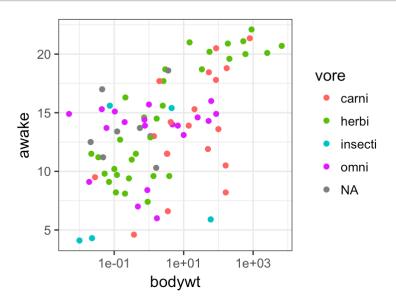
Lab Worksheet 2

We will be working with the msleep data set that is provided with ggplot2. The data set contains information about the sleep habits of 83 mammals. Enter ?msleep on the R command line to learn more about the dataset.

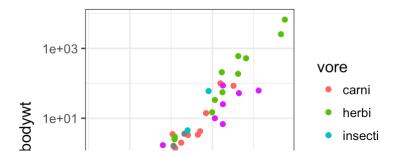
Problem 1: Make the following plots: (i) a plot of total time awake vs. body weight, colored by "vore" (carnivore, herbivore, etc.); (ii) a plot of body weight vs. brain weight, colored by "vore". When you plot body weight and/or brain weight, consider whether a linear scale or a logarithmic scale seems more appropriate, and explain your reasoning in 1-2 sentences. **HINT:** Use the functions scale_x_log10() and scale_y_log10() to change the scales.

 $\label{eq:ggplot} $$\gcd(x=bodywt, y=awake, color=vore)) + geom_point() + scale_x_log_{10}()$

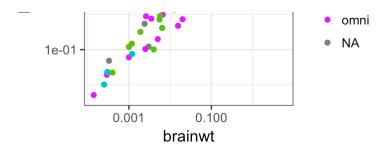


 $\label{eq:color_vore} $$ ggplot(msleep, aes(x=brainwt, y=bodywt, color=vore)) + geom_point() + scale_x_log10() + scale_y_log10() \\$

Warning: Removed 27 rows containing missing values (geom point).



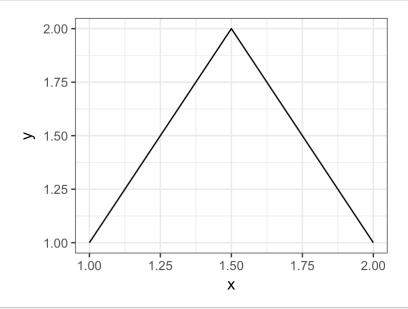
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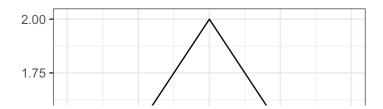
Log scales are more appropriate for both body weight and brain weight because there are a few species that have much larger values than most other species. If we were to use a linear scale, these outlying species would require axis ranges that are too wide to resolve any details for the majority of the species.

Problem 2: Explain the difference between <code>geom_line()</code> and <code>geom_path()</code>. Make up a simple data set (5-10 data points), plot it twice, once using <code>geom_line()</code> and once using <code>geom_path()</code>, and explain why each plot looks the way it does.

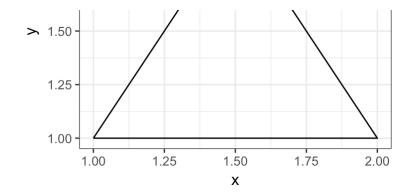
 $geom_line()$ connects data points in the order from smallest to largest x value. $geom_path()$, by contrast, connects data points in the order in which they appear in the data frame. The following data set produces an open triangle with $geom_line()$ and a closed triangle with $geom_path()$.







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