Exampl_t_ANOVA.Rmd

F. A. BarriosInstituto de Neurobiología UNAM

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Outline

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Examples Chap03 (Vittinghoff et al. book)

The examples for chapter 3 (Vittinghoff's book http://www.biostat.ucsf.edu/vgsm) using data from the heart and estrogen/progestin study (HERS), a clinical trial of hormone therapy (HT) for prevention of recurrent heart attacks and death among 2,763 post-menopausal women with existing coronary heart disease (CHD)

Introduction

t-Test example presented in Table 3.1 of the t-Test of difference in average glucose by exercise for the women that are not diabetic. These examples are to revisit some t-test R estimations and t-test function in R. And to remember that a Boxplot gives a good amount of information about a numerical variable: Centering described by the median Dispersion, measured by the hight of the box (interquartil distance). Observation range The presence of extreme values (outliers) And some information of the distribution "form" (skewness)

This last point bears further explanation. If the median is located toward the bottom of the box, then the data are right-skewed toward larger values. That is, the distance between the median and the 75th percentile is greater than that between the median and the 25th percentile. Likewise, right-skewness will be indicated if the upper whisker is longer than the lower whisker or if there are more outliers in the upper range. Both the boxplot and the histogram show evidence for right-skewness in the SBP data.

```
setwd("~/Dropbox/Fdo/ClaseStats/RegressionClass/RegressionR_code")
# To set the working directory at the user dir
library(tidyverse)
```

```
library(multcomp)
```

```
library(car)
```

```
library(emmeans)

hers <- read_csv("DataRegressBook/Chap3/hersdata.csv")
```

```
# Loading the HERS database in hers variable
summary(hers)
```

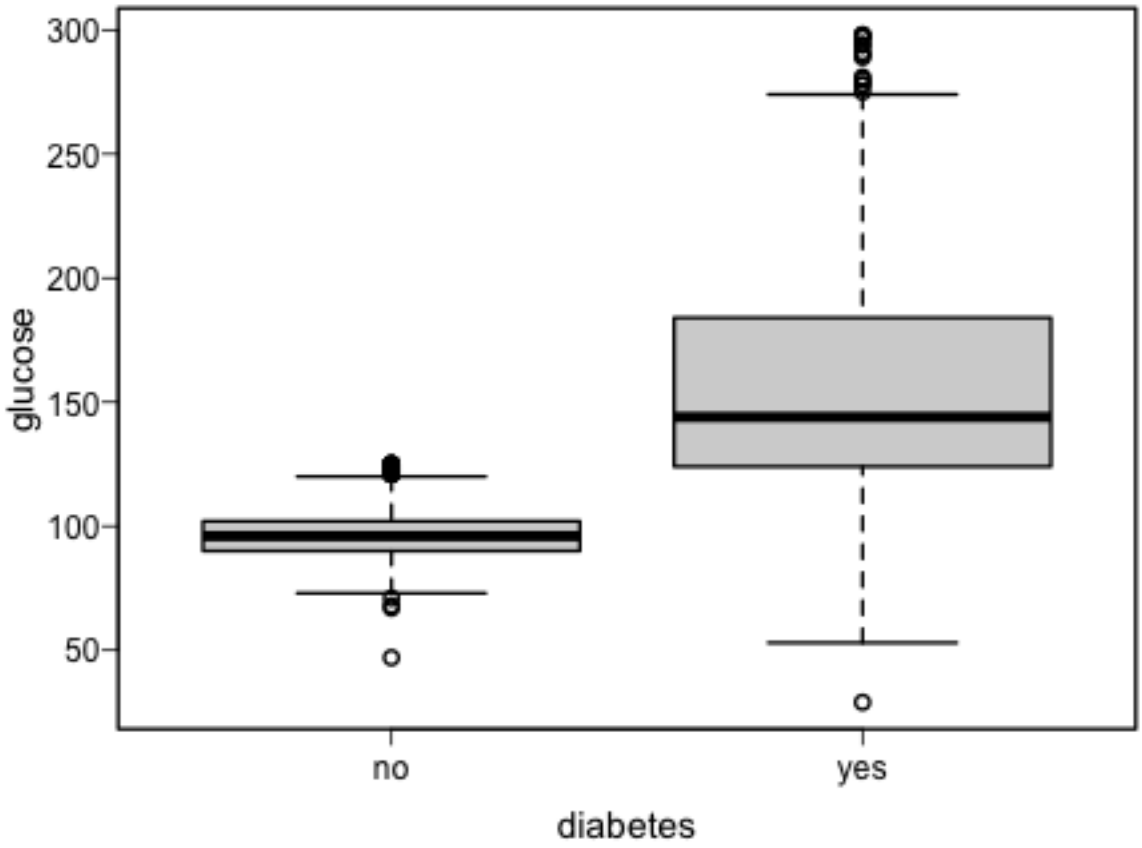
```
      HT                  age           raceth            nonwhite
 Length:2763        Min.   :44.00   Length:2763        Length:2763
 Class :character   1st Qu.:62.00   Class :character   Class :character
```

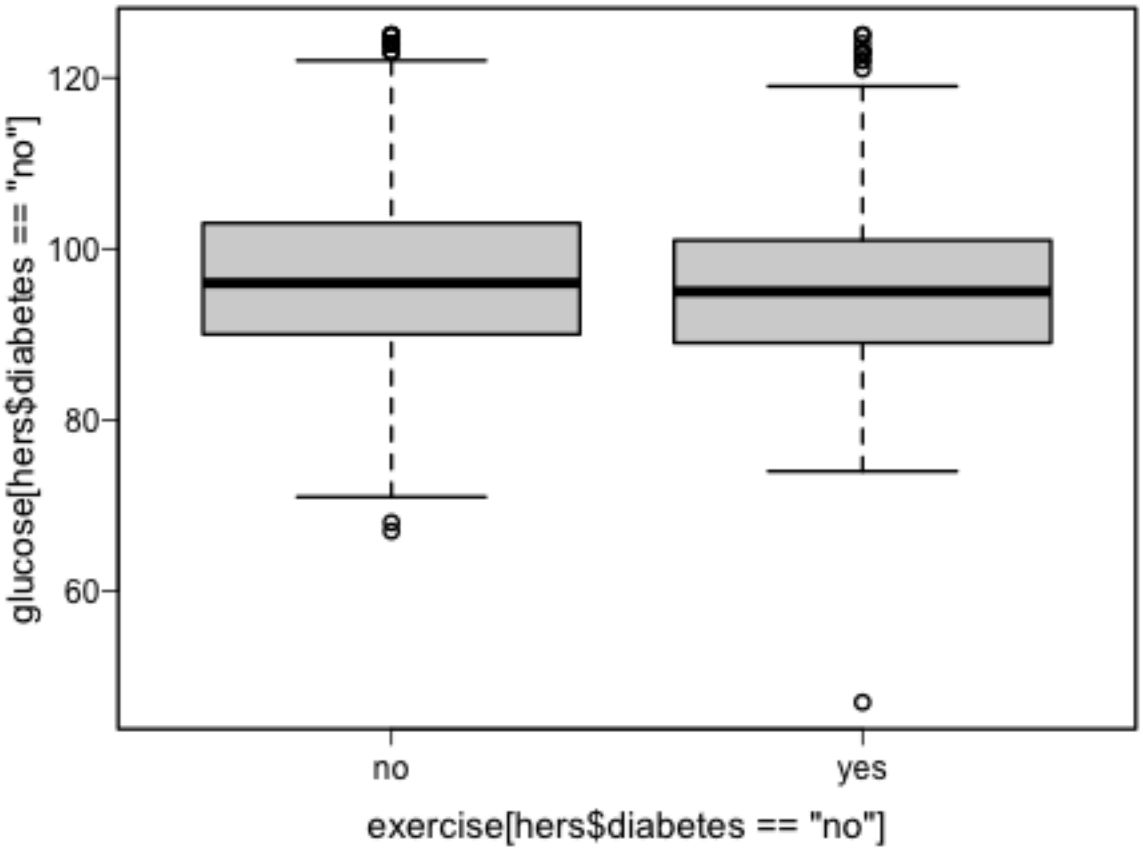
```
Mode  :character   Median :67.00   Mode  :character   Mode  :character
                   Mean   :66.65
                   3rd Qu.:72.00
                   Max.   :79.00

  smoking            drinkany           exercise           physact
Length:2763        Length:2763        Length:2763        Length:2763
Class :character   Class :character   Class :character   Class :character
Mode  :character   Mode  :character   Mode  :character   Mode  :character


  globrat            poorfair           medcond          htnmeds
Length:2763        Length:2763        Min.   :0.0000   Length:2763
Class :character   Class :character   1st Qu.:0.0000   Class :character
Mode  :character   Mode  :character   Median :0.0000   Mode  :character
                                      Mean   :0.3721
                                      3rd Qu.:1.0000
                                      Max.   :1.0000

  statins            diabetes           dmpills            insulin
Length:2763        Length:2763        Length:2763        Length:2763
Class :character   Class :character   Class :character   Class :character
Mode  :character   Mode  :character   Mode  :character   Mode  :character


    weight            BMI             waist             WHR
Min.   : 37.50   Min.   :15.21   Min.   : 56.90   Min.   :0.624
1st Qu.: 62.20   1st Qu.:24.64   1st Qu.: 82.00   1st Qu.:0.811
Median : 71.00   Median :27.75   Median : 90.50   Median :0.867
Mean   : 72.73   Mean   :28.58   Mean   : 91.74   Mean   :0.870
3rd Qu.: 81.40   3rd Qu.:31.73   3rd Qu.:100.30   3rd Qu.:0.923
Max.   :132.00   Max.   :54.13   Max.   :170.00   Max.   :1.218
NA's   :2        NA's   :5       NA's   :2        NA's   :3
   glucose          weight1           BMI1            waist1
Min.   : 29.0   Min.   : 37.70   Min.   :14.73   Min.   : 59.00
1st Qu.: 91.0   1st Qu.: 61.20   1st Qu.:24.34   1st Qu.: 81.30
Median : 99.0   Median : 70.40   Median :27.54   Median : 90.00
Mean   :112.2   Mean   : 72.04   Mean   :28.36   Mean   : 91.12
3rd Qu.:114.0   3rd Qu.: 80.90   3rd Qu.:31.54   3rd Qu.:100.00
Max.   :298.0   Max.   :142.00   Max.   :54.04   Max.   :142.00
                NA's   :150      NA's   :153     NA's   :151
     WHR1            glucose1          tchol             LDL
Min.   :0.6060   Min.   : 42.0   Min.   :110.0   Min.   : 36.8
1st Qu.:0.8100   1st Qu.: 91.0   1st Qu.:201.0   1st Qu.:119.6
Median :0.8630   Median :100.0   Median :224.0   Median :141.0
Mean   :0.8668   Mean   :114.5   Mean   :228.6   Mean   :145.0
3rd Qu.:0.9200   3rd Qu.:116.0   3rd Qu.:252.0   3rd Qu.:166.0
Max.   :1.1500   Max.   :440.0   Max.   :465.0   Max.   :393.4
NA's   :151      NA's   :150     NA's   :4       NA's   :11
     HDL               TG             tchol1           LDL1
```

```
 Min.   : 14.00   Min.   : 31.0   Min.   : 92.0   Min.   :-20.0
 1st Qu.: 41.00   1st Qu.:116.0   1st Qu.:193.0   1st Qu.:106.6
 Median : 49.00   Median :157.0   Median :214.0   Median :128.8
 Mean   : 50.26   Mean   :166.1   Mean   :219.2   Mean   :132.4
 3rd Qu.: 57.00   3rd Qu.:208.0   3rd Qu.:242.0   3rd Qu.:154.1
 Max.   :130.00   Max.   :476.0   Max.   :535.0   Max.   :450.2
 NA's   :11       NA's   :4       NA's   :150     NA's   :155
      HDL1             TG1              SBP             DBP
 Min.   : 14.00   Min.   :  31.0   Min.   : 83.0   Min.   : 45.00
 1st Qu.: 42.00   1st Qu.: 119.0   1st Qu.:122.0   1st Qu.: 67.00
 Median : 50.00   Median : 157.0   Median :134.0   Median : 72.00
 Mean   : 51.78   Mean   : 175.8   Mean   :135.1   Mean   : 73.15
 3rd Qu.: 59.00   3rd Qu.: 214.0   3rd Qu.:147.0   3rd Qu.: 80.00
 Max.   :124.00   Max.   :1016.0   Max.   :224.0   Max.   :102.00
 NA's   :155      NA's   :150                      NA's   :1
     age10
 Min.   :4.400
 1st Qu.:6.200
 Median :6.700
 Mean   :6.665
 3rd Qu.:7.200
 Max.   :7.900
```

```r
boxplot(glucose ~ diabetes, data=hers)
# Some graphical description of the glucose state
boxplot(glucose[hers$diabetes == "no"] ~ exercise[hers$diabetes == "no"], alternative="two.sided", data=
t.test(glucose[hers$diabetes == "no"] ~ exercise[hers$diabetes == "no"], data=hers, alternative="two.si
```

```
    Two Sample t-test

data:  glucose[hers$diabetes == "no"] by exercise[hers$diabetes == "no"]
t = 3.8685, df = 2030, p-value = 0.000113
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.8346242 2.5509539
sample estimates:
 mean in group no mean in group yes
         97.36104          95.66825
```


300
250
200
150
100
50
glucose
no
yes
diabetes



t-test examles

Examples of t-test from the exercises of the Daniel's book, Chap 7, section 3 number 3. Data can be downloaded from the WEB page of the Daniel's book

```
setwd("~/Dropbox/Fdo/ClaseStats/RegressionClass/RegressionR_code")
# Daniel's chap 7 t-test examples
# EXR_C07_S03_03
Ex733 = read.csv(file="DataOther/EXR_C07_S03_03.csv", header=TRUE)
names(Ex733)
```

```
[1] "Length" "Group"
```

```
summary(Ex733)
```

```
     Length          Group      
 Min.   : 88.25   Min.   :1.000  
 1st Qu.: 94.55   1st Qu.:1.000  
 Median :101.00   Median :1.000  
 Mean   :102.13   Mean   :1.413  
 3rd Qu.:109.47   3rd Qu.:2.000  
 Max.   :128.95   Max.   :2.000  
```

```
# In parts
NoOSAS = Ex733$Length[Ex733$Group == 1]
OSAS = Ex733$Length[Ex733$Group == 2]
#
boxplot(NoOSAS,OSAS)
```

```r
var.test(OSAS, NoOSAS)
```

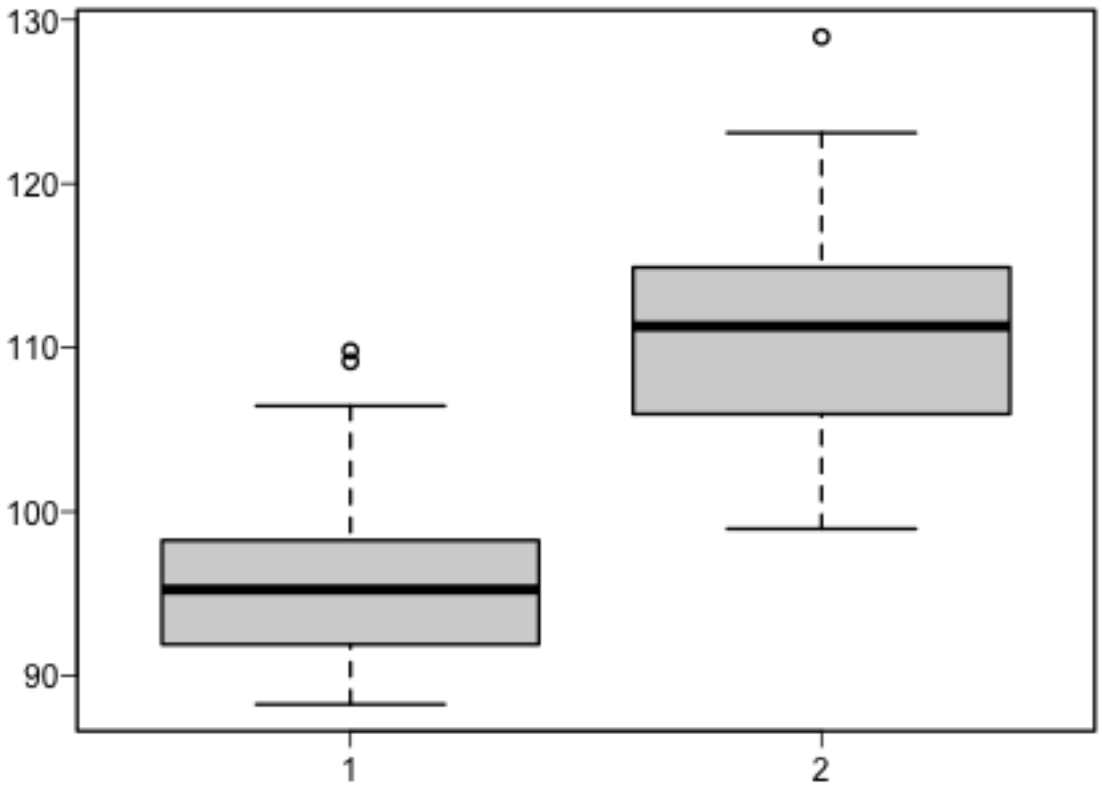
```
    F test to compare two variances

data:  OSAS and NoOSAS
F = 1.5494, num df = 25, denom df = 36, p-value = 0.2253
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.7606111 3.3152356
sample estimates:
ratio of variances
          1.549382
```

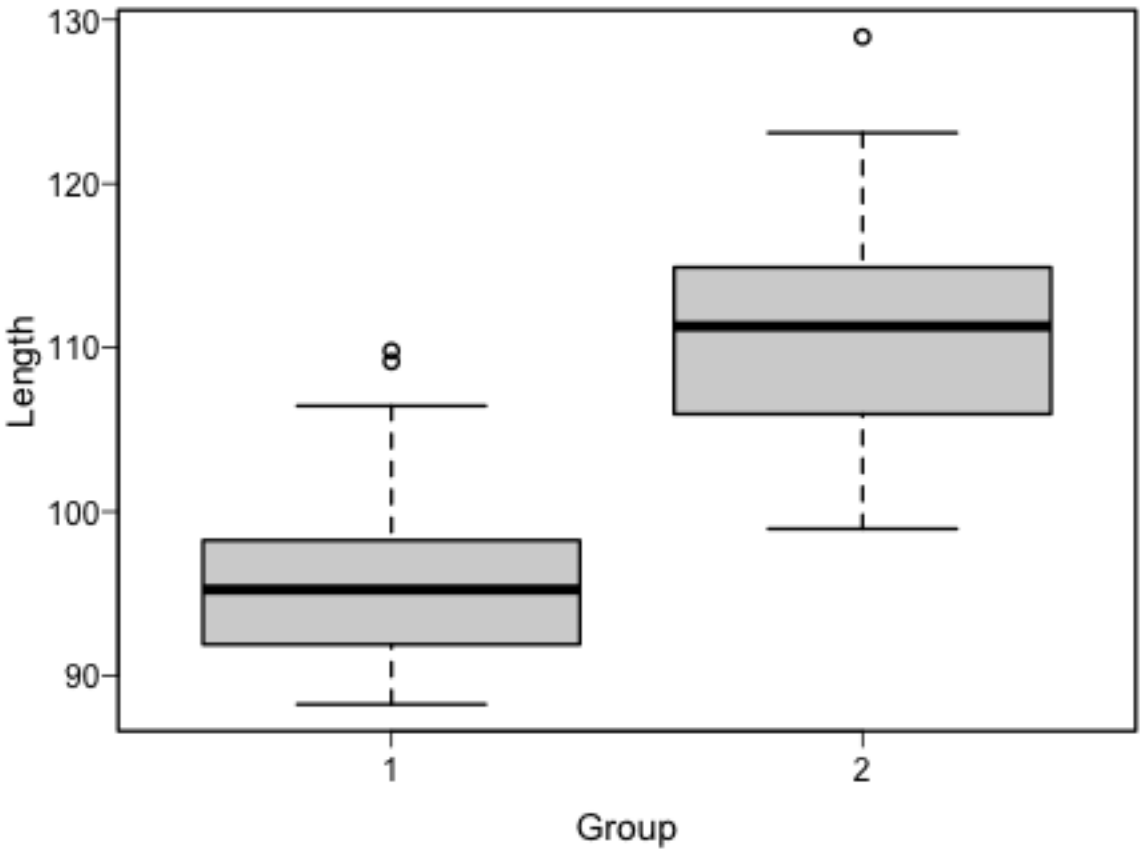
```r
t.test(NoOSAS, OSAS, alternative="less", conf.level=0.99)
```

```
    Welch Two Sample t-test

data:  NoOSAS and OSAS
t = -9.2441, df = 46.217, p-value = 2.229e-12
alternative hypothesis: true difference in means is less than 0
99 percent confidence interval:
      -Inf -11.24172
sample estimates:
mean of x mean of y
 95.85405 111.05962
```

```r
#
# Shorter and direct
boxplot(Length ~ Group, data=Ex733)
t.test(Length ~ Group, data=Ex733, alternative="less", conf.level=0.99)
```

```
    Welch Two Sample t-test

data:  Length by Group
t = -9.2441, df = 46.217, p-value = 2.229e-12
alternative hypothesis: true difference in means is less than 0
99 percent confidence interval:
      -Inf -11.24172
sample estimates:
mean in group 1 mean in group 2
       95.85405       111.05962
```


130
120
110
100
90
8
1
2



How it looks for several variables an ANOVA example using the HERS data refering to the diabetic participants.

```
#  Example of the HERS data for diabetic participants
hers_yesdi <- filter(hers, diabetes == "yes")
hers_yesdi <- mutate(hers_yesdi, physact = factor(physact, levels=c("much less active","somewhat less a

#  Example of ANOVA with HERS data for diabetic participants
#
ggplot(data = hers_yesdi, mapping = aes(x = physact, y = glucose)) + geom_boxplot(na.rm = TRUE)
glucose_yesdi_act <- lm(glucose ~ physact, data = hers_yesdi)
Anova(glucose_yesdi_act, type="II")
```

```
Anova Table (Type II tests)

Response: glucose
           Sum Sq  Df F value Pr(>F)
physact     17992   4   1.925 0.1044
Residuals 1696313 726
```

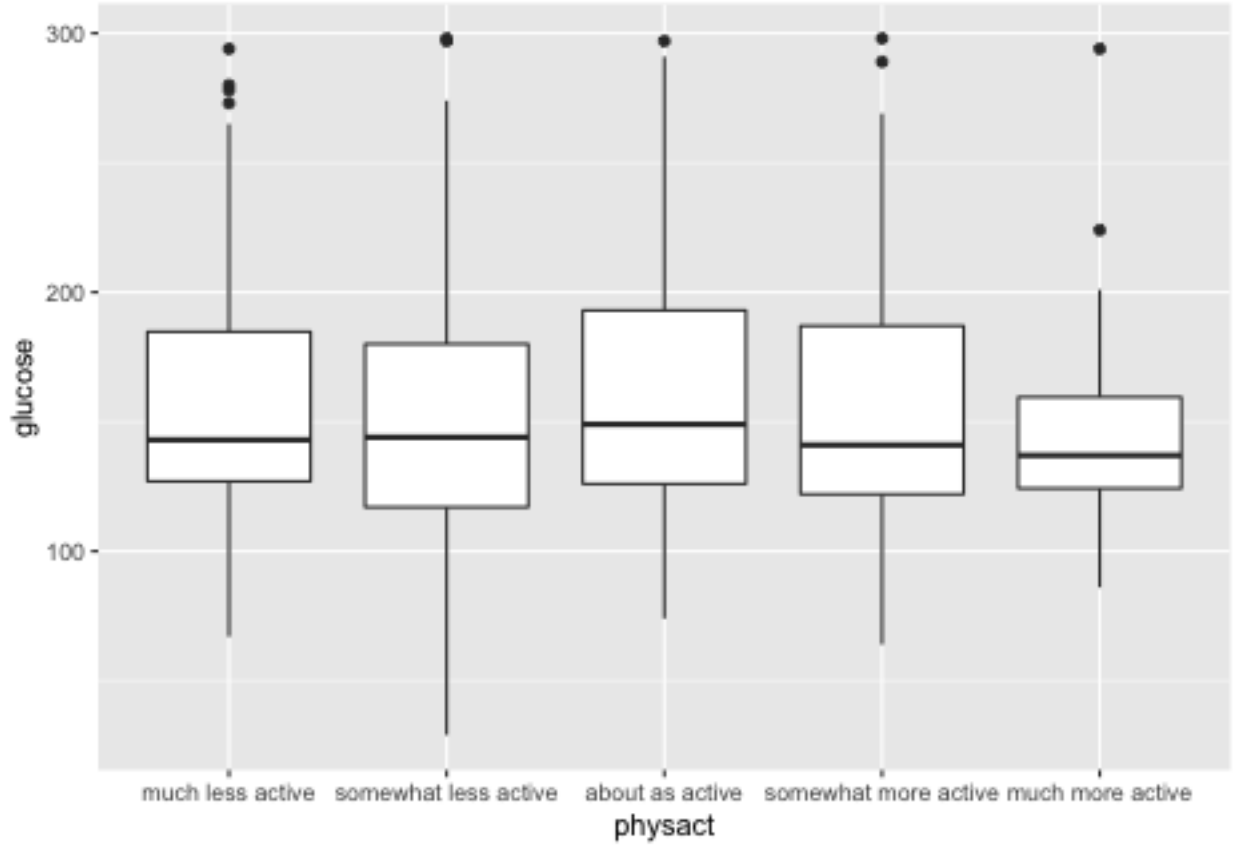
```
#
S(glucose_yesdi_act)
```

```
Call: lm(formula = glucose ~ physact, data = hers_yesdi)

Coefficients:
                           Estimate Std. Error t value Pr(>|t|)
(Intercept)                 155.789      5.095  30.575   <2e-16 ***
```

```
physactsomewhat less active   -4.590      6.235  -0.736    0.462
physactabout as active         5.191      5.958   0.871    0.384
physactsomewhat more active   -1.398      6.362  -0.220    0.826
physactmuch more active      -11.789      8.320  -1.417    0.157
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard deviation: 48.34 on 726 degrees of freedom
Multiple R-squared: 0.0105
F-statistic: 1.925 on 4 and 726 DF,  p-value: 0.1044
    AIC     BIC
7751.41 7778.98
```

```
glucose_emmeans <- emmeans(glucose_yesdi_act, "physact")
contrast(glucose_emmeans, adjust="sidak")
```

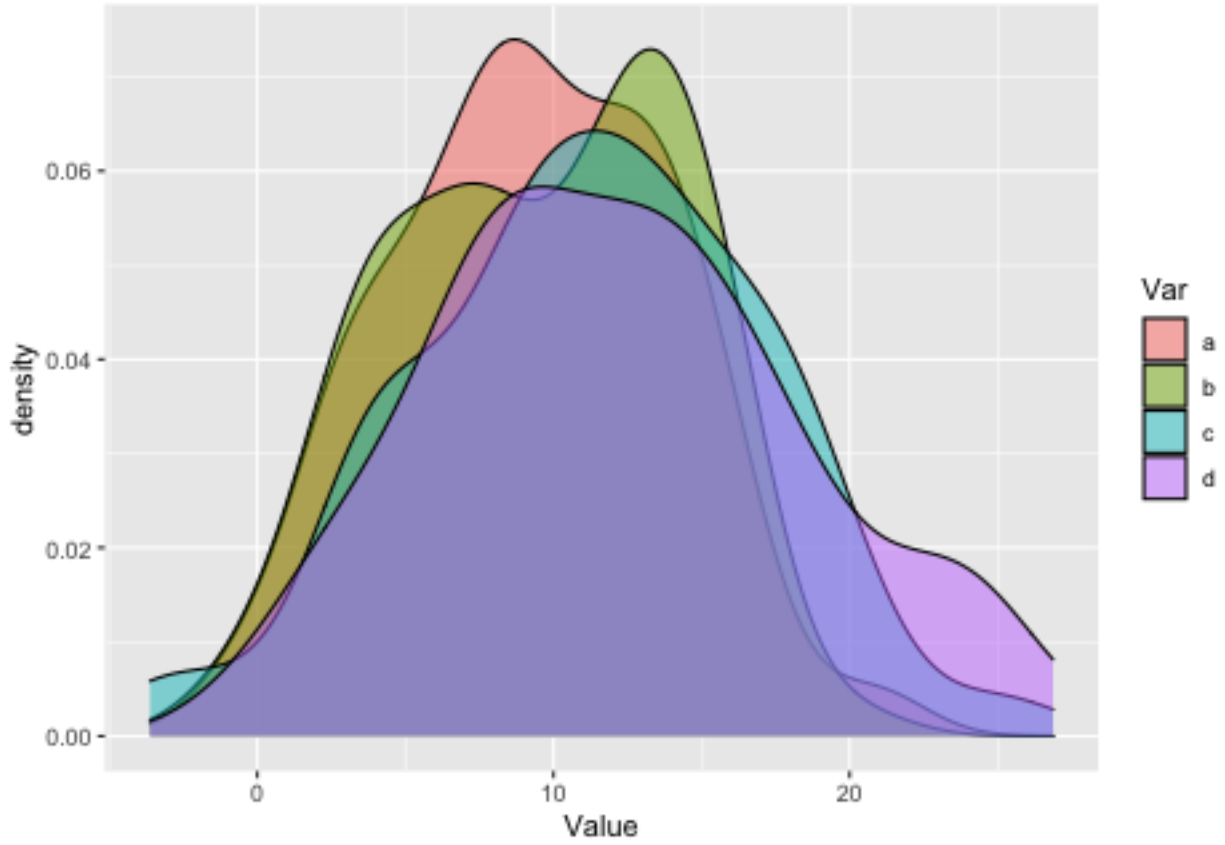
```
 contrast                    estimate   SE  df t.ratio p.value
 much less active effect         2.52 4.45 726  0.565  0.9856
 somewhat less active effect    -2.07 3.46 726 -0.599  0.9815
 about as active effect          7.71 3.16 726  2.441  0.0722
 somewhat more active effect     1.12 3.60 726  0.311  0.9991
 much more active effect        -9.27 5.50 726 -1.687  0.3830

P value adjustment: sidak method for 5 tests
```



Example from R-bloggers

First we build four random variables with two different distributions.

```
# Create the four groups
set.seed(10)
df1 <- data.frame(Var="a", Value=rnorm(100,10,5))
df2 <- data.frame(Var="b", Value=rnorm(100,10,5))
df3 <- data.frame(Var="c", Value=rnorm(100,11,6))
df4 <- data.frame(Var="d", Value=rnorm(100,11,6))

# merge them in one data frame
df<-rbind(df1,df2,df3,df4)

# convert Var to a factor
df$Var<-as.factor(df$Var)
df%>%ggplot(aes(x=Value, fill=Var))+geom_density(alpha=0.5)
```



The ANOVA (taken from R-bloggers)

ANOVA (ANalysis Of VAriance) is a statistical test used to compare two or more groups to see if they are significantly different. The ANOVA model and some examples. The null hypothesis in ANOVA is that there is no difference between means and the alternative is that the means are not all equal. This means that when we are dealing with many groups, we cannot compare them pairwise. We can simply answer if the means between groups can be considered as equal or not.

```r
# ANOVA
model1<-lm(Value~Var, data=df)
anova(model1)
```

```
Analysis of Variance Table

Response: Value
           Df  Sum Sq Mean Sq F value    Pr(>F)
Var         3   565.7 188.565   6.351 0.0003257 ***
Residuals 396 11757.5  29.691
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Tukey multiple comparisons

What about if we want to compare all the groups pairwise? In this case, we can apply the Tukey's HSD which is a single-step multiple comparison procedure and statistical test, Tukey's Honest Significant Difference (Tukey's HSD). It can be used to find means that are significantly different from each other.

```r
summary(glht(model1, mcp(Var="Tukey")))
```

```
     Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: lm(formula = Value ~ Var, data = df)

Linear Hypotheses:
           Estimate Std. Error t value Pr(>|t|)
b - a == 0   0.2079     0.7706   0.270  0.99312
c - a == 0   1.8553     0.7706   2.408  0.07727 .
d - a == 0   2.8758     0.7706   3.732  0.00129 **
c - b == 0   1.6473     0.7706   2.138  0.14298
d - b == 0   2.6678     0.7706   3.462  0.00329 **
d - c == 0   1.0205     0.7706   1.324  0.54795
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

Linear Regression

The term "regression" was introduced by Francis Galton (Darwin's nephew) during the XIX century to describe a biological phenomenon. The heights of the descendants of tall ancestors have the tendency to "return", come back, to the normal average high in the population, known as the regression to the media. (Mr. Galton was an Eugenics supporter)

Examples for "simple" linear regression

The general equation for the straight line is $y = mx + b_0$, this form is the "slope, intersection form". The slope is the rate of change the gives the change in y for a unit change in x. Remember that the slope formula for two pair of points (x_1, y_1) and (x_2, y_2) is:

$$m = \frac{(y_2 - y_1)}{(x_2 - x_1)}$$

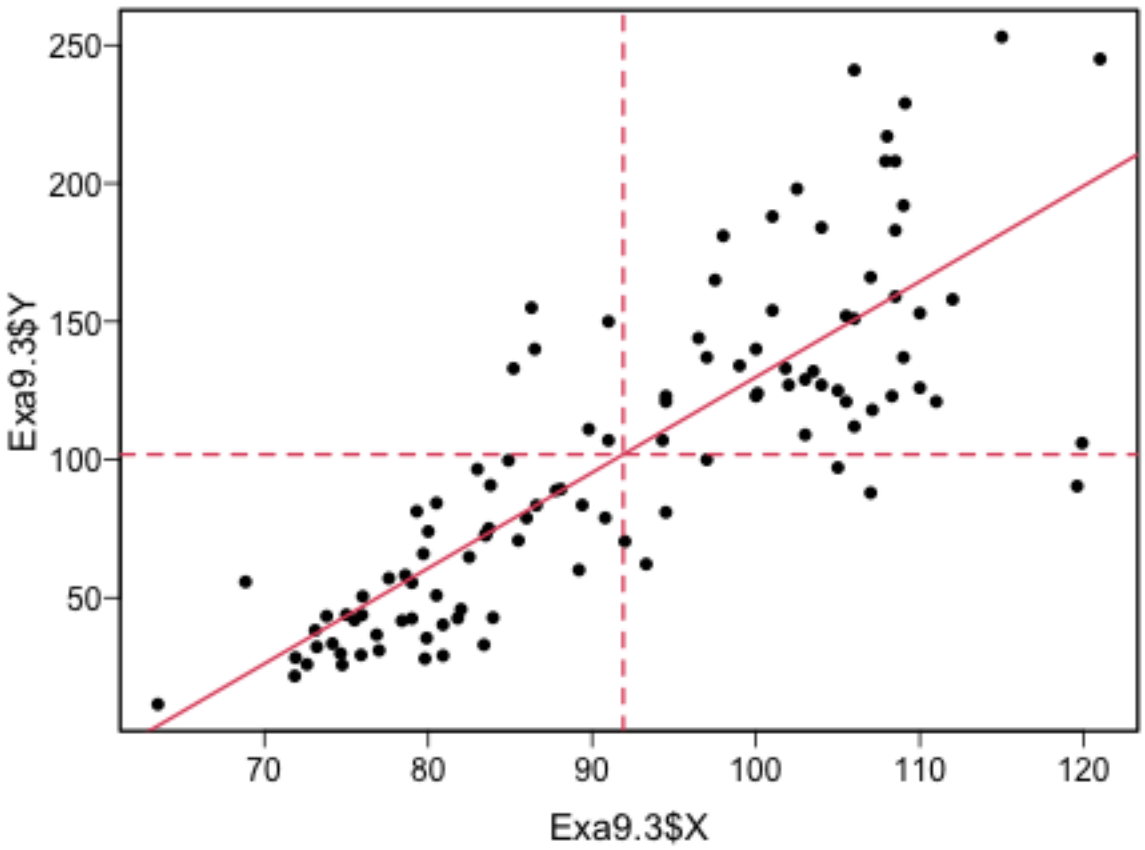
```r
setwd("~/Dropbox/Fdo/ClaseStats/RegressionClass/RegressionR_code")
# Changing wd to load the data file
Exa9.3 = read.csv(file="DataOther/EXA_C09_S03_01.csv", header=TRUE)
names(Exa9.3)
```

```
[1] "SUBJ" "X"    "Y"
```

```r
plot(Exa9.3$Y ~ Exa9.3$X, pch = 20)
Ybar=mean(Exa9.3$Y)
Xbar=mean(Exa9.3$X)
abline(h=Ybar, col = 2, lty = 2)
abline(v=Xbar, col = 2, lty = 2)
Lin9.3 = lm(Y ~ X, data=Exa9.3)
summary(Lin9.3)
```

```

Call:
lm(formula = Y ~ X, data = Exa9.3)

Residuals:
     Min       1Q   Median       3Q      Max
-107.288  -19.143   -2.939   16.376   90.342

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -215.9815    21.7963  -9.909   <2e-16 ***
X              3.4589     0.2347  14.740   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 33.06 on 107 degrees of freedom
Multiple R-squared:   0.67, Adjusted R-squared:  0.667
F-statistic: 217.3 on 1 and 107 DF,  p-value: < 2.2e-16
```

```r
abline(Lin9.3, col=2)
```


250
200
150
100
50
Exa9.3$Y
70
80
90
100
110
120
Exa9.3$X