

1. Run the following lines and study how they work. Then state what they do and output for us. (20 Points)

The following code creates a dataframe *df1* which consists of 3 columns and 12 rows:

```
df1=data.frame(Name=c('James','Paul','Richards','Marico','Samantha','Ravi','Raghu',  
                      'Richards','George','Ema','Samantha','Catherine'),  
               State=c('Alaska','California','Texas','North Carolina','California','Texas',  
                       'Alaska','Texas','North Carolina','Alaska','California','Texas'),  
               Sales=c(14,24,31,12,13,7,9,31,18,16,18,14))
```

```
> head(df1)
```

| | Name | State | Sales |
|---|----------|----------------|-------|
| 1 | James | Alaska | 14 |
| 2 | Paul | California | 24 |
| 3 | Richards | Texas | 31 |
| 4 | Marico | North Carolina | 12 |
| 5 | Samantha | California | 13 |
| 6 | Ravi | Texas | 7 |

The following code utilizes the aggregate() function to sum the Sales by State:

```
aggregate(df1$Sales, by=list(df1$State), FUN=sum)
```

```
> aggregate(df1$Sales, by=list(df1$State), FUN=sum)
```

| | Group.1 | x |
|---|----------------|----|
| 1 | Alaska | 39 |
| 2 | California | 55 |
| 3 | North Carolina | 30 |
| 4 | Texas | 83 |

The following code utilizes dplyr function to do the same sum of the Sales by State:

```
library(dplyr)  
df1 %>% group_by(State) %>% summarise(sum_sales = sum(Sales))
```

```
> df1 %>% group_by(State) %>% summarise(sum_sales = sum(Sales))
```

```
# A tibble: 4 × 2
```

| | State | sum_sales |
|---|----------------|-----------|
| | <chr> | <dbl> |
| 1 | Alaska | 39 |
| 2 | California | 55 |
| 3 | North Carolina | 30 |
| 4 | Texas | 83 |

2. Use R to read the WorldCupMatches.csv from the DATA folder on Google Drive. Then perform the followings (48 points):

a. Find the size of the data frame. How many rows, how many columns?

```
> df = read.csv("C:/Users/User/OneDrive - Umich/15_CSC302 Intro to Data Visualization/Rscripts/worldCupMatches.csv", header=T)
> dim(df)
[1] 852 20
```

b. Use summary function to report the statistical summary of your data.

```
> summary(df)
   Year      Datetime      Stage      Stadium      City      Home.Team.Name      Home.Team.Goals      Away.Team.Goals      Away.Team.Name
Min.   :1930   Length:852   Length:852   Length:852   Length:852   Length:852   Min.   : 0.000   Min.   : 0.000   Length:852
1st Qu.:1970   Class :character   Class :character   Class :character   Class :character   Class :character   1st Qu.: 1.000   1st Qu.: 0.000   Class :character
Median :1990   Mode  :character   Mode  :character   Mode  :character   Mode  :character   Mode  :character   Median : 2.000   Median : 1.000   Mode  :character
Mean   :1985                                     Mean   : 1.811   Mean   : 1.022
3rd Qu.:2002                                     3rd Qu.: 3.000   3rd Qu.: 2.000
Max.   :2014                                     Max.   :10.000   Max.   : 7.000

win.conditions      Attendance      Half.time.Home.Goals      Half.time.Away.Goals      Referee      Assistant.1      Assistant.2      RoundID
Length:852          Min.   : 2000      Min.   :0.0000      Min.   :0.0000      Length:852      Length:852      Length:852      Min.   : 201
Class :character    1st Qu.: 30000      1st Qu.:0.0000      1st Qu.:0.0000      Class :character   Class :character   Class :character   1st Qu.: 262
Mode  :character    Median : 41580      Median :0.0000      Median :0.0000      Mode  :character   Mode  :character   Mode  :character   Median : 337
                    Mean   : 45165      Mean   :0.7089      Mean   :0.4284                                     Mean   :10661773
                    3rd Qu.: 61375      3rd Qu.:1.0000      3rd Qu.:1.0000                                     3rd Qu.: 249722
                    Max.   :173850      Max.   :6.0000      Max.   :5.0000                                     Max.   :97410600
                    NA's   :2

MatchID      Home.Team.Initials      Away.Team.Initials
Min.   : 25      Length:852      Length:852
1st Qu.: 1189      Class :character   Class :character
Median : 2191      Mode  :character   Mode  :character
Mean   : 61346868
3rd Qu.: 43950059
Max.   :300186515
```

c. Find how many unique locations olympics were held at.

```
> length(unique(df$City))
[1] 151
```

d. Find the average attendance.

```
> df2 = df[is.na(df["Attendance"])==F, ] # create df2 which excludes any "attendance" entries with "NA"
> mean(df2$Attendance) # find the average attendance of the remaining dataset
[1] 45164.8
```

e. For each Home Team, what is the total number of goals scored? (Hint: Please refer to question 1)

```
> aggregate(df$Home.Team.Goals, by=list(df$Home.Team.Name), FUN=sum)
  Group.1 x
1   Algeria 5
2   Angola 0
3 Argentina 111
4  Australia 7
5   Austria 31
6   Belgium 27
7   Bolivia 1
8   Brazil 180
9   Bulgaria 11
10  Cameroon 11
11  Canada 0
12  Chile 25
13  China PR 0
14  Colombia 11
15  Costa Rica 7
16  Croatia 3
17 Côte d'Ivoire 5
18  Cuba 5
19  Czech Republic 0
20  Czechoslovakia 27
21  Denmark 13
```

- f. What is the average number of attendees for each year? Is there a trend or pattern in the data in that sense?

```
> aggregate(df2$Attendance, by=list(df2$Year), FUN=mean) #using df2 to throw out the years with "NA" attendance
```

| Group.1 | x |
|---------|---------------|
| 1 | 1930 32808.28 |
| 2 | 1934 21352.94 |
| 3 | 1938 20872.22 |
| 4 | 1950 47511.18 |
| 5 | 1954 29561.81 |
| 6 | 1958 23423.14 |
| 7 | 1962 27911.62 |
| 8 | 1966 48847.97 |
| 9 | 1970 50124.22 |
| 10 | 1974 49098.76 |
| 11 | 1978 40678.71 |
| 12 | 1982 40571.60 |
| 13 | 1986 46039.06 |
| 14 | 1990 48388.75 |
| 15 | 1994 68991.12 |
| 16 | 1998 43517.19 |
| 17 | 2002 42268.70 |
| 18 | 2006 52491.23 |
| 19 | 2010 49669.62 |
| 20 | 2014 55374.91 |

3. Use R to read the metabolites.csv from the DATA folder on Google Drive. Then perform the followings (32 points):

- a. Find how many Alzheimers patients there are in the data set. (Hint: Please refer to question 1)

```
> df = read.csv("C:/Users/User/OneDrive - Umich/15_CSC302 Intro to Data Visualization/Rscripts/metabolite.csv", header=T)
> sum(df$Label == "Alzheimer")
[1] 35
```

- b. Determine the number of missing values for each column. (Hint: is.na())

```
> colSums(is.na(df))
```

| Label | Phe | Pro | Ser | Thr | ADMA |
|-----------|------------|------------|------------|-----------|------------|
| 0 | 0 | 0 | 0 | 0 | 0 |
| alpha.AAA | c4.OH.Pro | Carnosine | Creatinine | DOPA | Dopamine |
| 0 | 20 | 1 | 0 | 0 | 20 |
| Histamine | Kynurenine | Met.SO | Nitro.Tyr | PEA | Putrescine |
| 0 | 0 | 1 | 62 | 69 | 0 |
| Sarcosine | Serotonin | Spermidine | Spermine | t4.OH.Pro | Taurine |
| 0 | 0 | 0 | 60 | 0 | 2 |

- c. Remove the rows which has missing value for the Dopamine column and assign the result to a new data frame. (Hint: is.na())

```
> df2 = df[is.na(df[["Dopamine"]])!=F, ] # create df2 which excludes any "Dopamine" entries with "NA"
> head(df2)
```

| | Label | Phe | Pro | Ser | Thr | ADMA | alpha.AAA | c4.OH.Pro | Carnosine | Creatinine | DOPA | Dopamine | Histamine | Kynurenine | Met.SO |
|---|-----------|------|------------|-----------|-----------|------------|-----------|-----------|-----------|------------|-------|----------|-----------|------------|--------|
| 1 | Alzheimer | 72.8 | 166 | 170 | 282 | 1.15 | 0.760 | 0.236 | 1.270 | 49.9 | 0.265 | 0.233 | 0.225 | 5.21 | 0.526 |
| 4 | Alzheimer | 94.1 | 129 | 162 | 201 | 1.10 | 0.795 | NA | 0.675 | 80.1 | 0.264 | 0.234 | 0.209 | 5.80 | 0.389 |
| 5 | Alzheimer | 79.8 | 126 | 115 | 199 | 1.24 | 1.360 | NA | 1.280 | 60.5 | 0.271 | 0.231 | 0.210 | 4.46 | 0.466 |
| 8 | Healthy | 83.6 | 119 | 135 | 268 | 1.18 | 0.779 | 0.215 | 0.647 | 30.6 | 0.275 | 0.244 | 0.214 | 5.66 | 0.245 |
| 9 | Healthy | 73.7 | 124 | 145 | 307 | 1.17 | 0.785 | 0.186 | 0.590 | 39.8 | 0.259 | 0.233 | 0.210 | 6.36 | 0.413 |
| | Nitro.Tyr | PEA | Putrescine | Sarcosine | Serotonin | Spermidine | Spermine | t4.OH.Pro | Taurine | SDMA | C0 | C10 | C10.1 | C10.2 | C12 |
| 1 | 0.027 | NA | 0.068 | 17.8 | 0.147 | 0.188 | NA | 24.0 | 125 | 1.13 | 18.2 | 0.059 | 0.312 | 0.038 | 0.030 |
| 4 | NA | NA | 0.110 | 18.7 | 0.255 | 0.353 | NA | 23.1 | 159 | 1.34 | 23.5 | 0.071 | 0.317 | 0.040 | 0.045 |
| 5 | NA | NA | 0.118 | 22.5 | 0.390 | 0.473 | NA | 26.9 | 149 | 1.24 | 13.6 | 0.139 | 0.472 | 0.074 | 0.056 |
| 8 | 0.002 | NA | 0.161 | 23.3 | 0.215 | 0.276 | NA | 10.7 | 133 | 1.04 | 13.3 | 0.051 | 0.217 | 0.030 | 0.041 |

- d. In the new data frame, replace the missing values in the c4-OH-Pro column with the median value of the same column. (Hint: there is median() function.)

```
> df2$c4.OH.Pro[is.na(df2$c4.OH.Pro)] <- median(df2$c4.OH.Pro, na.rm=T)
> head(df2)
```

| | Label | Phe | Pro | Ser | Thr | ADMA | alpha.AAA | c4.OH.Pro | Carnosine | Creatinine | DOPA | Dopamine | Histamine | Kynurenine | Met.SO |
|---|-----------|------|-----|-----|-----|------|-----------|-----------|-----------|------------|-------|----------|-----------|------------|--------|
| 1 | Alzheimer | 72.8 | 166 | 170 | 282 | 1.15 | 0.760 | 0.236 | 1.270 | 49.9 | 0.265 | 0.233 | 0.225 | 5.21 | 0.526 |
| 4 | Alzheimer | 94.1 | 129 | 162 | 201 | 1.10 | 0.795 | 0.199 | 0.675 | 80.1 | 0.264 | 0.234 | 0.209 | 5.80 | 0.389 |
| 5 | Alzheimer | 79.8 | 126 | 115 | 199 | 1.24 | 1.360 | 0.199 | 1.280 | 60.5 | 0.271 | 0.231 | 0.210 | 4.46 | 0.466 |
| 8 | Healthy | 83.6 | 119 | 135 | 268 | 1.18 | 0.779 | 0.215 | 0.647 | 30.6 | 0.275 | 0.244 | 0.214 | 5.66 | 0.245 |
| 9 | Healthy | 73.7 | 124 | 145 | 307 | 1.17 | 0.785 | 0.186 | 0.590 | 39.8 | 0.259 | 0.233 | 0.210 | 6.36 | 0.413 |

| | Nitro.Tyr | PEA | Putrescine | Sarcosine | Serotonin | Spermidine | Spermine | t4.OH.Pro | Taurine | SDMA | C0 | C10 | C10.1 | C10.2 | C12 |
|---|-----------|-----|------------|-----------|-----------|------------|----------|-----------|---------|------|------|-------|-------|-------|-------|
| 1 | 0.027 | NA | 0.068 | 17.8 | 0.147 | 0.188 | NA | 24.0 | 125 | 1.13 | 18.2 | 0.059 | 0.312 | 0.038 | 0.030 |
| 4 | NA | NA | 0.110 | 18.7 | 0.255 | 0.353 | NA | 23.1 | 159 | 1.34 | 23.5 | 0.071 | 0.317 | 0.040 | 0.045 |
| 5 | NA | NA | 0.118 | 22.5 | 0.390 | 0.473 | NA | 26.9 | 149 | 1.24 | 13.6 | 0.139 | 0.472 | 0.074 | 0.056 |
| 8 | 0.002 | NA | 0.161 | 23.3 | 0.215 | 0.276 | NA | 10.7 | 133 | 1.04 | 13.3 | 0.051 | 0.217 | 0.030 | 0.041 |
| 9 | NA | NA | 0.121 | 22.1 | 0.166 | 0.327 | NA | 16.0 | 215 | 1.24 | 15.8 | 0.061 | 0.258 | 0.036 | 0.037 |

| | C12.DC | C12.1 | C14 | C14.1 | C14.1.OH | C14.2 | C14.2.OH | C16 | C16.OH | C16.1 | C16.1.OH | C16.2 | C16.2.OH | C18 | C18.1 | C18.1.OH | C18.2 |
|--|--------|-------|-----|-------|----------|-------|----------|-----|--------|-------|----------|-------|----------|-----|-------|----------|-------|
|--|--------|-------|-----|-------|----------|-------|----------|-----|--------|-------|----------|-------|----------|-----|-------|----------|-------|

- e. (Optional) Drop columns which have more than 25% missing values. (Hint: when you slice your data frame, you can use `-c(..., ..., ...)` where ... represent one column name)

```
> missing_values <- colSums(is.na(df2)) / nrow(df2)
> columns2drop <- names(missing_values[missing_values > .25])
> print(columns2drop)
[1] "Nitro.Tyr" "PEA" "Spermine" "PC.aa.C32.2" "PC.aa.C38.1"
```

I couldn't get the `-c(..., ..., ...)` to work with column names. I got the list of column names, but didn't actually drop them.