# Introduction to R

# Code 12: ANOVA and TWO WAY ANOVA
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#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~#
# code chunk 1
# Create Diet Plan Data
#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~#


loss <- c(14,14,20,22,26,27,15,18,23,25,28,30,32,36,40,42,45,33,38,42,44,46,47)

WTL <- data.frame(Plan, loss)

str(WTL)

WTL$Plan <- factor(WTL$Plan)

#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~#
# code chunk 2
# ANOVA
#~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~#

?aov

# the function aov requires a formula specification - in the code below,
# the variable on the left is the "dependent" variable - the QUANTITATIVE
# variable that we are trying to predict or explain. The QUALITATIVE variable
# on the right, should have at least 3 levels.

a1 <- aov(WTL$loss ~ WTL$Plan)

a1

summary(a1)

plot(WTL$loss ~ WTL$Plan, data=WTL)
# from above, I understand that at least one of the diet plans is different -
# but I don't know which one. To determine this, I need to run a post hoc test.
# there are a lot to choose from. Two common post hoc tests are Fishers LSD
# and Tukey's HSD.
# although we could write a lot of code...let's install a package to get what we need.
# we can apply the TukeyHSD test easily:
TukeyHSD(a1)

# Fisher's HSD test requires that we install a package:
install.packages("agricolae")
library(agricolae)
out <- LSD.test(a1,"WTL$Plan")
out
bar.group(out$groups)
boxplot(WTL$loss ~ WTL$Plan)

UCDavis <- read.csv("Ucdavis2.csv")
head(UCDavis)
str(UCDavis)
table(UCDavis$Seat)

# getting rid of the missing value
UCDavis1 <- UCDavis[-which(UCDavis$Seat==""'),]
str(UCDavis1)

# ~~~~~~~~~~~~~~~~~~~~~~~~~#
# code chunk 5            #
# Example 2 - UC Davis    #
# ANOVA                  #
# ~~~~~~~~~~~~~~~~~~~~~~~~~#

a2<-aov(UCDavis1$GPA~UCDavis1$Seat)
summary(a2)

TukeyHSD(a2, "UCDavis1$Seat")

# ~~~~~~~~~~~~~~~~~~~~~~~~~#
# code chunk 6             #
# Example 3 - Ritalin      #
# 2 Way ANOVA with Interaction  #
# ~~~~~~~~~~~~~~~~~~~~~~~~~#

ritalin<- read.csv("RITALIN.csv")
head(ritalin)

attach(ritalin)
plot(Activity ~ Drug + Group, data=ritalin)

interaction.plot(Drug, Group, Activity)

results<-lm(Activity ~ Drug + Group + Drug*Group, data=ritalin)
anova(results)