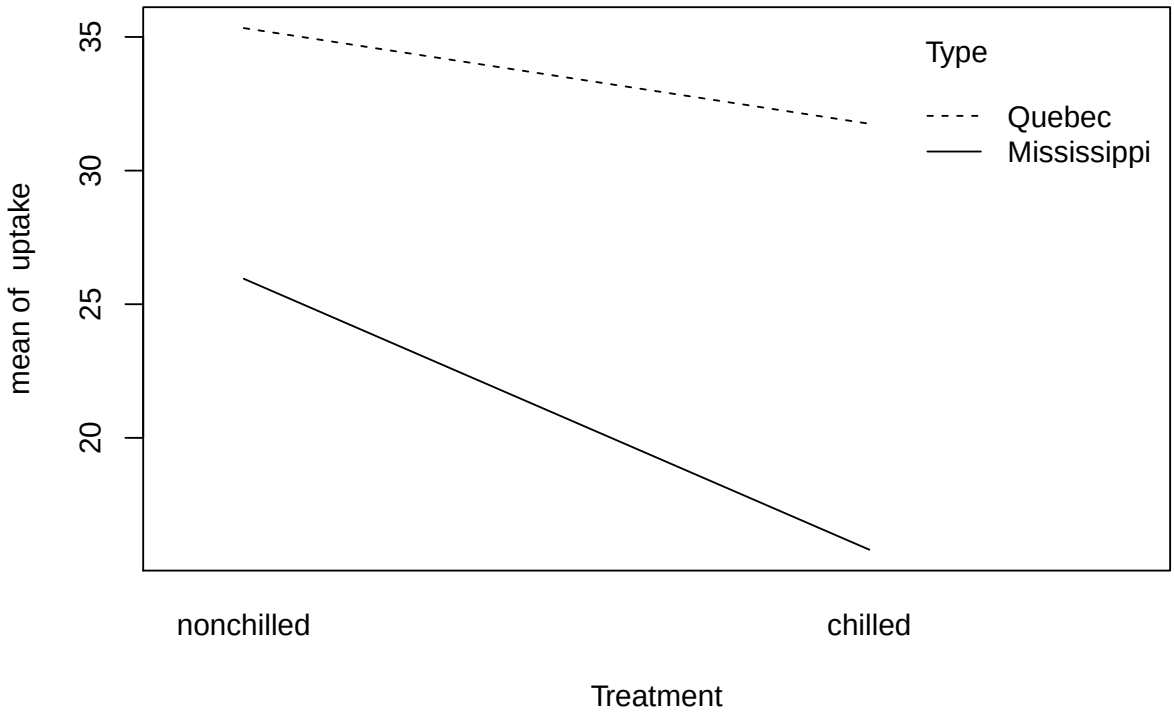
3c. Interaction Effects, continued.

We need to know the statistically significant differences between each Treatment-Type combinations. We've done something similar in Question 1d; but now we also need to have a plot of the interactions.

```
TukeyHSD(CO2_anova)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = uptake ~ Treatment * Type, data = CO2)
##
## $Treatment
##                          diff       lwr       upr     p adj
## chilled-nonchilled -6.859524 -10.33624 -3.382808 0.0001817
##
## $Type
##                          diff       lwr       upr p adj
## Mississippi-Quebec -12.65952 -16.13624 -9.182808     0
##
## $`Treatment:Type`
##                                                    diff       lwr         upr
## chilled:Quebec-nonchilled:Quebec            -3.580952 -10.06369   2.9017869
## nonchilled:Mississippi-nonchilled:Quebec    -9.380952 -15.86369  -2.8982131
## chilled:Mississippi-nonchilled:Quebec      -19.519048 -26.00179 -13.0363083
## nonchilled:Mississippi-chilled:Quebec       -5.800000 -12.28274   0.6827393
## chilled:Mississippi-chilled:Quebec         -15.938095 -22.42083  -9.4553560
## chilled:Mississippi-nonchilled:Mississippi -10.138095 -16.62083  -3.6553560
##                                                p adj
## chilled:Quebec-nonchilled:Quebec           0.4727714
## nonchilled:Mississippi-nonchilled:Quebec   0.0015893
## chilled:Mississippi-nonchilled:Quebec      0.0000000
## nonchilled:Mississippi-chilled:Quebec      0.0959830
## chilled:Mississippi-chilled:Quebec         0.0000000
## chilled:Mississippi-nonchilled:Mississippi 0.0005553
```

```
with(CO2, interaction.plot(Treatment, Type, uptake))
```



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