Lab 2 — Mammal Sleep Behavior

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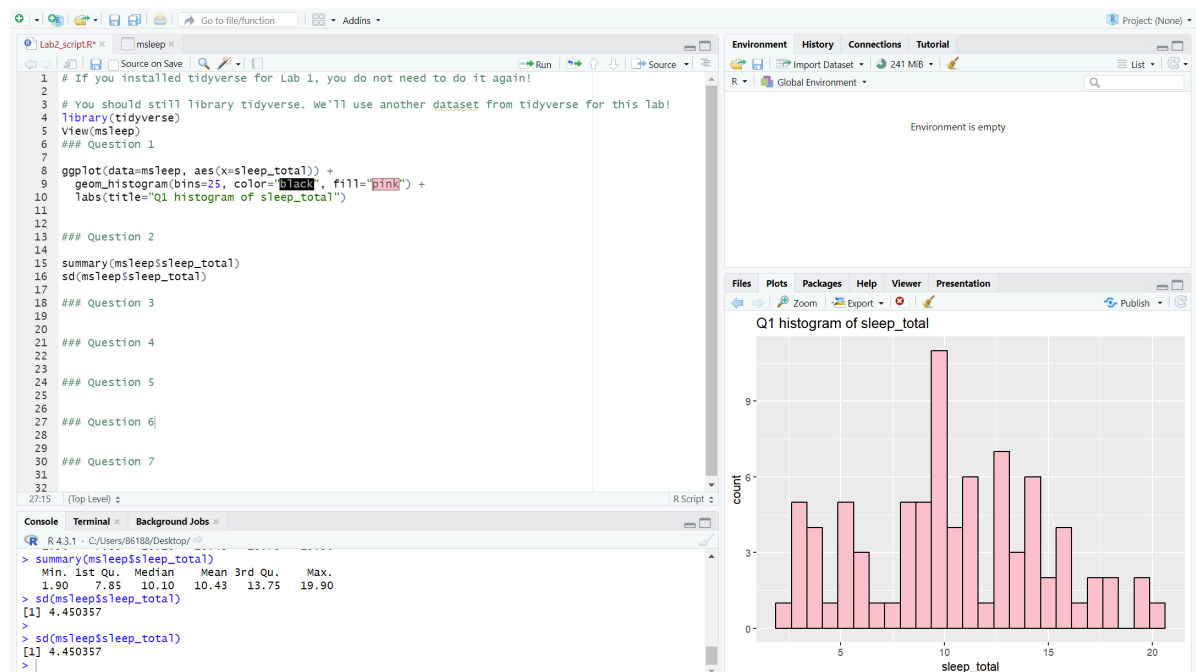
Q1.
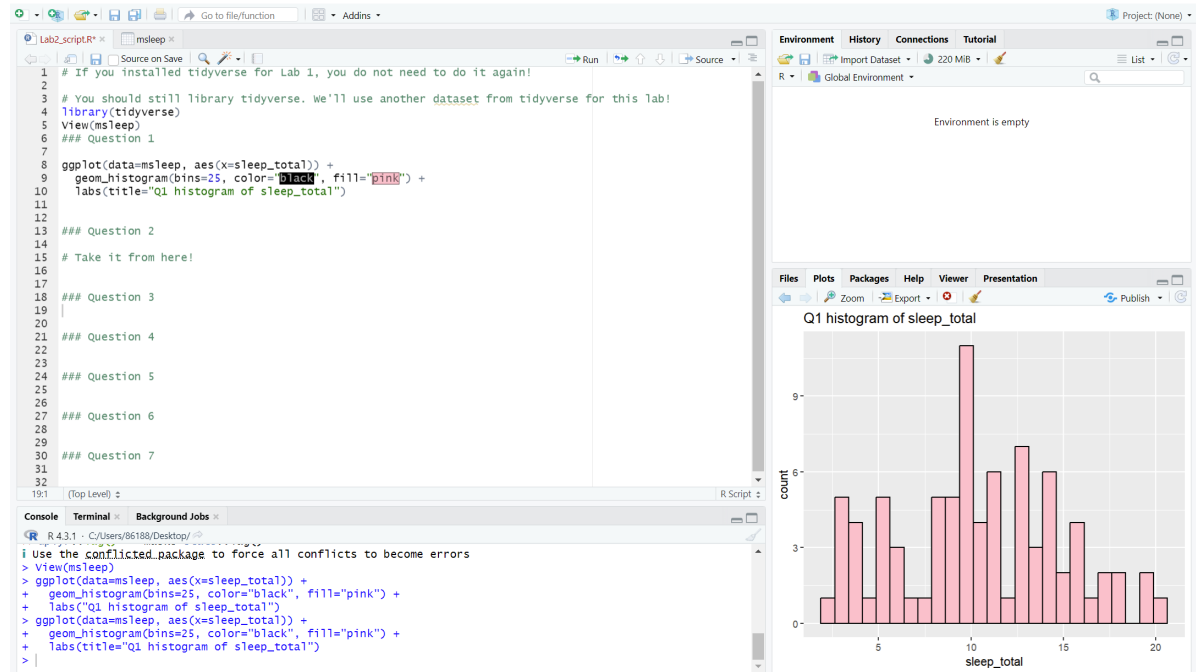
Q2.

min	Q1	Q2	mean	Q3	max
1.90	7.85	10.10	10.43	13.75	19.90

standard_deviation: 4.450357

Q3.

1. The typical amount (median) of sleep for a mammal species is 10.10

2. The lowest amount of sleep is 1.9, the highest is 19.9

```
16  sd(msleep$sleep_total)
17
18  ### Question 3
19
20  max(msleep$sleep_total)
21  min(msleep$sleep_total)
22
23  ### Question 4
24
25:1    (Top Level) ÷
```

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```
    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    1.90    7.85   10.10   10.43   13.75   19.90
>
> summary(msleep$sleep_total)
    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    1.90    7.85   10.10   10.43   13.75   19.90
> summary(msleep$sleep_total)
    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    1.90    7.85   10.10   10.43   13.75   19.90
> sd(msleep$sleep_total)
[1] 4.450357
>
> sd(msleep$sleep_total)
[1] 4.450357
> max(msleep$sleep_total)
[1] 19.9
> min(msleep$sleep_total)
[1] 1.9
```
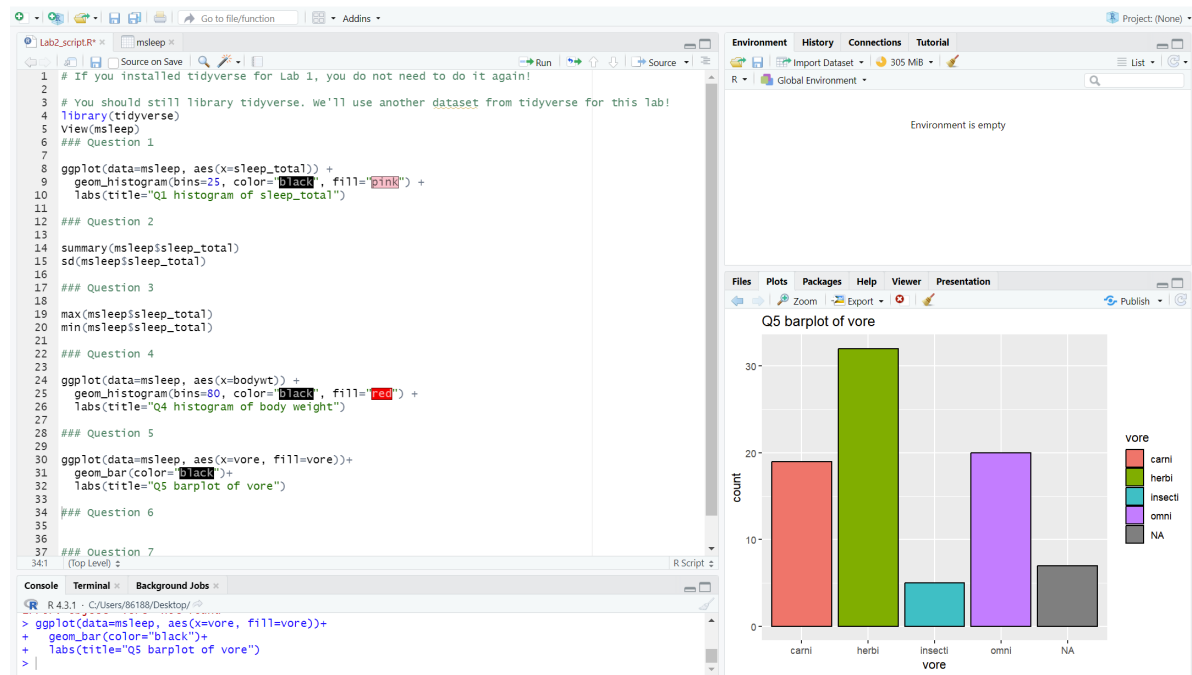
3. The average deviation from the mean (standard deviation) is 4.450357

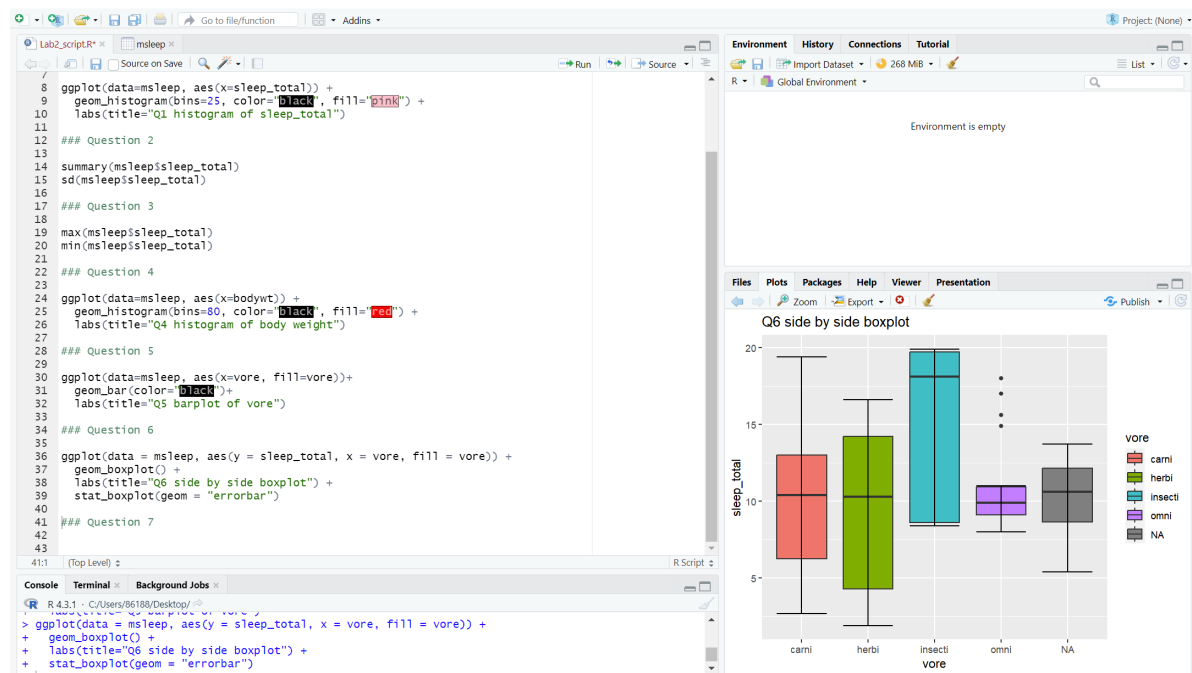4. The range of middle 50% is 7.85~13.75

Q4.
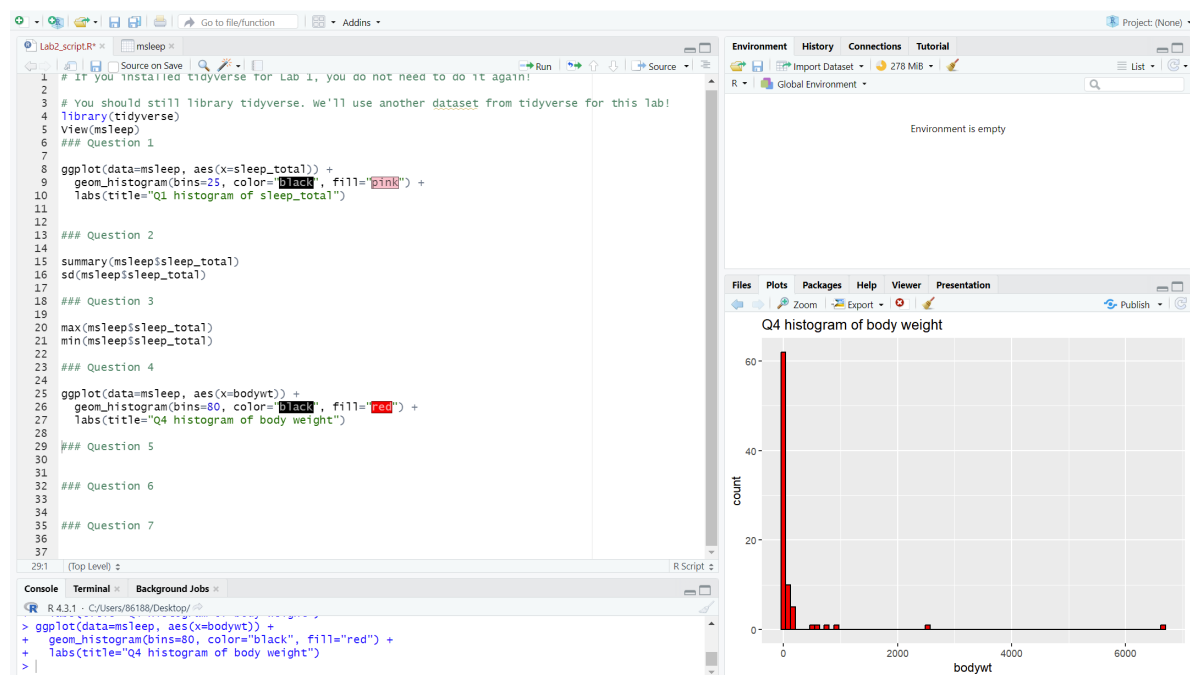
This distribution seems to be highly right skewed, while the distribution of sleep_total is a little skewed. And the size of data from "bodywt" varies greatly from one to another, yet "sleep_total" is more centralized.

Q5.

The "herbi" appears the most.

Q6.

Q7.

1. The "insecti" appears to get the most sleep.
2. In different "vore" types, the "sleep_total" varies a lot. For example, in "omni" and "NA", the sleep hour does not vary a lot, but in the other three vore types, the distribution covers a wide range (the min and max are very different, a relatively large proportion has low total sleep), so I think high total sleep is not a consistent feature of all animals.
3. (I'm sorry I made this so long)I think "vore" is a helpful way to explain variability in total sleep across mammals. Because if I only look at the msleep dataset, I can see many columns (genus, vore, order, conservation...) If I click the column header, the column will be grouped(sorted). I think grouping the "vore" has three advantages: (1) limited total group

numbers (only five vore type) , (2) each group has enough data (for example in "conservation" column, there are only 2 "cd" type, which is a very small number). (3) in the side by side boxplot, each type of "vore" does have its own characteristics. Therefore, "vore" classification can be helpful in the msleep dataset. But in some vore types, like "carni", it's hard to determine exactly how long "carni" sleep(compared to "omni") because sleep_total of "carni" varies from "less than 5" to "close to 20". So maybe use some other classification will be a little better? (but I don't think a boxplot should be used just to determine a specific value and "vore" classification is good).