# Butter

### RM | May 2021

 $I'm\ the\ nice\ guy$ 

### Hey

- Knit this Rmd file to see if you can make a html or pdf. If you couldn't, just use RStudio Cloud or the Binder RStudio in the lab note homepage. Po loves RStudio. Everything you need is on the Cloud.
- Edit, add, delete the codes as you need. Delete and insert words/writings as you need.

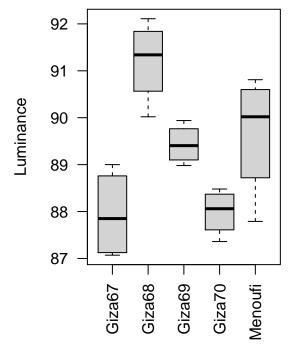
### Codes in LabAssignment6.Rmd

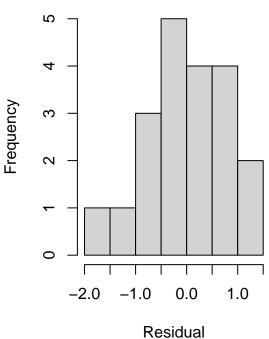
#### Part 1

```
Load data and peek.
```

```
#### Part I
ec <- read.csv("egyptianCotton.csv")</pre>
head(ec)
  Luminance Variety
1
      89.94 Giza69
2
      89.59 Giza69
3
      89.22 Giza69
      88.98 Giza69
4
5
      89.00
             Giza67
6
      88.52 Giza67
Fit ANOVA model
fittedModel <- aov(Luminance ~ Variety,</pre>
                    data = ec
Model diagnostic
        data = ec,
        xlab="",
```

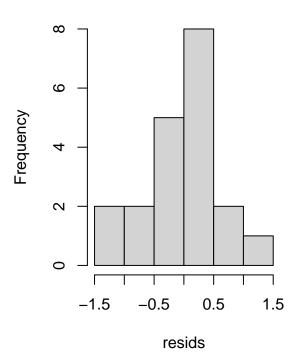






```
normalData <- rnorm(dim(ec)[1])
resids <- aov(normalData~Variety, data=ec)$residuals
hist(resids)</pre>
```

### **Histogram of resids**

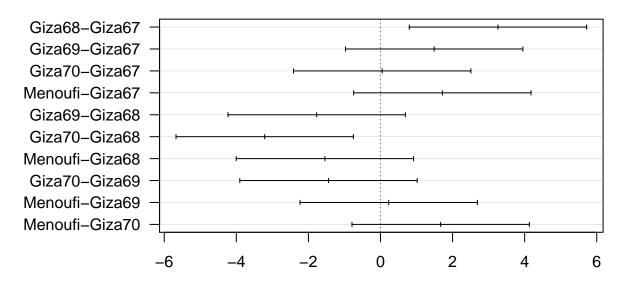


Compute/show cool statistics things

anova(fittedModel)

```
Analysis of Variance Table
```

# 99% family-wise confidence level



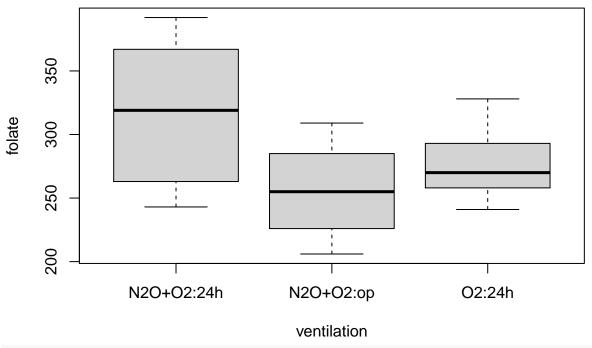
Differences in mean levels of Variety

#### Part II

```
Data is Anesthesia Ventilation.csv
```

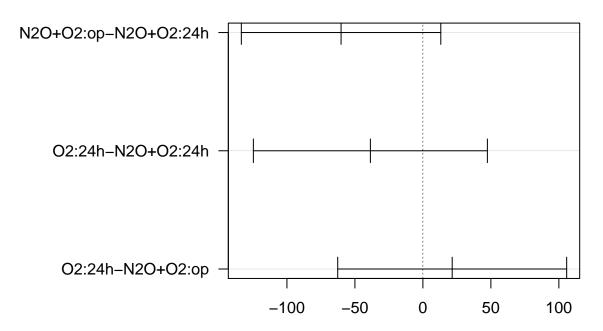
```
av <- read.csv("AnesthesiaVentilation.csv")</pre>
 \# \ \textit{Or} \ \textit{read.csv}("http://www.stat.ucdavis.edu/~affarris/AnesthesiaVentilation.csv") \\
head(av, 10)
   folate ventilation
      243 N20+02:24h
1
2
      251 N20+02:24h
3
      275 N20+02:24h
4
      291
           N20+02:24h
      347 N20+02:24h
5
      354 N20+02:24h
7
      380 N20+02:24h
8
      392 N20+02:24h
9
      206
             N20+02:op
      210
             N2O+02:op
boxplot(folate ~ ventilation,
        data = av,
        main = "Po is a nice guy."
```

## Po is a nice guy.



Analysis of Variance Table

## 99% family-wise confidence level



Differences in mean levels of ventilation

### Appendix: R Script

```
#### Part I
ec <- read.csv("egyptianCotton.csv")</pre>
head(ec)
fittedModel <- aov(Luminance ~ Variety,</pre>
                    data = ec
                    )
par(mfrow=c(1,2)) ## two side-by-side plots
boxplot(Luminance ~ Variety,
        data = ec,
        xlab="",
        las = 2 ## vertical labels
hist(fittedModel$residuals,
     ylab="Frequency",
     xlab="Residual",
     main=""
     )
normalData <- rnorm(dim(ec)[1])</pre>
resids <- aov(normalData~Variety, data=ec)$residuals
hist(resids)
anova(fittedModel)
tuky <- TukeyHSD(fittedModel,</pre>
                  conf.level = 0.99
par(mar=c(5,6,4,1)+1.2) ## so that labels don't get cut off
plot(tuky,
     las=1 ## horizontal labels
av <- read.csv("AnesthesiaVentilation.csv")</pre>
# Or read.csv("http://www.stat.ucdavis.edu/~affarris/AnesthesiaVentilation.csv")
head(av, 10)
boxplot(folate ~ ventilation,
        data = av,
        main = "Po is a nice guy."
fittedModel <- aov(folate ~ ventilation,</pre>
                    data = av
anova(fittedModel)
tuky <- TukeyHSD(fittedModel,</pre>
                  conf.level = 0.99
par(mar=c(5,12,4,2)+0.1)
plot(tuky,
     las=1 ## horizontal labels
```