Lab 4 - In class exercise - Answers

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1. Import the fastfood data set explored in class. Load the packages dplyr, ggplot2, and descriptr

2. Following the code covered in class, write a function that takes as input a vector of data (say a variable from a data frame) The function should compute the mean, standard deviation, variance, and median of such variable. The output of the function should be a data frame with 4 columns: Mean, Median, SD, and Variance.

There are two potential answers for this. Using base R and summarize from dplyr.

fastfood <- rio::import(file = "fastfood.csv", header = TRUE) %>% tibble()

Load fast food

```
# Base R
descriptive_stats <- function(data){

# Compute the Descriptive Statistics using base R functions
mean <- mean(data, na.rm = TRUE)
median <- median(data, na.rm = TRUE)
sd <- sd(data, na.rm = TRUE)
var <- var(data, na.rm = TRUE)

# Save output as data frame (tibble object)
# note: I capitalize the variable names just to avoid confusion with the objects defined inside the f
# you can assign them the same name as the objects and it works fine
table <- tibble(
    Mean = mean,</pre>
```

```
Median = median,
   SD = sd,
   VAR = var
  # Return Table
 return(table)
# test the function
descriptive_stats(
  data = fastfood$calories
## # A tibble: 1 x 4
     Mean Median
                     SD
##
     <dbl> <int> <dbl> <dbl>
## 1 531.
             490 282. 79770.
# solution 2: using summarize from dplyr
desc_table2 <- function(data){</pre>
  # the key difference here is that data is not a vector, but a data frame
  # verify the data used as input is a data frame object (tibble).
 df <- tibble(variable = data)</pre>
  # create the table with desc stats
  table <- df %>%
   summarize(
     Mean = mean(variable, na.rm = TRUE),
     Median = median(variable, na.rm = TRUE),
     SD = sd(variable, na.rm = TRUE),
     VAR = var(variable, na.rm = TRUE)
   )
 return(table)
# test the function
desc_table2(
  data = fastfood$calories
## # A tibble: 1 x 4
                   SD
##
     Mean Median
                           VAR
     <dbl> <int> <dbl> <dbl>
## 1 531.
             490 282. 79770.
```

3. Use your user written function to obtain the descriptive statistics of the variables: i) calories, ii) cholesterol, iii) protein, and iv) sugar. Use lapply and bind_rows to visualize the output in one data frame. Add a column with the variable names to identify the output of each row.

```
## [[1]]
## # A tibble: 1 x 4
     Mean Median SD
##
    <dbl> <int> <dbl> <dbl>
## 1 531. 490 282. 79770.
##
## [[2]]
## # A tibble: 1 x 4
   Mean Median SD
                        VAR
   <dbl> <int> <dbl> <dbl> <
##
## 1 72.5 60 63.2 3989.
##
## [[3]]
## # A tibble: 1 x 4
    Mean Median
                   SD
                        VAR
   <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 27.9 24.5 17.7 313.
##
## [[4]]
## # A tibble: 1 x 4
##
     Mean Median SD
                       VAR.
    <dbl> <int> <dbl> <dbl> <dbl>
## 1 7.26
          6 6.76 45.7
```

4. Use the function ds_summary_stats() from descriptr to compute the descriptive statistics of this new data frame. Compare the results with the output of your user written function.

```
descriptr::ds_summary_stats(fastfood %>% select(calories, cholesterol, protein, sugar))
## ------
##
##
Univariate Analysis
```

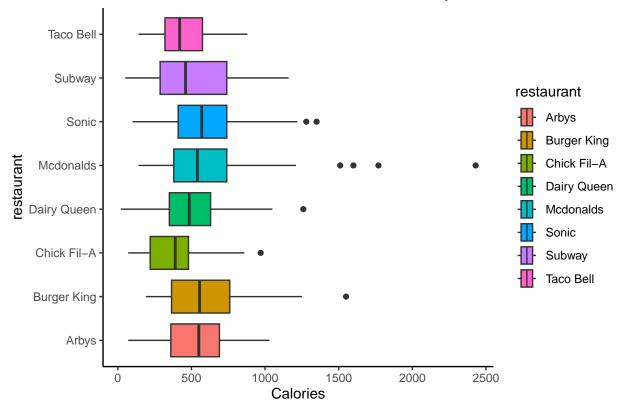
##									
##	N		515.00	Var	riance	79770.18			
##	Missing		0.00	Sto	l Deviation	282.44			
##	Mean		530.91	Ran	ıge	2410.00			
##	Median		490.00		erquartile Rang	ge 360.00			
##	Mode		350.00	Unc	corrected SS	186164000.00			
##	Trimmed Mean		512.13		rected SS	41001871.07			
##	Skewness		1.41		eff Variation	53.20			
##	Kurtosis		4.72	Sto	l Error Mean	12.45			
##									
##			Ųu	antiles	\$				
##		0			17.	-1			
## ##		Quantile			Và	alue			
##		Max			2/15	30 00			
##		99%		2430.00					
##		95%		1340.20					
##		90%	1033.00 886.00						
##		Q3		886.00 690.00					
##		Median		490.00					
##		Q1 330.00							
##		10%			2:	10.00			
##		5%		170.00					
##		1%		110.00					
##		Min			20	0.00			
##									
##			Extr	eme Val	ues				
##									
##		Low			I	High			
##	01		17- 7		O1		17 - 7		
##	Obs		Val 20		Obs		Value 2430		
## ##	303 393		50		40 45		2430 1770		
##	73		70		48		1600		
##	188		70		193		1550		
##	128		10		39		1510		
##									
##									
##									
##			Variabl	e: chol	esterol				
##									
##			Univariate	Analys	sis				
##						0000 04			
##	N		515.00	Varia		3989.24			
##	Missing		0.00		eviation	63.16			
##	Mean		72.46	Range		805.00			
## ##	Median Mode		60.00 40.00		rquartile Range	60.00 4754175.00			
##	Trimmed Mean		40.00 65.69		rected SS	2050467.77			
##	Skewness		4.42		Variation	87.17			
##	Kurtosis		38.89		Error Mean	2.78			
##			22.30	~ 0 tu L		20			
##	Quantiles								
##			•						

##	Quantile		Value			
##	M		005.00			
##	Max		805.00			
##	99%		282.20			
##	95%		175.00			
##	90%		130.00			
##	Q3		95.00			
##	Median		60.00			
## ##	Q1 10%		35.00			
##	10% 5%		20.00 10.00			
##	1%		0.00			
##	ı,₀ Min		0.00			
##	HIII		0.00			
##		Fytrom	ne Values			
##		LA CI CII	ac values			
##	Low		High			
##	20.1		0			
##	Obs	Value	o Obs	Value		
##	49	0	193	805		
##	112	0	40	475		
##	113	0	206	335		
##	279	0	39	295		
##	303	0	45	295		
##						
##						
##						
##		Varia	ble: protein			
##						
##		Univariate	Analysis			
##						
##	N	515.00	Variance 312.72			
##	Missing	1.00	Std Deviation 17.68			
##	Mean	27.89	Range 185.00			
##	Median	24.50	Interquartile Range 20.00			
##	Mode	23.00	Uncorrected SS 560272.00			
##	Trimmed Mean	26.27	Corrected SS 160425.90			
## ##	Skewness Kurtosis	2.81 16.49	Coeff Variation 63.40 Std Error Mean 0.78			
##	Kurtosis	10.49	Std Effor Mean 0.76			
##		Quant	iles			
##		quano	1105			
##	Quantile		Value			
##	4					
##	Max		186.00			
##	99%		96.61			
##	95%		56.35			
##	90%		46.70			
##	Q3		36.00			
##	Median		24.50			
##	Q1		16.00			
##	10%		12.00			
##	5%		9.00			
##	1%		6.00			

##	Min		1.0	00				
##								
##		Extreme Values						
##	-							
## ##	I	LOW	Hig	Ç n				
##	Obs	Value	e Obs		Value			
##	302	1	40		186			
##	392	3	193		134			
##	188	5	39		115			
##	233	5	70		103			
##	135	6	45		98			
##								
##								
## ##		Va	riable: sugar					
##		V d.	riabie. Sugar					
##		Univariate	Analysis					
##			J					
##	N	515.00	Variance	45.72				
##	Missing	0.00	Std Deviation	6.76				
##	Mean	7.26	Range	87.00				
##	Median	6.00	Interquartile Range					
## ##	Mode Trimmed Mean	7.00 6.63	Uncorrected SS Corrected SS					
##	Skewness	4.61	Coeff Variation					
##	Kurtosis	42.28	Std Error Mean	0.30				
##								
##		Quant	tiles					
##								
##	Quar	ntile	Value	:				
## ##	Max		87.00	,				
##	99%		33.44					
##	95%		16.00					
##	90%		14.00					
##	Q3		9.00)				
##	Media	an	6.00					
##	Q1		3.00					
##	10%		1.00 0.70					
## ##	5% 1%		0.70					
##	Min		0.00					
##			0.00					
##		Extreme	e Values					
##								
##	Lo	W	High	ı				
##	Ob ~	17-7	Ob ~		<i>V</i> = 1			
## ##	0bs 35	Value O	0bs 48		Value 87			
##	41	0	47		52			
##	42	0	230		37			
##	43	0	352		36			
##	44	0	46		35			

5. Create a box plot for the distribution of calories on the fast food items across restaturants. On the x-axis show the distribution of "calories" and on the y-axis represent the restaurant. Use appropriate labels, coloring, and other graphics best practices.

Distribution of Calories on Fast Food Items by Restaurant

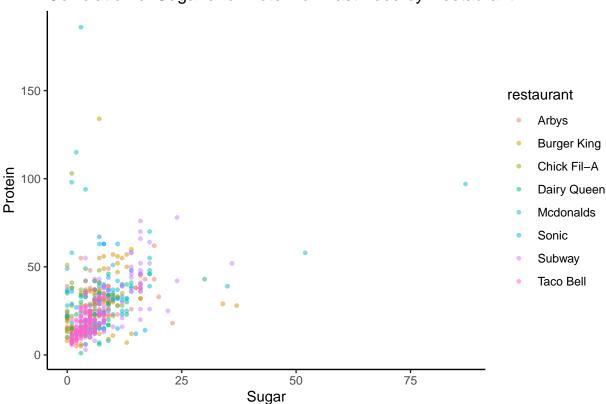


6. Create a scatter plot that shows the correlation between sugar (x-axis) and protein (y-axis) by restaurants on the same panel. Add a specific color for the observations of each restaurant. Use appropriate labels, coloring, and other graphics best practices. Save this graph in your environment. Hint: where in the aesthetic mapping should you specify that the graph will vary across restaurants?

```
theme_classic()
scatter_sugar_protein
```

Warning: Removed 1 row containing missing values or values outside the scale range
('geom_point()').

Correlation of Sugar and Protein on Fast Food by Restaurant



7. Add two lines to your previous scatterplot. A vertical line with the mean of variable sugar, and a horizontal line with the mean of variable cholesterol. Use geom_vline and geom_hline. For these functions you need to specify the xintercept and yintercept as parameters, respectively.

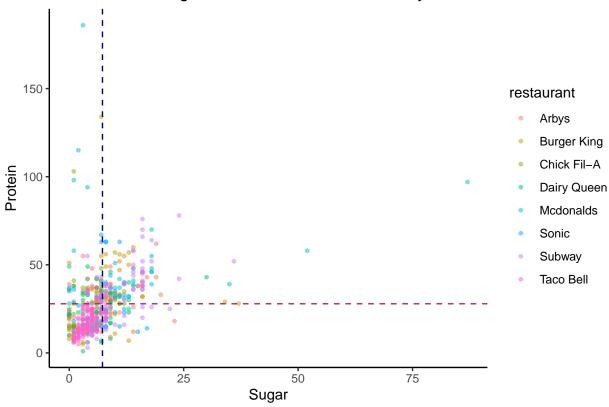
```
mean_sugar <- fastfood$sugar %>% mean(na.rm = TRUE)
mean_protein <- fastfood$protein %>% mean(na.rm = TRUE)

scatter_sugar_protein_improved <- scatter_sugar_protein +
   geom_vline(xintercept = mean_sugar, color = "navy", linetype = "dashed") +
   geom_hline(yintercept = mean_protein, color = "maroon", linetype = "dashed")

scatter_sugar_protein_improved</pre>
```

Warning: Removed 1 row containing missing values or values outside the scale range
('geom_point()').





8. Export this graph using ggsave into your folder.

```
ggsave(filename = "scatter_protein_sugar.jpg",
    plot = scatter_sugar_protein_improved)
```

```
## Saving 6.5 \times 4.5 in image
```

Warning: Removed 1 row containing missing values or values outside the scale range
('geom_point()').