Lesson 07 - Advanced Plotting

Jul 25, 2016

In this lesson we will learn how to use the ggplot2 (based on the Grammar of Graphics) package to plot data in R. Although ggplot2 is complicated at first, it uses a very logical approach to plotting.

You can install ggplot2 with `install.packages("ggplot2")` and load it into your environment with `library(ggplot2)`.

Code for this lesson can be found here.

Why ggplot2?

We just learned about plotting in base R. ggplot2 is another package by Hadley Wickham, that allows for plotting with a different approach than in base R, using a grammar of graphics (hence the package name).

Advantages

- *More intuitive approach to plotting:* ggplot2 makes it easy to create different plots with the same data, changing the plotting method or the grouping variable(s). It can also easily create plots that would require “hacky” code in base R (such as comparing density distributions).
- *Creates better plots:* ggplot2 makes it easier to create publication-quality plots, with fewer lines of code. It also **creates legends automatically and easily** for color, point size, and line type

(among others), making it easy to compare different variables in a plot.[1]
- *Enforces good plotting standards:* The package is structured to enforce proper plotting techniques (for example, it does not support two different y-axes, or two different color scales on the same plot), which helps make sure plots are understandable.

Disadvantages

- *Different syntax than base R plotting:* All plotting functions in ggplot2 are used with different commands, which requires learning new functions in order to create good plots. Fortunately, there's a cheat sheet.
- *Requires structured, tidy data:* Because ggplot2 requires that data be in a data frame, basic plots are still easier in base R than ggplot2. In addition, you have to make sure your data is tidy (long) before being able to plot in ggplot2.
- *Enforces good plotting standards:* Sometimes you want to make a plot that ggplot2 can't/won't support.

ggplot2's support for legends is enough to make it worth learning, but in addition its versatility makes it really useful for creating detailed plots.

Plotting

ggplot2 takes a data frame (in tidy format) as an argument, and maps features of the data set onto the graph using *aesthetics*.

Scatter plots

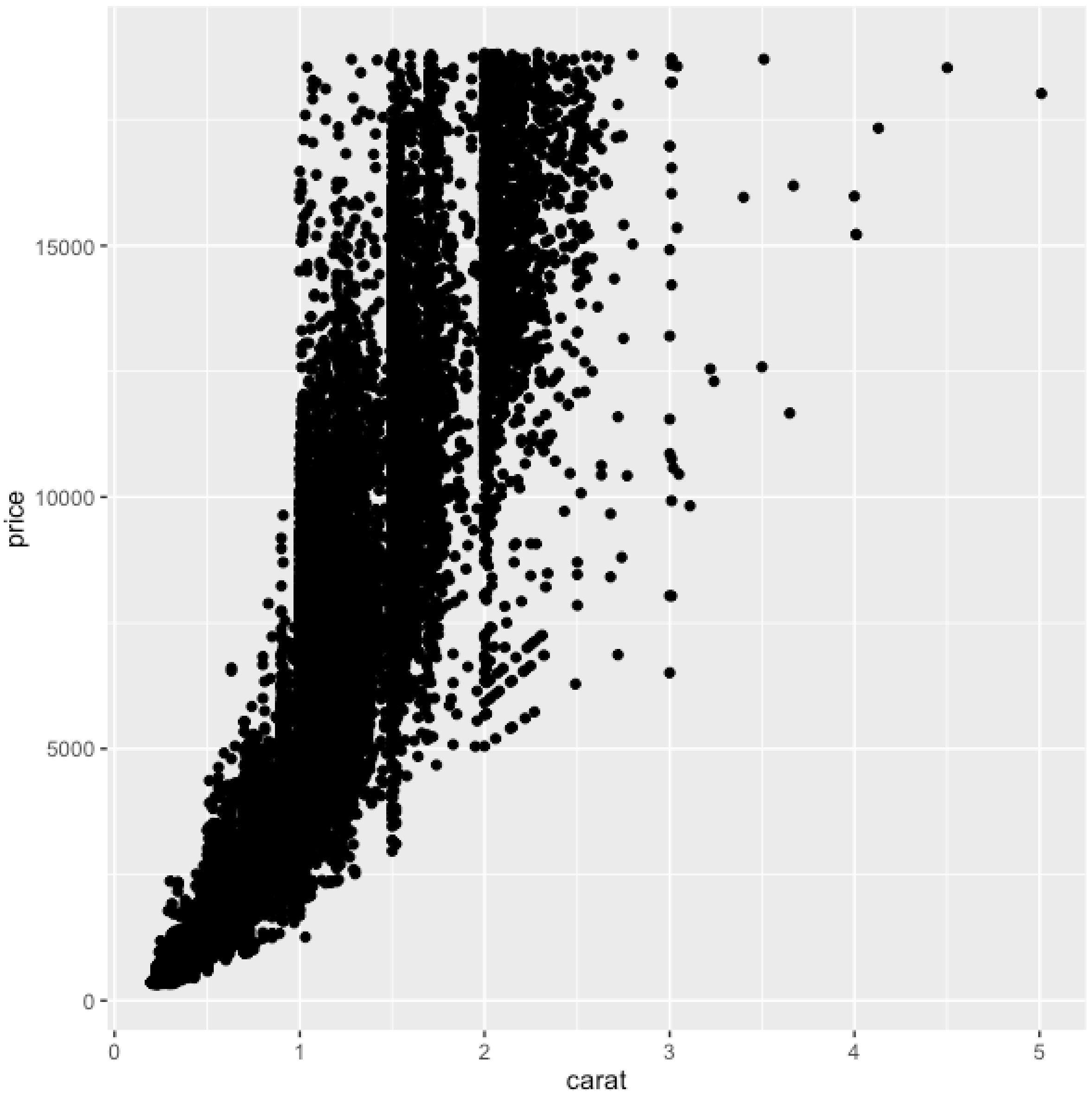
Let's start off with one of ggplot2's default data set, `diamonds`, that lists diamond prices.

```
library(ggplot2)
> diamonds
# A tibble: 53,940 x 10
   carat       cut color clarity depth table price     x     y     z
   <dbl>     <ord> <ord>   <ord> <dbl> <dbl> <int> <dbl> <dbl> <dbl>
1   0.23     Ideal     E     SI2  61.5    55   326  3.95  3.98  2.43
2   0.21   Premium     E     SI1  59.8    61   326  3.89  3.84  2.31
3   0.23      Good     E     VS1  56.9    65   327  4.05  4.07  2.31
4   0.29   Premium     I     VS2  62.4    58   334  4.20  4.23  2.63
5   0.31      Good     J     SI2  63.3    58   335  4.34  4.35  2.75
6   0.24 Very Good     J    VVS2  62.8    57   336  3.94  3.96  2.48
7   0.24 Very Good     I    VVS1  62.3    57   336  3.95  3.98  2.47
8   0.26 Very Good     H     SI1  61.9    55   337  4.07  4.11  2.53
9   0.22      Fair     E     VS2  65.1    61   337  3.87  3.78  2.49
10  0.23 Very Good     H     VS1  59.4    61   338  4.00  4.05  2.39
```

```
# ... with 53,930 more rows
```

To plot carat vs. price using ggplot2, we call the `ggplot` function with our data set, and give it an aesthetic for the x and y axes. We also add a *geom*: how we want to visualize the data.

```
ggplot(diamonds, aes(x=carat, y=price)) +
    geom_point()
```



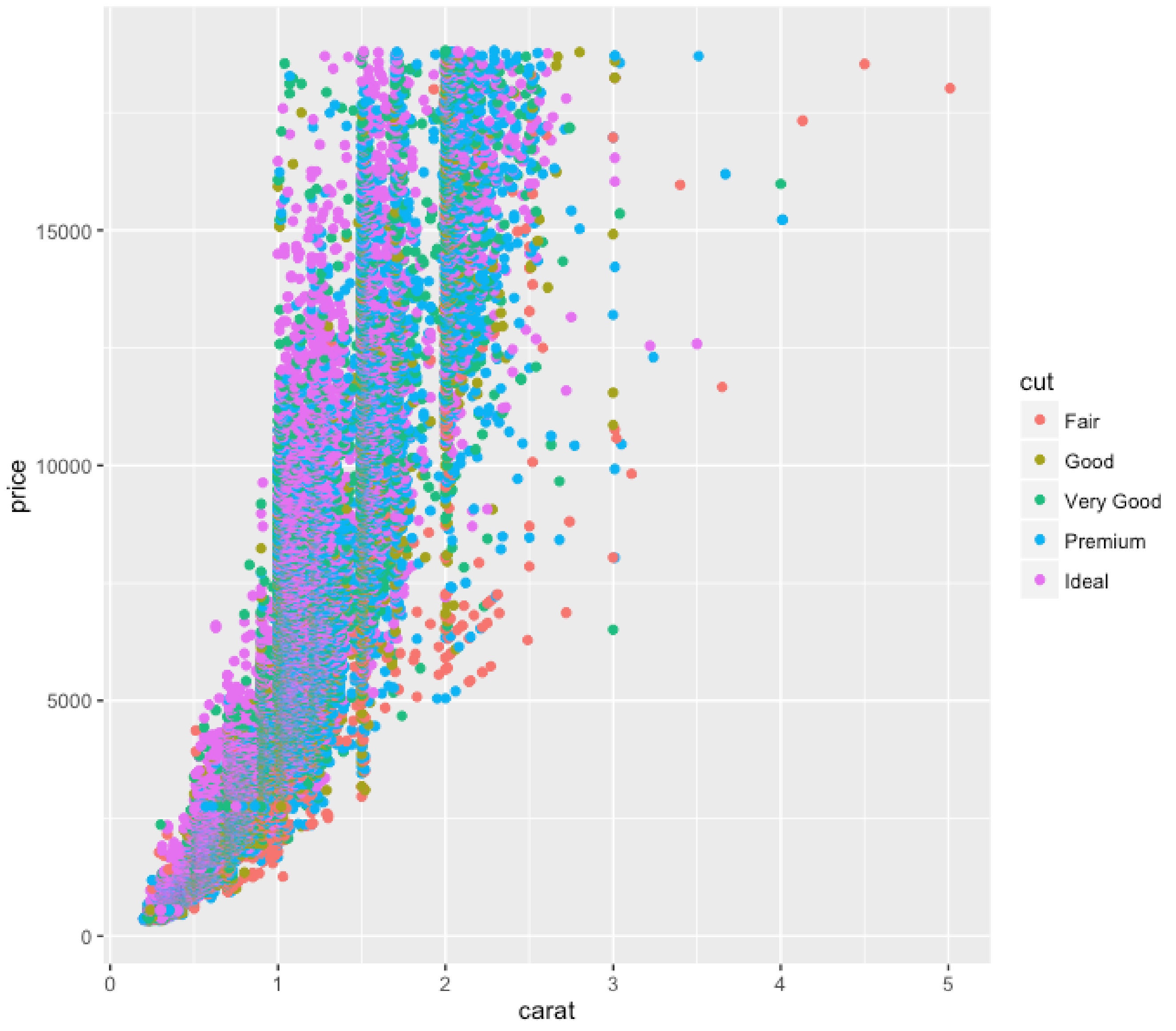
All plots in ggplot2 are created this way: with the first line being a data set (and optional aesthetics), and “adding” additional geoms or graphical parameters to the command.

Here, we’re defining the x and y aesthetics (with `aes`) in the ggplot2 call.

Adding plot variables

We can also define aesthetics within geom calls–for example, we can color by different aspects using the `colour` argument within `aes`.

```
ggplot(diamonds, aes(x=carat, y=price)) +
    geom_point(aes(colour=cut))
```



So easy!

References to columns in the data frame must be within calls to `aes`, or else you will get an error something like this:

```
> ggplot(diamonds, aes(x=carat, y=price)) +
+     geom_point(colour=cut)
Error in rep(value[[k]], length.out = n) :
  attempt to replicate an object of type 'closure'
```

The `geom` functions (e.g. `geom_point`) take other parameters in addition to `aes`. For example, try changing the transparency of the points using the following:

```
ggplot(diamonds, aes(x=carat, y=price)) +
    geom_point(aes(colour=cut), alpha=0.5)
```

Only mapping columns in a data frame to a graphical parameter should be *inside* of `aes`.

Axes

changing axis ranges

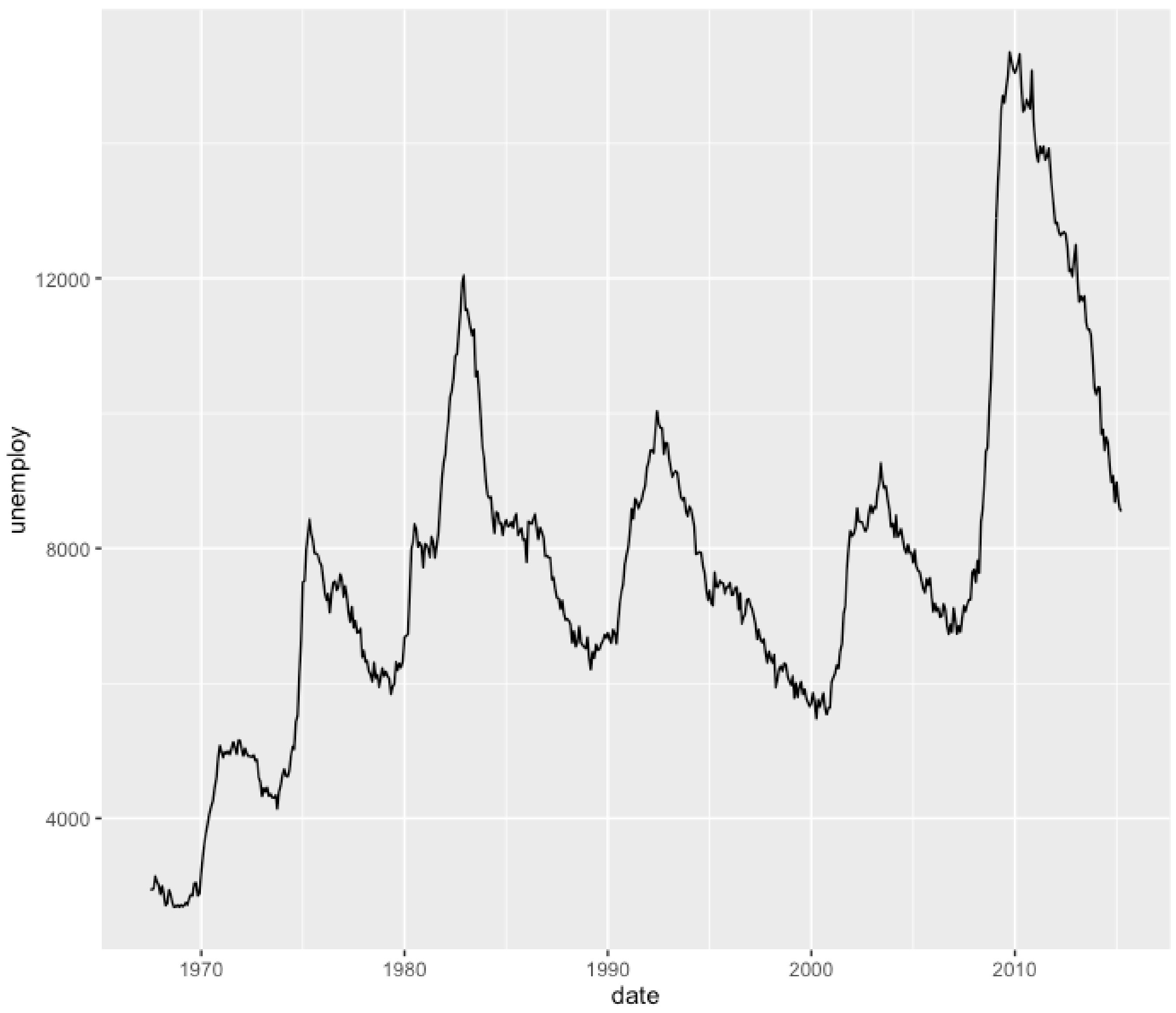
ggplot2 has a lot of commands for refining the plot axis.

Let’s take a look at some economics data:

```
> economics
# A tibble: 574 x 6
         date   pce    pop psavert uempmed unemploy
       <date> <dbl>  <int>   <dbl>   <dbl>    <int>
1  1967-07-01 507.4 198712    12.5     4.5     2944
2  1967-08-01 510.5 198911    12.5     4.7     2945
3  1967-09-01 516.3 199113    11.7     4.6     2958
4  1967-10-01 512.9 199311    12.5     4.9     3143
5  1967-11-01 518.1 199498    12.5     4.7     3066
6  1967-12-01 525.8 199657    12.1     4.8     3018
7  1968-01-01 531.5 199808    11.7     5.1     2878
8  1968-02-01 534.2 199920    12.2     4.5     3001
9  1968-03-01 544.9 200056    11.6     4.1     2877
10 1968-04-01 544.6 200208    12.2     4.6     2709
# ... with 564 more rows
```

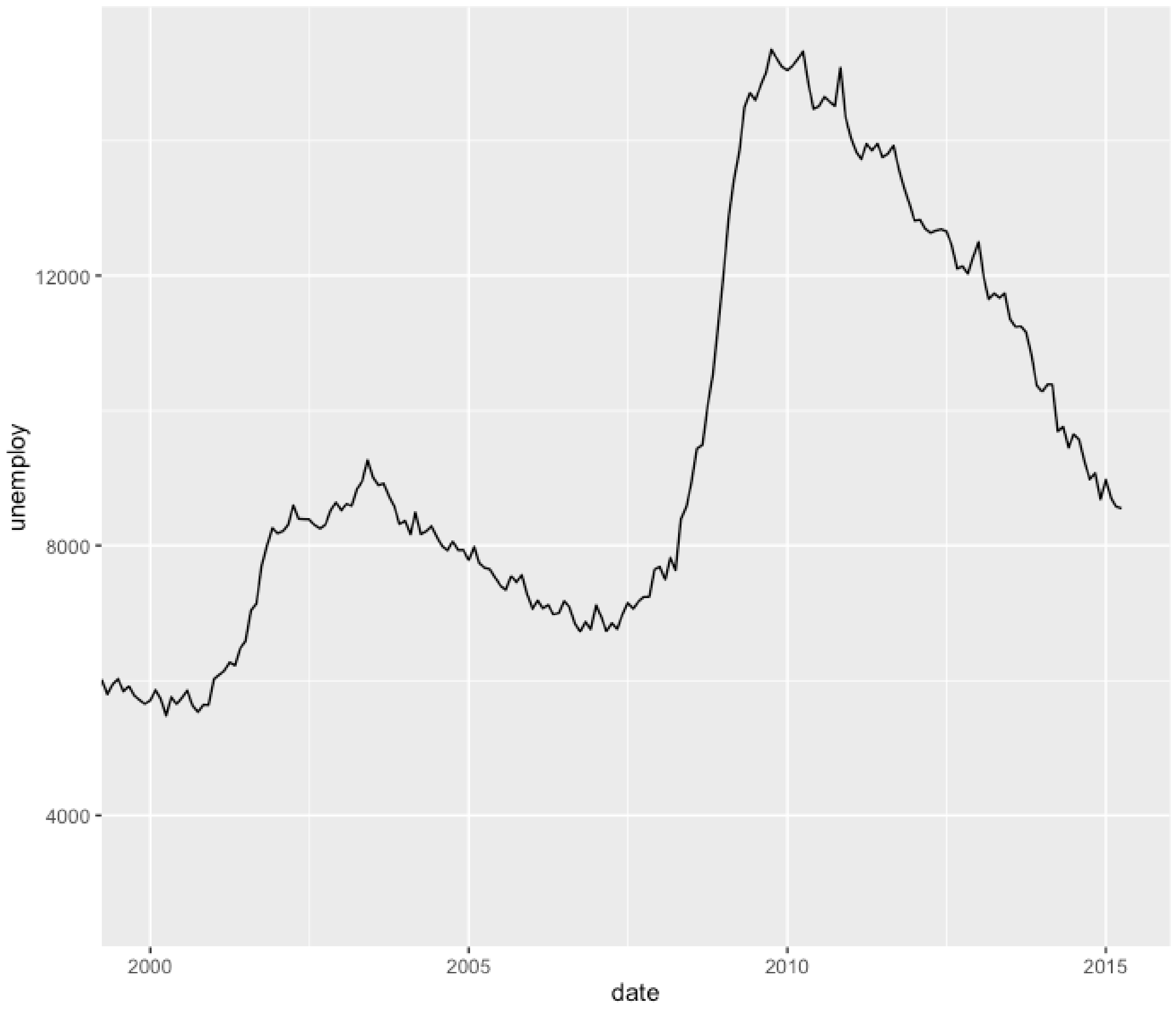
We can use `geom_line` to plot unemployment data over time.

```
ggplot(economics, aes(x=date, y=unemploy)) +
    geom_line()
```



If we’re only interested in the last 16 years, we can change the plotting limits using the `coord_cartesian` function:

```
ggplot(economics, aes(x=date, y=unemploy)) +
    geom_line() +
    coord_cartesian(xlim=c(as.Date("2000-01-01"), as.Date("2015-04-01")))
```



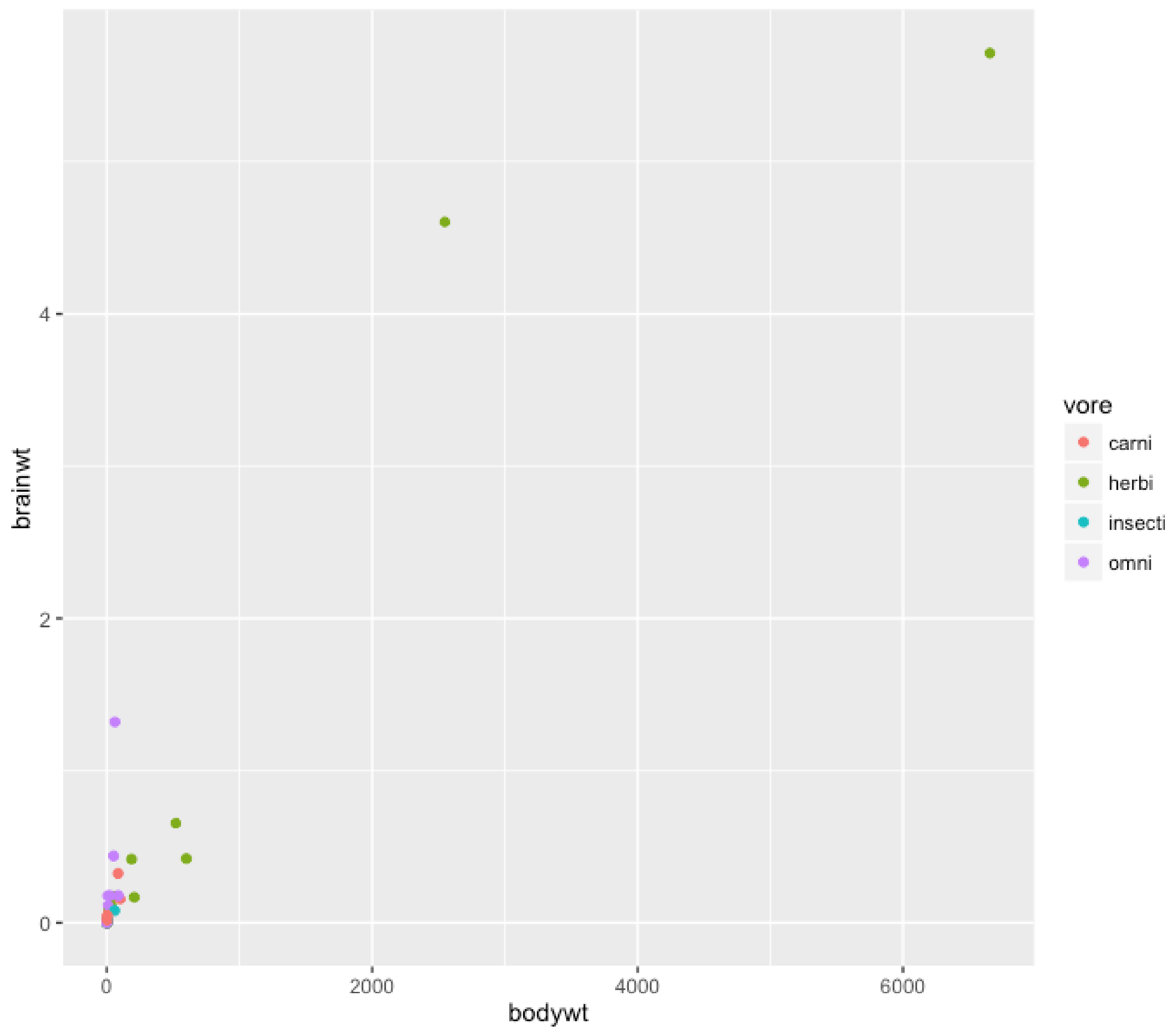
Because the `date` column is in Date format, we have to coerce the strings into Dates to adjust the plotting limits via the `xlim` argument.

How can we adjust the y-axis so that the y-axis range includes 0?

log scales

Using the data set `msleep`, which contains mammalian sleep data, we can plot body weight vs. brain weight:

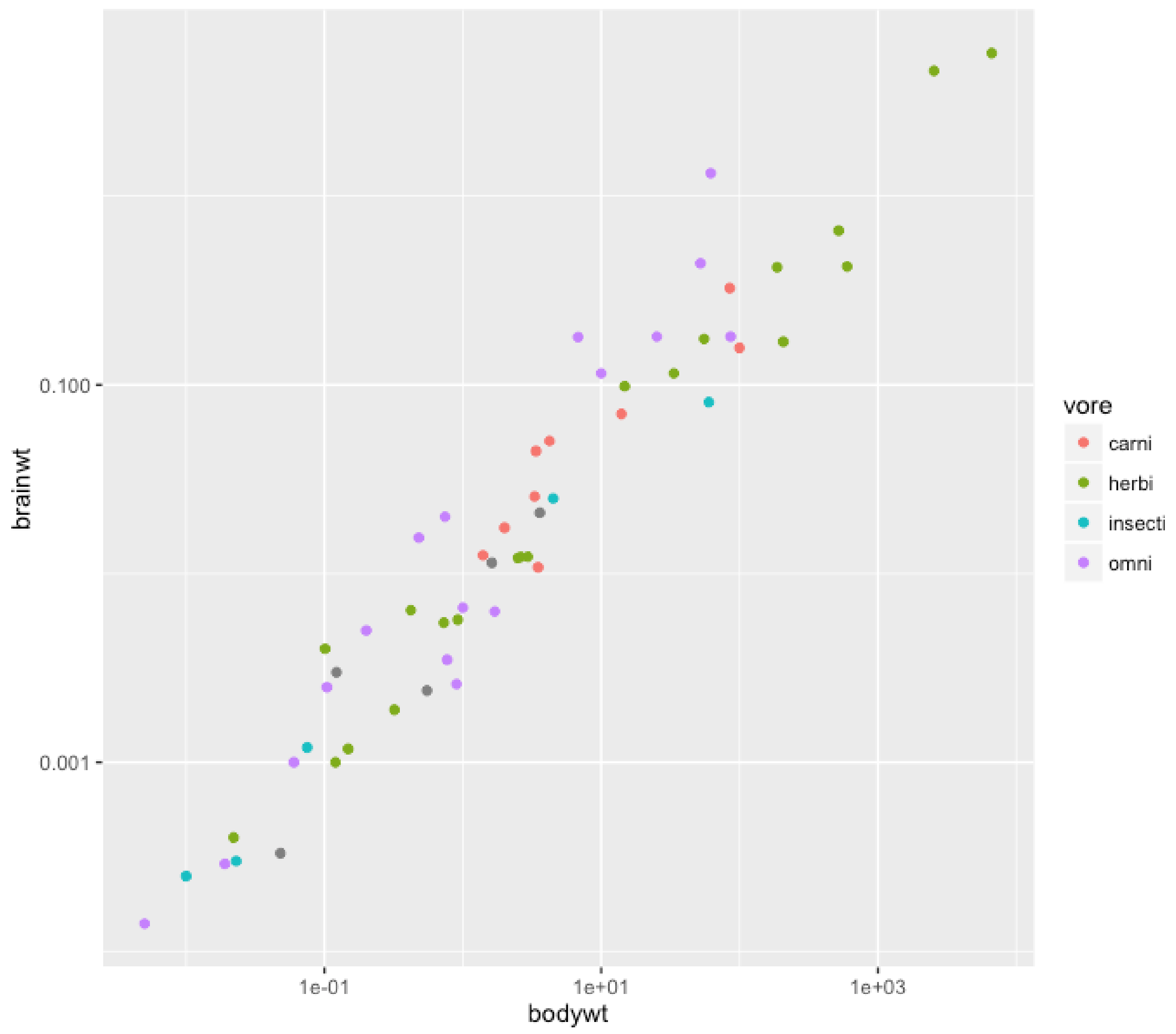
```
ggplot(msleep, aes(x=brainwt, y=bodywt)) +
    geom_point(aes(colour=vore))
```



This data doesn’t look good on a scatter plot–probably because both the body weight and brain weight fall into an exponential distribution. Log-transforming this data will make visualizing it much better.

ggplot2 has the commands `scale_x_log10` and `scale_y_log10` to automatically change the scale of the axis without having to transform the data manually.

```
ggplot(msleep, aes(x=bodywt, y=brainwt)) +
    geom_point(aes(colour=vore)) +
    scale_x_log10() +
    scale_y_log10()
```

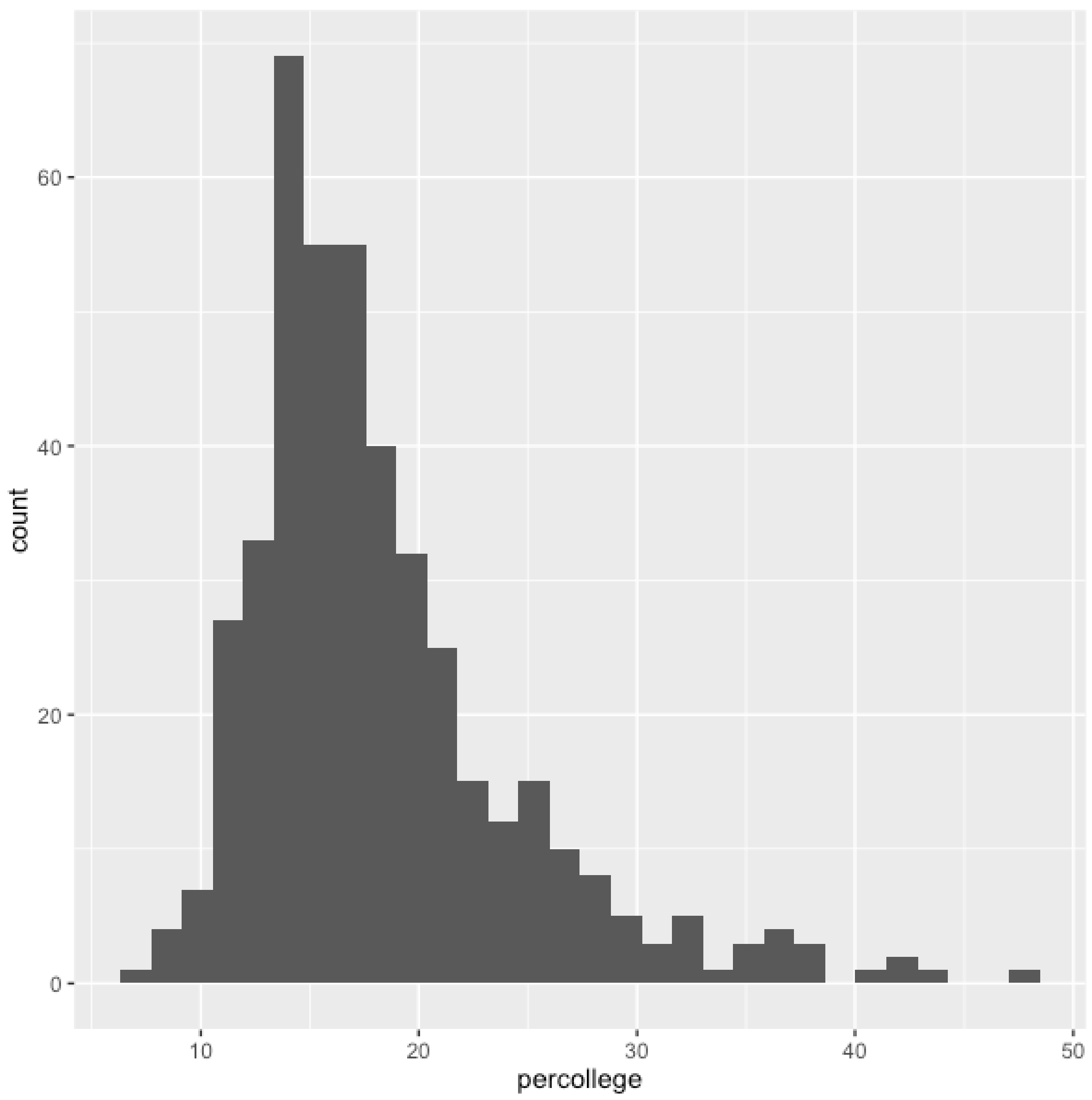


The plot looks much cleaner, and the relationship between body weight and brain weight is evident.

Density plots and histograms

ggplot2 also can display data as a histogram, much like the `hist()` function. Let's look at another data set, `midwest`, that has demographic information about some Midwestern states. What percent of people are college-educated?

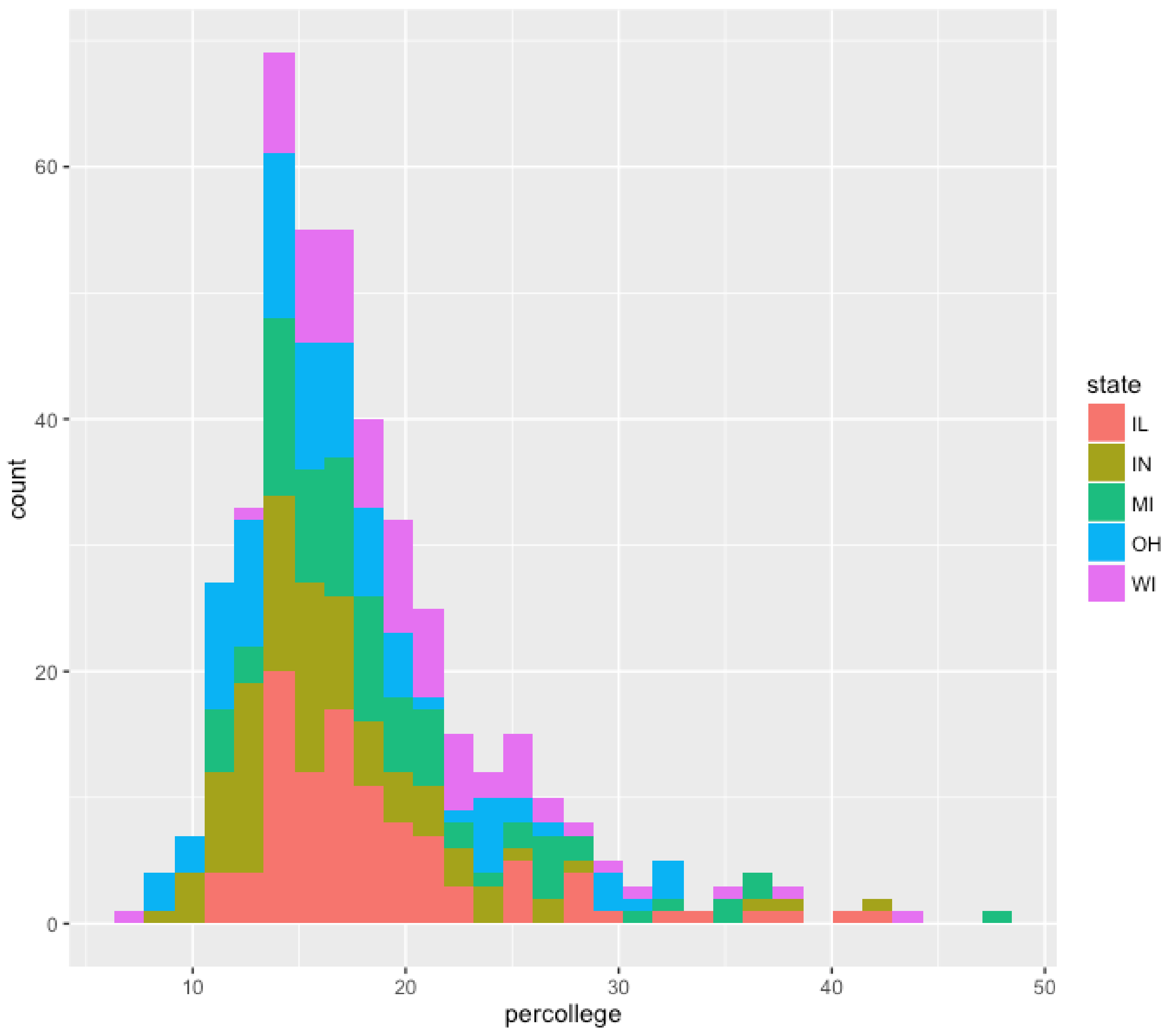
```
ggplot(midwest, aes(x=percollege)) +
    geom_histogram()
```



We can change the bin width using the `binwidth` argument, but for this plot the default width seems fine.

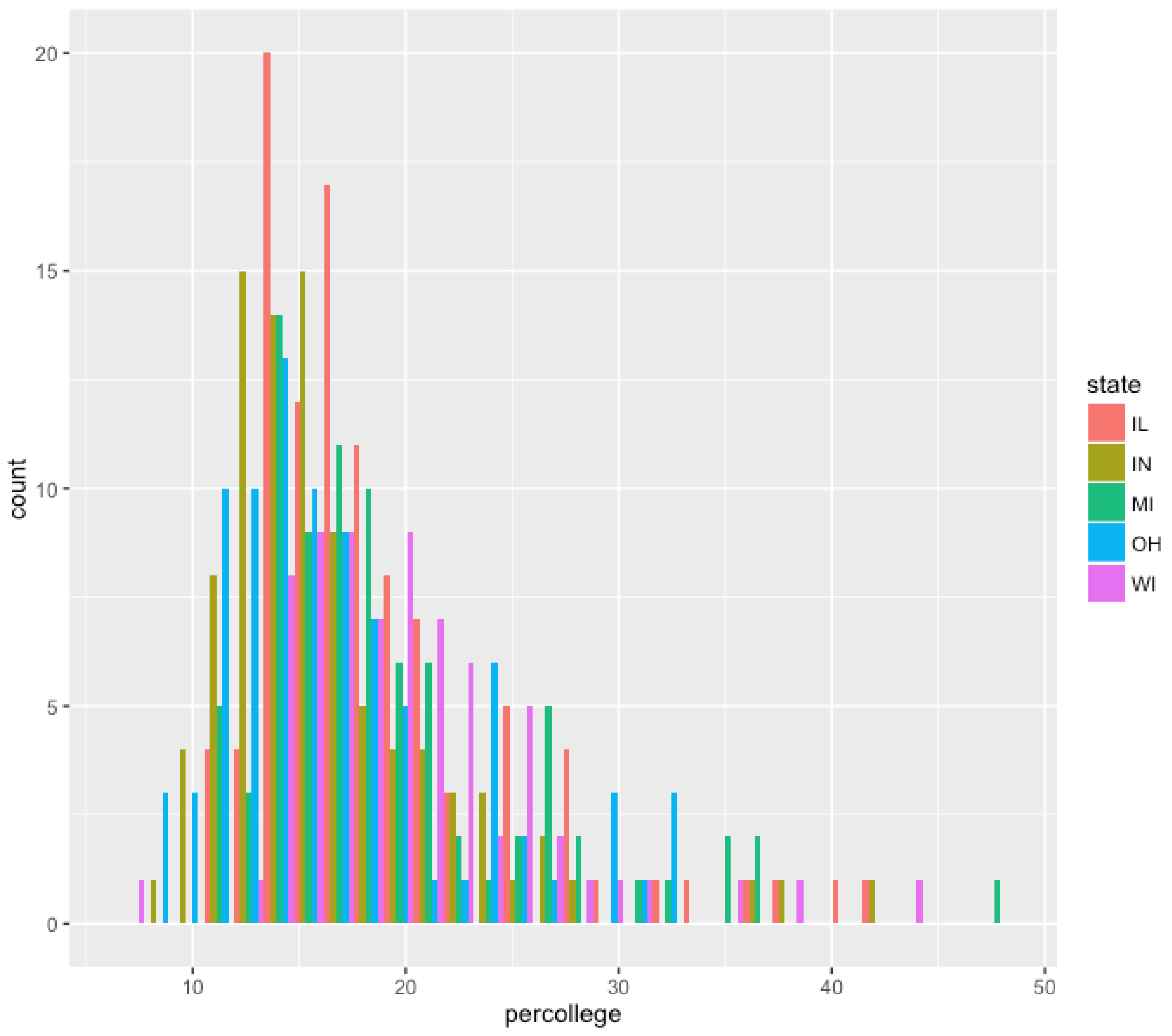
We can color the bars by state using the `fill` option, which functions very similarly to `colour`:

```
ggplot(midwest, aes(x=percollege)) +
    geom_histogram(aes(fill=state))
```



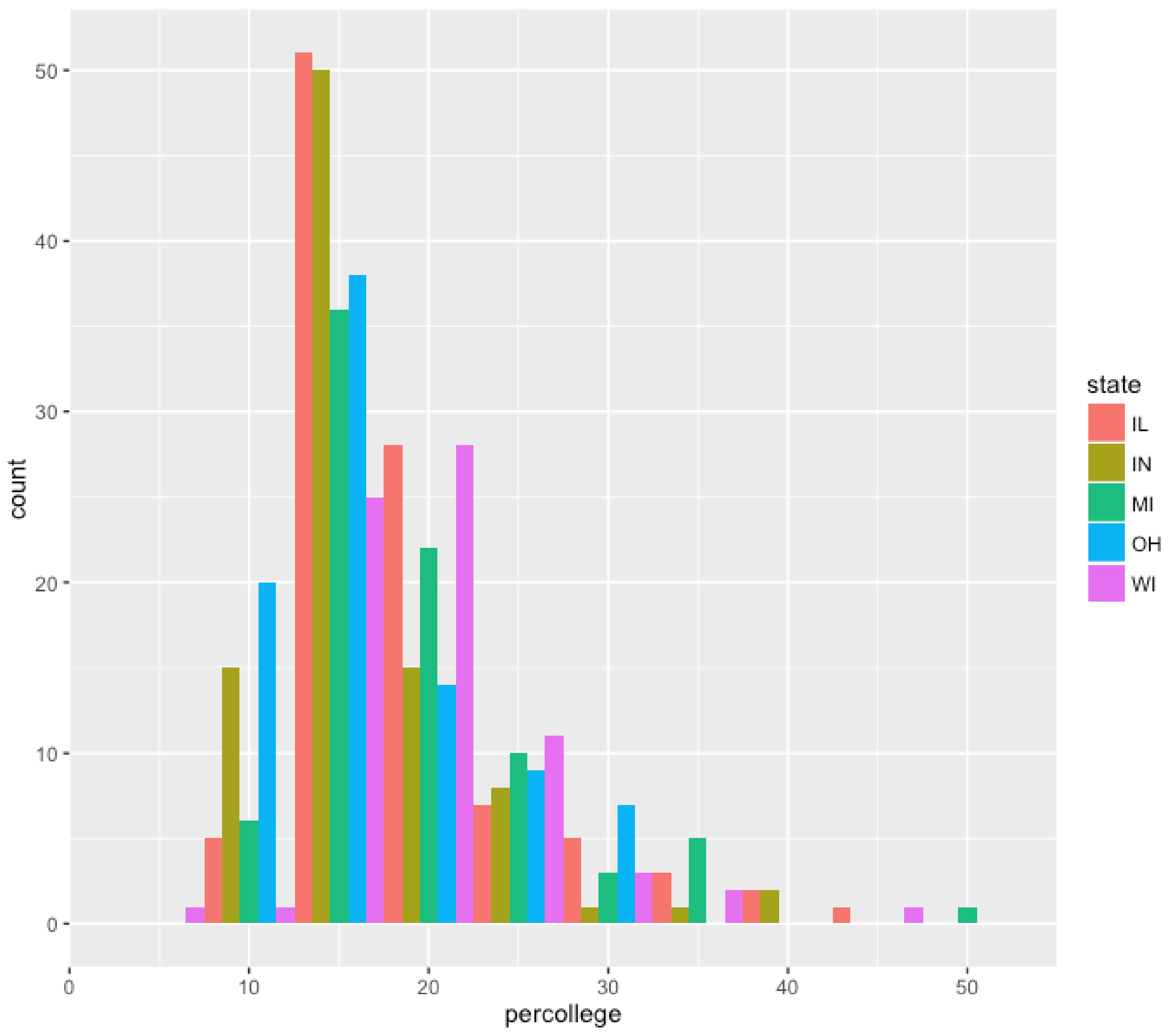
This method of plotting, with stacked bars, makes it difficult to see all the data. We can change that using the option `position="dodge"` inside the histogram call, which places the bars next to each other instead of stacked.

```
ggplot(midwest, aes(x=percollege)) +
    geom_histogram(aes(fill=state), position='dodge')
```



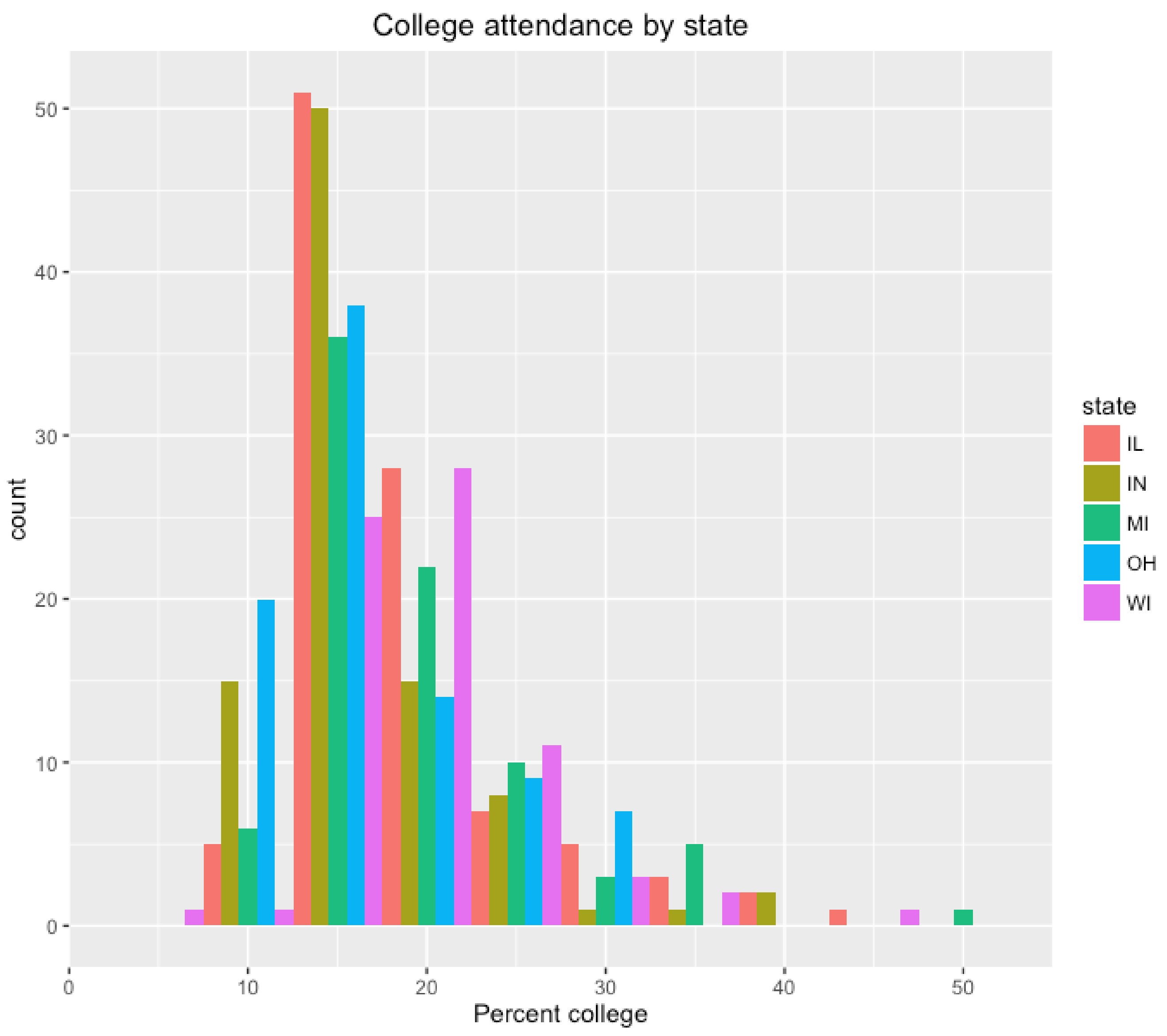
The resolution on this is too fine to see a difference. We can make the same plot, but change the bin size:

```
ggplot(midwest, aes(x=percollege)) +
    geom_histogram(aes(fill=state), position='dodge', binwidth=5)
```



Great! This is looking, if not publication-worthy, at least good enough to send to collaborators. However, the graph doesn't have a title, and the x-axis label is not very descriptive. We can change the plot title and the axis labels using the `labs` function:

```
ggplot(midwest, aes(x=percollege)) +
    geom_histogram(aes(fill=state), position='dodge', binwidth=5) +
    labs(title='College attendance by state', x='Percent college')
```

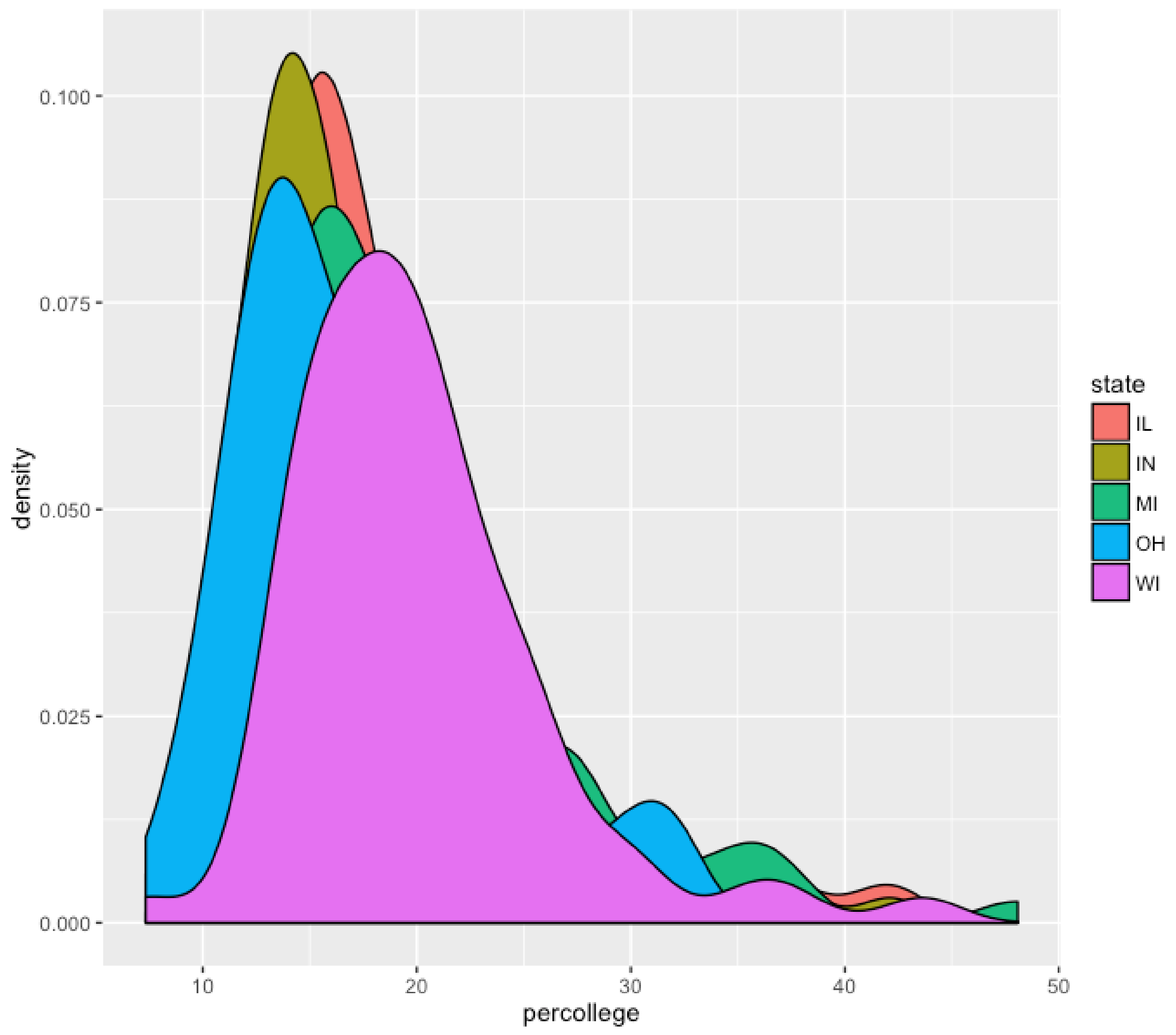


Note that here we're adding another command to our ggplot2 set of function calls, again using `+`.

How would we change the y-axis label?

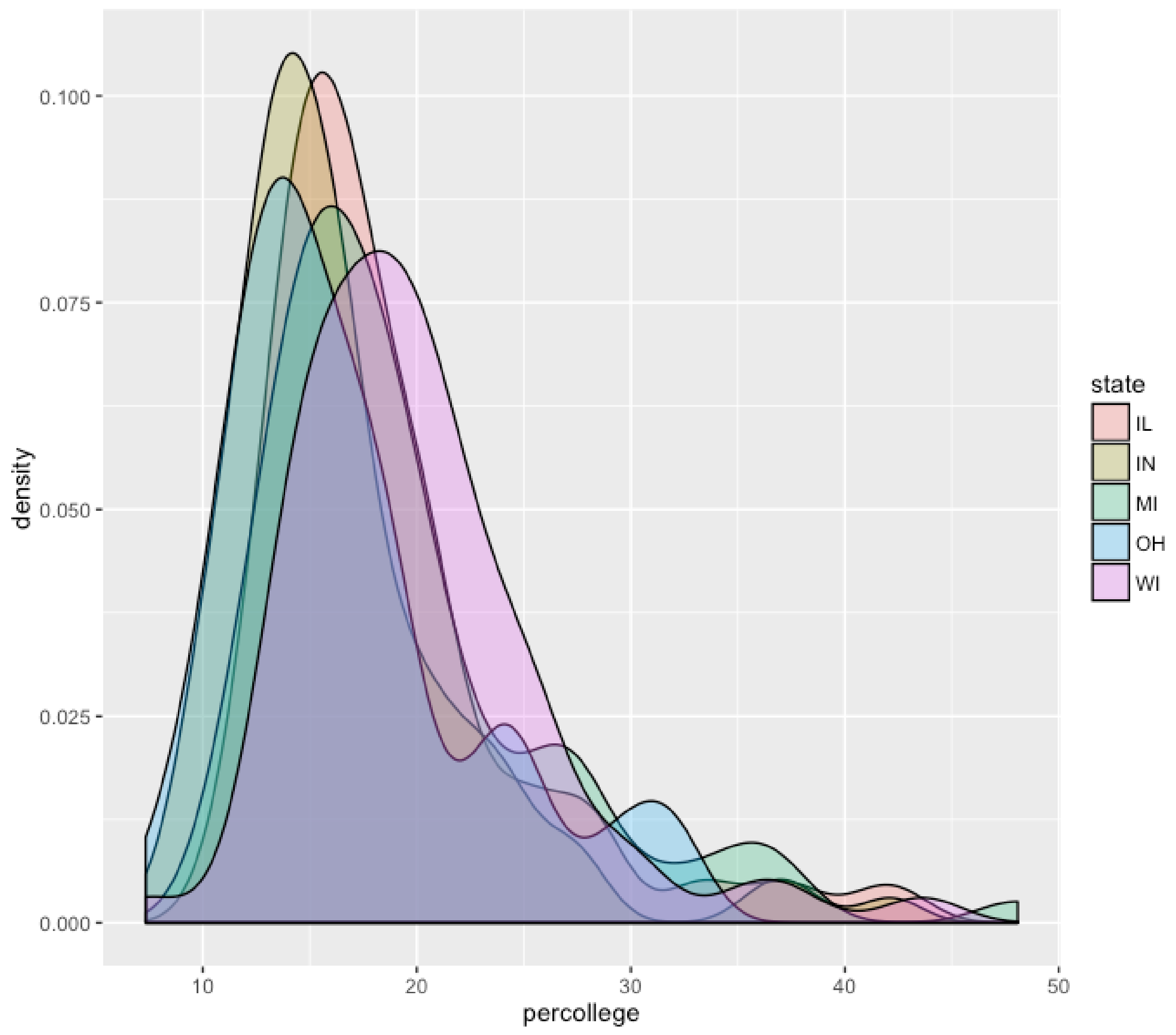
We can also create density plots using `geom_density`, using the fill option by state:

```
ggplot(midwest, aes(x=percollege)) +
    geom_density(aes(fill=state))
```



Unfortunately, these density plots overlap each other, so we need to add transparency:

```
ggplot(midwest, aes(x=percollege)) +
    geom_density(aes(fill=state), alpha=0.3)
```



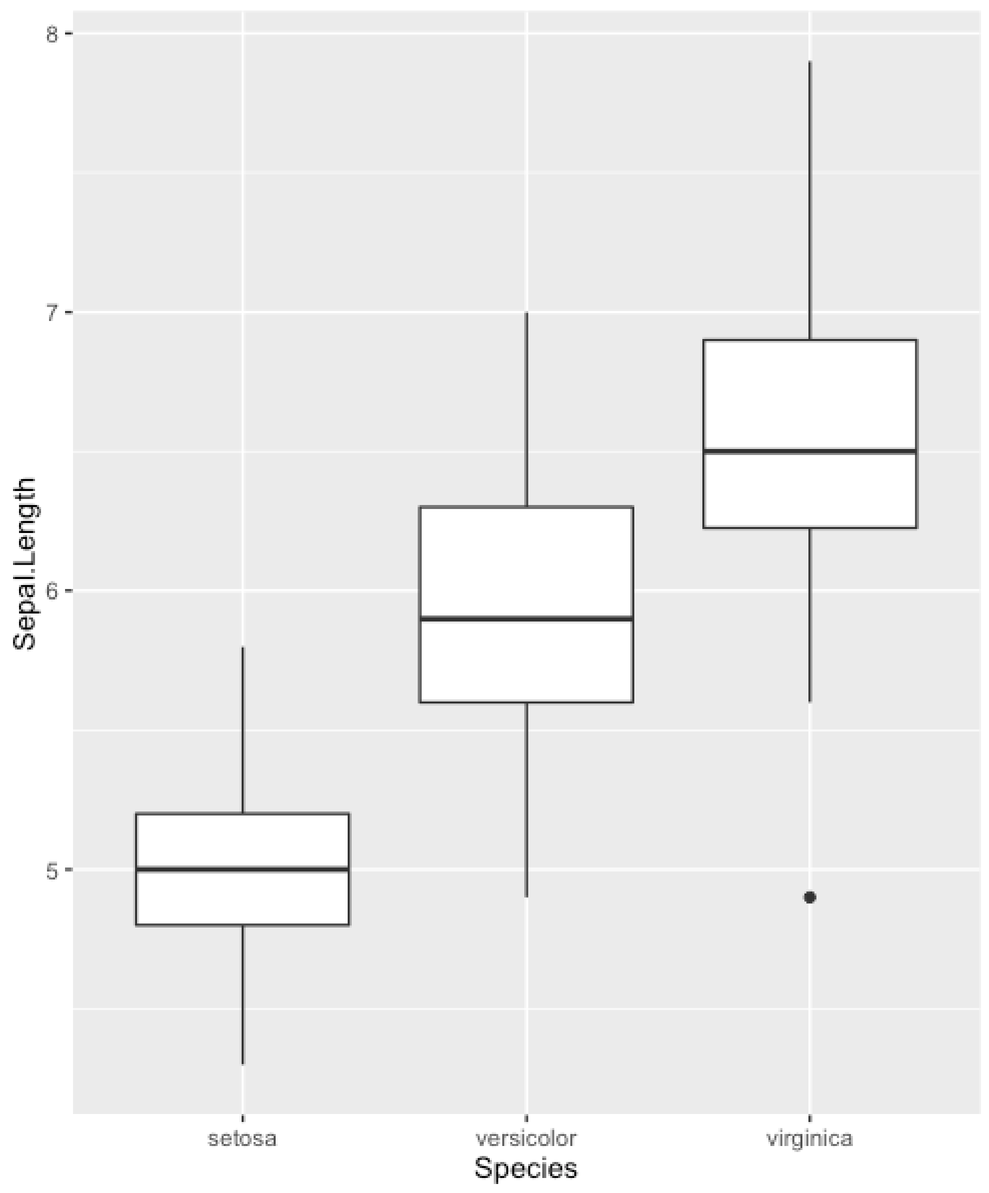
It seems like Wisconsin is the most-educated state out of these five.

What happens when you use `colour` instead of `fill`?

Boxplots

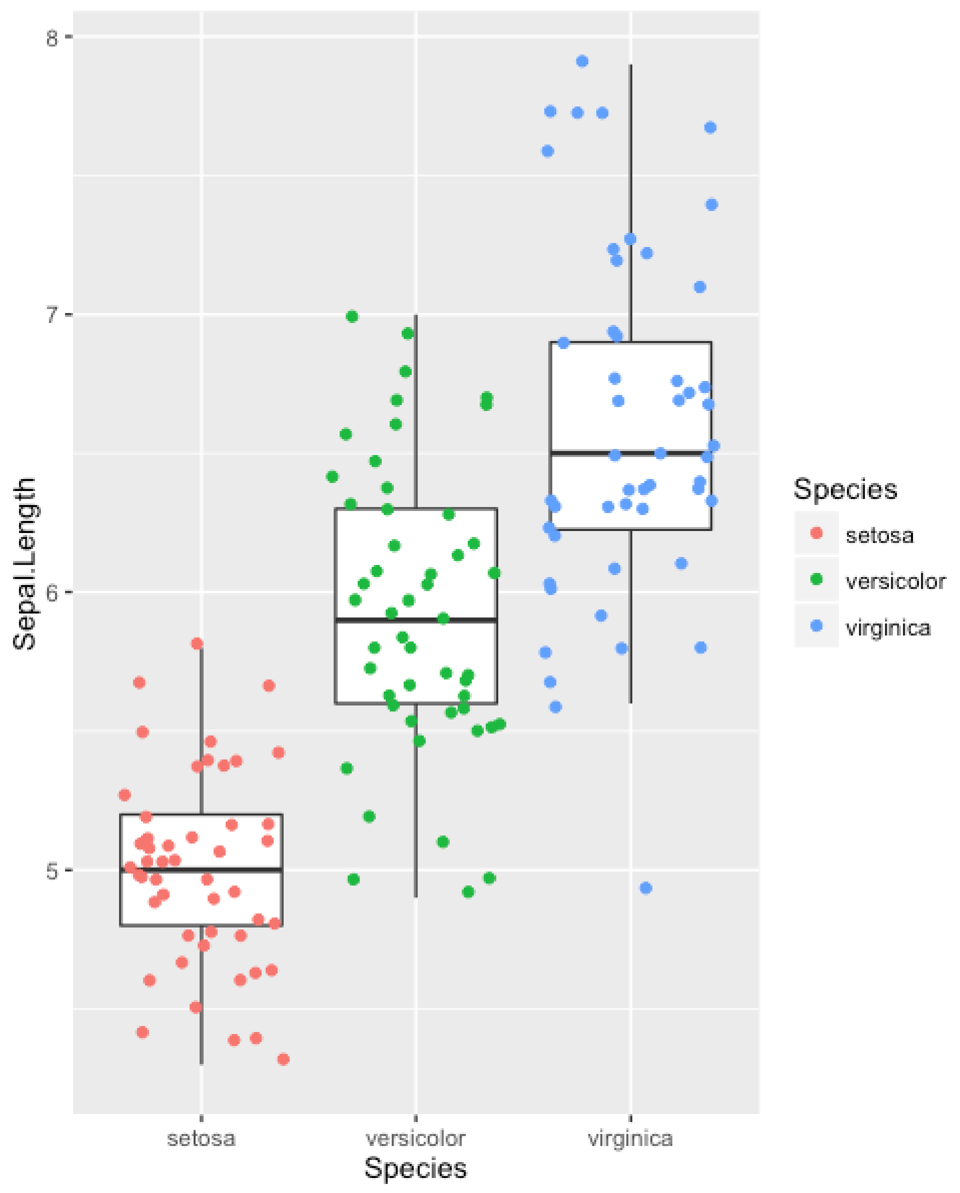
We can use the `geom_boxplot` function to create boxplots. For example, we can go back to our iris data:

```
ggplot(iris, aes(x=Species, y=Sepal.Length)) +
    geom_boxplot()
```



Using ggplot2, we can layer multiple geoms on the same plot. Boxplots let us see the distributions of the data, but we can add individual data points with `geom_jitter` (a “jittered” extension of `geom_point`).

```
ggplot(iris, aes(x=Species, y=Sepal.Length)) +
    geom_boxplot(outlier.color=NA) +
    geom_jitter(aes(colour=Species))
```



Displaying individual data points, in this organized fashion, gives a complete and easily-interpretable picture of the data.

Homework

1. Add another geom that labels the species name for each point on the body weight vs. brain weight plot. (Hint: look at the examples in `?geom_text`.)
2. Create a new plot displaying iris Sepal Length by Species, using `geom_violin` instead of a boxplot. Try coloring by species, and then filling by species.

Resources

- ggplot2 cheat sheet
- Become a superhero, handle your data with R

- Introduction to R graphics with ggplot2

1. Base R, surprisingly, does not have good support for legends. You have to create legends manually (`?legend`) and keep track of values between your legend arguments and the plot. ↩