GY7702 CW1

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```
library(tidyverse)
library(knitr)
```

Question 1:

Create the vector of 25 numbers between 1 and 7 listed below, using the function c. Assume those values represent the answers to a survey question, following the scale presented further below.

```
[1] NA 3 4 4 5 2 4 NA 6 3 5 4 0 5 7 5 NA 5 2 4 NA 3 3 5 NA

1 = completely disagree

2 = disagree

3 = somehow disagree

4 = neither agree nor disagree

5 = somehow agree
```

6 = agree

7 = completely agree

NA = missing value

Question 1.1: write the code necessary to check whether all participants to the survey either completely disagree or completely agree, once the missing values are excluded.

```
#First make the vector containing all the answers to the question
survey_answer <- c(NA, 3, 4, 4, 5, 2, 4, NA, 6, 3, 5, 4, 0, 5, 7, 5, NA, 5, 2, 4, NA, 3, 3, 5, NA)

#Before doing anything you must remove NA values from the vector
survey_answer = survey_answer[
   !is.na(survey_answer)]
```

```
#1 = completely disagree so this asks the vector if all values are equal to 1.
print(paste(
   "Do all participants completely disagree?", all(survey_answer == 1)
   ))

## [1] "Do all participants completely disagree? FALSE"

#7 = completely agree, same as above.
print(paste(
   "Do all participants completely agree?", all(survey_answer == 7)
   ))
```

[1] "Do all participants completely agree? FALSE"

Question 1.2: write the code necessary to extract the indexes related to the participants in the survey who at least somehow agree or more.

```
#the which function used to extract 5, 6 and 7 (in the vector c) out of the survey_answer vetor
which(survey_answer %in% c(5,6,7))
## [1] 4 7 9 12 13 14 15 20
```

Question 2:

1 Gentoo Biscoe
2 Gentoo Biscoe

Question 2.1: Install the library palmerpenguins.

```
#install.packages("palmerpenguins")
pengtable <- palmerpenguins::penguins #create a variable for the table of data to be called from
#View(pengtable)

library(palmerpenguins) #install palmer penguins library
library(dplyr) #install dplyr library
library(tidyverse) #install tidyverse library</pre>
```

Question 2.2: write the code necessary to create a table showing species, island, bill length and body mass of the 10 Gentoo penguins in the penguins table with the highest body mass.

```
pengtable %>%
  na.omit(pengtable) %>% #remove na values
  dplyr::select(species, island, bill_length_mm, body_mass_g) %>% #select the variables required out of
  dplyr::filter(species == "Gentoo") %>% #filter so only work with the species "Gentoo"
  dplyr::slice_max(body_mass_g, n = 10) #display the top 10 values for body mass
## # A tibble: 11 x 4
## species island bill_length_mm body_mass_g
## <fct> <fct> <dbl> <int>
```

6300

6050

49.2

59.6

```
## 3 Gentoo Biscoe
                              51.1
                                          6000
                              48.8
                                         6000
## 4 Gentoo Biscoe
## 5 Gentoo Biscoe
                              45.2
                                         5950
                              49.8
## 6 Gentoo Biscoe
                                         5950
   7 Gentoo Biscoe
                              48.4
                                         5850
## 8 Gentoo Biscoe
                              49.3
                                         5850
## 9 Gentoo Biscoe
                              55.1
                                         5850
## 10 Gentoo Biscoe
                              49.5
                                         5800
## 11 Gentoo Biscoe
                              48.6
                                          5800
```

Question 2.3: write the code necessary to create a table showing the average bill length per island, ordered by average bill length.

```
pengtable %>%
  na.omit(pengtable) %>% #remove na values
  dplyr::select(bill_length_mm, island) %>% #select the variables required out of pengtable
  dplyr::group_by(island) %>% #group the coloumns by island
  dplyr::summarise(
    avg_bill_length_mm = mean(bill_length_mm), .groups = 'keep' #create a new column and calculate ave
    ) %>% #.groups = 'keep' keeps the same grouping after the summarise and stops any friendly errors i
  dplyr::arrange(avg_bill_length_mm) #arrange in accending avg_bill_length_mm
## # A tibble: 3 x 2
## # Groups: island [3]
##
    island
              avg_bill_length_mm
     <fct>
                            <dbl>
## 1 Torgersen
                             39.0
## 2 Dream
                             44.2
## 3 Biscoe
                             45.2
```

Question 2.4: write the code necessary to create a table showing the minimum, median and maximum proportion between bill length and bill depth by species.

```
pengtable %>%
   na.omit(pengtable) %>% #remove na values
   dplyr::select(bill_length_mm, bill_depth_mm, species) %>% #select the variables required out of pen
    dplyr::group_by(species) %>% #group columns by species
    dplyr::mutate(
     min_proportion = min(bill_length_mm) / min(bill_depth_mm) #create new column for minimum proporti
    ) %>%
   dplyr::mutate(
     med_proportion = median(bill_length_mm) / median(bill_depth_mm) #create new column for median pro
   ) %>%
   dplyr::mutate(
     max_proportion = max(bill_length_mm) / max(bill_depth_mm) #create new column for maximum proporti
    ) %>%
   dplyr::summarise(
     min_proportion, med_proportion, max_proportion, .groups = 'keep' #remove bill length and depth fr
   ) %>% #.groups = 'keep' keeps the same grouping after the summarise and stops any friendly errors i
    dplyr::slice_head(n = 1) # remove rows with repeated data, only 1 row per species
```

```
## # A tibble: 3 x 4
## # Groups: species [3]
    species min_proportion med_proportion max_proportion
    <fct>
##
                      <dbl>
                                     <dbl>
## 1 Adelie
                        2.07
                                      2.11
                                                     2.14
## 2 Chinstrap
                        2.49
                                      2.69
                                                     2.79
## 3 Gentoo
                        3.12
                                      3.16
                                                     3.45
```

Question 3

Question 3.1:write the code necessary to load the data from covid19_cases_20200301_202010 to a variable named covid_data.

the code line below doesn't work in rserver.

I uploaded the file using the upload button in the files tab.

read_csv("C:Users/mirif/OneDrive/Desktop/MASTERS/R/covid19_cases_20200301_20201017.csv")

```
library(readr) # load readr library
covid_data <- read_csv("covid19_cases_20200301_20201017.csv") #Using this code i can import the uploade
#View(covid_data) #view(data) has been commented out as errors occur when trying to knit</pre>
```