

DA5020 – Assignment 2

This and all subsequent assignments must be done using R Markdown Notebooks. Be sure to properly "chunk" your code and add comments to each chunk. Make it clear which question you are answering, and each chunk of code should accomplish a small well-defined task.

Using the built-in dataset **msleep**, answer the following questions and demonstrate the use of dplyr verbs and pipes. Use the help function to learn more about the dataset e.g. `?msleep`

Question 1 — (+5 bonus points)

Load the **msleep** dataset and inspect the dimensions and properties of the data e.g. what type of observations are recorded in the dataset, are any missing, etc. Summarize your findings/understanding about the dataset based on what you have observed.

Question 2 — (5 points)

Create a bar chart showing the **conservation** status of the mammals in this dataset. Comment on the results.

Question 3 — (10 points)

Filter the data to extract carnivores and herbivore. Hint: `vore == 'herbi'` and `vore == 'carni'`. Calculate the mean **sleep_rem** for each group (i.e. you are calculating the mean REM sleep for Carnivores and Herbivores). Explain your findings. Hint: you may need to filter NA when calculating the mean.

Question 4 — (10 points)

Create a scatterplot showing the relationship between **bodywt** and **brainwt**. Comment on any correlation that is visually apparent. Tip: if you rescale the x and y axis using a logarithmic scale, it may help you to interpret the visualization better e.g. you can append the following to `ggplot()`: `scale_x_log10()` and `scale_y_log10()`.

Question 5 — (10 points)

Calculate the Pearson coefficient of correlation in R, to evaluate the strength of the correlation between **bodywt** and **brainwt**. Did the results support your original assumptions from question 4?

Question 6 — (15 points)

Determine which mammals are outliers in terms of **sleep_total**. Outliers, for the sake of this question, are defined as values that are more than 1.5 standard deviations from the mean. Display the **name** and **sleep_total** of the mammals which are outliers.

Submission Details

- **Your submission must contain two files: the .Rmd file and a knitted PDF or HTML (from the .rmd).** Name your .Rmd file, `DA5020.A2.FirstName.LastName.Rmd` and your PDF/HTML `DA5020.A2.FirstName.LastName.{pdf,html}`, where *FirstName.LastName* is your first and last name.

- The .Rmd file must be fully commented and properly "chunked" R code and detailed explanations. Make sure that it is easy to recognize which question you answer and that your code runs from beginning to end (because that is how we will test it.) Code that doesn't execute, stops, throws errors will receive no points. If the TAs have to "debug" your code or spend any effort getting it to run, substantial points will be deducted.
- Not submitting a knitted PDF or HTML will result in reduction of 30 points.
- Not submitting the .Rmd file (or both) will result in a score of 0.

**** Note: Do not merely print the output for each question but always explain the results from your code. Points will be deducted for any missing explanation and any visualizations that are not clearly labeled.**