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")
head(ec)
```

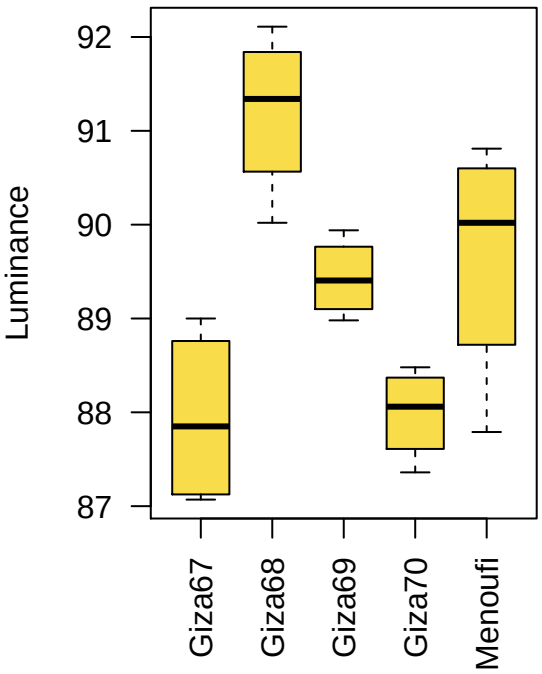
```
  Luminance Variety
1     89.94  Giza69
2     89.59  Giza69
3     89.22  Giza69
4     88.98  Giza69
5     89.00  Giza67
6     88.52  Giza67
```

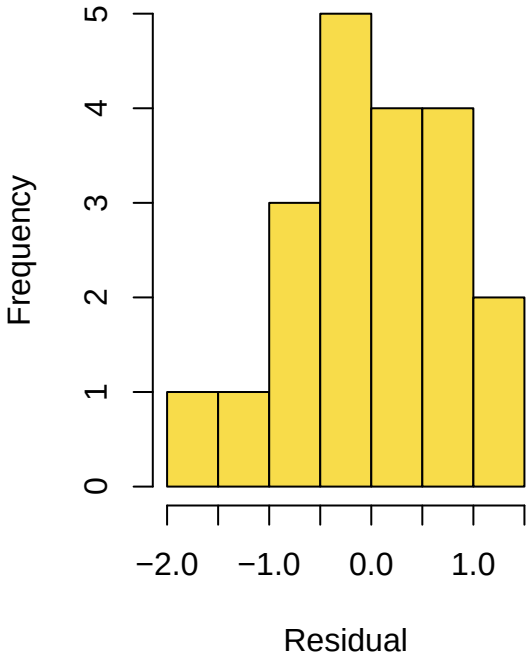
Fit ANOVA model

```
fittedModel <- aov(Luminance ~ Variety,
                   data = ec
                   )
```

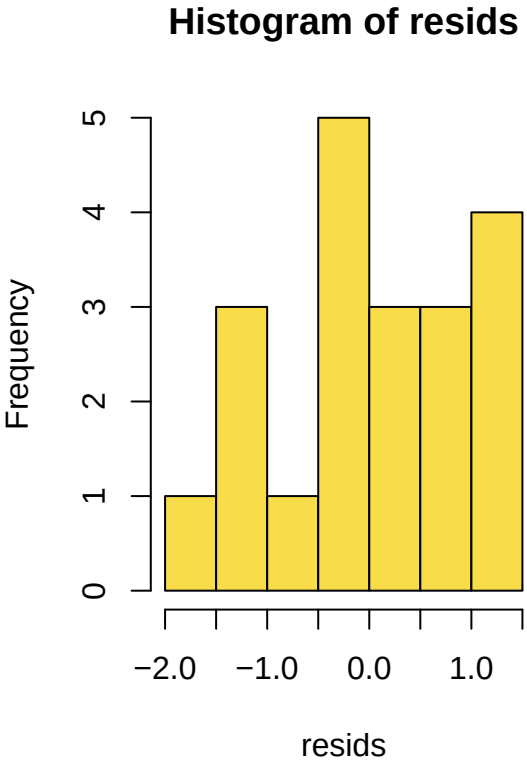
Model diagnostic

```
par(mfrow=c(1,2)) ## two side-by-side plots
boxplot(Luminance ~ Variety,
        data = ec,
        xlab="",
        las = 2, ## vertical labels
        col = "#F8DC4A"
        )
hist(fittedModel$residuals,
     ylab="Frequency",
     xlab="Residual",
     main="",
     col = "#F8DC4A"
     )
```






```
normalData <- rnorm(dim(ec)[1])
resids <- aov(normalData~Variety, data=ec)$residuals
hist(resids, col = "#F8DC4A")
```



Compute/show cool statistics things

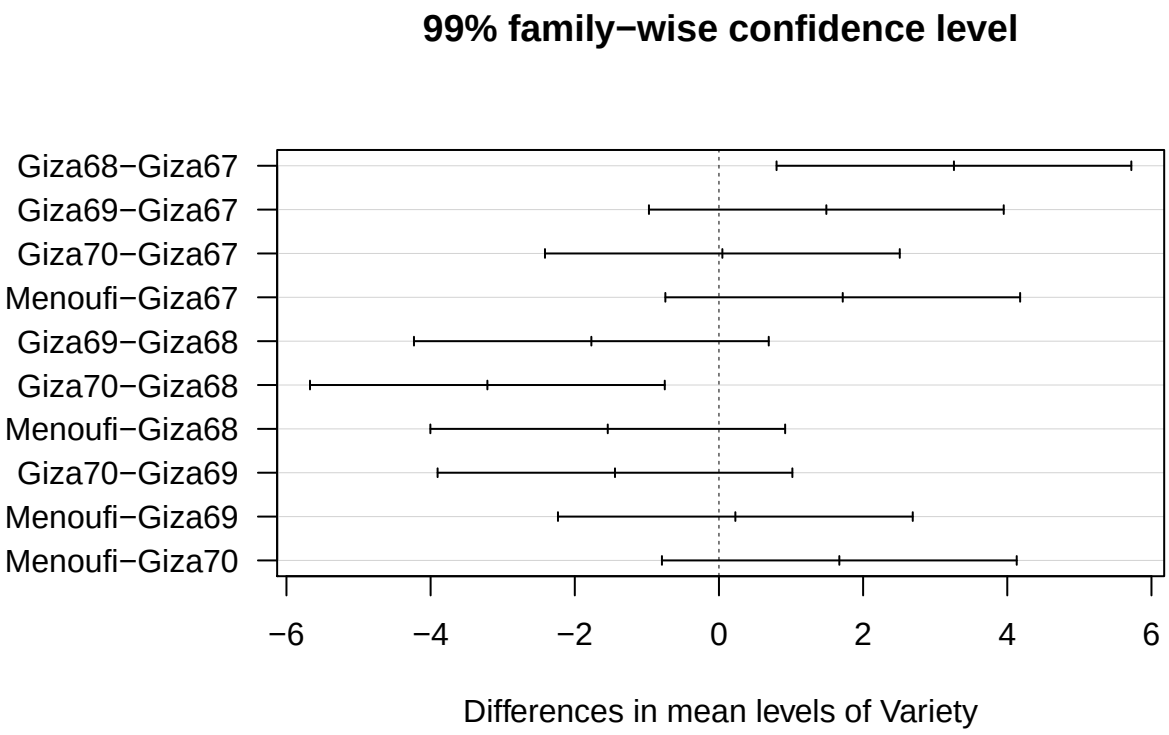
```
anova(fittedModel)
```

```
Analysis of Variance Table

Response: Luminance
          Df Sum Sq Mean Sq F value    Pr(>F)
```

```
Variety    4 29.243  7.3107  9.3158 0.0005455 ***
Residuals 15 11.771  0.7848
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
tuky <- TukeyHSD(fittedModel,
                 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
     )
```



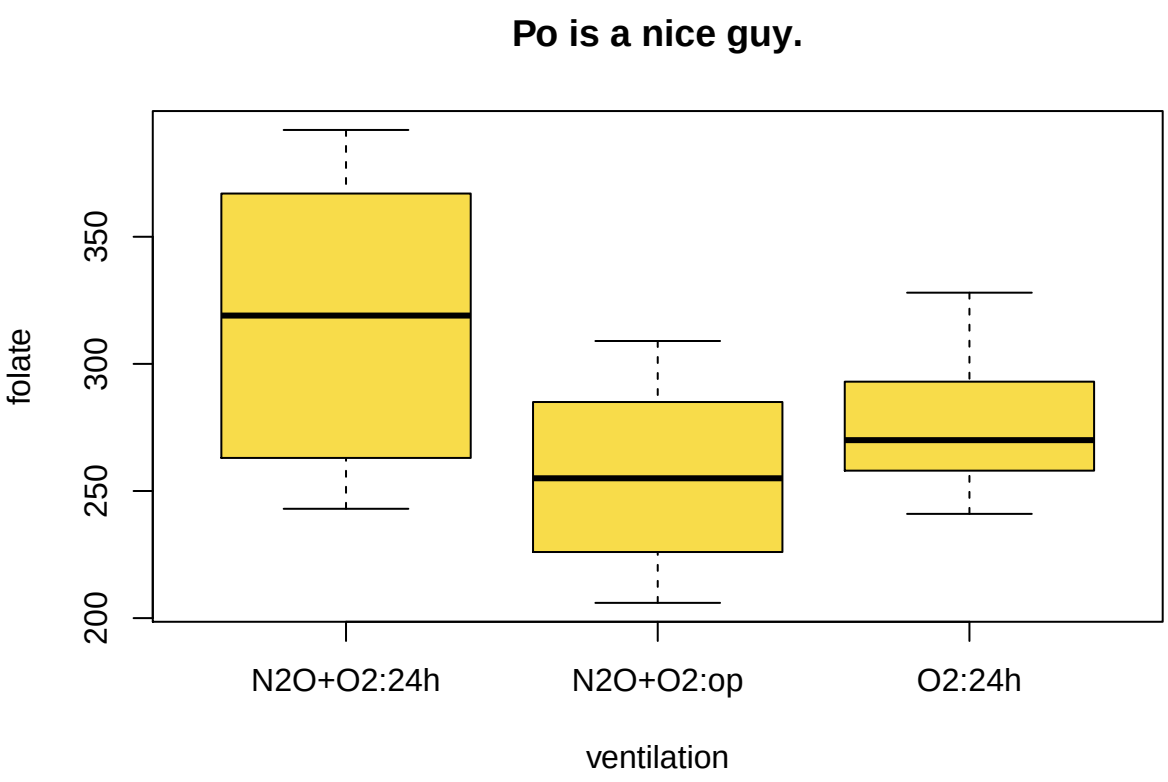
Part II

Data is AnesthesiaVentilation.csv

```
av <- read.csv("AnesthesiaVentilation.csv")
# Or read.csv("http://www.stat.ucdavis.edu/~affarris/AnesthesiaVentilation.csv")
head(av, 10)
```

```
   folate ventilation
1     243  N2O+O2:24h
2     251  N2O+O2:24h
3     275  N2O+O2:24h
4     291  N2O+O2:24h
5     347  N2O+O2:24h
6     354  N2O+O2:24h
7     380  N2O+O2:24h
8     392  N2O+O2:24h
9     206   N2O+O2:op
10    210   N2O+O2:op
```

```
boxplot(folate ~ ventilation,
        data = av,
        main = "Po is a nice guy.",
        col = "#F8DC4A"
        )
```



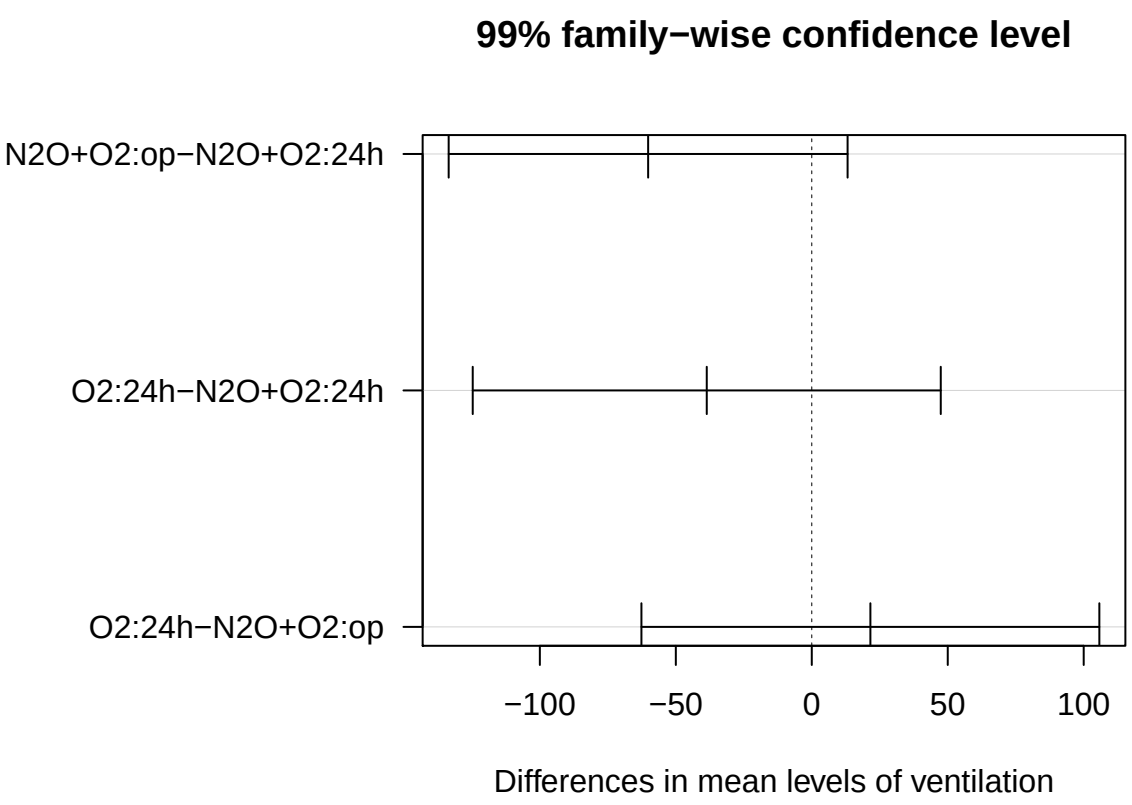

```
fittedModel <- aov(folate ~ ventilation,
                   data = av
                   )
anova(fittedModel)
```

```
Analysis of Variance Table

Response: folate
            Df Sum Sq Mean Sq F value  Pr(>F)
```

```
ventilation  2  15516  7757.9  3.7113 0.04359 *
Residuals   19  39716  2090.3
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
tuky <- TukeyHSD(fittedModel,
                 conf.level = 0.99
                 )
par(mar=c(5,12,4,2)+0.1)
plot(tuky,
     las=1 ## horizontal labels
     )
```



Appendix: R Script

```
#### Part I
ec <- read.csv("egyptianCotton.csv")
head(ec)
fittedModel <- aov(Luminance ~ Variety,
                   data = ec
                   )
par(mfrow=c(1,2)) ## two side-by-side plots
boxplot(Luminance ~ Variety,
        data = ec,
        xlab="",
        las = 2, ## vertical labels
        col = "#F8DC4A"
        )
hist(fittedModel$residuals,
     ylab="Frequency",
     xlab="Residual",
     main="",
     col = "#F8DC4A"
     )
normalData <- rnorm(dim(ec)[1])
resids <- aov(normalData~Variety, data=ec)$residuals
hist(resids, col = "#F8DC4A")
anova(fittedModel)
tuky <- TukeyHSD(fittedModel,
                 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")
# 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.",
        col = "#F8DC4A"
        )
fittedModel <- aov(folate ~ ventilation,
                   data = av
                   )
anova(fittedModel)
tuky <- TukeyHSD(fittedModel,
                 conf.level = 0.99
                 )
par(mar=c(5,12,4,2)+0.1)
plot(tuky,
     las=1 ## horizontal labels
     )
```