4: Exploring `geom` Functions

Ellen Bledsoe

2026-02-19

Plotting in `ggplot2`

Data Visualization Types and When to Use Them

Let's practice making different kinds of plots with various `geom` functions to see how they work.

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.2
## v ggplot2   4.0.0     v tibble    3.3.0
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.1.0
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
fish <- read_csv("../data/fish_sick_data.csv")
```

```
## Rows: 50 Columns: 7
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (1): species
## dbl (6): tank_id, avg_daily_temp, num_fish, day_length, tank_volume, num_sick
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Plotting in `ggplot2`

First, let's remind ourselves of the general structure of how we make plots using the `ggplot2` syntax.

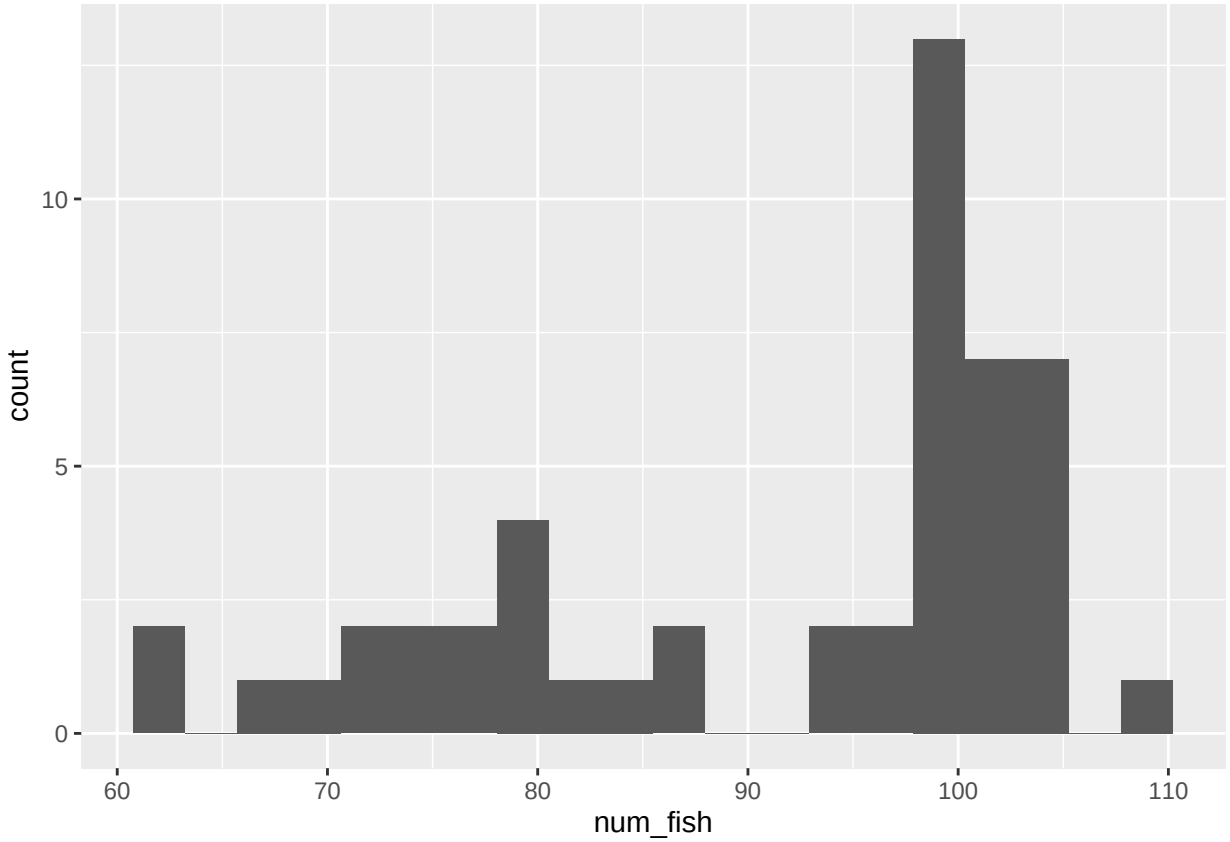
```
# ggplot(data = <DATA>, mapping = aes(x = <COLUMN1>, y = <COLUMN2)) +
  # geom_function() +
  # labs() +
  # theme()
```

Histograms

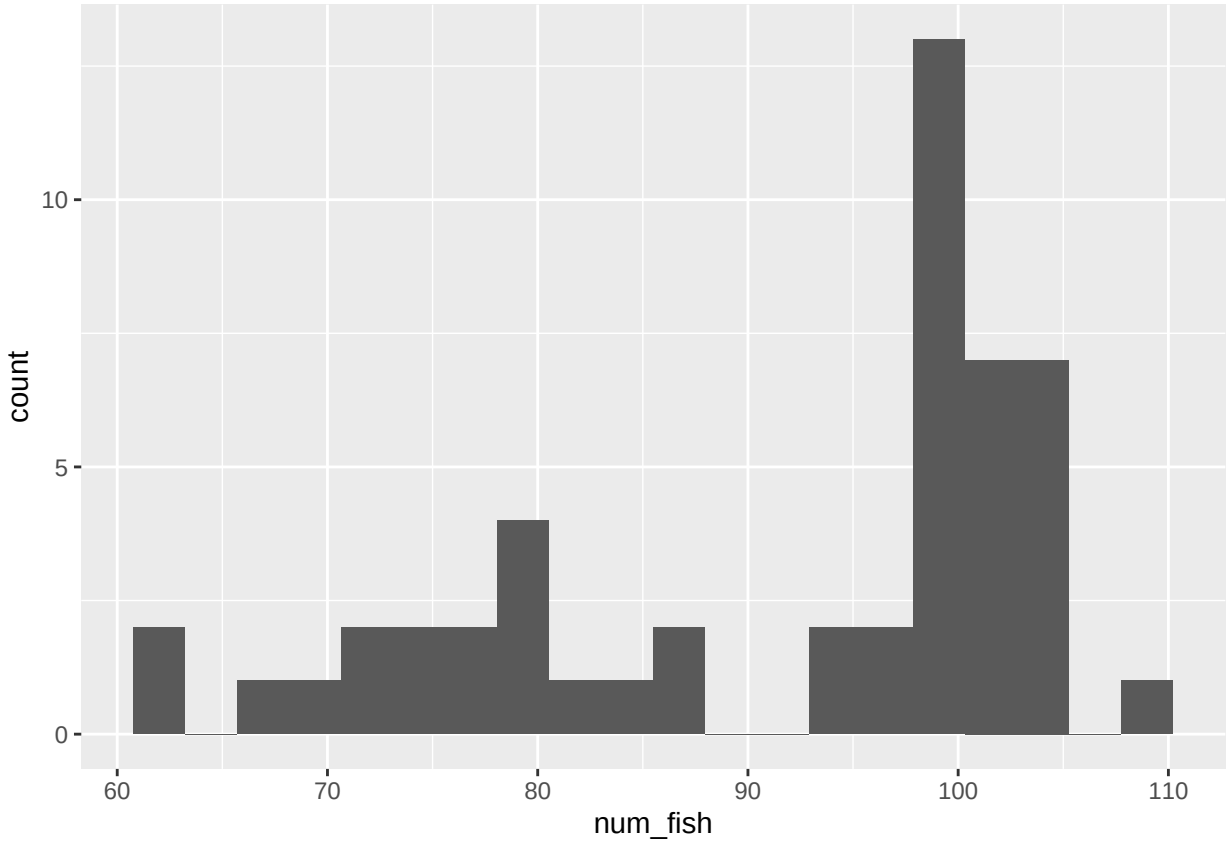
As we learned last modules, histograms are plots which let us look at *one numeric variable.*

They help us get a feel for the distribution of that data. To make histograms in `ggplot2`, we use the `geom_histogram()` function. Let's look at the number of fish.

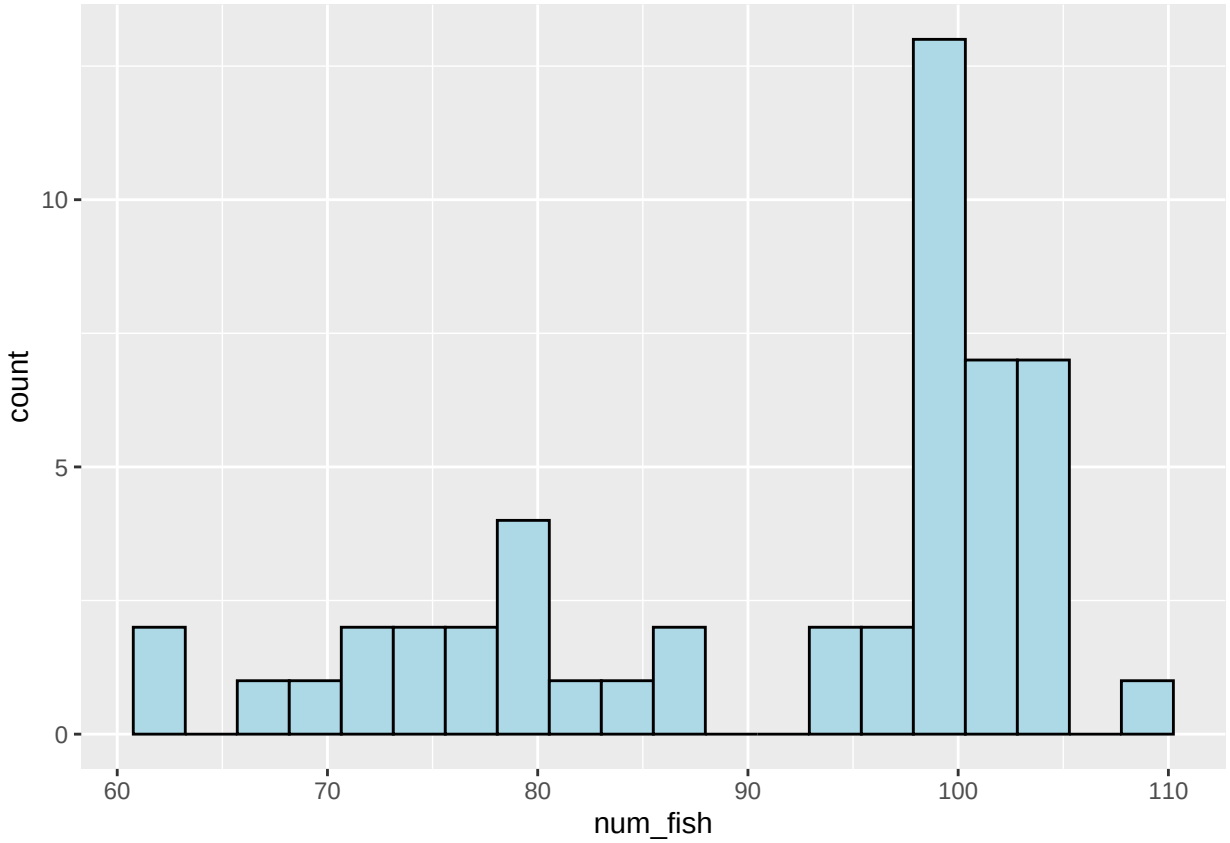
```r
ggplot(fish, aes(x = num_fish)) +
  geom_histogram(bins = 20)
```




```r
# we can change the number of bins (essentially, the number of columns) by modifying the bins argument
ggplot(fish, aes(x = num_fish)) +
  geom_histogram(bins = 20)
```



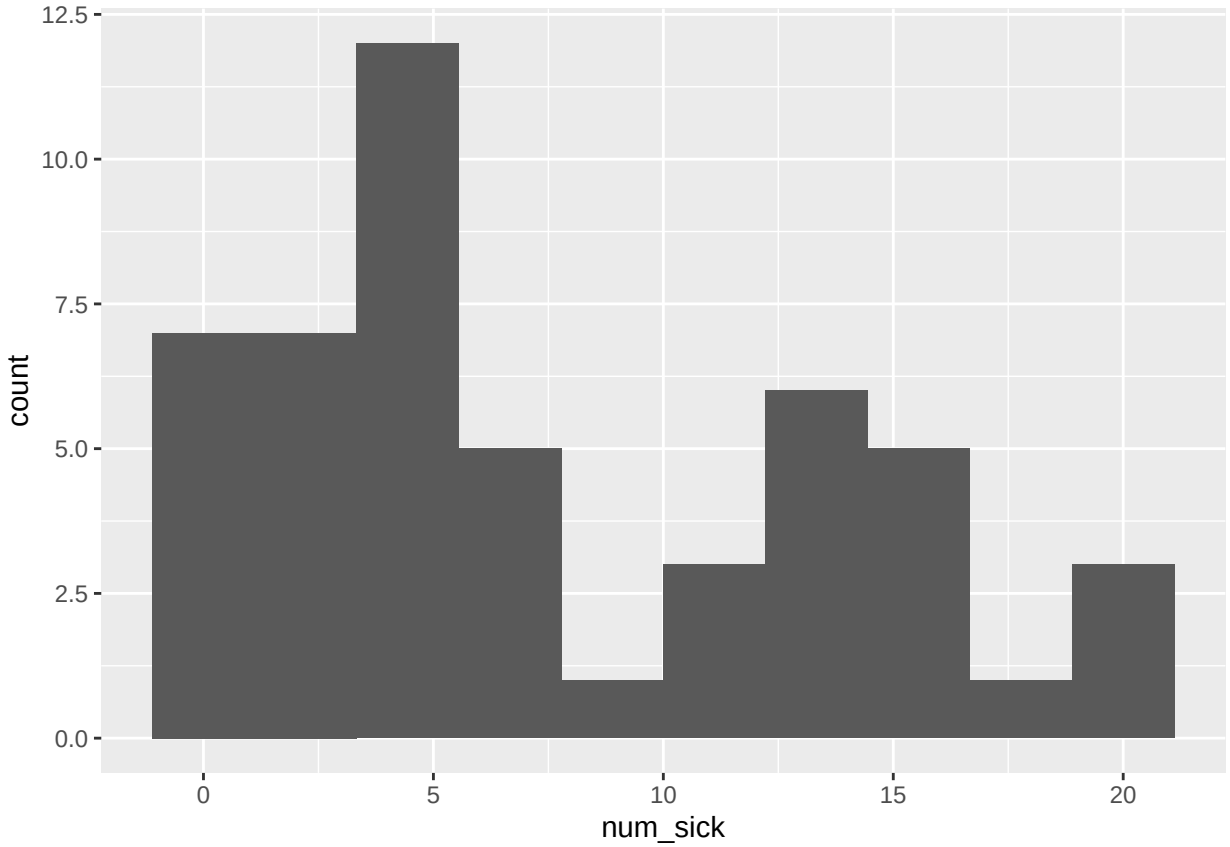

```
# we can also modify the colors, if we want
ggplot(fish, aes(x = num_fish)) +
  geom_histogram(bins = 20, fill = "lightblue", color = "black")
```



Let's Practice

Make a histogram of the number of sick fish in the tanks. Create the histogram with 10 bins (10 groupings).

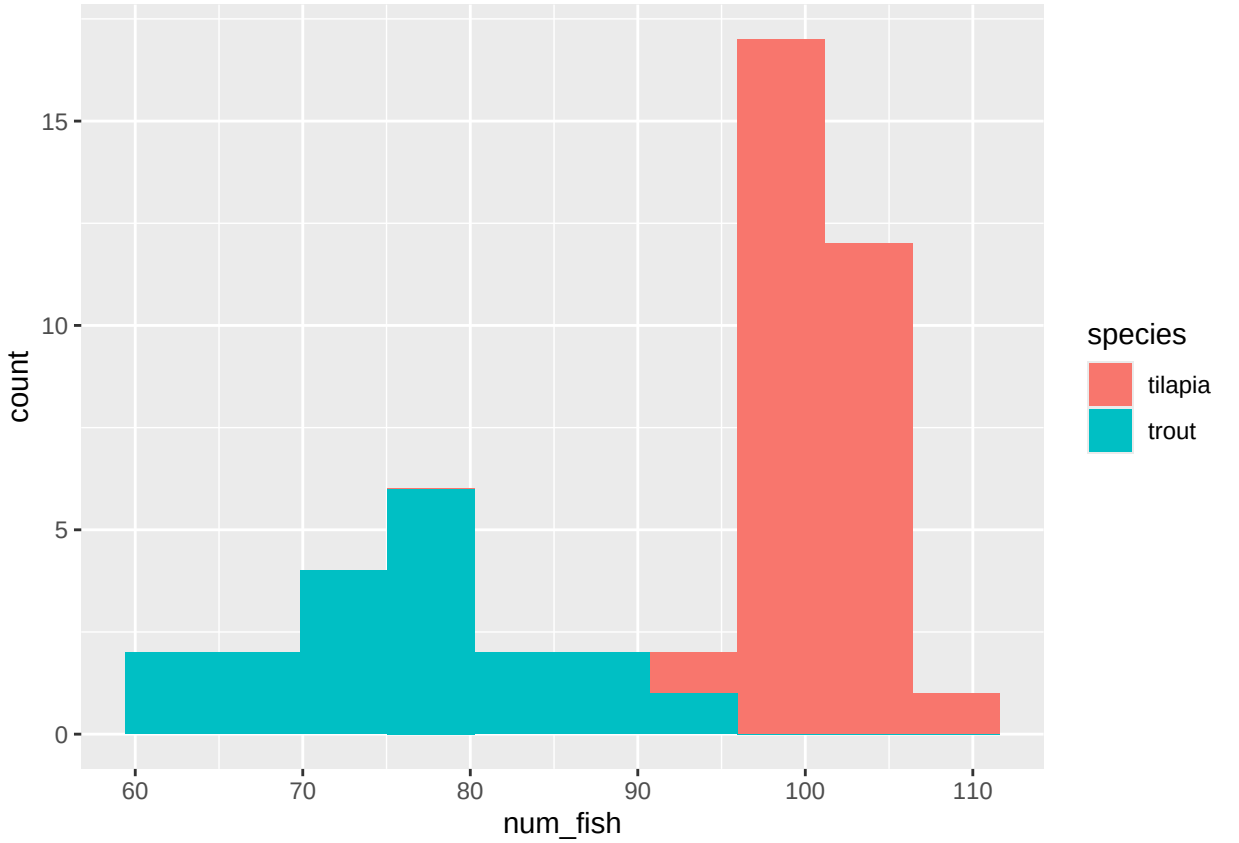
```
ggplot(fish, aes(x = num_sick)) +
  geom_histogram(bins = 10)
```



Multiple Histograms (with `geom_histogram()`)

When we create a multiple histogram, we have to add one additional argument to `geom_histogram()`. Let's see what happens if we just specify `fill`.

```
ggplot(fish, aes(x = num_fish, fill = species)) +
  geom_histogram(bins = 10)
```

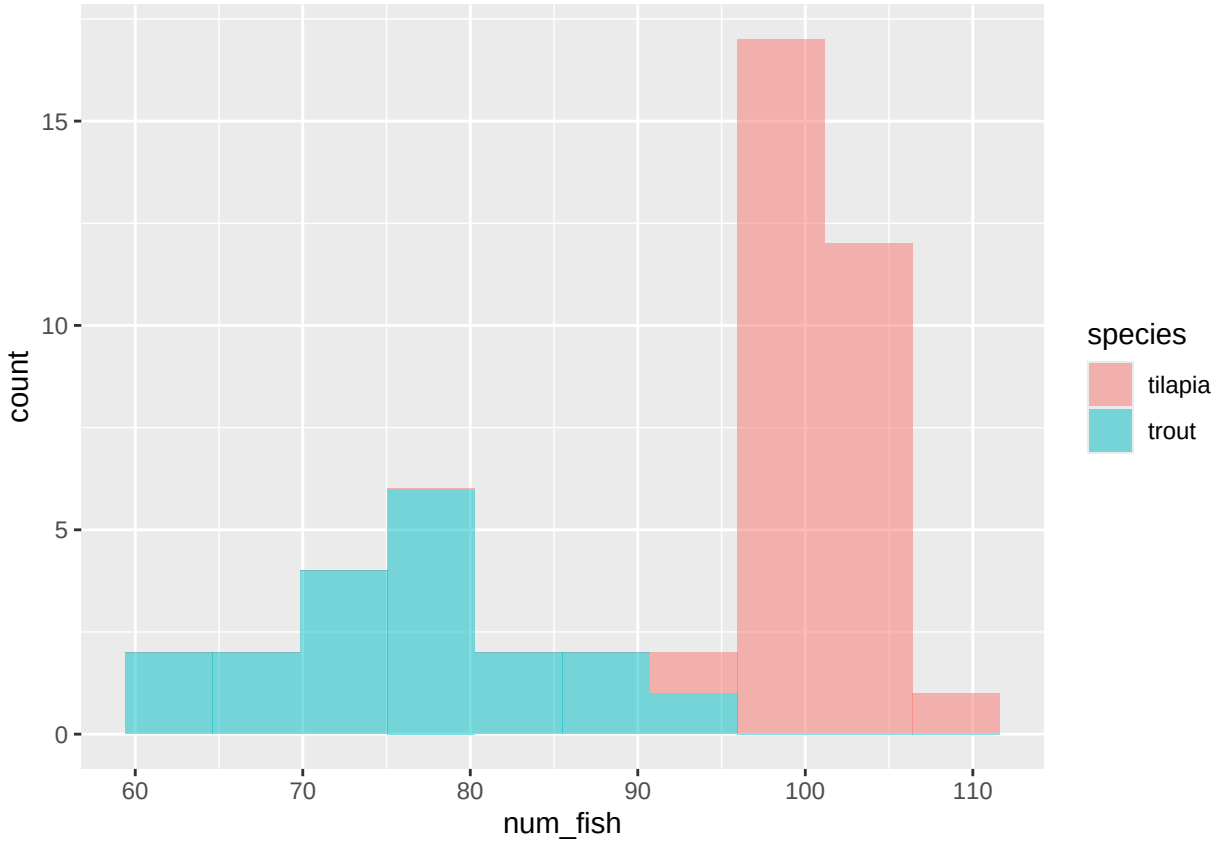


What is happening in the column with both green and red? Perhaps the teal histogram is in front of the red histogram and as blocking us from seeing some red?

Let's change the transparency using an argument called `alpha`, which allows us to make layers transparent. The scale for `alpha` goes from 0 (completely transparent) to 1 (not transparent at all).

We can set the transparency to 0.5 to see if there is any overlap.

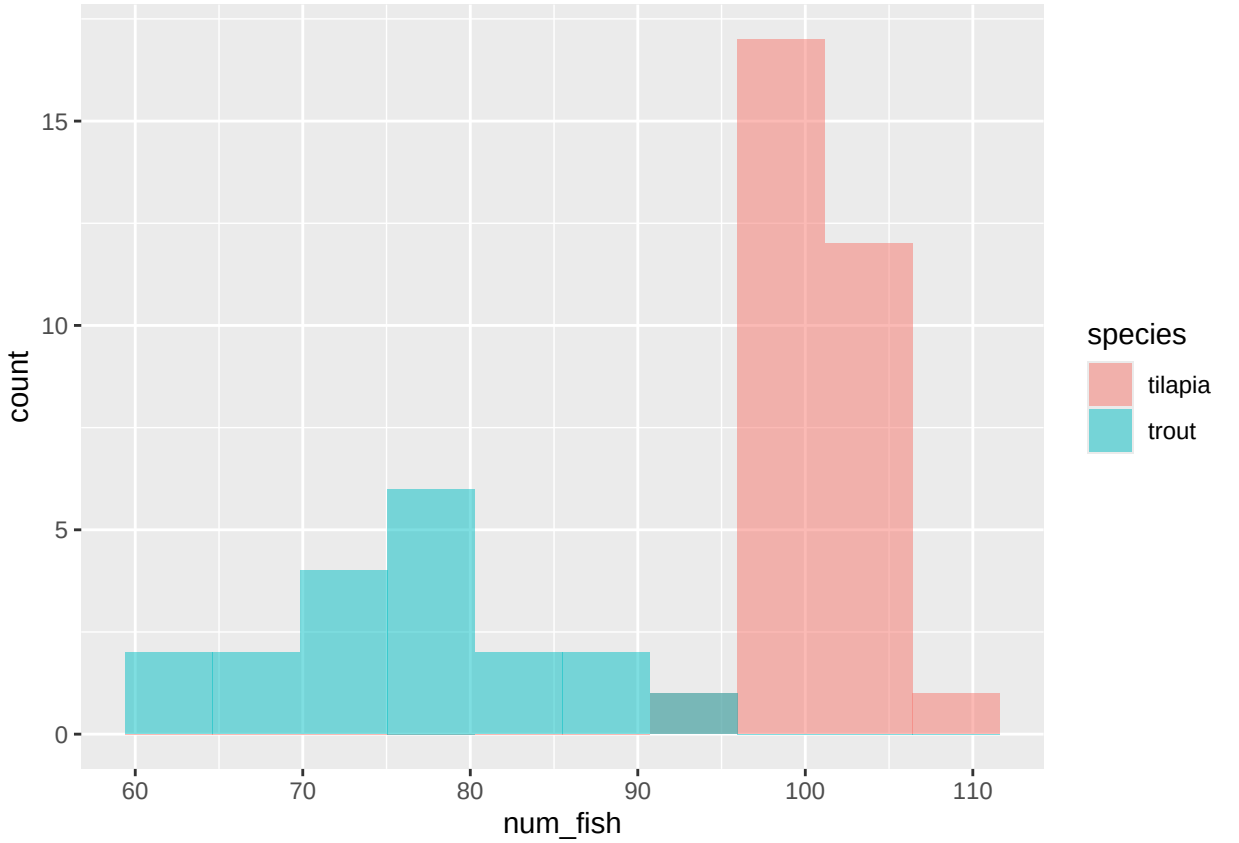
```
ggplot(fish, aes(x = num_fish, fill = species)) +
  geom_histogram(bins = 10, alpha = 0.5)
```



Not too much changed. It still doesn't look like we can see any red points behind the teal. Perhaps the teal values and red values are stacked on top of one another?

Let's take a look at what happens when we add the argument `position = "identity"`.

```
ggplot(fish, aes(x = num_fish, fill = species)) +
  geom_histogram(bins = 10, alpha = 0.5, position = "identity")
```



Aha! This is different from above. Instead of red being stacked vertically on top of teal, we can now see that the red values start at 0 on the y-axis and are overlapping with the teal.

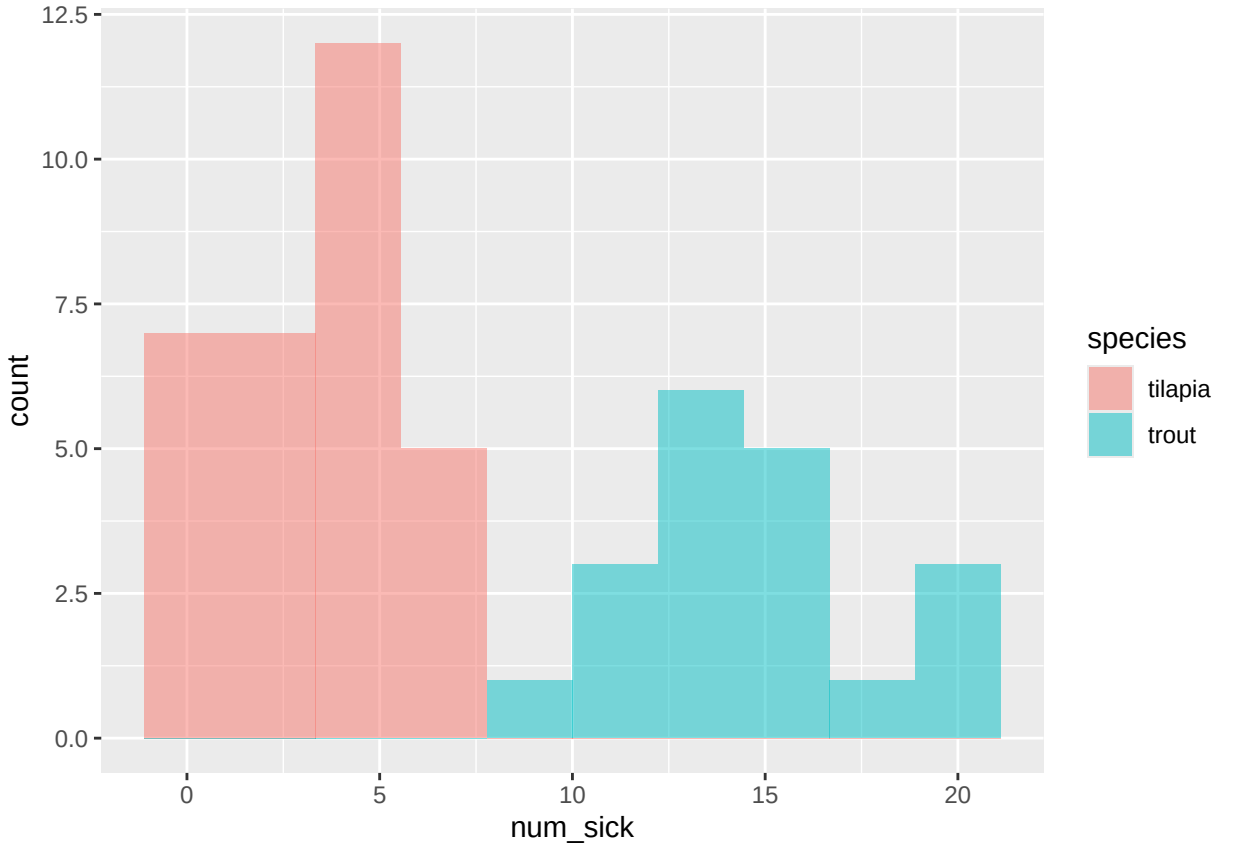
The `position = "identity"` argument tell `geom_histogram` to plot the data for each group starting from 0 in the y-axis rather than stacking values from the same group, which is the default.

Any time we plot a multiple histogram, we need to change the transparency and add `position = "identity"` when creating a multiple histogram; if we don't, we won't see potential overlap!

Let's Practice!

Make a multiple histogram of the number of sick fish per species. Make sure your plot has 10 bins, is partially transparent, and the data are *not* stacked.

```
ggplot(fish, aes(x = num_sick, fill = species)) +
  geom_histogram(bins = 10, alpha = 0.5, position = "identity")
```



The powerful and pesky `aes()` function

A quick note about the `aes()` function. It's one of the more confusing bits of `ggplot2`.

When do I put the `color` (or `size` or `linetype` or `fill` or whatever) inside the `aes()` function versus in the `geom` function but outside of `aes()`? When we made our multiple histogram plots, why did the `fill` argument go inside of `aes()` but `alpha` went outside?

Essentially, it boils down to this:

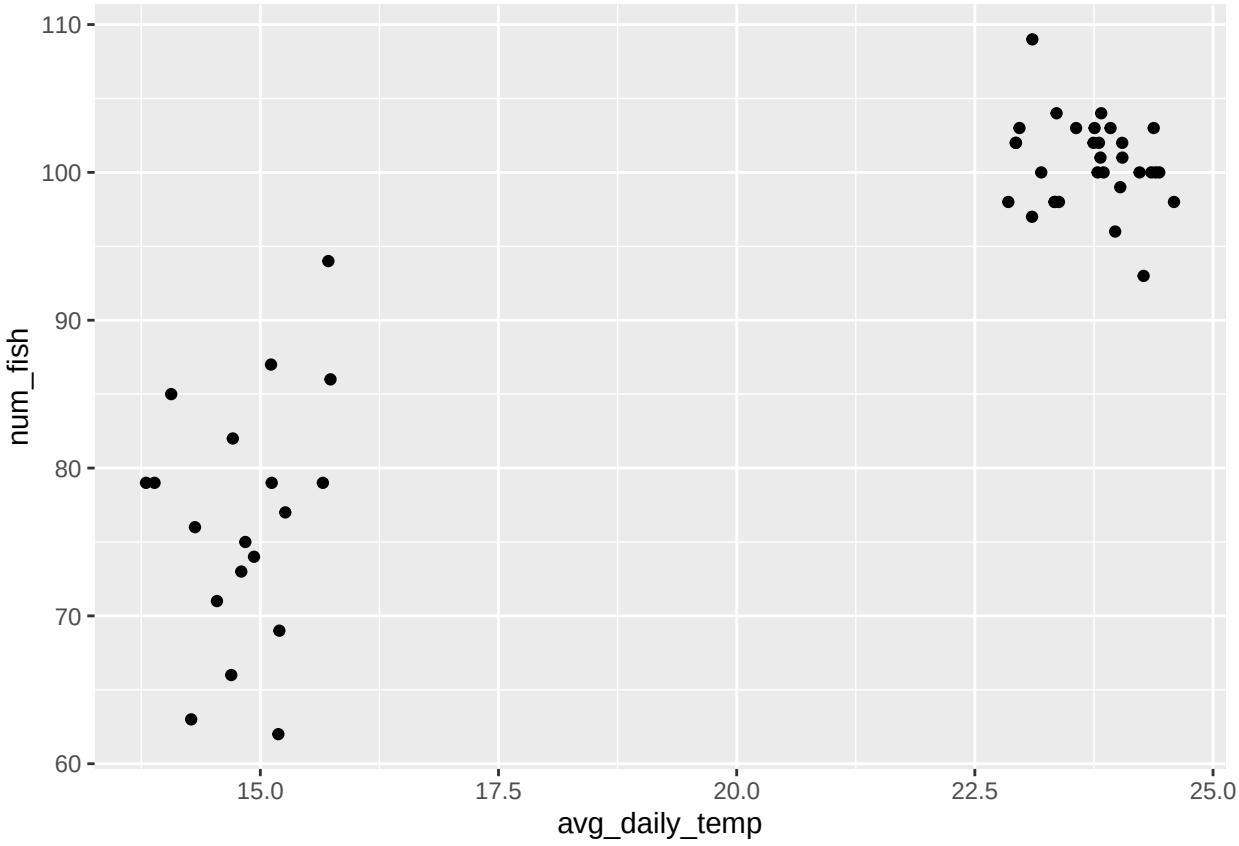
- if you want something (color, size, etc.) on your plot to change based on a **variable** from a data frame, you will want to put the argument *within* the `aes()` function.
- if you want something (color, size, etc.) on the plot to be **constant**, you will specify it *outside* of the function.

For some additional examples and explanation, check out this Stack Overflow page.

Scatter Plot

As a reminder, we use the `geom_point()` function to make a scatter plot of the relationship between *two numeric variables*.

```
ggplot(fish, aes(avg_daily_temp, num_fish)) +
  geom_point()
```

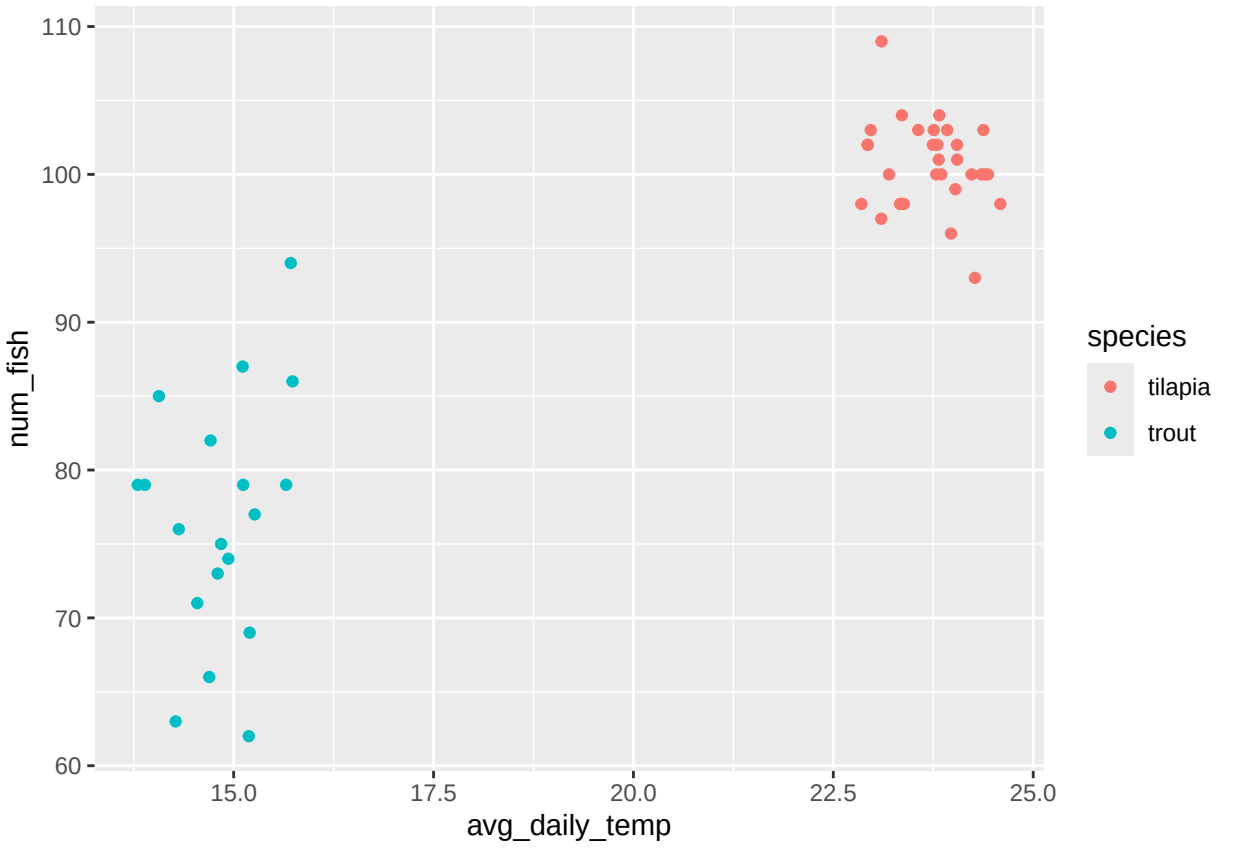


Let's Practice: Multiple Scatterplot

Using what you've learned about making histograms, see if you can create a "multiple scatterplot," where the color of the points are determined by the fish species.

Hint: you'll want to use an argument called `color`.

```
ggplot(fish, aes(avg_daily_temp, num_fish, color = species)) +
  geom_point()
```

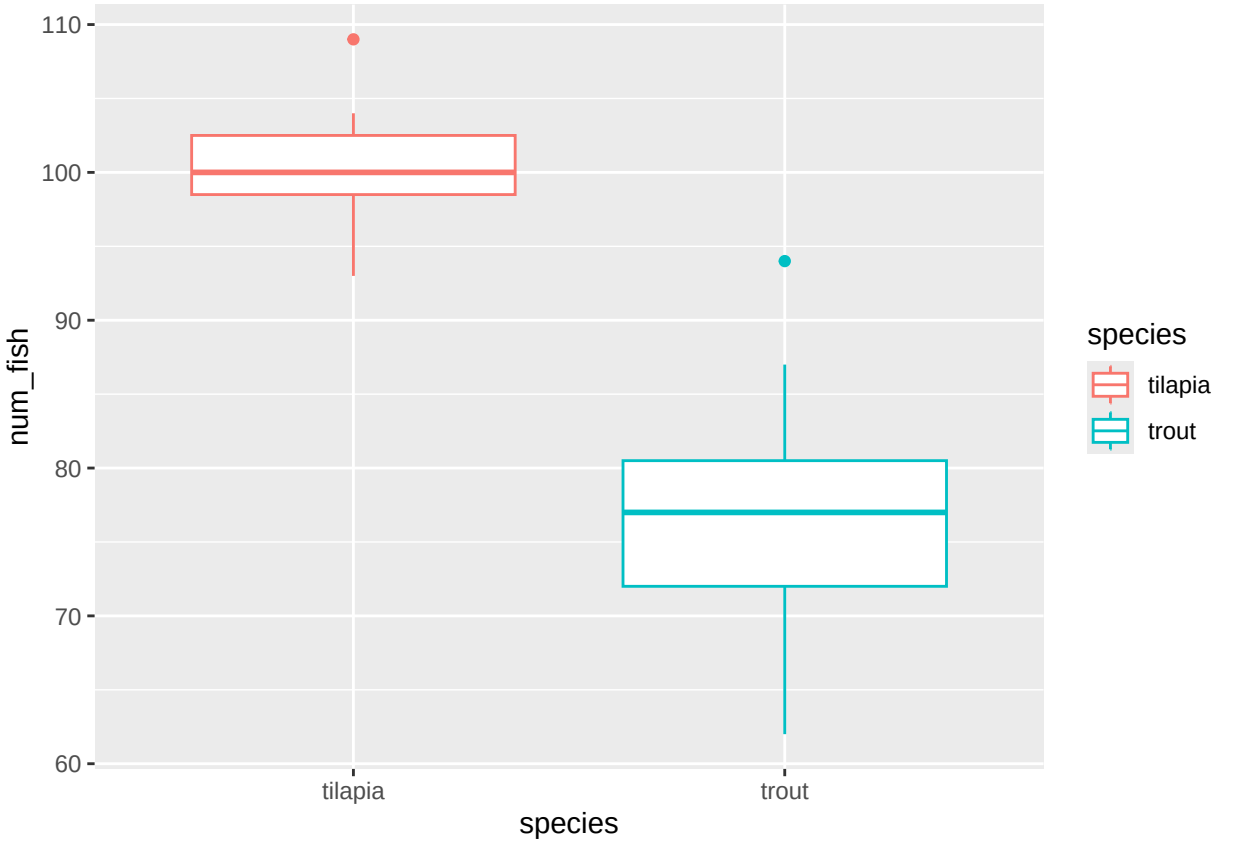


Box-and-Whisker Plots

Box-and whisker-plots (also known as box plots) are another great option for looking at one *numeric* variable and one or more *categorical* variables. They are particularly nice when you want to see measures of central tendency and variation in the same plot.

Let's build one and then talk through what each component means. We use `geom_boxplot` to make these types of plots.

```
ggplot(fish, aes(species, num_fish, color = species)) +
  geom_boxplot()
```



So what does the box represent? And the whiskers?

- the **box** represents the *middle 50% of the values* in the data set.
- the line that runs through the middle of the box represents the *median (**middle value**)* of the data
- the **whiskers** represent the *spread of the data* (we won't get into the mathematical details of exactly how they are calculated) and are roughly comparable to 95% confidence intervals (we will cover this in another module)
- values that fall outside of the whiskers can be considered outliers and are plotted individually

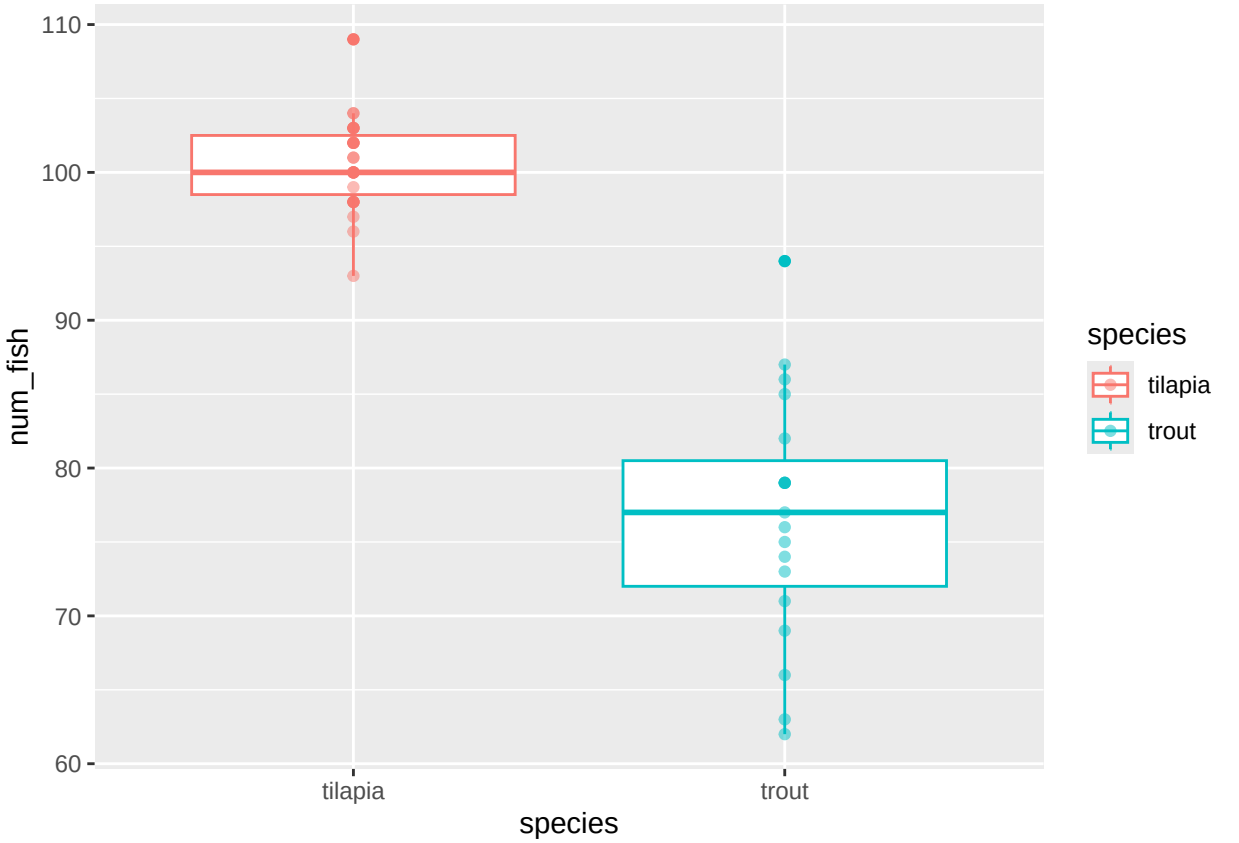
Layering

One of the beautiful parts of working with `ggplot2` is that you can add multiple layers to each plot.

One of the key things missing from box-and-whisker plots is any indication of how many data points we have. In the plot above, there could be 5 tanks per species or 500 tanks per species.

How can we add an indication of how many points there are? We can layer each individual data point on top of the boxes!

```
ggplot(fish, aes(species, num_fish, color = species)) +
  geom_boxplot() +
  geom_point(alpha = 0.5)
```

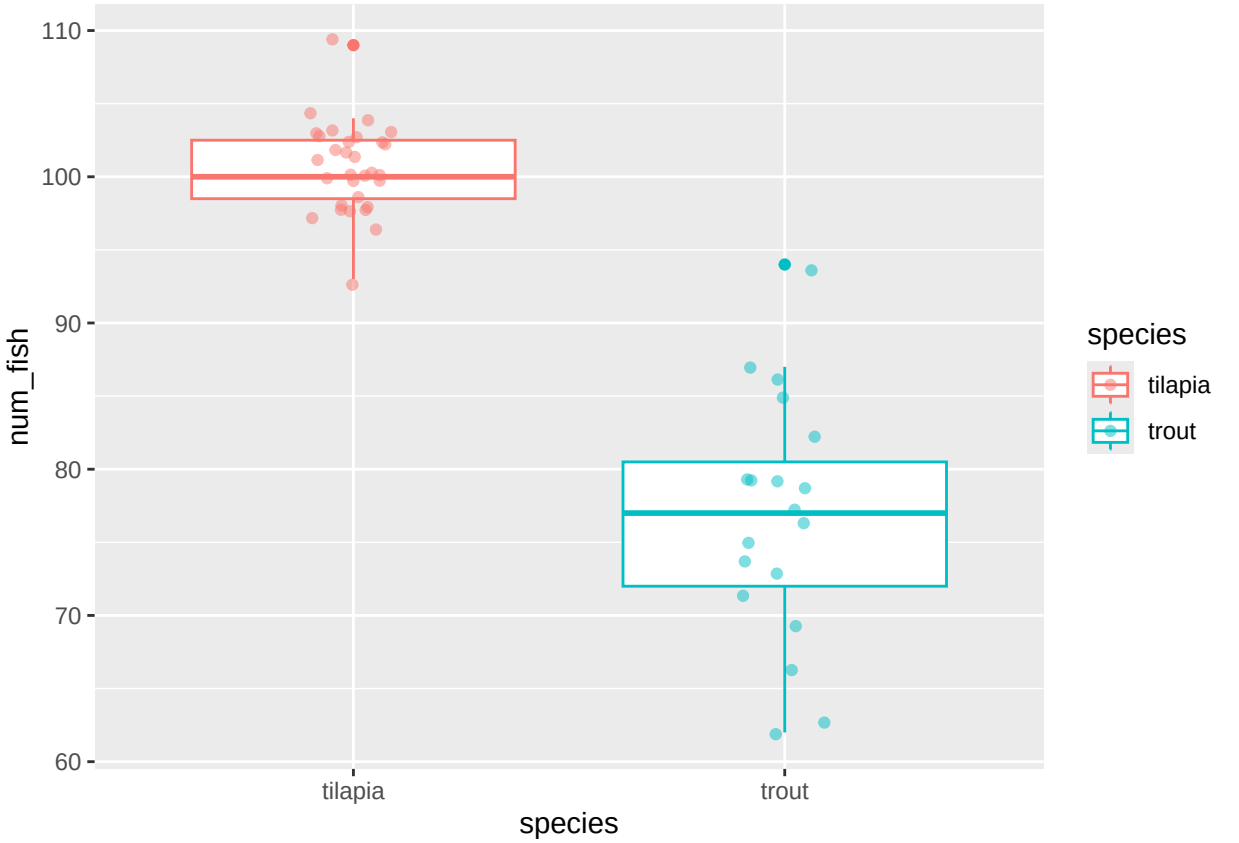


This is nice, but there is still some overlap in points that makes it hard for us to see exactly how many points are there.

The `geom_jitter()` function is a special version of `geom_point()`. It adds a little bit of randomness to the points (both horizontally and vertically) so that they don't overlap as much.

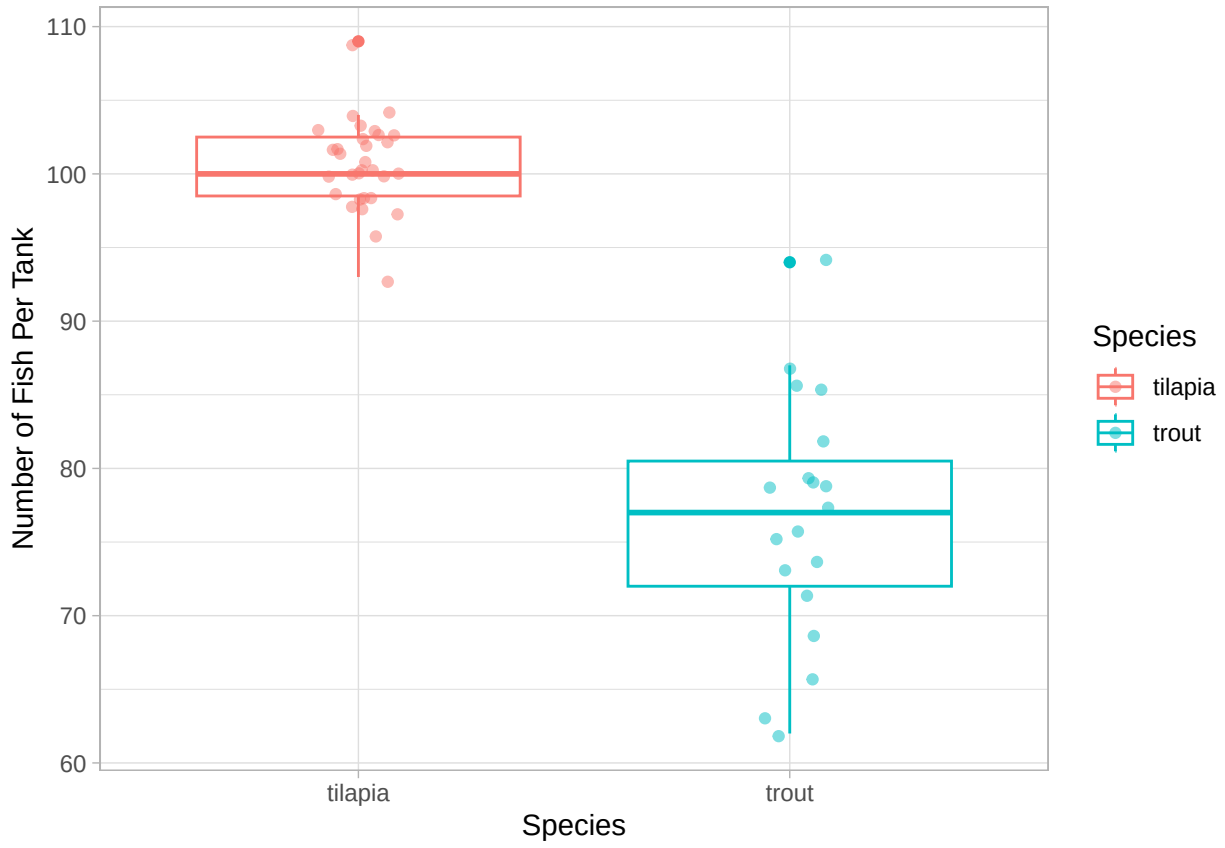
We can control how much randomness we allow with the `width` and/or `height` arguments. I usually ignore `height` and set the `width` argument to 0.1.

```
ggplot(fish, aes(species, num_fish, color = species)) +
  geom_boxplot() +
  geom_jitter(alpha = 0.5, width = 0.1)
```



That is looking really nice! We can keep improving it, though, with better labels for the axes and the legend as well as a nice `theme`.

```
ggplot(fish, aes(species, num_fish, color = species)) +
  geom_boxplot() +
  geom_jitter(alpha = 0.5, width = 0.1) +
  labs(x = "Species",
       y = "Number of Fish Per Tank",
       color = "Species") +
  theme_light()
```



`color` and `fill`

We have used two different arguments in the `aes()` function to specify that we want to colors in our plots to change based on one of the columns in our dataset. When do you want to use which one?

`color` For the most part, the `color` argument refers to the color of the lines in a plot (e.g., in box plots, the colors of the lines change).

The one exception to this is in `geom_point()`. We change the color of the points with the `color` argument, as well.

`fill` When there is space that we want to fill in with color depending on the values in a column, we want to use the `fill` argument.

For histograms, the `fill` argument changes the color inside the bins. If we use `color` in a histogram instead, only the outlines of the columns will change, but the columns will remain filled with gray.

In boxplots, the inside area of the box will be filled with color, but the lines will stay black.

In Labels

If we have specified either `color` or `fill` (or both) in the `aes()` function, `ggplot` will automatically create a legend for us. The key is determined by whichever argument we used.

So, if you use the `color` argument in the `aes()` function, you would want to use the `color` argument in the `labs()` function to change the title of the legend. If you used the `fill` argument, you would then use the `fill` argument in the `labs()` function.

If you have both `color` and `fill` in `aes()`, you will need to add both arguments to the `labs()` function. If you give the same label to each, it will create one key.

Let's Practice!

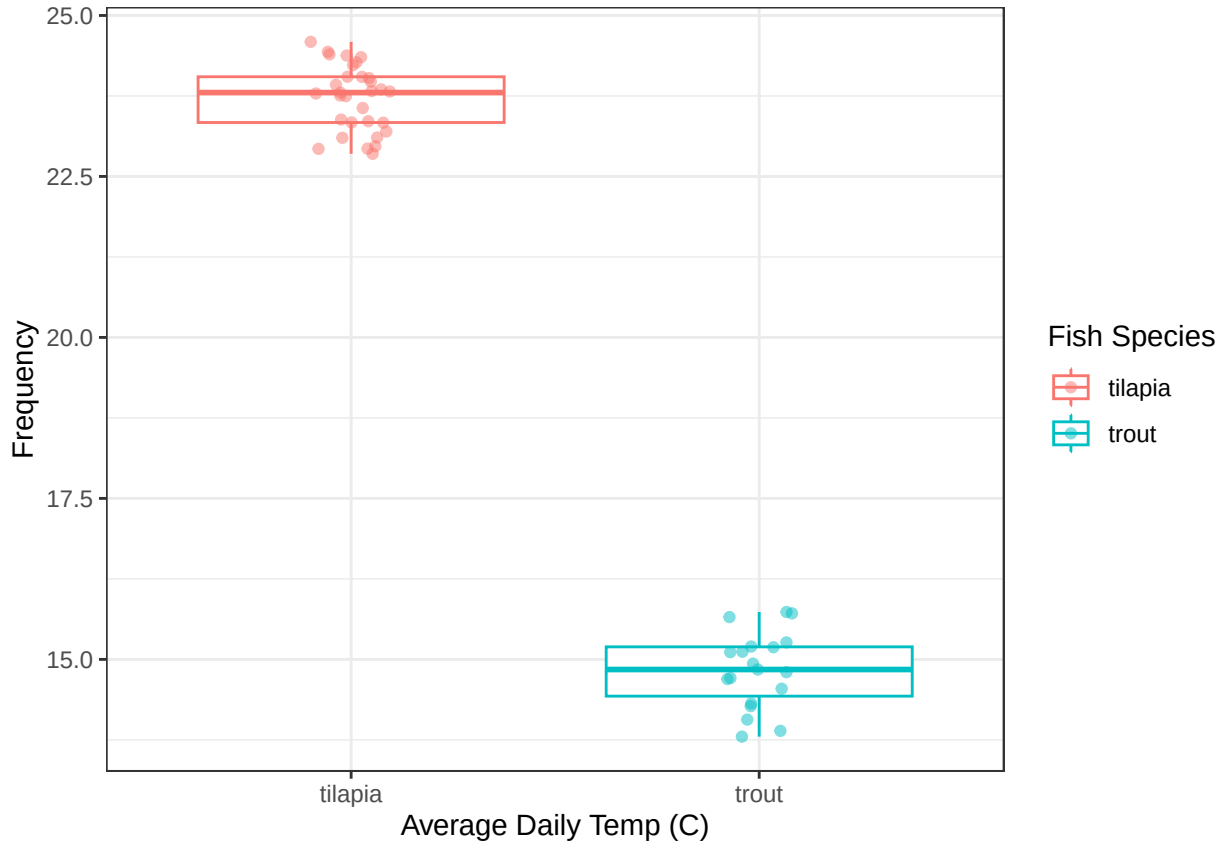
Make 2 different types of plots with the same data: the average daily temperature of the tanks and fish species.

First, think about the variables we are plotting. How many are there? Are they categorical or numeric?

Based on those answers, determine which plot types you can produce for those variable types.

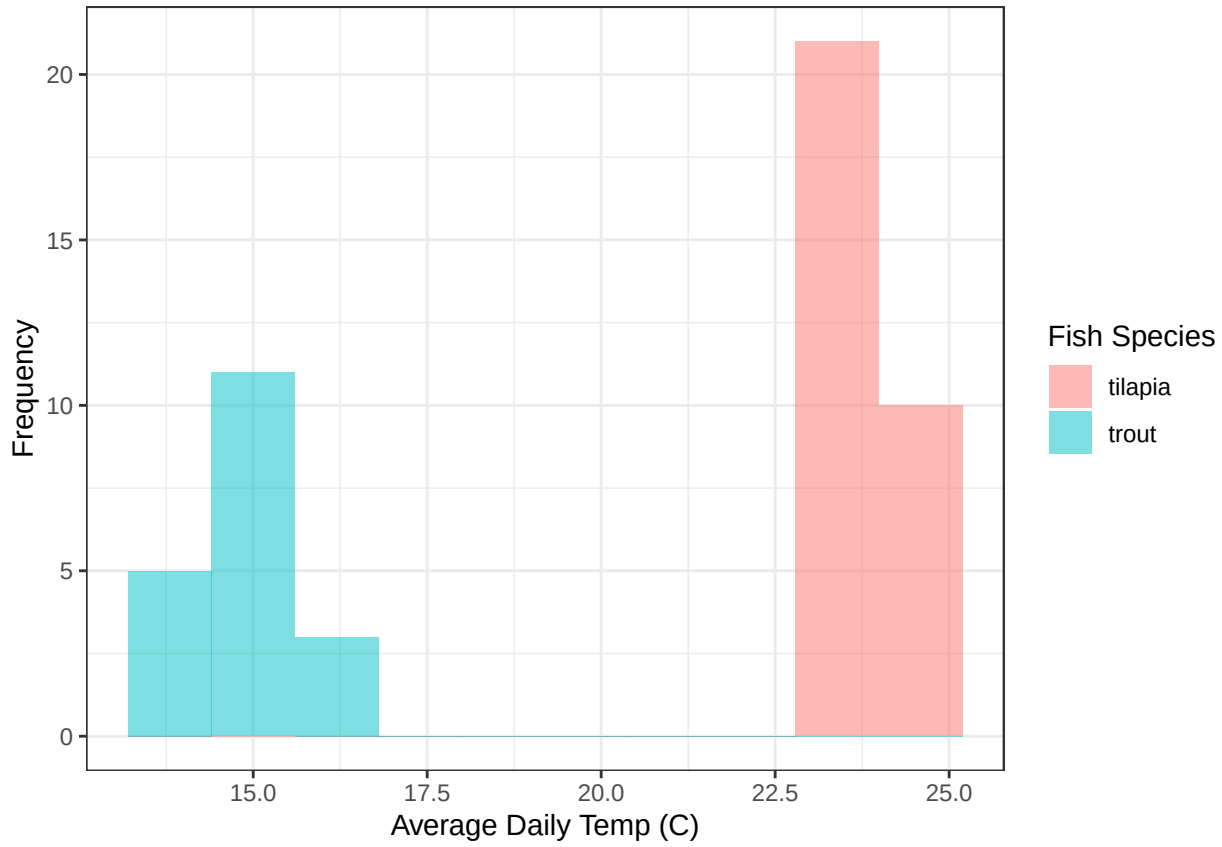
Now, make your two plot! To each, add labels and a theme.

```
# boxplot
ggplot(fish, aes(species, avg_daily_temp, color = species)) +
  geom_boxplot() +
  geom_jitter(alpha = 0.5, width = 0.1) +
  labs(x = "Average Daily Temp (C)",
       y = "Frequency",
       color = "Fish Species") +
  theme_bw()
```



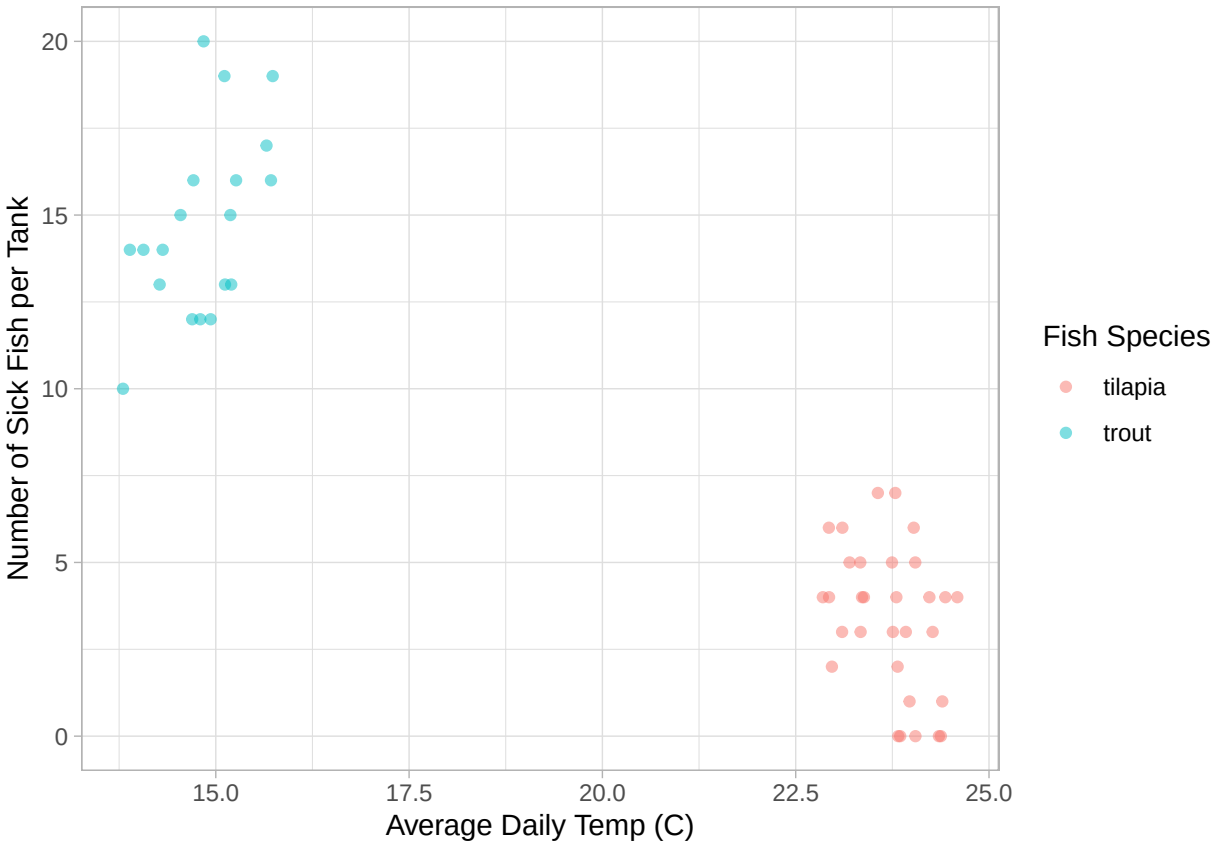

```
# histogram
ggplot(fish, aes(avg_daily_temp, fill = species)) +
  geom_histogram(bins = 10, alpha = 0.5, position = "identity") +
  labs(x = "Average Daily Temp (C)",
```

```
       y = "Frequency",
       fill = "Fish Species") +
  theme_bw()
```



Finished? Let's add another variable. Now, we want to plot average daily temperatures, the number of sick fish, and the fish species. Work through the same steps as above.

```
ggplot(fish, aes(avg_daily_temp, num_sick, color = species)) +
  geom_point(alpha = 0.5) +
  labs(x = "Average Daily Temp (C)",
       y = "Number of Sick Fish per Tank",
       color = "Fish Species") +
  theme_light()
```



Summary

Let's summarize some of what we've learned in this module

Data Visualization Types and When to Use Them

Histogram

Good for looking at the distribution of one numeric variable

- one numeric variable (x-axis)

Multiple Histogram

Good for looking at differences in the distributions of one numeric variable based on a categorical variable

- one numeric variable (x-axis)
- one categorical variable via the `fill` or `color` argument in the `aes()` function
- we always want to add transparency (`alpha`) and, for histograms, `position = "identity"`

Scatter Plot

Good for looking for the relationship between two numeric variables

- two numeric variables (x-axis and y-axis)
- can add in a categorical variable via `aes()`, but the main relationship is between the two numeric variables

Box Plot

Good for looking at measures of central tendency and variation for a numeric variable and the differences between those measures between categories

- one numeric variable (y-axis)
- at least one categorical (x-axis and additional via `aes()`)

Layering

We can add multiple layers to ggplots, which is part of what makes them so useful!

- we can add multiple `geom` functions to a single plot
- we use the `labs()` function to rename axes labels and legends
- we use a `theme` function to make the plot more aesthetically pleasing and easier to understand