

CMTH 642 Data Analytics: Advanced Methods

Assignment 1 (10%)

[Daria Yip]

[DHA - Student#500721106]

1. Read the csv files in the folder. (3 points)

```
csvdata1 <- read.csv("C:/Users/samda/Documents/Ryerson/CIND 642 -  
R/Macronutrients1.csv", header = T, sep = ",")  
csvdata2 <- read.csv("C:/Users/samda/Documents/Ryerson/CIND 642 -  
R/USDA_Micronutrients2.csv", header = T, sep = ",")
```

2. Merge the data frames using the variable "ID". Name the Merged Data Frame "USDA". (6 points)

```
USDA <- merge(csvdata1, csvdata2, by = "ID") #merge function to merge two  
dataframes by a common variable
```

```
head(USDA)
```

```
##      ID      Description Calories Protein TotalFat Carbohydrate  
Sodium  
## 1 1001      BUTTER,WITH SALT      717      0.85      81.11      0.06  
714  
## 2 1002 BUTTER,WHIPPED,WITH SALT      717      0.85      81.11      0.06  
827  
## 3 1003      BUTTER OIL,ANHYDROUS      876      0.28      99.48      0.00  
2  
## 4 1004      CHEESE,BLUE      353      21.40      28.74      2.34  
1,395  
## 5 1005      CHEESE,BRICK      371      23.24      29.68      2.79  
560  
## 6 1006      CHEESE,BRIE      334      20.75      27.68      0.45  
629  
##      Cholesterol Sugar Calcium Iron Potassium VitaminC VitaminE VitaminD  
## 1      215      0.06      24 0.02      24      0      2.32      1.5  
## 2      219      0.06      24 0.16      26      0      2.32      1.5  
## 3      256      0.00      4 0.00      5      0      2.80      1.8  
## 4      75      0.50      528 0.31      256      0      0.25      0.5  
## 5      94      0.51      674 0.43      136      0      0.26      0.5  
## 6      100      0.45      184 0.50      152      0      0.24      0.5
```

3. Check the datatypes of the attributes. Delete the commas in the Sodium and Potassium records. Assign Sodium and Potassium as numeric data types. (6 points)

```
str(USDA) #Check the datatypes of the attributes, you can also use  
sapply(USDA, class)
```

```
## 'data.frame':    7057 obs. of  15 variables:
## $ ID            : int  1001 1002 1003 1004 1005 1006 1007 1008 1009 1010
...
## $ Description   : chr   "BUTTER,WITH SALT" "BUTTER,WHIPPED,WITH SALT"
"BUTTER OIL,ANHYDROUS" "CHEESE,BLUE" ...
## $ Calories      : int   717 717 876 353 371 334 300 376 403 387 ...
## $ Protein       : num   0.85 0.85 0.28 21.4 23.24 ...
## $ TotalFat      : num   81.1 81.1 99.5 28.7 29.7 ...
## $ Carbohydrate  : num   0.06 0.06 0 2.34 2.79 0.45 0.46 3.06 1.28 4.78 ...
## $ Sodium        : chr    "714" "827" "2" "1,395" ...
## $ Cholesterol   : int   215 219 256 75 94 100 72 93 105 103 ...
## $ Sugar         : num   0.06 0.06 0 0.5 0.51 0.45 0.46 NA 0.52 NA ...
## $ Calcium       : int    24 24 4 528 674 184 388 673 721 643 ...
## $ Iron          : num   0.02 0.16 0 0.31 0.43 0.5 0.33 0.64 0.68 0.21 ...
## $ Potassium     : chr    "24" "26" "5" "256" ...
## $ VitaminC      : num    0 0 0 0 0 0 0 0 0 0 ...
## $ VitaminE      : num   2.32 2.32 2.8 0.25 0.26 0.24 0.21 NA 0.29 NA ...
## $ VitaminD      : num    1.5 1.5 1.8 0.5 0.5 0.5 0.4 NA 0.6 NA ...

USDA$Sodium <- as.numeric(gsub(",", "", USDA$Sodium)) #delete commas in Sodium
and assign
USDA$Potassium <- as.numeric(gsub(",", "", USDA$Potassium)) #delete commas in
Potassium & #assign to numeric

class(USDA$Sodium) #check class

## [1] "numeric"

class(USDA$Potassium) #check class

## [1] "numeric"

head(USDA) #check that commas have been removed from both

##      ID              Description Calories Protein TotalFat Carbohydrate
Sodium
## 1 1001      BUTTER,WITH SALT      717    0.85    81.11      0.06
714
## 2 1002 BUTTER,WHIPPED,WITH SALT      717    0.85    81.11      0.06
827
## 3 1003      BUTTER OIL,ANHYDROUS      876    0.28    99.48      0.00
2
## 4 1004              CHEESE,BLUE      353   21.40    28.74      2.34
1395
## 5 1005              CHEESE,BRICK      371   23.24    29.68      2.79
560
## 6 1006              CHEESE,BRIE      334   20.75    27.68      0.45
629
##      Cholesterol Sugar Calcium Iron Potassium VitaminC VitaminE VitaminD
## 1           215   0.06      24 0.02          24         0     2.32     1.5
## 2           219   0.06      24 0.16          26         0     2.32     1.5
```

```
## 3      256  0.00      4 0.00      5      0      2.80      1.8
## 4       75  0.50     528 0.31     256      0      0.25      0.5
## 5       94  0.51     674 0.43     136      0      0.26      0.5
## 6      100  0.45     184 0.50     152      0      0.24      0.5
```

4. Remove records (rows) with missing values in more than 4 attributes (columns). How many records remain in the data frame? (6 points)

```
missing <- rowSums(is.na(USDA))
USDA <- USDA[!missing > 4,]
nrow(USDA)
```

```
## [1] 6887
```

#Therefore, there are 6887 records that remain in the dataframe #that do not have rows with missing values more than 4 #attributes.

5. For records with missing values for Sugar, Vitamin E and Vitamin D, replace missing values with mean value for the respective variable. (6 points)

```
mean.sugar <- mean(USDA$Sugar, na.rm = TRUE)
USDA$Sugar[is.na(USDA$Sugar)] = mean.sugar
```

```
mean.vitd <- mean(USDA$VitaminD, na.rm=TRUE)
USDA$VitaminD[is.na(USDA$VitaminD)] = mean.vitd
```

```
mean.vite <- mean(USDA$VitaminE, na.rm=TRUE)
USDA$VitaminE[is.na(USDA$VitaminE)] = mean.vite
```

```
check <- sum(is.na(USDA$Sugar)) + sum(is.na(USDA$VitaminE)) +
sum(is.na(USDA$VitaminD)) #double check #no more missing values in these
columns
check
```

```
## [1] 0
```

6. With a single line of code, remove all remaining records with missing values. Name the new Data Frame "USDAclean". How many records remain in the data frame? (6 points)

```
USDAclean <- na.omit(USDA) #single line of code to remove all remaining
missing values
```

```
nrow(USDAclean) #remaining is 6310 from the original 6887 in Question 4
```

```
## [1] 6310
```

7. Which food has the highest sodium level? (6 points)

```
USDAclean[which(USDAclean$Sodium == max(USDAclean$Sodium)),]
```

```
##      ID Description Calories Protein TotalFat Carbohydrate Sodium
Cholesterol
## 265 2047  SALT, TABLE      0      0      0      0 38758
0
##      Sugar Calcium Iron Potassium VitaminC VitaminE VitaminD
## 265      0      24 0.33      8      0      0      0
```

```
#can also use the which.max #USDAclean[which.max(USDAclean$Sodium),]
```

#Therefore, salt has the highest sodium level.

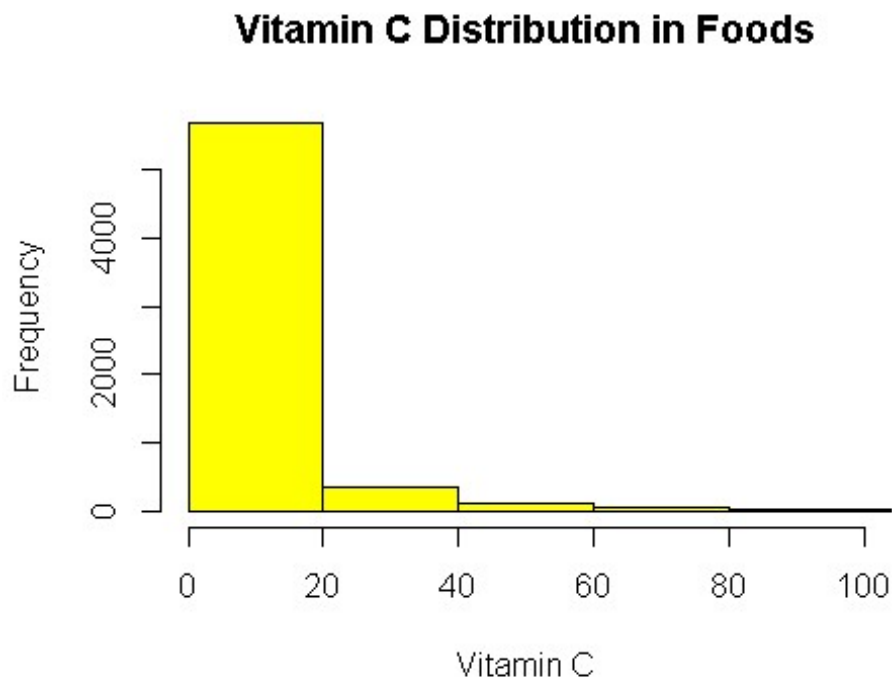
8. Create a histogram of Vitamin C distribution in foods. (6 points)

```
summary(USDAclean$VitaminC) #take a look at the column to see
```

```
##      Min.   1st Qu.   Median     Mean   3rd Qu.    Max.
##    0.000    0.000    0.000    9.284    3.000 2400.000
```

#what kind of axis limits we need

```
hist(USDAclean$VitaminC, breaks = 100, xlim = c(0, 100),
     xlab = "Vitamin C", col = "yellow", main = "Vitamin C Distribution in
Foods")
```

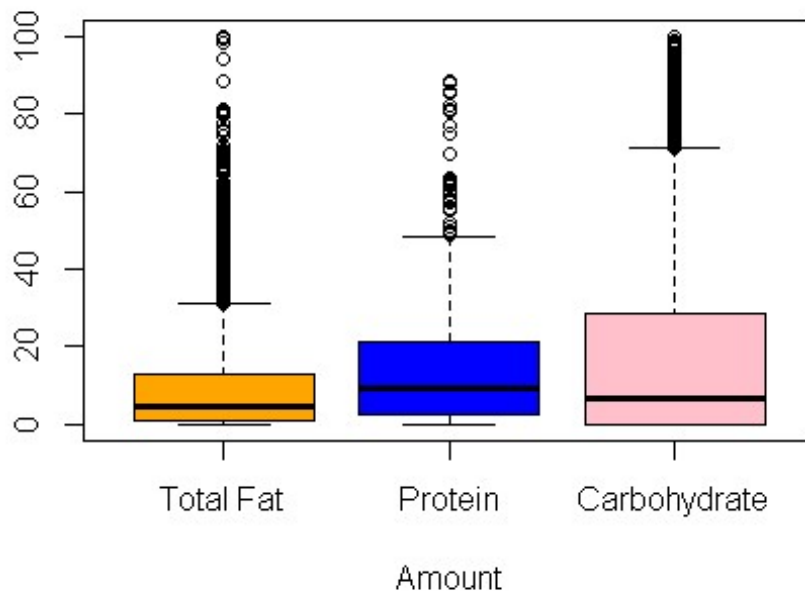


```
#breaks is very important to include here so R knows how we
#want the histogram to be broken up
```

9. Create a boxplot to illustrate the distribution of values for TotalFat, Protein and Carbohydrate. (6 points)

```
boxplot(USDAclean$TotalFat, USDAclean$Protein, USDAclean$Carbohydrate, names
= c("Total Fat", "Protein", "Carbohydrate"), col = c("orange", "blue",
"pink"), xlab = "Amount", main = "Distribution of Values for Total Fat,
Protein, and Carbohydrates", horizontal = FALSE)
```

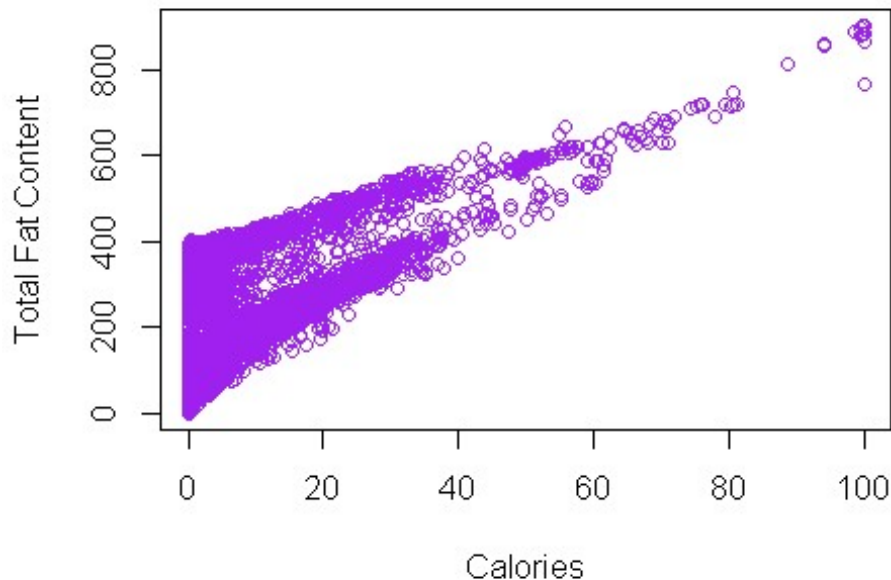
tribution of Values for Total Fat, Protein, and Carboh



10. Create a scatterplot to illustrate the relationship between a food's TotalFat content and its Calorie content. (6 points)

```
plot(USDAclean$Calories~USDAclean$TotalFat, main = "Relationship between  
Calories and Total Fat Content", xlab = "Calories", ylab = "Total Fat  
Content", col = "purple")
```

Relationship between Calories and Total Fat Conte



11. Add a variable to the data frame that takes value 1 if the food has higher sodium than average, 0 otherwise. Call this variable HighSodium. Do the same for High Calories, High Protein, High Sugar, and High Fat. How many foods have both high sodium and high fat? (8 points)

```
HighSodium <- 0 #Initialize
HighCalories <- 0
HighProtein <- 0
HighSugar <- 0
HighFat <- 0

USDAclean <- cbind(USDAclean, HighSodium) #add column
USDAclean <- cbind(USDAclean, HighCalories, HighProtein,
                  HighSugar, HighFat) #add columns

#For loop to calculate the if and else for High Sodium #condition
for(i in 1:length(USDAclean$Description))
{
  if(USDAclean$Sodium[i] > mean(USDAclean$Sodium))
  {
    USDAclean$HighSodium[i] = 1
  }
  else
  {
    USDAclean$HighSodium[i] = 0
  }
}
```

```

#High Calories, using extraction
USDAclean$HighCalories[USDAclean$Calories > mean(USDAclean$Calories)] <- 1
USDAclean$HighCalories[USDAclean$Calories <= mean(USDAclean$Calories)] <- 0

#HighProtein, using if else statement instead of for loop
USDAclean$HighProtein <- ifelse(USDAclean$Protein >
mean(USDAclean$Protein),1,0)

#HighSugar
USDAclean$HighSugar <- ifelse(USDAclean$Sugar > mean(USDAclean$Sugar),1,0)

#HighFat
USDAclean$HighFat <- ifelse(USDAclean$TotalFat >
mean(USDAclean$TotalFat),1,0)

index <- USDAclean[which(USDAclean$HighFat == 1 & USDAclean$HighSodium ==
1),]
nrow(index) #High Sodium & High Fat foods

## [1] 644

#Therefore, there are 644 foods that have high sodium and high
#fat content.

head(USDAclean) #take a look at the data

##      ID          Description Calories Protein TotalFat Carbohydrate
Sodium
## 1 1001      BUTTER,WITH SALT      717    0.85    81.11      0.06
714
## 2 1002 BUTTER,WHIPPED,WITH SALT      717    0.85    81.11      0.06
827
## 3 1003      BUTTER OIL,ANHYDROUS      876    0.28    99.48      0.00
2
## 4 1004          CHEESE,BLUE      353   21.40    28.74      2.34
1395
## 5 1005          CHEESE,BRICK      371   23.24    29.68      2.79
560
## 6 1006          CHEESE,BRIE      334   20.75    27.68      0.45
629
##      Cholesterol Sugar Calcium Iron Potassium VitaminC VitaminE VitaminD
## 1          215  0.06      24 0.02          24          0      2.32      1.5
## 2          219  0.06      24 0.16          26          0      2.32      1.5
## 3          256  0.00       4 0.00           5          0      2.80      1.8
## 4           75  0.50     528 0.31        256          0      0.25      0.5
## 5           94  0.51     674 0.43        136          0      0.26      0.5
## 6          100  0.45     184 0.50        152          0      0.24      0.5
##      HighSodium HighCalories HighProtein HighSugar HighFat
## 1              1           1           0           0           1

```

```
## 2      1      1      0      0      1
## 3      0      1      0      0      1
## 4      1      1      1      0      1
## 5      1      1      1      0      1
## 6      1      1      1      0      1
```

12. Calculate the average amount of iron, for high and low protein foods. (8 points)

```
highavg <- mean(USDAclean$Iron[USDAclean$HighProtein == 1]) #high #protein
foods average iron
highavg
```

```
## [1] 3.069541
```

```
lowavg <- mean(USDAclean$Iron[USDAclean$HighProtein == 0]) #Low
#protein foods average iron
lowavg
```

```
## [1] 2.696634
```

```
ironmean <- cbind(highavg, lowavg)
colnames(ironmean) <- c("High Protein", "Low Protein")
rownames(ironmean) <- c("Average Iron")
ironmean
```

```
##           High Protein Low Protein
## Average Iron    3.069541    2.696634
```

*#The average amount of iron for high protein foods is 3.069541
#for High Protein Levels and 2.696634 for Low protein foods.*

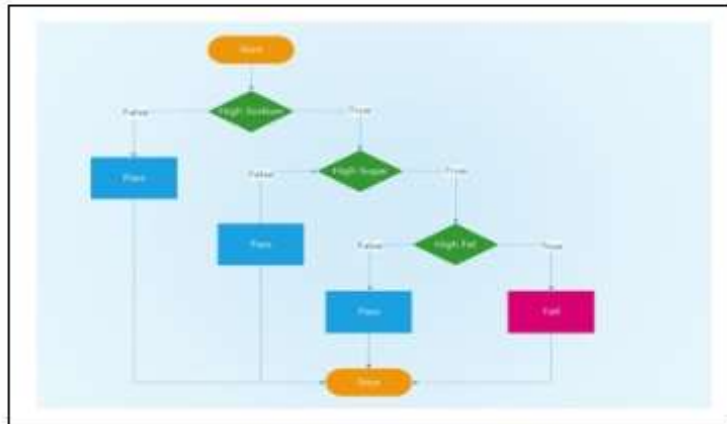
*#You can also do this using the aggregate function,
#aggregate(USDAclean\$Iron), list(USDAclean\$HighProtein) where #the FUN =
mean.*

13. Create a script for a “HealthCheck” program to detect unhealthy foods. Use the algorithm flowchart below as a basis for this script. (8 points)

```
require(jpeg)
```

```
## Loading required package: jpeg
```

```
img<-readJPEG("HealthCheck.jpg")
plot(1:4, ty = 'n', ann = F, xaxt = 'n', yaxt = 'n')
rasterImage(img,1,1,4,4)
```

```

HC <- function(x,y,z)
{
  ifelse(x == 1 & y == 1 & z == 1, "Fail", "Pass")
}
HC(0,1,1) #Testing
## [1] "Pass"

```

14. Add a new variable called HealthCheck to the data frame using the output of the function. (8 points)

```

HealthCheck <- 0 #Initialize
USDaclean <- cbind(USDaclean, HealthCheck) #add column

USDaclean$HealthCheck <-
HC(USDaclean$HighSodium,USDaclean$HighSugar,USDaclean$HighFat)

head(USDaclean)

```

ID	Description	Calories	Protein	TotalFat	Carbohydrate
1001	BUTTER,WITH SALT	717	0.85	81.11	0.06
1002	BUTTER,WHIPPED,WITH SALT	717	0.85	81.11	0.06
1003	BUTTER OIL,ANHYDROUS	876	0.28	99.48	0.00
1004	CHEESE,BLUE	353	21.40	28.74	2.34

```

1395
## 5 1005          CHEESE,BRICK      371  23.24  29.68      2.79
560
## 6 1006          CHEESE,BRIE      334  20.75  27.68      0.45
629
##   Cholesterol Sugar Calcium Iron Potassium VitaminC VitaminE VitaminD
## 1          215  0.06      24 0.02          24          0      2.32      1.5
## 2          219  0.06      24 0.16          26          0      2.32      1.5
## 3          256  0.00       4 0.00           5          0      2.80      1.8
## 4           75  0.50     528 0.31        256          0      0.25      0.5
## 5           94  0.51     674 0.43        136          0      0.26      0.5
## 6          100  0.45     184 0.50        152          0      0.24      0.5
##   HighSodium HighCalories HighProtein HighSugar HighFat HealthCheck
## 1           1           1           0           0           1      Pass
## 2           1           1           0           0           1      Pass
## 3           0           1           0           0           1      Pass
## 4           1           1           1           0           1      Pass
## 5           1           1           1           0           1      Pass
## 6           1           1           1           0           1      Pass

```

15. How many foods in the USDAclean data frame fail the HealthCheck? (8 points)

```
sum(USDAclean$HealthCheck == "Fail")
```

```
## [1] 237
```

16. Save your final data frame as "USDAclean_[your last name]." (3 points)

```
USDAclean_Yip <- USDAclean
```

This is the end of Assignment 1

Ceni Babaoglu, PhD