Pretty plots with ggplot2

Though this is technically a course on high-performance computing. I would be doing newcomers a disservice if we did not at least quickly cover how plotting works in R. We'll also be profiling some `ggplot2` code in the next section as an example.

`ggplot2` is a plotting framework that is (relatively) easy to use, powerful, AND it looks good.

```
library(ggplot2)

# Load the example data
data <- msleep
str(data)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    83 obs. of  11 variables:
##  $ name        : chr  "Cheetah" "Owl monkey" "Mountain beaver" "Greater short-tailed shrew" ...
##  $ genus       : chr  "Acinonyx" "Aotus" "Aplodontia" "Blarina" ...
##  $ vore        : chr  "carni" "omni" "herbi" "omni" ...
##  $ order       : chr  "Carnivora" "Primates" "Rodentia" "Soricomorpha" ...
##  $ conservation: chr  "lc" NA "nt" "lc" ...
##  $ sleep_total : num  12.1 17 14.4 14.9 4 14.4 8.7 7 10.1 3 ...
##  $ sleep_rem   : num  NA 1.8 2.4 2.3 0.7 2.2 1.4 NA 2.9 NA ...
##  $ sleep_cycle : num  NA NA NA 0.133 0.667 ...
##  $ awake       : num  11.9 7 9.6 9.1 20 9.6 15.3 17 13.9 21 ...
##  $ brainwt     : num  NA 0.0155 NA 0.00029 0.423 NA NA NA 0.07 0.0982 ...
##  $ bodywt      : num  50 0.48 1.35 0.019 600 ...
```

It's sleep data of some kind. Anyhow, let's start. `ggplot2` revolves around a certain kind of variable: the ggplot2 object. What is a ggplot2 object? Basically it is your data + information on how to interpret it + the actual geometry it uses to plot it.

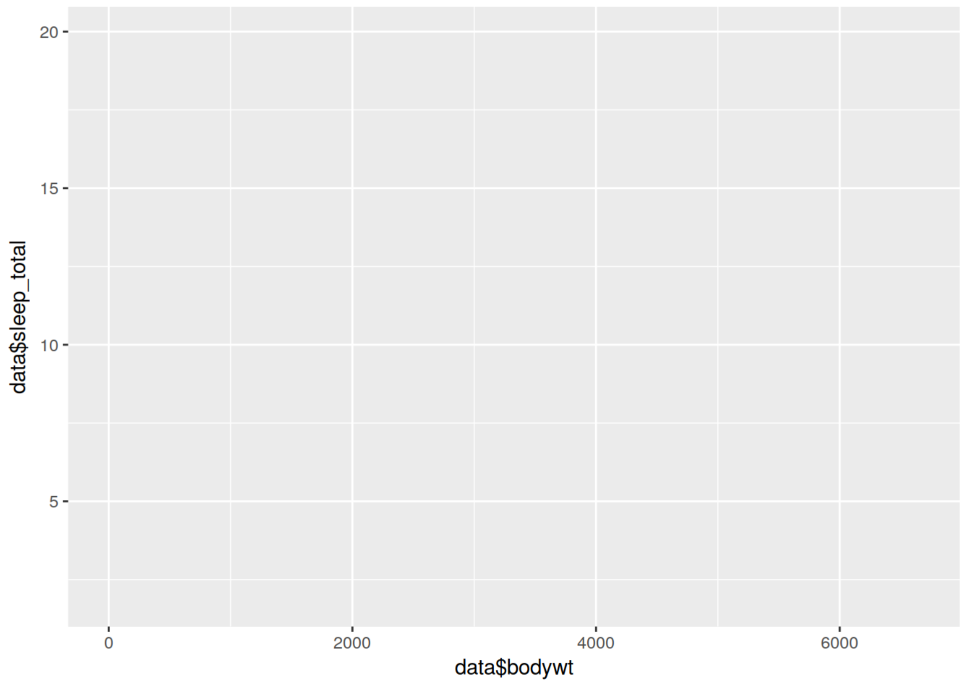
How to create ggplot2 objects:

You can add as much data in the inital function call as you want. All of these work, but the final version is the only "complete" object that fully specifies the data used for the plot.

```
ref <- ggplot()
ref <- ggplot(data)
ref <- ggplot(data, aes(x = bodywt, y = sleep_total))
# This is the same thing as the line above:
ref <- ggplot(data, aes(x = data$bodywt, y = data$sleep_total))
```

To store an object (to add to it later/plot it on demand), just give it a reference. Simply typing the reference will display the plot (if you've provided enough information to make it.)

```
ref
```



As you can see, we haven't specified everything we need yet. There are 3 components to making a plot with a ggplot object: your data, the aesthetic mappings of your data, and the geometry. If you are missing one, you won't get a functional plot.

Your data should be a dataframe with everything you want to plot. Note that it is possible to put data from multiple sources (ie. different dataframes) in the same plot, but it's easier if everything is in the same 2-dimensional dataframe.

```
ref <- ggplot(data)
```

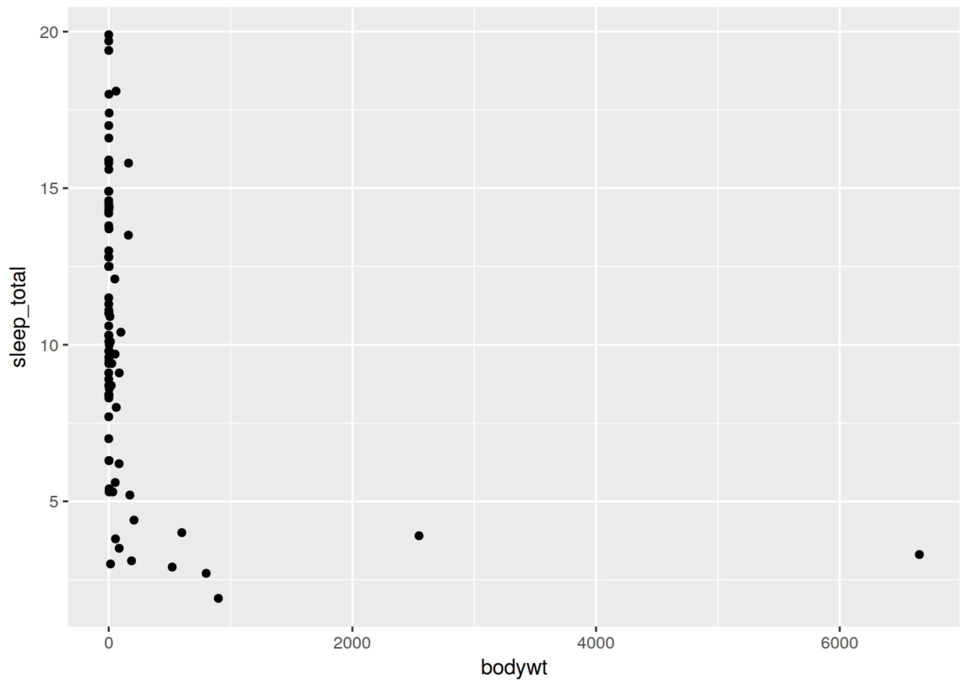
The aesthetic mappings tell ggplot2 how to interpret your data. Which values in your dataframe are the y-values, x-values, what should be used for colors, etc.

```
ref <- ggplot(data, aes(x = bodywt, y = sleep_total))
```

The geometry is the actual stuff that goes on the plot. You can specify any geometry as long as you have supplied the values it needs. If you've specified the required aesthetic mappings (which data corresponds to x, y, etc.), all you need to do is tell ggplot2 to create a certain geometry- for instance a scatterplot.

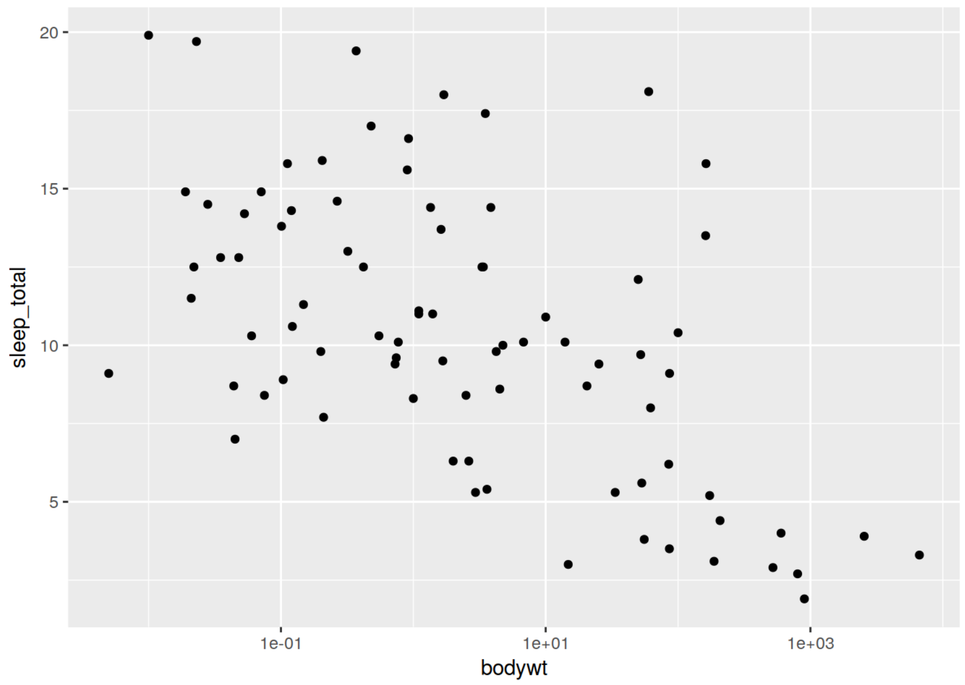
Just add the geometry you want to your object. In this case, we are making a scatterplot.

```
ref <- ggplot(data, aes(x = bodywt, y = sleep_total)) + geom_point()
ref
```



All you need to do to add more information to your plot/change things is add on more elements. Lets add a logarithmic scale on the x axis.

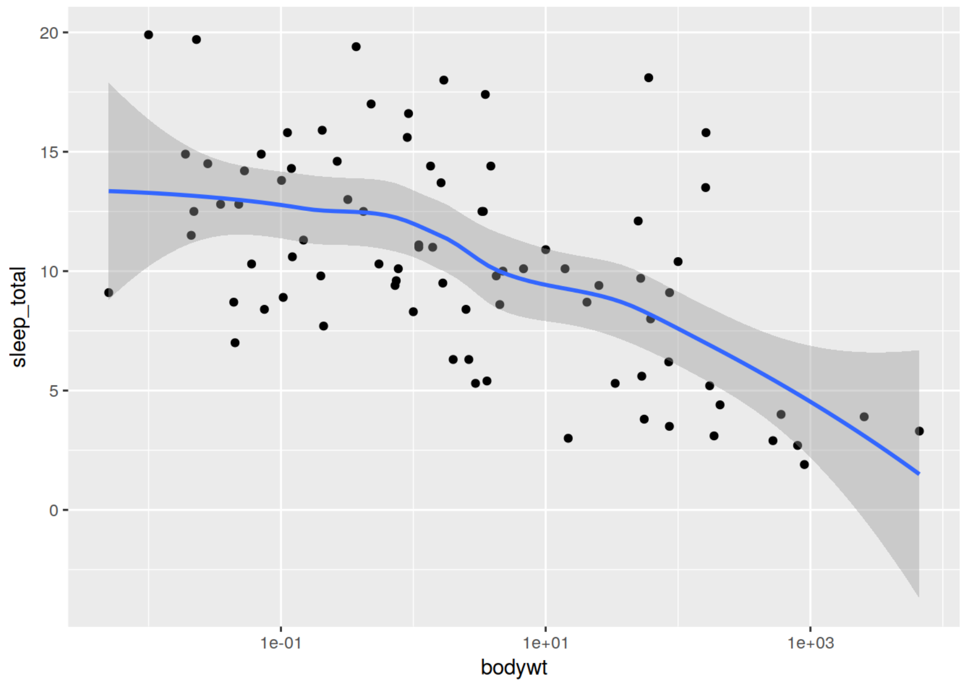
```
ref <- ggplot(data, aes(x = bodywt, y = sleep_total)) + geom_point() + scale_x_log10()
ref
```



Lets add a smoothed mean.

```
ref + geom_smooth()
```

```
## `geom_smooth()` using method = 'loess'
```



You can also specify aesthetics inside the call to create geomtery.

```
ggplot(data) + geom_point(aes(x = bodywt, y = sleep_total)) + scale_x_log10() + geom_smooth()
```

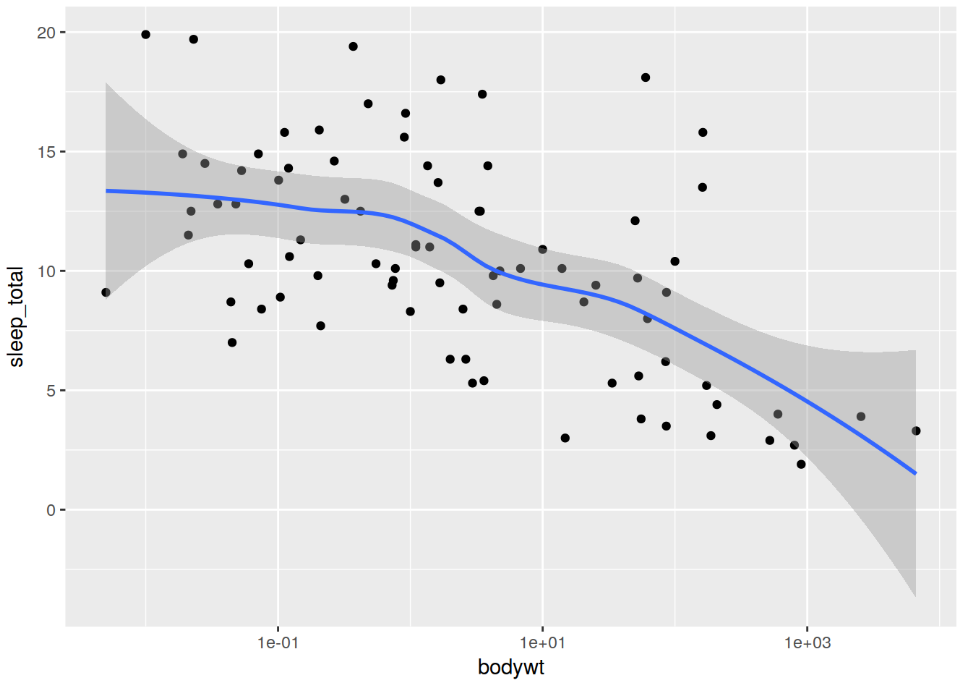
```
Error: stat_smooth requires the following missing aesthetics: x, y
```

Why didn't that work? This is because when we specfy aesthetics inside a call to geomtery it only applies for that layer (only geom_point got the x and y values). The only information that gets passed to all geometery calls is aethetics specified in the initial creation of the ggplot object.

So if we wanted that to work, we'd have to do this:

```
ggplot(data) + scale_x_log10() +
  geom_point(aes(x = bodywt, y = sleep_total)) +
  geom_smooth(aes(x = bodywt, y = sleep_total))
```

```
## `geom_smooth()` using method = 'loess'
```

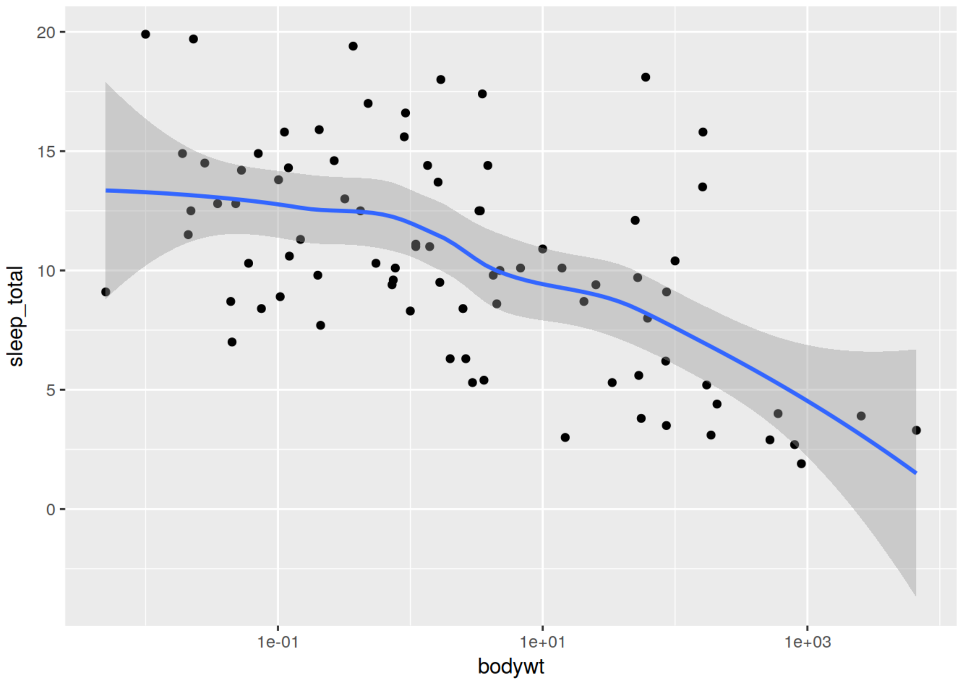


It’s important to note that geometry will automatically use any aesthetic mappings that it understands, and ignore ones it doesn’t. So if you specify as much stuff as you can in the inital call that can be used, it’ll save you work.

Like this:

```
ggplot(data, aes(x = bodywt, y = sleep_total)) + scale_x_log10() + geom_point() + geom_smooth()
```

```
## `geom_smooth()` using method = 'loess'
```



Exercise - Creating a plot of our own:

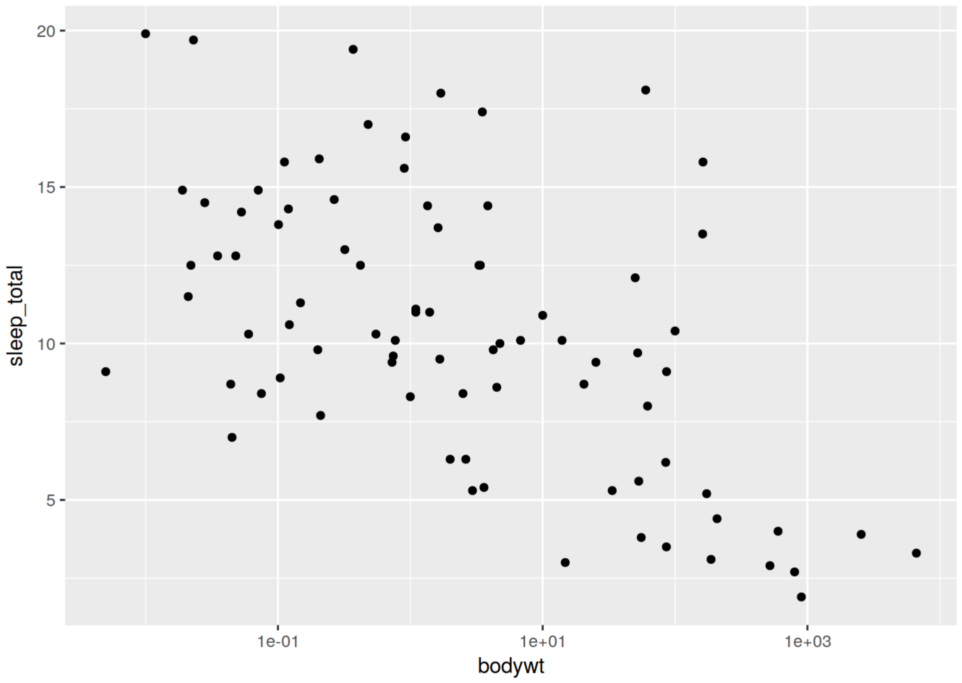
Make a scatterplot of conservation status vs. time spent awake

Hint: conservation status is `data$conservation` and time awake is `data$awake`. To make a scatterplot, use `geom_point()`.

Let’s follow up with a few very common plot/geometry types and mappings you might be interested in:

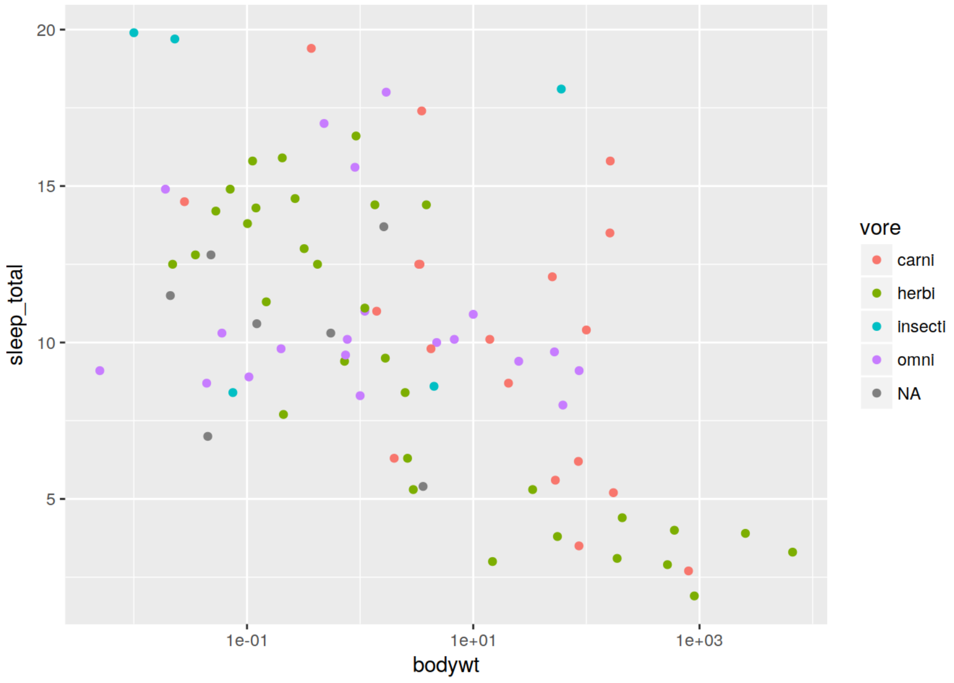
These x and y mappings (and the log scale on the x axis will be used for all later plots).

```
plot <- ggplot(data, aes(x = bodywt, y = sleep_total)) + scale_x_log10()
plot + geom_point()
```



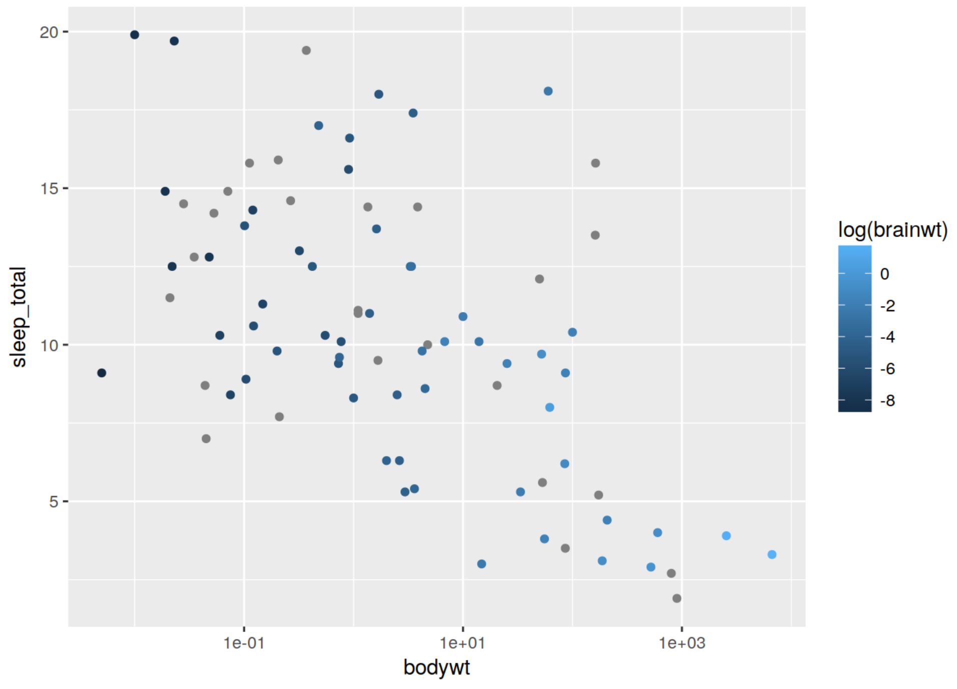
First lets add color based on what things eat. Note that it automatically adds a legend.

```
plot + geom_point(aes(color = vore))
```



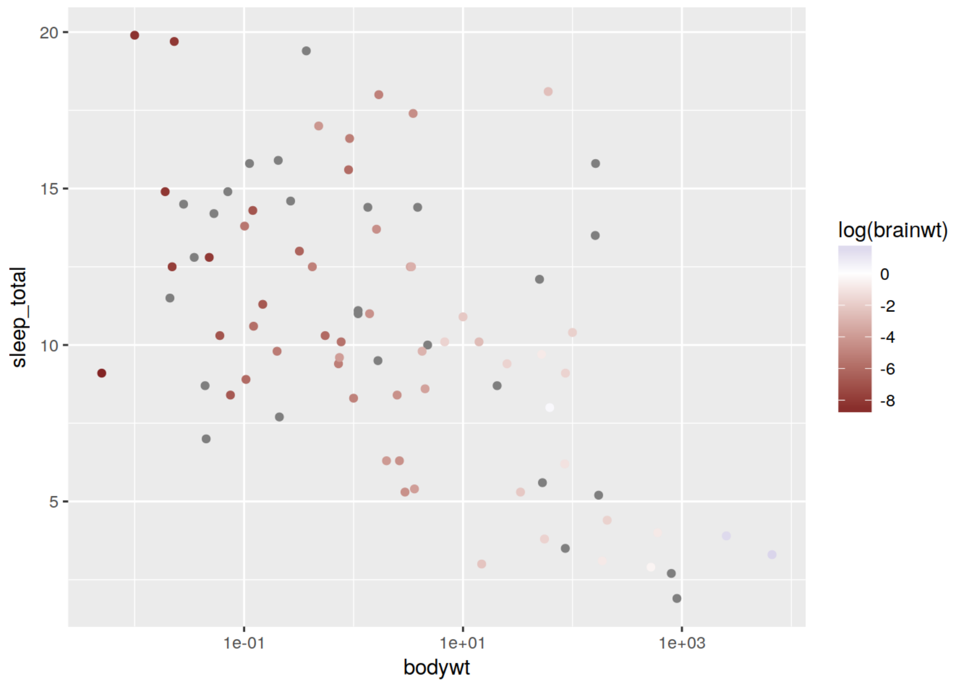
We used a factor there, but we can also use a continuous variable for color as well.

```
plot + geom_point(aes(color = log(brainwt)))
```



We can change the legend to change the colors in this case.

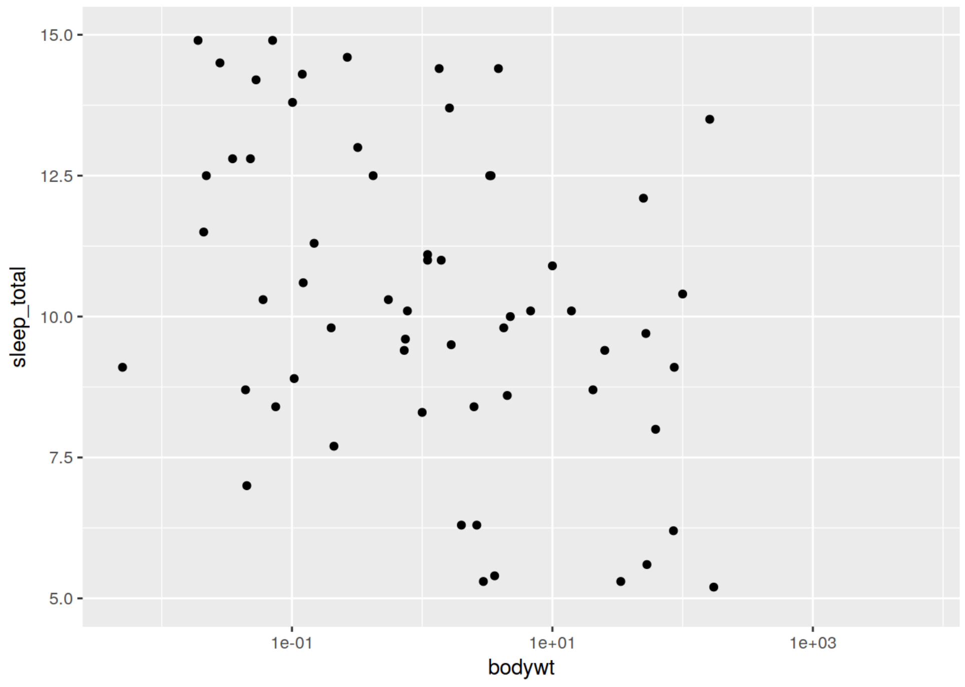
```
plot + geom_point(aes(color = log(brainwt))) + scale_color_gradient2()
```



Set the limits of a scale

```
plot + geom_point() + scale_y_continuous(limits = c(5, 15))
```

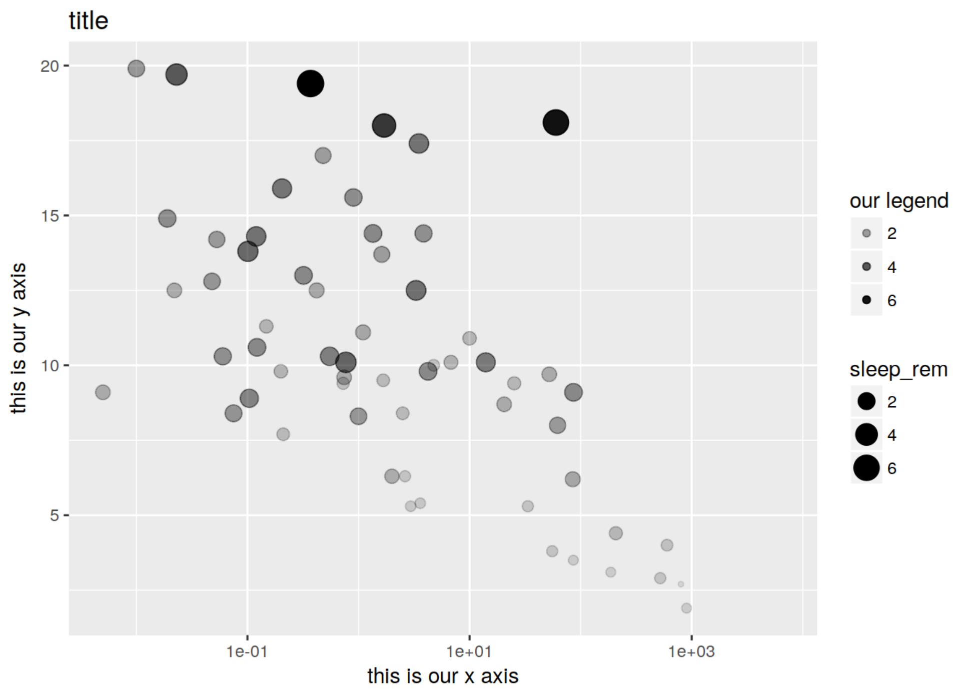
```
## Warning: Removed 23 rows containing missing values (geom_point).
```



Changing size and alpha works the same way:

```
plot + geom_point(aes(size = sleep_rem, alpha = sleep_rem)) +
  xlab("this is our x axis") + ylab("this is our y axis") + ggtitle("title") + scale_alpha("our legend")
```

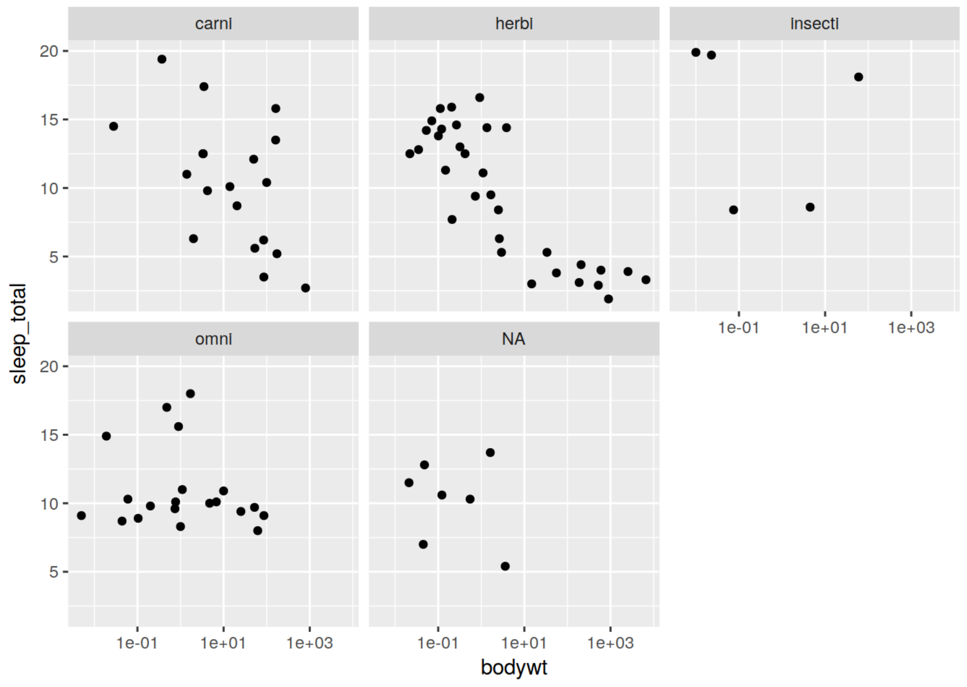
```
## Warning: Removed 22 rows containing missing values (geom_point).
```



If we want to simply change a plot value like marker shape or size without mapping it to data, just specify it outside the call to aesthetics. plot + geom_point(aes(shape = vore), size = 6, color = “orange”)

Let’s facet our data by a factor:

```
plot + geom_point() + facet_wrap(~vore)
```



Exercise - Another plot example:

How would I make a scatterplot of conservation status (`data$conservation`) vs time awake (`data$awake`), with the color mapped to vore (`data$vore`) and the ize mapped to the log of brain weight (`log(data$brainwt)`). Bonus points if you add axis labels and a title.

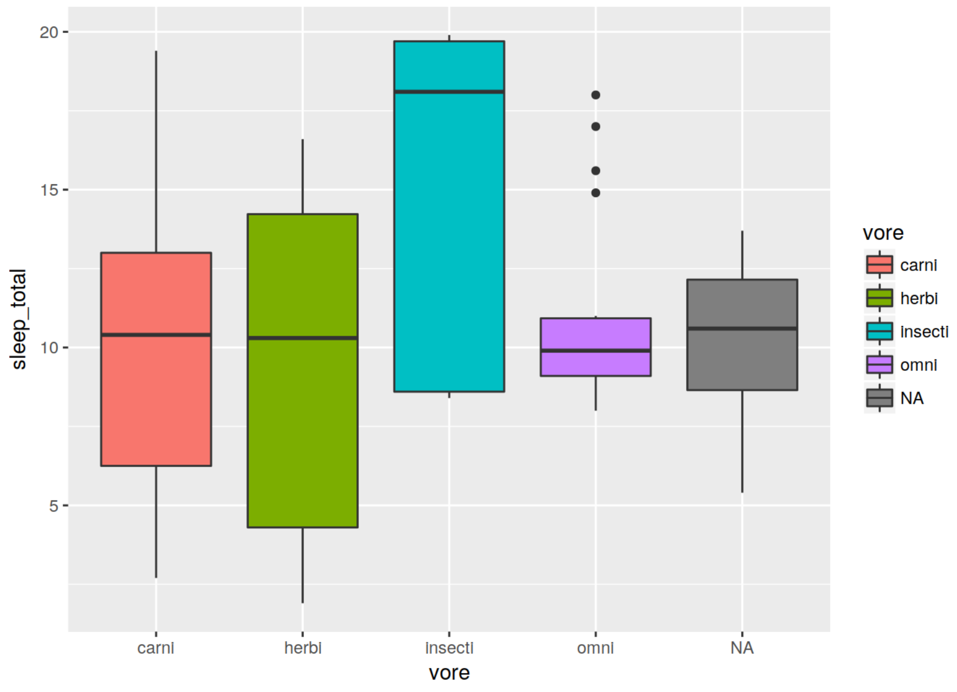
Other types of plots

All other types of plots work identically to the scatterplot - let's see a few examples…

Boxplot

Note that stats are automatically performed.

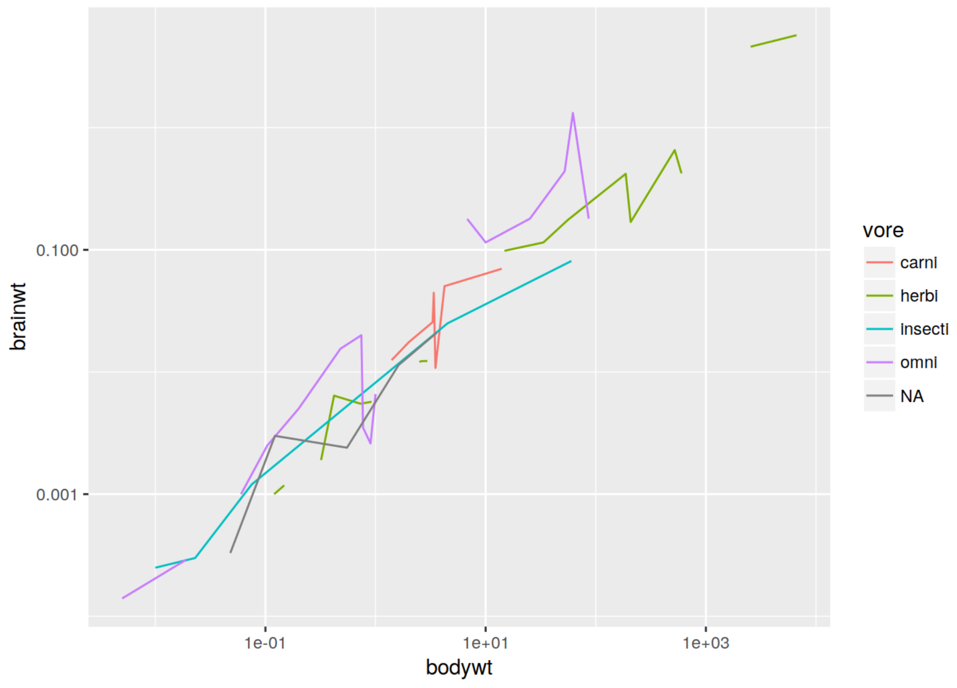
```
ggplot(data, aes(x = vore, y = sleep_total, fill = vore)) + geom_boxplot()
```



Line plot with different groups

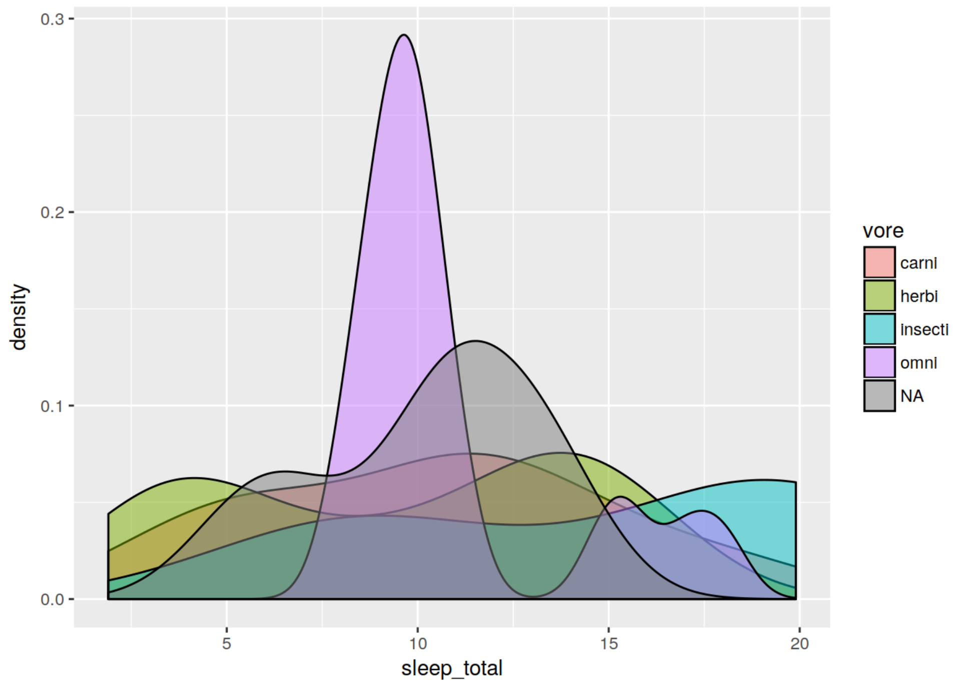
```
ggplot(data, aes(x = bodywt, y = brainwt, group = vore, color = vore)) +
  geom_line() + scale_x_log10() + scale_y_log10()
```

```
## Warning: Removed 8 rows containing missing values (geom_path).
```



1D density

```
ggplot(data, aes(x = sleep_total, fill = vore)) + geom_density(alpha = 0.5)
```

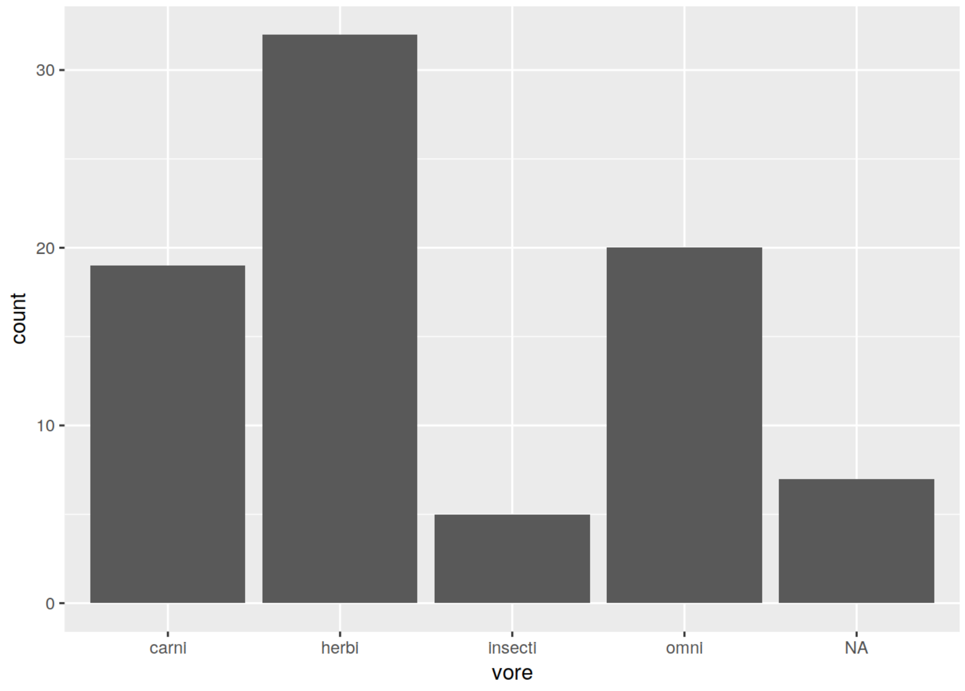


Violin plot

ggplot(data, aes(x = vore, y = sleep_total)) + geom_violin()

Bar plot

```
ggplot(data, aes(x = vore)) + geom_bar()
```



Note that it automatically is binning the number of values in “vore”. To get a bar plot to simply plot the values you feed it, use `geom_bar(stat = "identity")`.

Exercise - making other types of plots:

Make a box plot of the amount of sleep (`data$sleep_total`) per conservation status (`data$conservation`). Fill in the box plot colors by conservation status (`data$conservation`).

Hint: you will need the following aesthetics: x, y, and fill. The geometry you want to use is `geom_boxplot()`

Next section