Exploratory data analysis: Data visualization with {ggplot2}

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One key part of exploratory data analysis is making plots that let you visually inspect the data. This lesson will focus on graphics.

R has three major graphing systems: the base system, lattice, and ggplot2. Each system has its benefits and drawbacks and each is also very versatile with many, many options for creating and adjusting plots.

Unfortunately, there isn't enough time to go through all three graphing systems. After describing a few base R graphing functions, this lesson will focus on {ggplot2} since it allows users to build plots using the grammar of graphics and integrates well with the tidyverse.

Setup

We're using three libraries today:

- {ggplot2}
- {haven}
- {labelled}

The {ggplot2} library is part of the {tidyverse}, so we don't need to load it separately (we can just use `library(tidyverse)` as always).

We're also going to use {haven}, which allows us to read in data files from other software. We'll use it to read in a Stata (`*.dta`) version of the HSLS data we've used before. Though {haven} is part of the {tidyverse} and should have been installed when you installed {tidyverse}, we'll have to explicitly call it

The {labelled}, however, is not part of the {tidyverse}, meaning that we will need to install it first and then load separately.

QUICK EXERCISE Using the console, install the new package "labelled".

```r
## ---------------------------
## libraries
## ---------------------------

library(tidyverse)
```

```
── Attaching packages ─────────────────────────────────────── tidyverse 1.3.0 ──

✔ ggplot2 3.3.0     ✔ purrr   0.3.3
✔ tibble  2.1.3     ✔ dplyr   0.8.5
✔ tidyr   1.0.2     ✔ stringr 1.4.0
✔ readr   1.3.1     ✔ forcats 0.5.0

── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
```

```
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
```

```r
library(haven)
library(labelled)
```

```r
## ---------------------------
## directory paths
## ---------------------------

## assume we're running this script from the ./scripts subdirectory
dat_dir <- file.path("..", "data")
tsc_dir <- file.path(dat_dir, "sch_test")
```

```r
## ---------------------------
## input data
## ---------------------------

## assume we're running this script from the ./scripts subdirectory
df_hs <- read_dta(file.path(dat_dir, "hsls_small.dta"))
df_ts <- read_csv(file.path(tsc_dir, "all_schools.csv"))
```

```
Parsed with column specification:
cols(
  school = col_character(),
  year = col_double(),
  math = col_double(),
  read = col_double(),
  science = col_double()
)
```

Plots using base R

Even though users have developed new graphics libraries, the base R graphics system is still very powerful. It's also very easy to use in a pinch. When I want a quick visual of a data distribution that's just for me, I generally use base R.

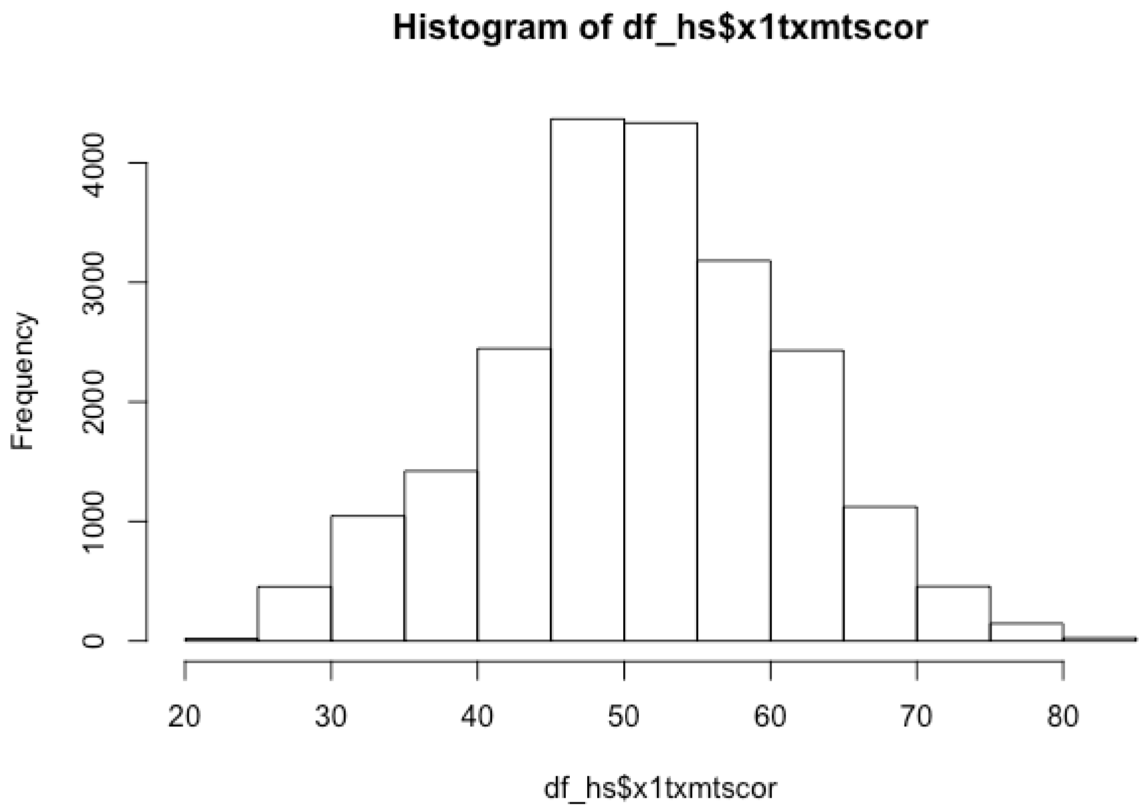
Note that for the next few plots, I'm not much concerned with how they look. Specifically, the axis labels won't be very nice or useful. We could spend time learning to make really nice base R plots for publication, but I'd rather we spend that time with {ggplot2} graphics.

Also note that we'll switch to using the base R data frame `$` notation to pull out the columns we want.

Histogram

For continuous variables, a histogram is a useful plot. Though the `hist()` function has many options to adjust how it looks, the defaults work really well.

```r
## histogram of math scores
hist(df_hs$x1txmtscor)
```



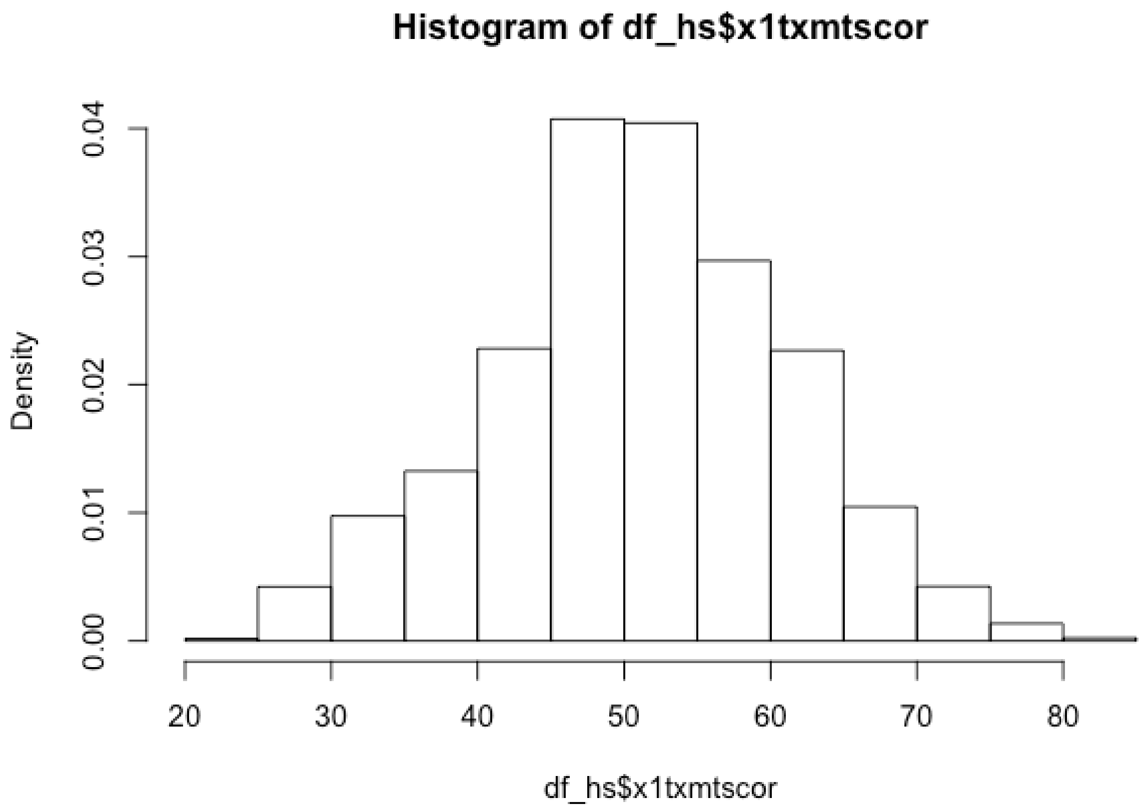
Quick exercise Check the distribution of the students' socioeconomic score (SES).

Density

Density plots are also really helpful. R doesn't have single density plot function, but you can get a density plot in one of two ways, each of which will give a slightly different result.

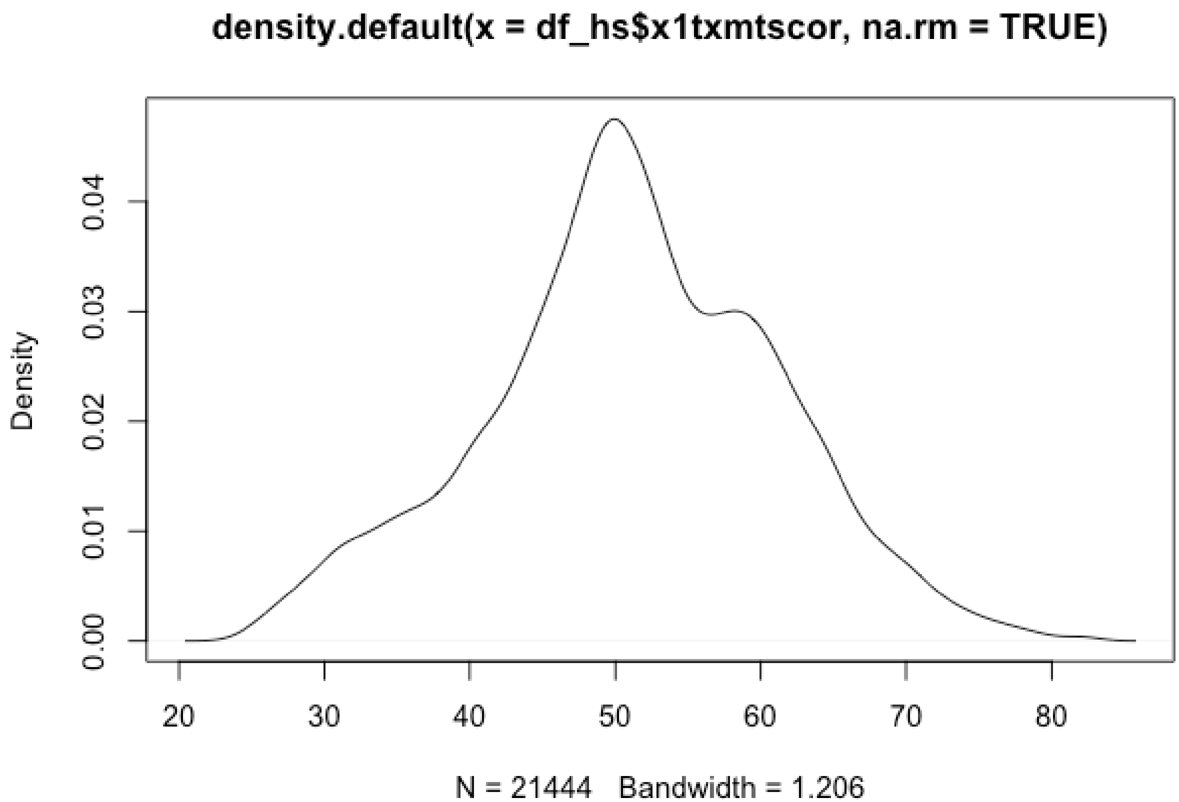
First, you can adjust the `hist()` function to add the `freq = FALSE` argument. It looks like the first histogram above, but notice that the y-axis now represents density rather than counts.

```
## density plot of math scores with hist() function
hist(df_hs$x1txmtscor, freq = FALSE)
```



Second, you can `plot()` the `density()` of a continuous variable. Unlike `hist()`, however, `density()` doesn't automatically ignore missing values, so we have to tell it to remove `NA`s.

```r
## density plot of math scores
plot(density(df_hs$x1txmtscor, na.rm = TRUE))
```



Quick exercise Plot the density of SES. Next, try to use the `col` argument in `plot()` to change the color of the line to `'red'`.

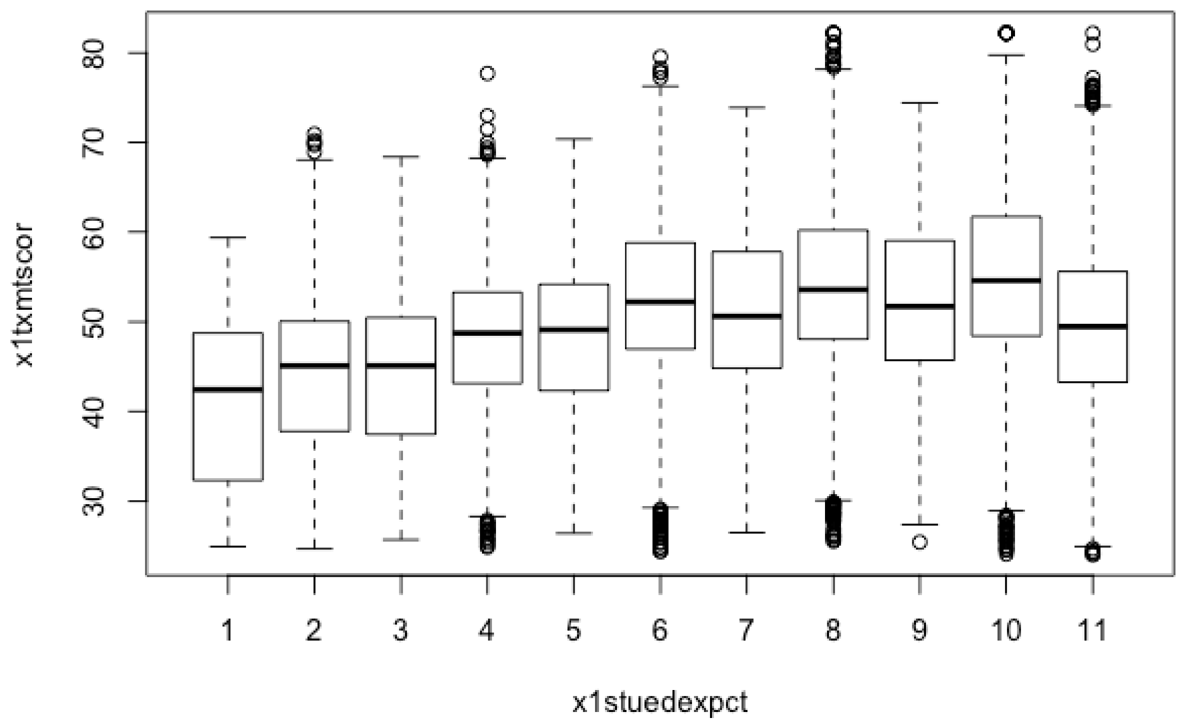
Box plot

Call a box plot using the `boxplot()` function. This one is a little trickier because it uses the R formula construction to set the continuous variable against the group. The formula uses a tilde, ~, and should be constructed like this:

- `<var> ~ <group var>`

Notice how we can use the `data` argument instead of adding `df$` in front of the variable names.

```
## box plot of math scores against student expectations
boxplot(x1txmtscor ~ x1stuedexpct, data = df_hs)
```



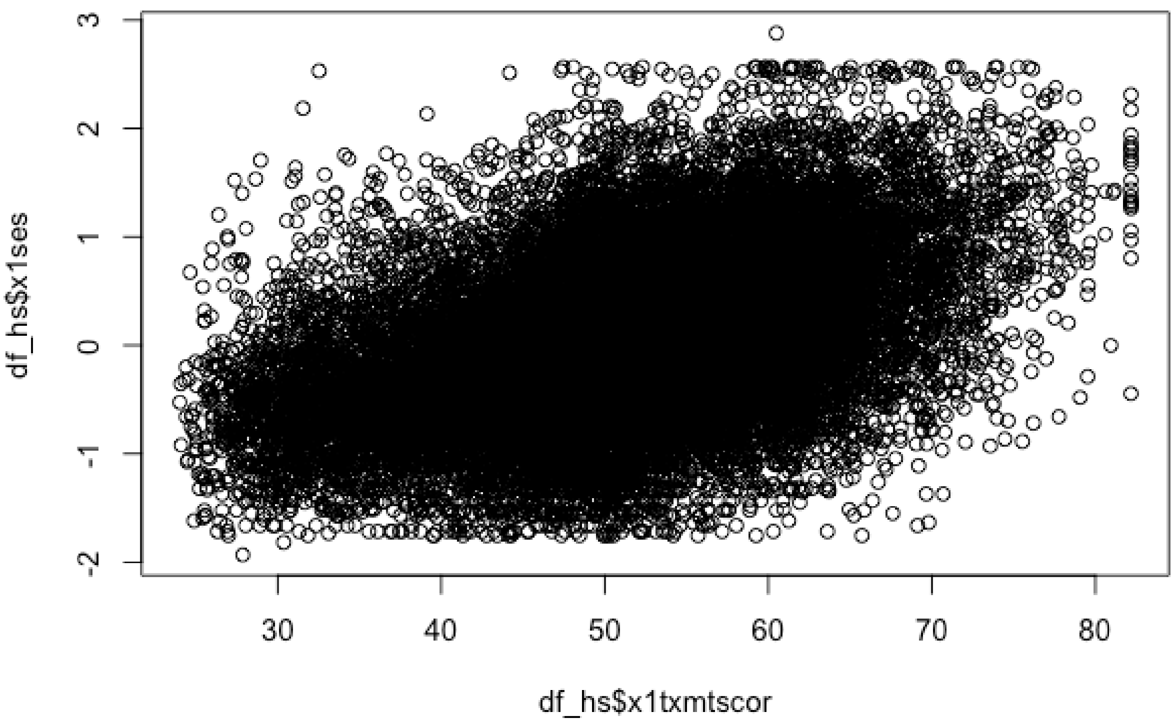
Scatter

Finally, plot continuous variables against one another using the base `plot()` function. There are two primary ways to make a scatter plot using `plot()`:

- `plot(x, y)`
- `plot(y ~ x)`

With both, `x` is the variable that will go on the x-axis and `y` the one that will go on the y-axis. It's really a matter of which makes sense to you. We'll use the first.

```
## scatter plot of math against SES
plot(df_hs$x1txmtscor, df_hs$x1ses)
```



Quick exercise Rerun the above plot, but this time store it in an object. Next, plot math scores against SES using the second formula method and store it in another object. Visually compare the two, but for a more formal test, use `identical(plot_1, plot_2)` on the two plot objects to prove they are the same.

Plots using ggplot2

The first few times I tried to use ggplot2, I didn't quite get it. But once I did (and it doesn't take too long!), I really started to like it. It's now my go-to system for making plots.

The ggplot2 system is too involved to cover in all of its details, but that's kind of the point of the grammar of graphics: once you see how it's put together, you can anticipate the commands you need to build your plot.

We'll start by covering the same plots as above.

Histogram

As the main help site says, all ggplot2 plots need three things:

- **[data]**: The source of the variables you want to plot
- **[aesthetics]**: How variables in the data map onto the plot (*e.g.*, what's on the x-axis? what's on the y-axis?)

- **[geom]**: The geometry of the figure or the kind of figure you want to make (*e.g.*, what do you want to **do** with those data and mappings? A line graph? A box plot?…)

Depending on the plot you want to make, each of these pieces may be called at different points in the command structure, which is usually made up of linked functions like other tidyverse libraries. The key difference between {ggplot2} and {dplyr}, for example, is that while {dplyr} uses the pipe (`%>%`) to connect different functions, {ggplot2} uses a plus sign (`+`).

It may help you remember the difference:

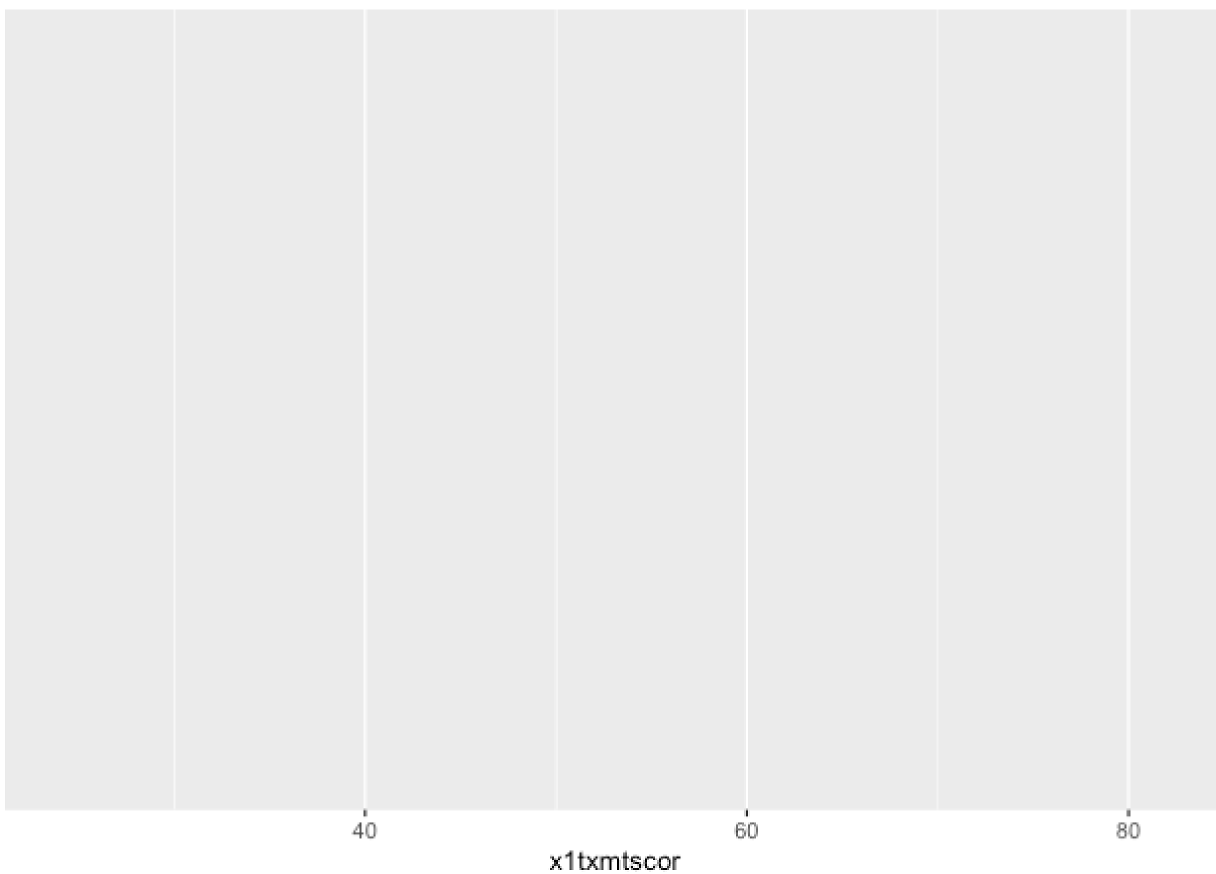
- {dplyr} *moves* output from left to the input in the right and so needs a **pipe**
- {ggplot2} *adds* layer upon layer to build up the final figure and so needs a +

We'll start by making a histogram again. To help make these pieces clearer, I'll use the argument names when possible. The first function, which initializes the plot is `ggplot()`. Its first argument is the data.

The aesthetic mappings, that is, which variables go where or how they function on the plot, go inside the `aes()` function. Since we only have one variable, `x1txmtscor`, it is assigned to `x`.

If we stop there and print…

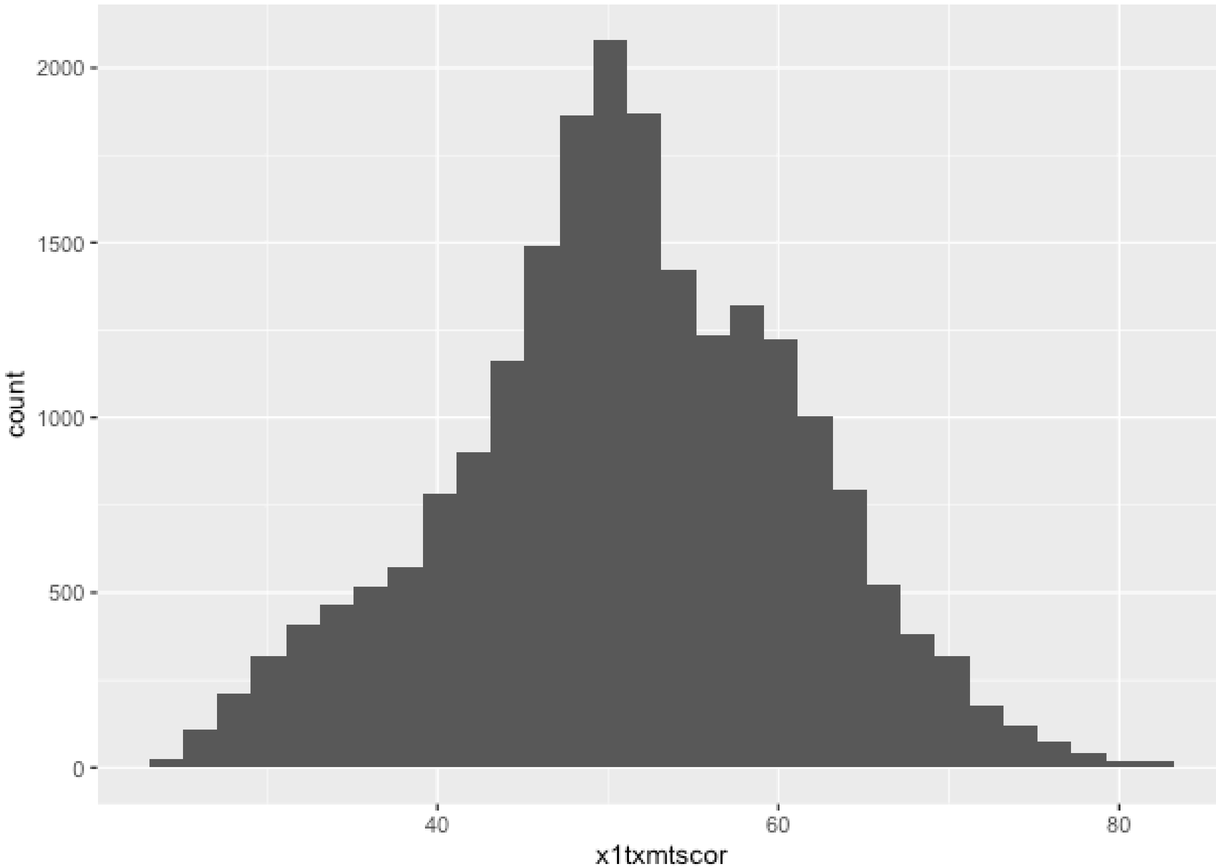
```
## init ggplot
p <- ggplot(data = df_hs, mapping = aes(x = x1txmtscor))
p
```



…nothing! Well, not nothing, but no histogram. That's because the plot object `p` knows the data and the key variable mapping but doesn't know what do with them. What do we want?

Since we want a histogram, we add the `geom_histogram()` function to the existing plot object. Trying again…

```r
## add histogram instruction
p <- p + geom_histogram()
p
```



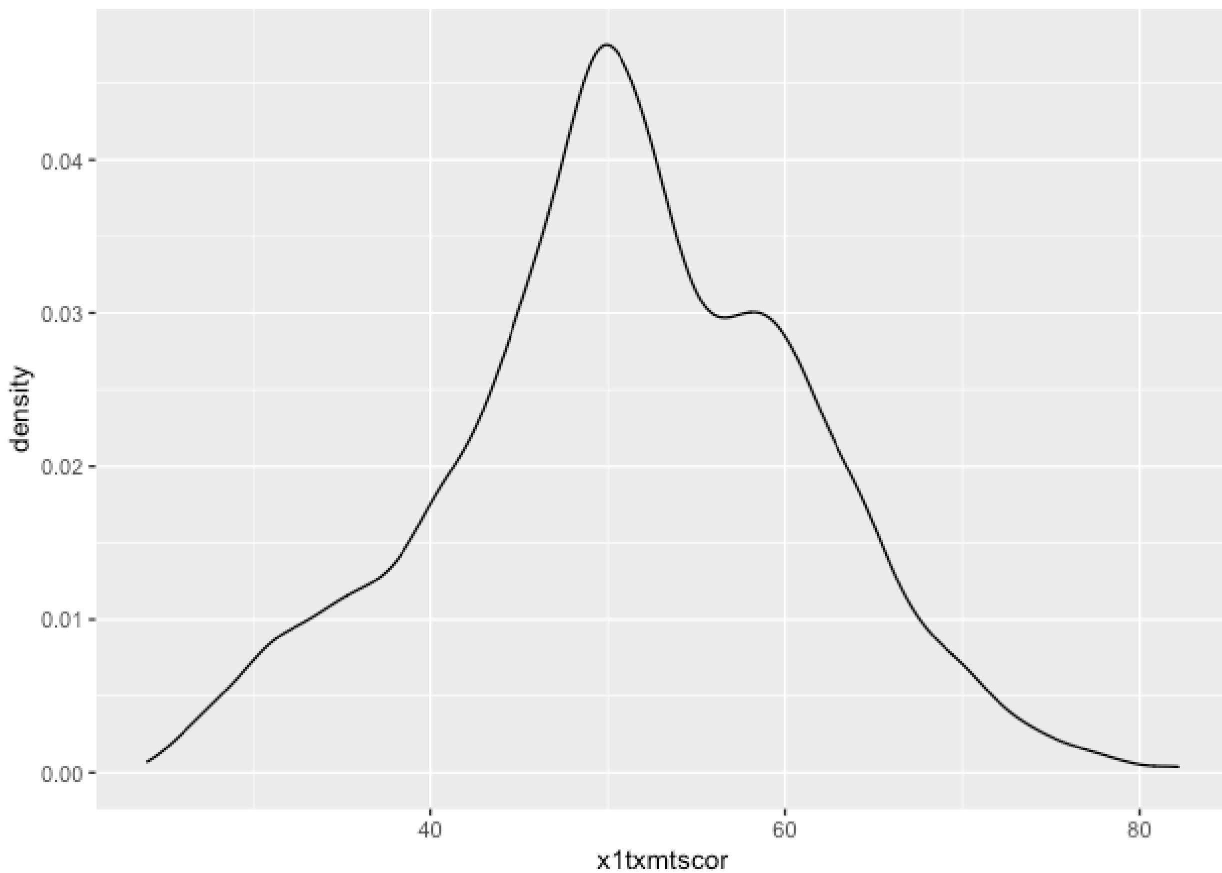
Success!

Density

Unlike the base R graphics system, {ggplot2} does have a density plotting command, `geom_density()`. Instead of building up the figure piecemeal, we'll go ahead and chain the geom to the first command and print.

Notice how the function chain is the mostly the same as above, but (1) written in a single linked chain and (2) using a different `geom_*()` command at the end to indicate that we want something different.

```r
## density
p <- ggplot(data = df_hs, mapping = aes(x = x1txmtscor)) +
    geom_density()
p
```

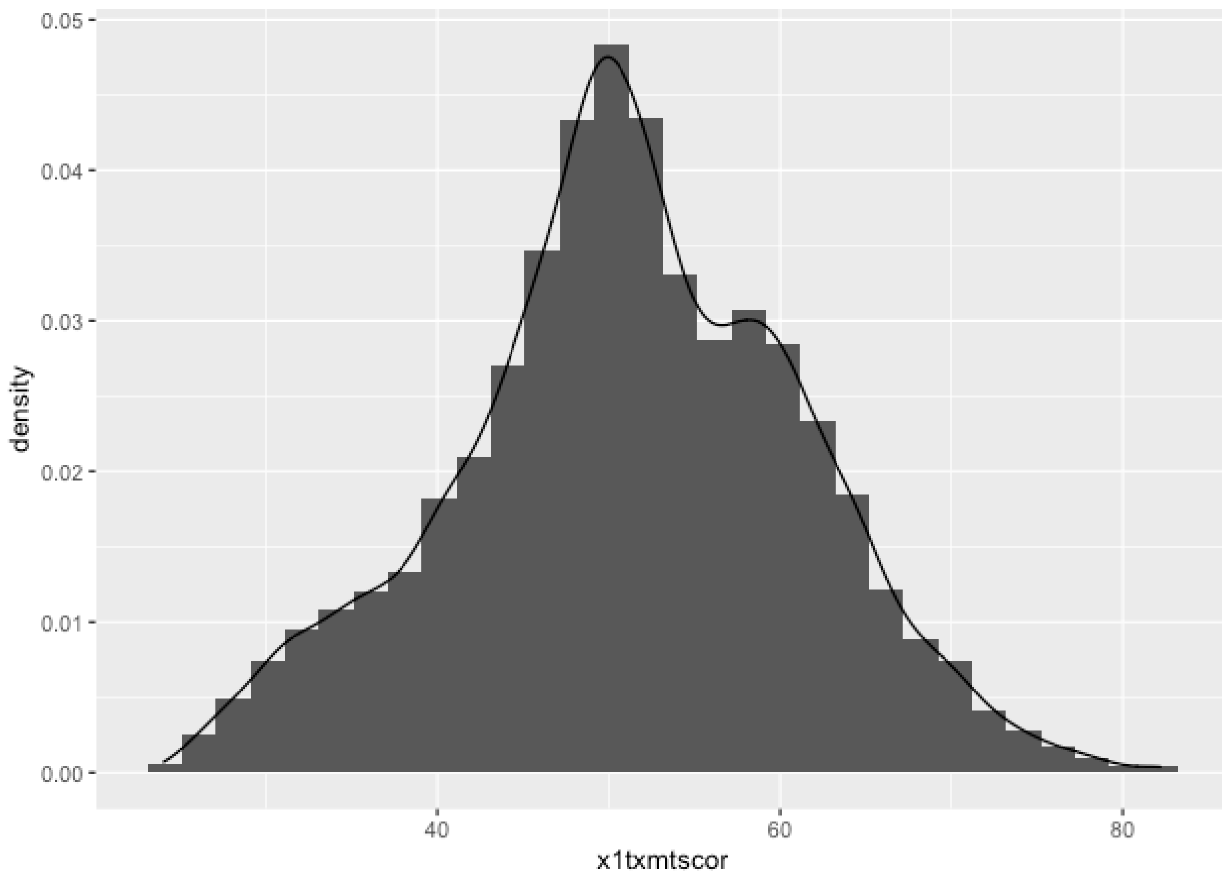


Quick exercise Make a density plot of SES.

If we want to superimpose the density plot over the histogram, we only need chain the two commands together with a slight modification in how the histogram is made. This way, the histogram and the density will be on the same scale.

The change happens in the `geom_histogram()` function, where we add a new mapping: `aes(y = ..density..)`. (**NOTE:** this is similar to what we did above in base R to make a histogram on a density scale.)

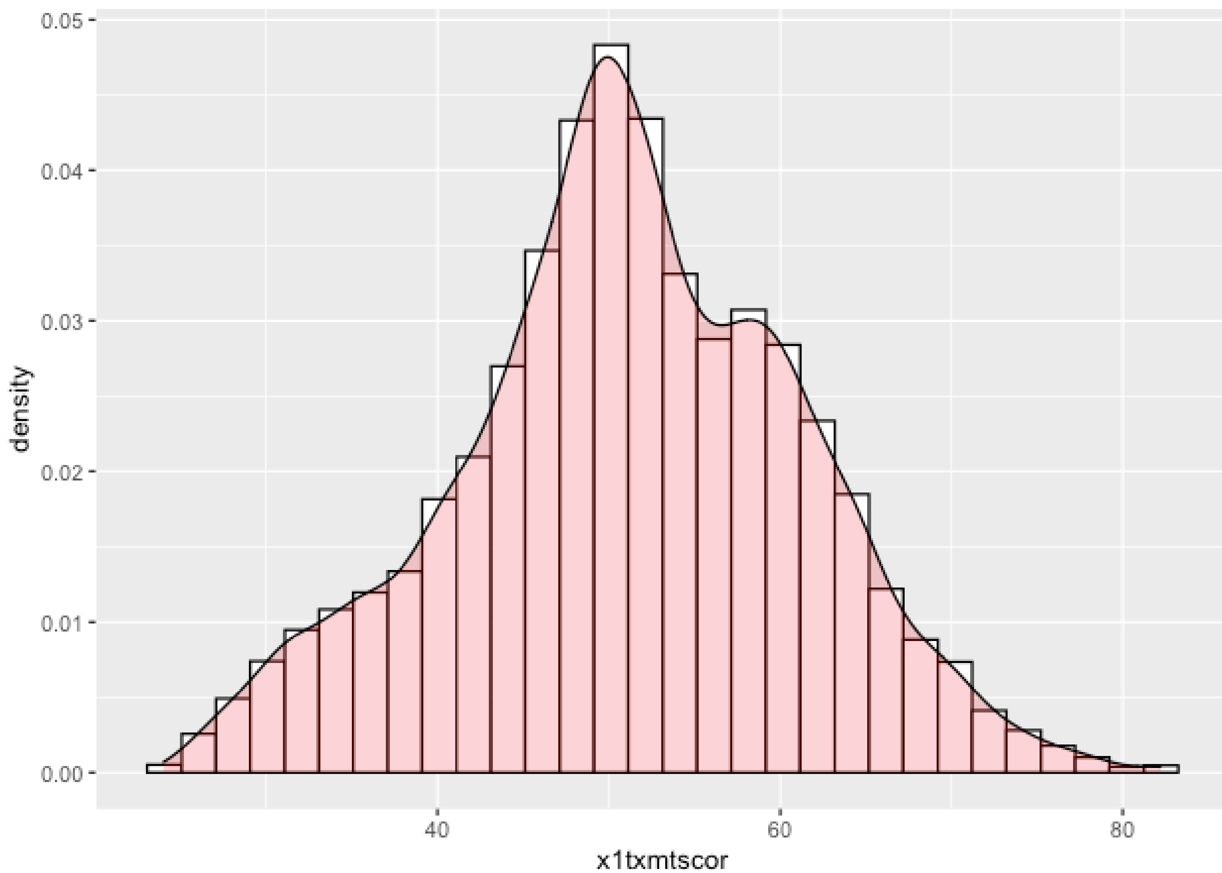
```
## histogram with density plot overlapping
p <- ggplot(data = df_hs, mapping = aes(x = x1txmtscor)) +
    geom_histogram(mapping = aes(y = ..density..)) +
    geom_density()
p
```



It worked, but it's not the greatest visual since the colors are the same and the density plot is thin with no fill.

Adding to what came before, the `geom_histogram()` and `geom_density()` both take on new arguments that change the defaults. Now the resulting plot should look nicer and be easier to read.

```
## histogram with density plot overlapping (add color to see better)
p <- ggplot(data = df_hs, mapping = aes(x = x1txmtscor)) +
    geom_histogram(mapping = aes(y = ..density..),
                   color = "black",
                   fill = "white") +
    geom_density(fill = "red", alpha = 0.2)
p
```



Quick exercise Try changing some of the arguments in the last plot. What happens when you change `alpha` (keep the value between 0 and 1)? What does the `color` argument change? And `fill`? What happens if you switch the `geom_*()` functions, call `geom_histogram()` after you call `geom_density()`?

Two-way

Plotting the difference in a continuous distribution across groups is a common task. Let's see the difference between student math scores between students with parents who have any postsecondary degree and those without.

Since we're using data that was labelled in Stata, we'll first use `val_labels()` to check the `x1paredu` variable.

```
## get parental education levels, use `val_labels()` to show them
df_hs %>% select(x1paredu) %>% val_labels
```

```
$x1paredu
                                Missing
                                     -9
                      Unit non-response
                                     -8
                Item legitimate skip/NA
                                     -7
No bio/adoptive/step-parent in household
                                      0
```

```
                         Less than high school
                                             1
                    High school diploma or GED
                                             2
                             Associate's degree
                                             3
                              Bachelor's degree
                                             4
                                Master's degree
                                             5
 Ph.D/M.D/Law/other high lvl prof degree
                                             7
```

We can see that all values of `x1paredu` greater than 2 represent parents with some college credential. Since we want only two distinct groups, we can use the operator `>=` to make a new 0/1 binary variable. If a value of `x1paredu` is above 3, then the new indicator `pared_coll` will be 1; if not, 0.

The `ggplot()` function doesn't need to use our full data. In fact, our data needs to be set up a bit differently to make this plot. We'll make a new temporary data object that only has the data we need.

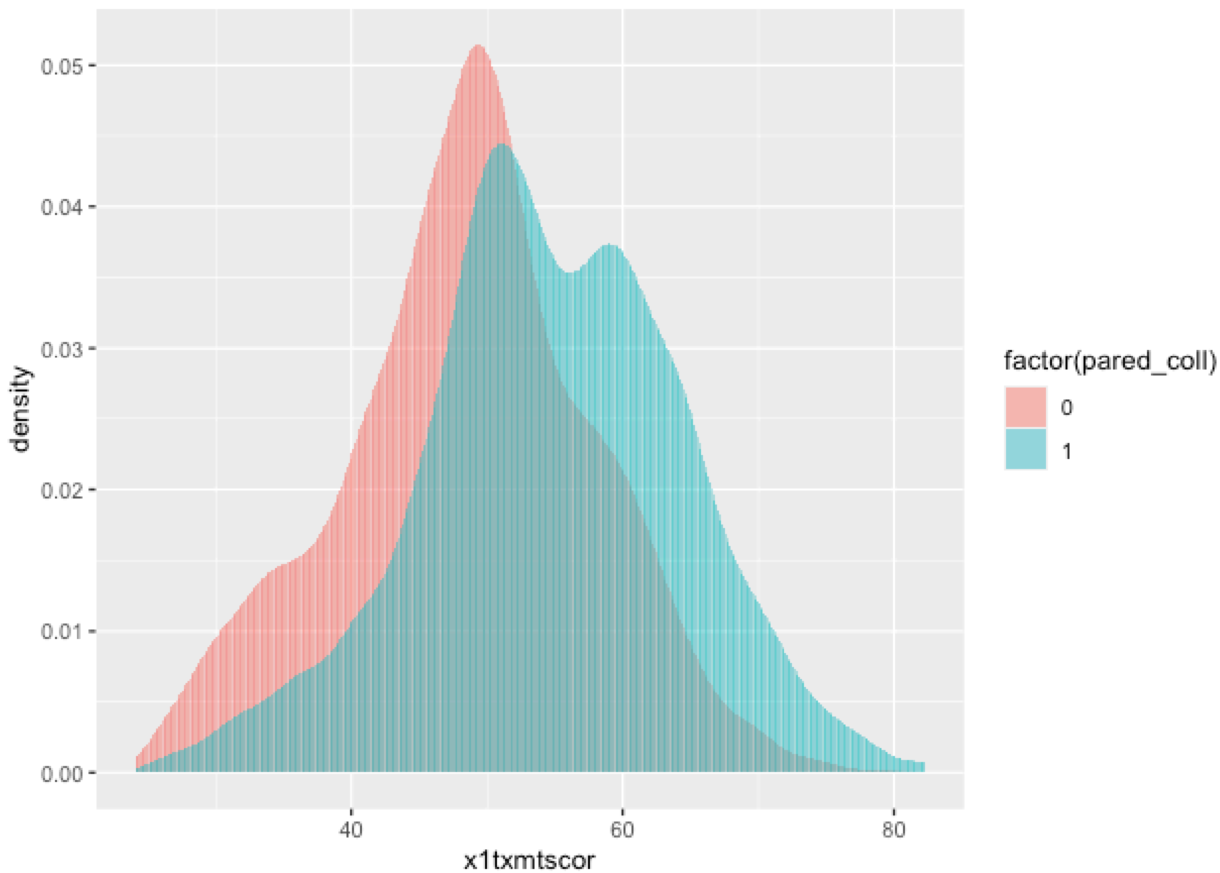
```r
## need to set up data
plot_df <- df_hs %>%
    select(x1paredu, x1txmtscor) %>%
    drop_na() %>%                      # can't plot NA so will drop
    mutate(pared_coll = ifelse(x1paredu >= 3, 1, 0)) %>%
    select(-x1paredu)

## show
head(plot_df)
```

```
# A tibble: 6 x 2
  x1txmtscor pared_coll
   <dbl+lbl>      <dbl>
1       59.4          1
2       47.7          1
3       64.2          1
4       49.3          1
5       62.6          1
6       58.1          1
```

To plot against the two groups we've made, we need to add it to the aesthetic feature, `aes()`. The math score, `x1txmtscor`, is still mapped to `x`, but since we want two side-by-side histograms, we set the `fill` aesthetic to our new indicator variable. So the function knows that it's a group (and not just a continuous number with only two values), we wrap it in the `factor()` function.

Finally, we add some changes to the `geom_histogram()` function so that each group is on the same scale.

```r
## two way histogram
p <- ggplot(data = plot_df,
            aes(x = x1txmtscor, fill = factor(pared_coll))) +
    geom_histogram(alpha = 0.5, stat = "density", position = "identity")
p
```

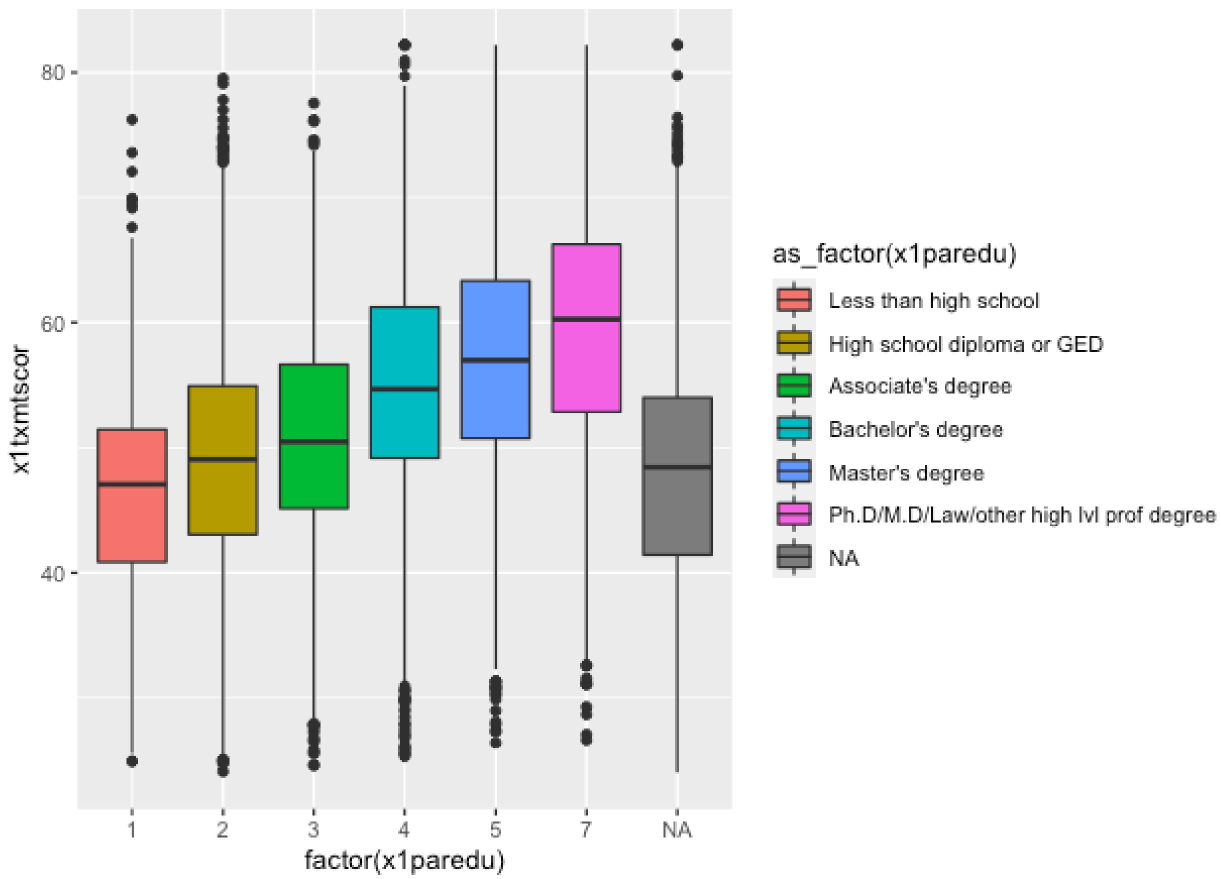


Quick exercise Remove some of the new arguments in `geom_histogram()`. How does the resulting plot change? Remove the `factor()` function from around `pared_coll`: what happens?

Box plot

By this point, you're hopefully seeing the pattern in how {ggplot2} figures are put together. To make a box plot, we need to add a `y` mapping to the `aes()` in addition to the `x` mapping. We don't have to, but we've also added the same variable to `fill` as we did to `x`. We do this so that in addition to having different box and whisker plots along the x-axis, each plot is given its own color.

```
## box plot using both factor() and as_factor()
p <- ggplot(data = df_hs,
            mapping = aes(x = factor(x1paredu),
                          y = x1txmtscor,
                          fill = as_factor(x1paredu))) +
    geom_boxplot()
p
```

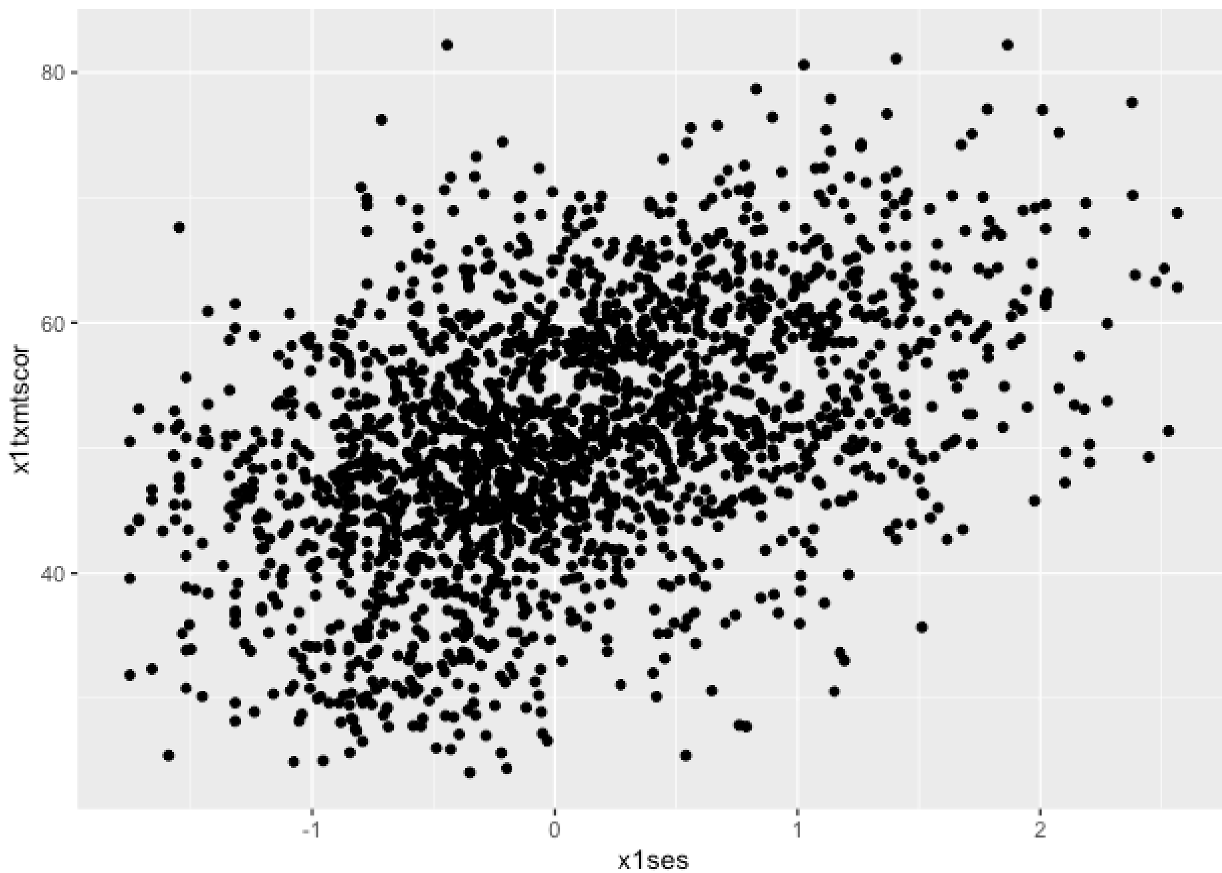


Quick exercise Change the `as_factor()` and `factor()` functions above. How does the plot change?

Scatter

To make a scatter plot, make sure that the `aes()` has mappings for the `x` axis and `y` axis and then use `geom_point()` to plot. To make things easier to see, we'll first reduce the data to 10% of the full sample using `sample_frac()` from dplyr.

```
## sample 10% to make figure clearer
df_hs_10 <- df_hs %>% sample_frac(0.1)

## scatter
p <- ggplot(data = df_hs_10, mapping = aes(x = x1ses, y = x1txmtscor)) +
    geom_point()
p
```



Now that we have our scatter plot, let's say that we want to add a third dimension. Specifically, we want to change the color of each point based on whether a student plans to earn a Bachelor's degree or higher. That means we need a new dummy variable that is 1 for those with BA/BS plans and 0 for others.

We can look at the student base year expectations with `count()`:

```
## see student base year plans
df_hs %>%
    count(x1stuedexpct)
```

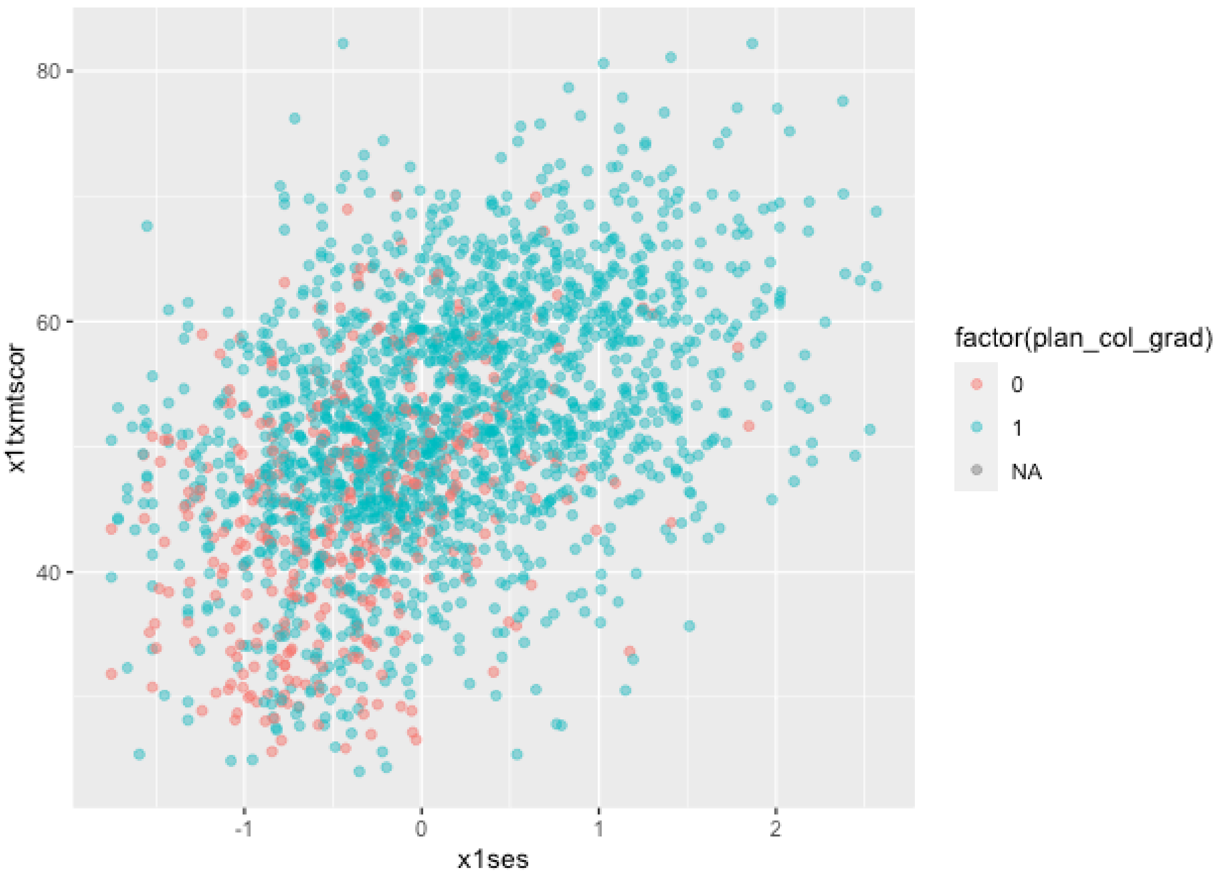
```
# A tibble: 12 x 2
                                   x1stuedexpct     n
                                      <dbl+lbl> <int>
 1  1 [Less than high school]                      93
 2  2 [High school diploma or GED]               2619
 3  3 [Start an Associate's degree]               140
 4  4 [Complete an Associate's degree]           1195
 5  5 [Start a Bachelor's degree]                 115
 6  6 [Complete a Bachelor's degree]             3505
 7  7 [Start a Master's degree]                   231
 8  8 [Complete a Master's degree]               4278
 9  9 [Start Ph.D/M.D/Law/other prof degree]      176
10 10 [Complete Ph.D/M.D/Law/other prof degree]  4461
11 11 [Don't know]                               4631
12 NA                                            2059
```

We see that `x1stuedexpct >= 6` means a student plans to earn a Bachelor's degree or higher. Let's create that.

```
## create variable for students who plan to graduate from college
df_hs_10 <- df_hs_10 %>%
    mutate(plan_col_grad = ifelse(x1stuedexpct >= 6, 1, 0))
```

Now that we have our new variable `plan_col_grad`, we can add it the `color` aesthetic, `aes()` in `geom_point()`. Don't forget to use `factor()` so that ggplot knows to treat it like a group!

```
## scatter
p <- ggplot(data = df_hs_10,
            mapping = aes(x = x1ses, y = x1txmtscor)) +
    geom_point(mapping = aes(color = factor(plan_col_grad)), alpha = 0.5)
p
```



Quick exercise Change how you make `plan_col_grad` so that instead of 1 and 0, you use 'yes' and 'no'. Make your figure again. What changes?

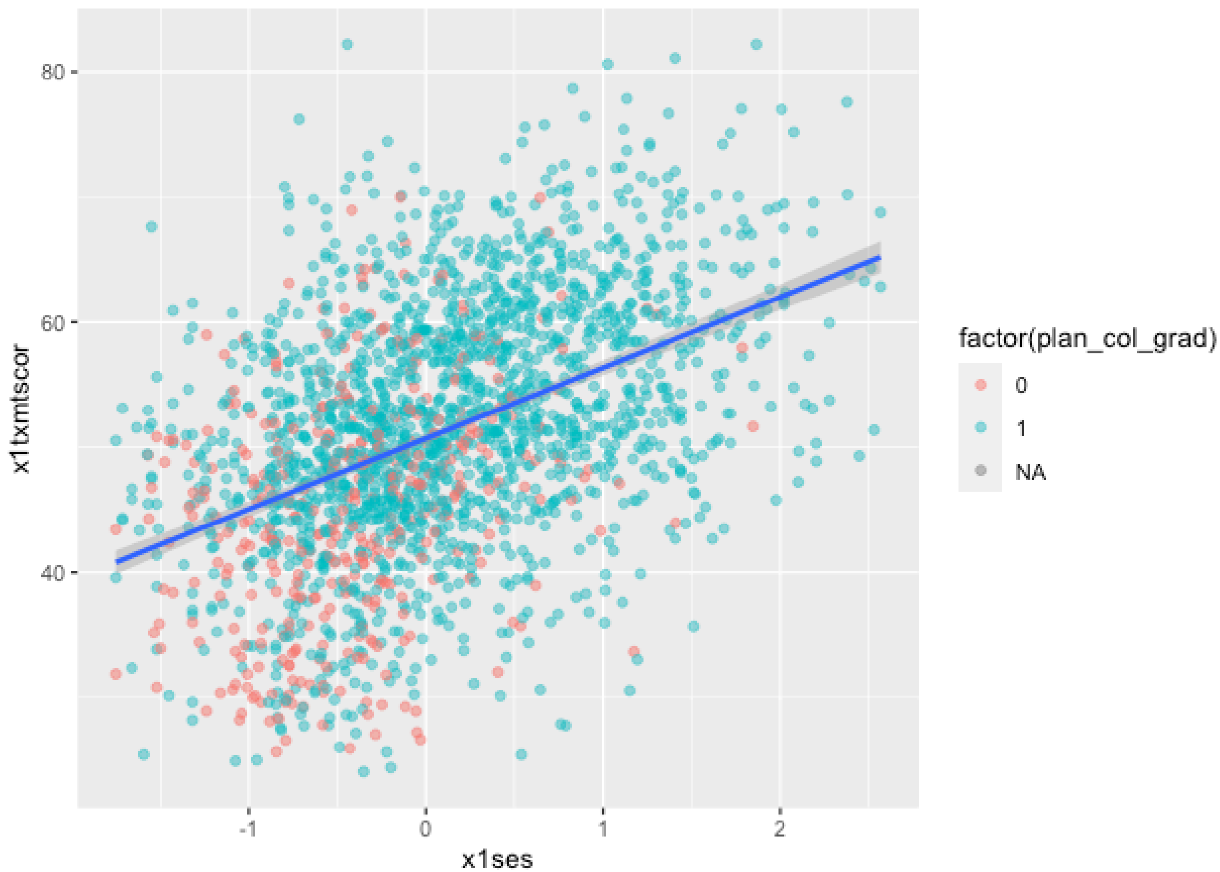
Fitted lines

It's often helpful to plot fitted lines against a scatter plot to help see the underlying trend. There are a number of ways to do this with the `geom_smooth()` function.

Linear fit

Setting `method = lm` in `geom_smooth()` will fit a simple straight line with 95% confidence interval shaded around it.

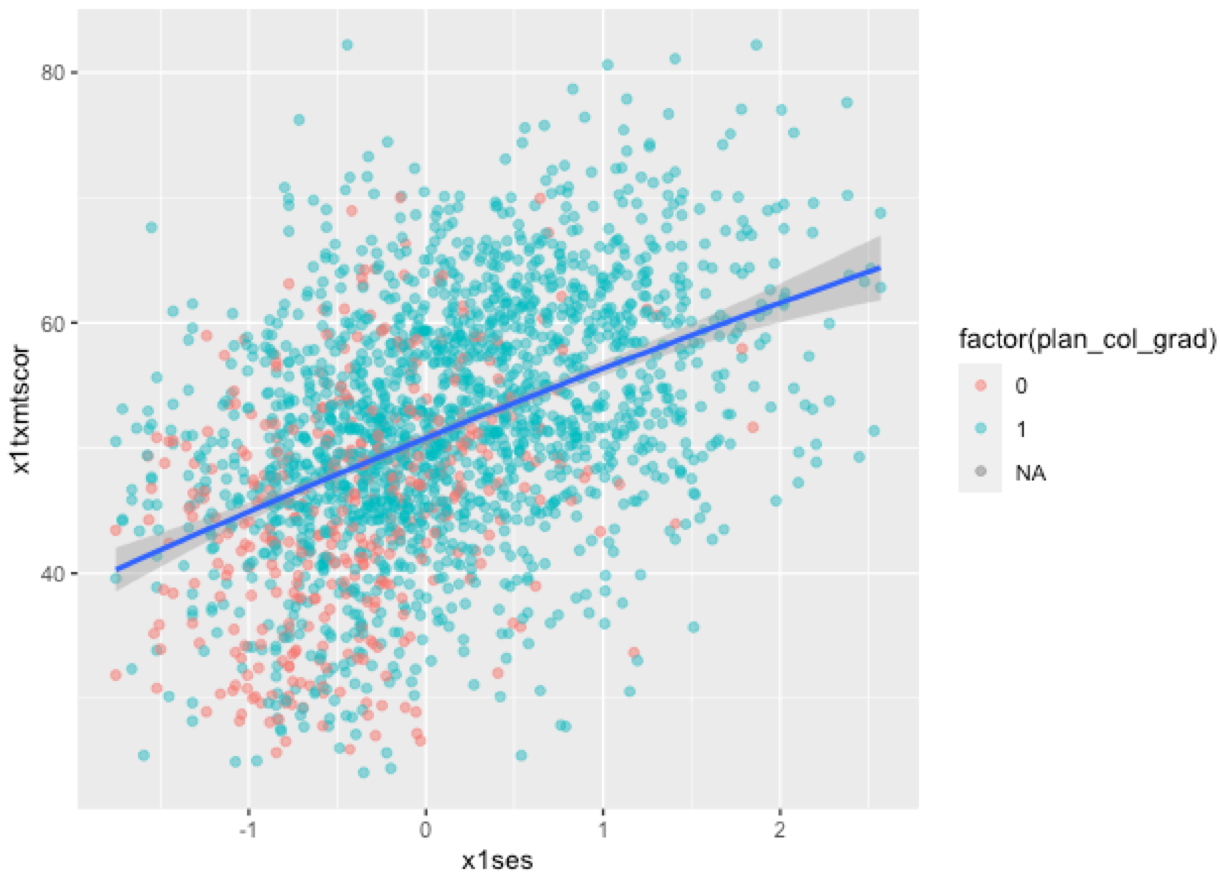
```
## add fitted line with linear fit
p <- ggplot(data = df_hs_10, mapping = aes(x = x1ses, y = x1txmtscor)) +
    geom_point(mapping = aes(color = factor(plan_col_grad)), alpha = 0.5) +
    geom_smooth(method = lm)
p
```



Linear fit with polynomials

In addition to the `method`, we can add a `formula` to allow the fitted line to take a non-linear shape. Using the `aes()` values of `x` and `y`, the argument below uses an R formula, `y ~ x`, but with the addition of the `poly()` function. Setting the second argument in `poly()` to 2 gives the line an extra quadratic term, which allows it to take a more curved shape.

```
## add fitted line with polynomial linear fit
p <- ggplot(data = df_hs_10, mapping = aes(x = x1ses, y = x1txmtscor)) +
    geom_point(mapping = aes(color = factor(plan_col_grad)), alpha = 0.5) +
    geom_smooth(method = lm, formula = y ~ poly(x,2))
p
```

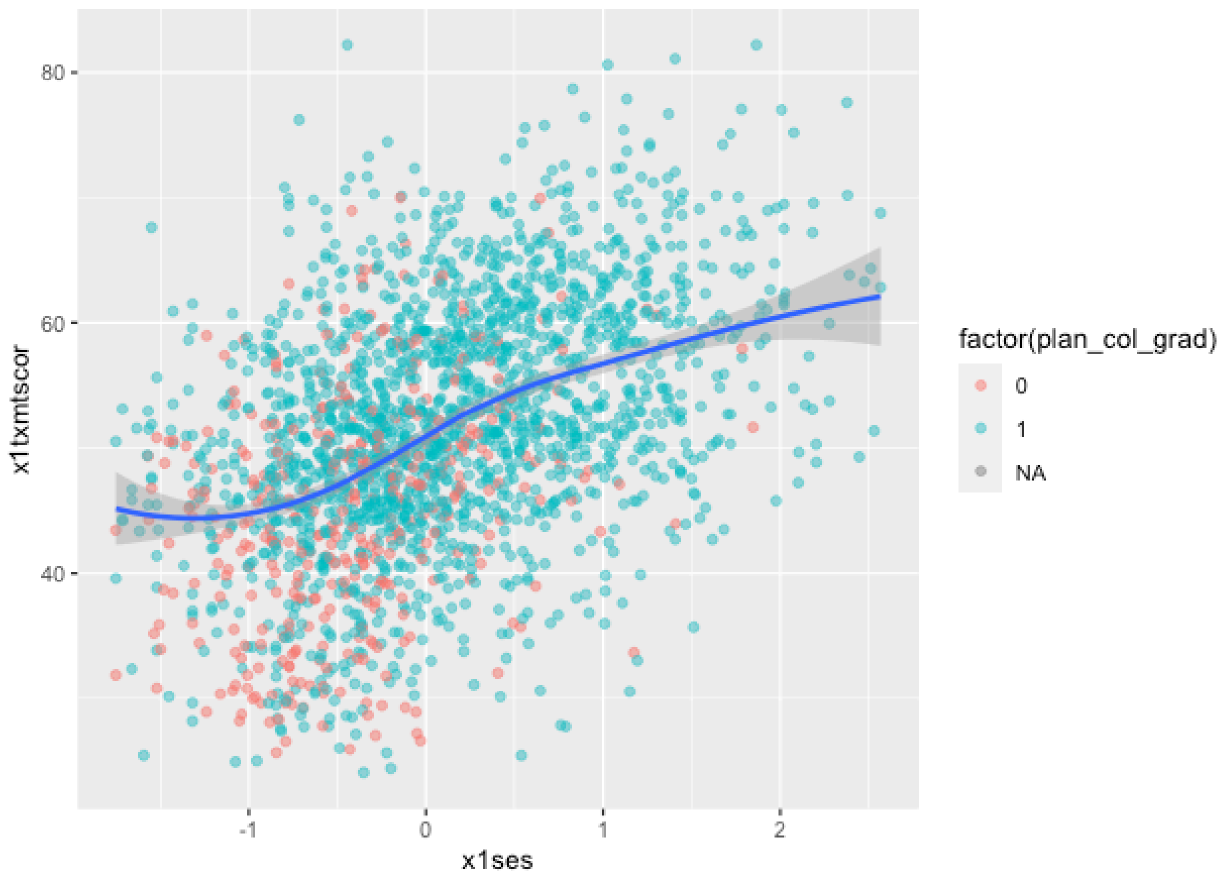


Quick exercise Change the value in `poly()` to higher numbers. How does the line change?

Loess

Finally, we can skip trying to adjust a linear line and just fit a loess.

```
## add fitted line with loess
p <- ggplot(data = df_hs_10, mapping = aes(x = x1ses, y = x1txmtscor)) +
    geom_point(mapping = aes(color = factor(plan_col_grad)), alpha = 0.5) +
    geom_smooth(method = loess)
p
```



To be clear, these semi-automated lines of best fit should not be used to draw final conclusions about the relationships in your data. You will want to do **much more** analytic work to make sure any correlations you observe aren't simply spurious and that fitted lines are telling you something useful. That said, fitted lines via {ggplot2} can be useful when first trying to understand your data or to more clearly show observed trends.

Line graph

When you want to show changes in one variable as a function of another variable, *e.g.*, changes in test scores over time, then a line graph is typically your best choice. Since our `hsls_small` data is cross-sectional, we'll shift to using our school test score data. Remember that test score data show three sets of test scores (math, science, and reading) for four schools over a period of six years. This data frame is long in year, but wide in test type. It looks like this:

```
## show test score data
df_ts
```

```
# A tibble: 24 x 5
   school        year  math  read science
   <chr>        <dbl> <dbl> <dbl>   <dbl>
 1 Bend Gate     1980   515   281     808
 2 Bend Gate     1981   503   312     814
 3 Bend Gate     1982   514   316     816
 4 Bend Gate     1983   491   276     793
 5 Bend Gate     1984   502   310     788
 6 Bend Gate     1985   488   280     789
```

```
 7 East Heights  1980   501   318     782
 8 East Heights  1981   487   323     813
 9 East Heights  1982   496   294     818
10 East Heights  1983   497   306     795
# … with 14 more rows
```

To keep it simple for our first line polot, we'll filter our plot data to keep only scores for one school.

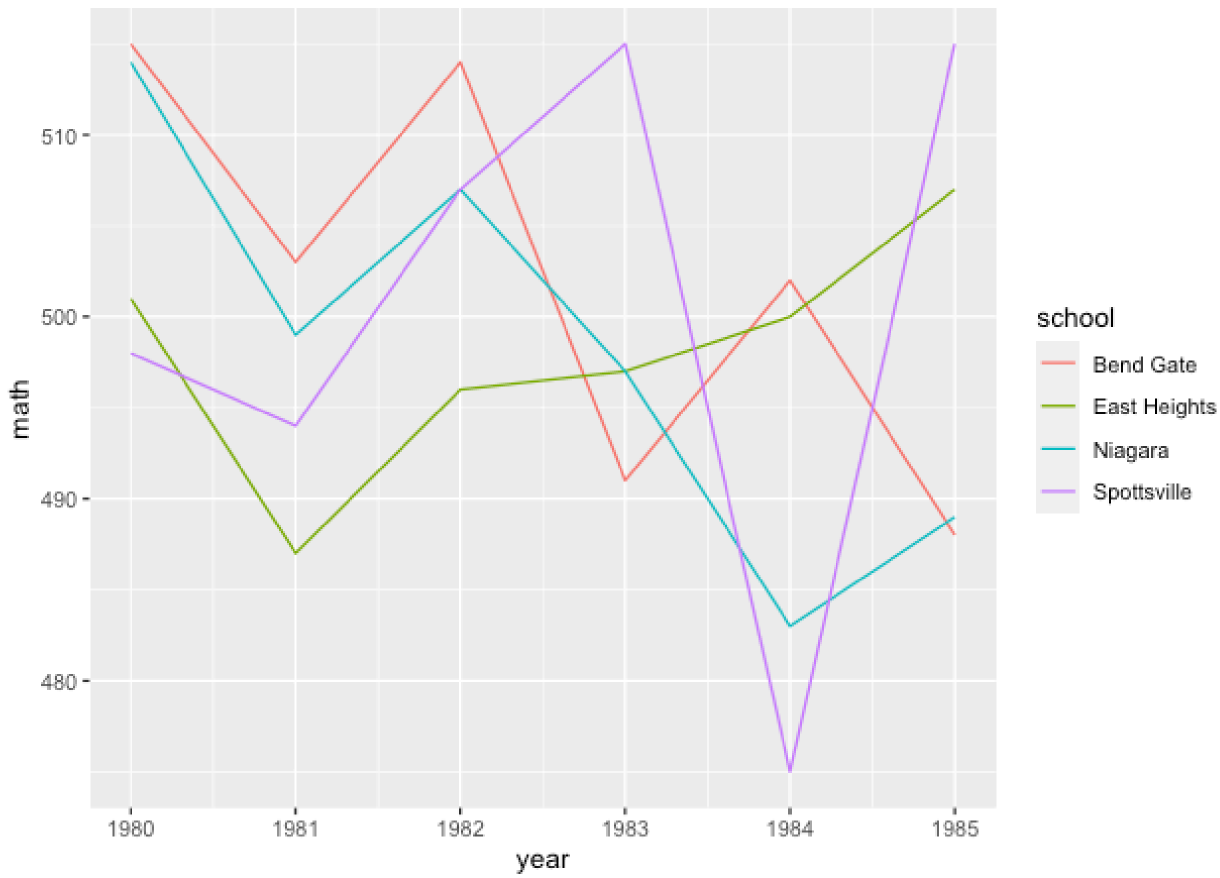
```r
## subset to Spottsville
plot_df <- df_ts %>%
    filter(school == "Spottsville")
```

We want to see changes in test scores over time, so we'll map `year` to the `x` axis and, for now, `math` to the `y` axis. To see a line graph, we add `geom_line()`.

```r
## line graph
p <- ggplot(data = plot_df,
            mapping = aes(x = year, y = math)) +
    geom_line()
p
```

Easy enough, but let's say that we want to add a third dimension — to show math scores for each school in the same plot area. To do this, we can map a third aesthetic to `school`. Looking at the help file for `geom_line()`, we see that lines (a version of a path) can take `colour`, which means we can change line color based on a variable. The code below is almost exactly the same as before, with the addition of `colour = school` inside `aes()`.

```r
## line graph for math scores at every school over time
p <- ggplot(data = df_ts,
            mapping = aes(x = year, y = math, colour = school)) +
    geom_line()
p
```

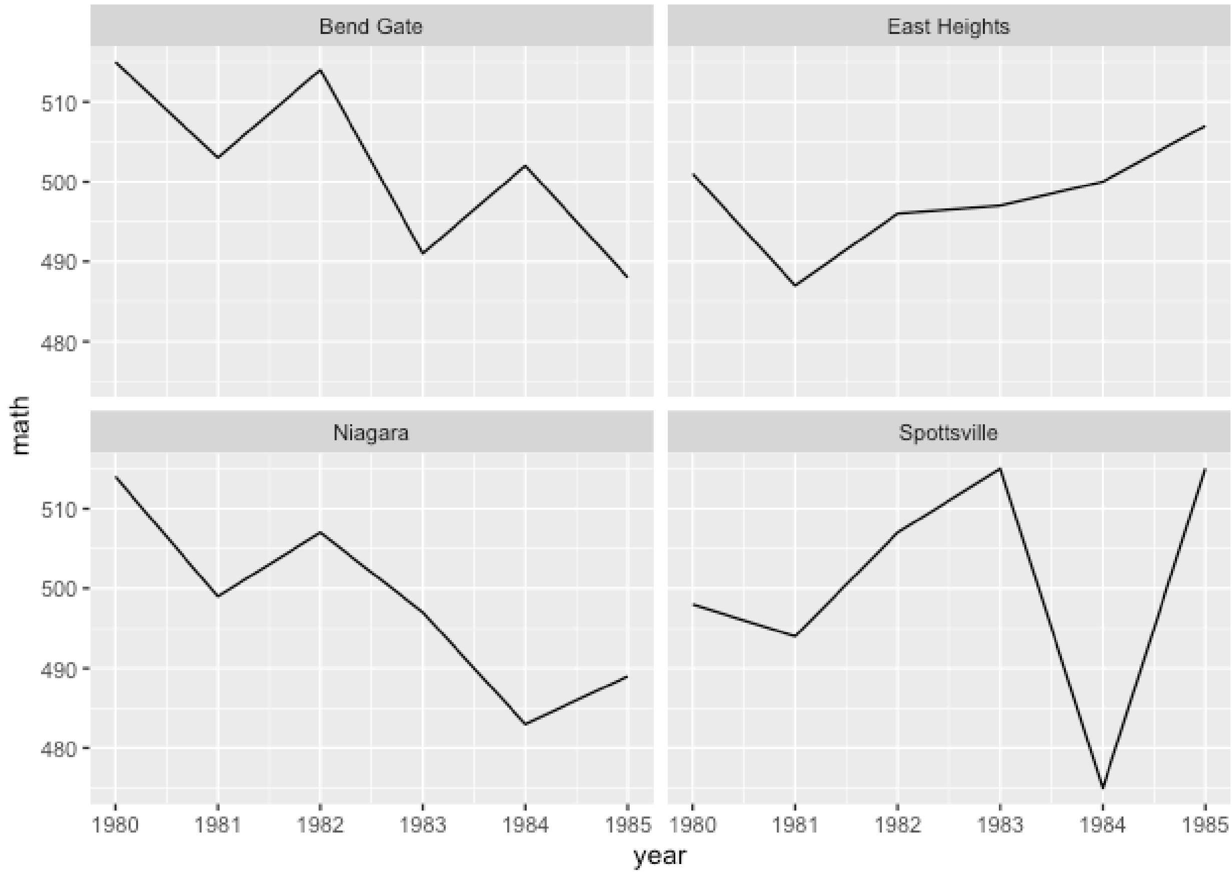


This is nice (though maybe a little messy at the moment) because it allows us to compare math scores across time across schools. But we have two more test types — reading and science — that we would like to include as well. One approach is to use facets.

Facets

With facets, we can put multiple plots together, each showing some subset of the data. For example, instead of plotting changes in math scores across schools over time on the same plot area (only changing the color), we can use `facet_wrap()` to give each school it's own little plot. Compared to the code just above, notice how we've removed `colour = school` from `aes()` and included `facet_wrap(~ school)`. The tilde (~) works like the tilde in `plot(y ~ x)` above: it means "plot against or by X".

```r
## facet line graph
p <- ggplot(data = df_ts,
            mapping = aes(x = year, y = math)) +
    facet_wrap(~ school) +
    geom_line()
p
```



Is this facetted plot better than the color line plot before it? To my eyes, it's a little clearer, but not so much so that I couldn't be convinced to use the first one. Whether you use the first or the second would largely depend on your specific data and presentational needs.

Facetting has a clearer advantage, however, when you want to include the fourth level of comparison: (1) scores across (2) time across (3) schools from (4) different tests. To make this comparison, we first need to reshape our data, which is only long in `year`, to be long in `test`, too. As we've already seen in a past lesson, we'll use `pivot_longer()` to place each test type in its own column (`test`) with the `score` next to it.

```
## reshape data long
df_ts_long <- df_ts %>%
    pivot_longer(cols = c("math","read","science"),
                 names_to = "test",
                 values_to = "score")

## show
df_ts_long
```

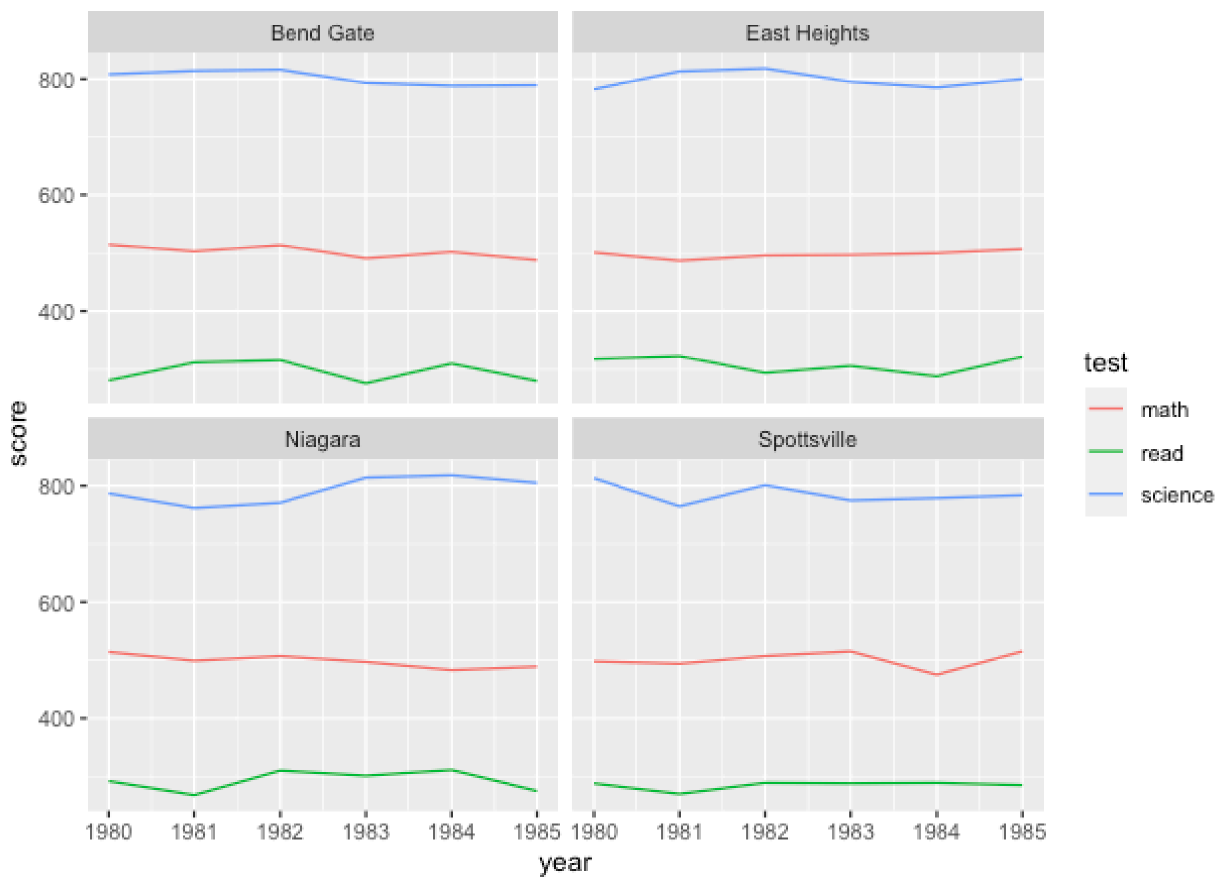
```
# A tibble: 72 x 4
   school      year test    score
   <chr>      <dbl> <chr>   <dbl>
 1 Bend Gate   1980 math      515
 2 Bend Gate   1980 read      281
 3 Bend Gate   1980 science   808
 4 Bend Gate   1981 math      503
 5 Bend Gate   1981 read      312
 6 Bend Gate   1981 science   814
```

```
 7 Bend Gate  1982 math      514
 8 Bend Gate  1982 read      316
 9 Bend Gate  1982 science   816
10 Bend Gate  1983 math      491
# … with 62 more rows
```

QUICK EXERCISE If we have 4 schools, 6 years, and 3 tests, how many observations should `df_ts_long` have in total? Does it?

With our reshaped data frame, we now reintroduce `colour` into the `aes()`, this time set to `test`. We make one other change: `y = score` now, since that's the column for test scores in our reshaped data. All else is the same.

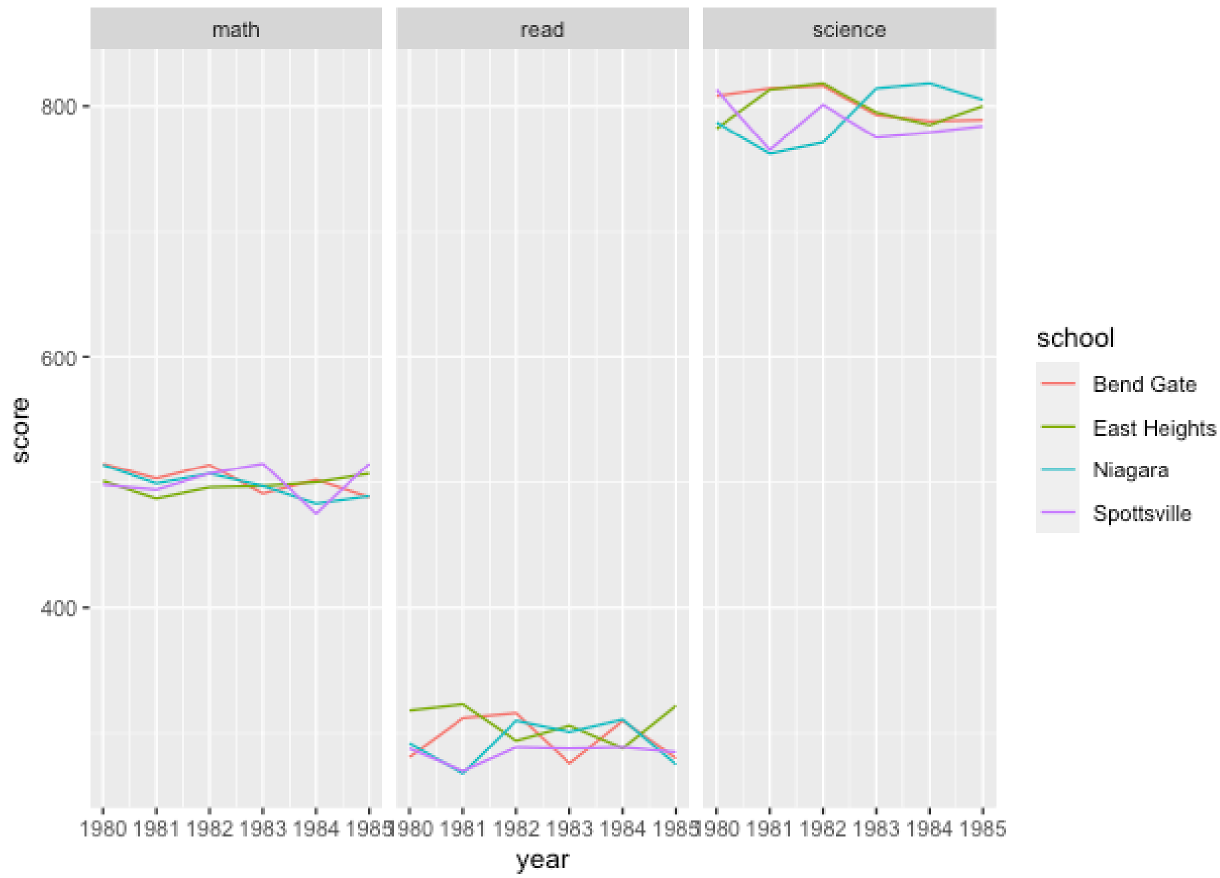
```
## facet line graph
p <- ggplot(data = df_ts_long,
            mapping = aes(x = year, y = score, colour = test)) +
    facet_wrap(~ school) +
    geom_line()
p
```



Well, it worked…we can see each school's different test score trends over time, with each school in its own facet and test scores a different color. But the result is a bit underwhelming. Because the different test types are such different scales, within-test changes seem rather flat over time.

Let's try something different: in the next figure, we'll swap the variables we give to `colour` and within `facet_wrap()`. This means that each test should have it's own facet and each line will represent a different school.

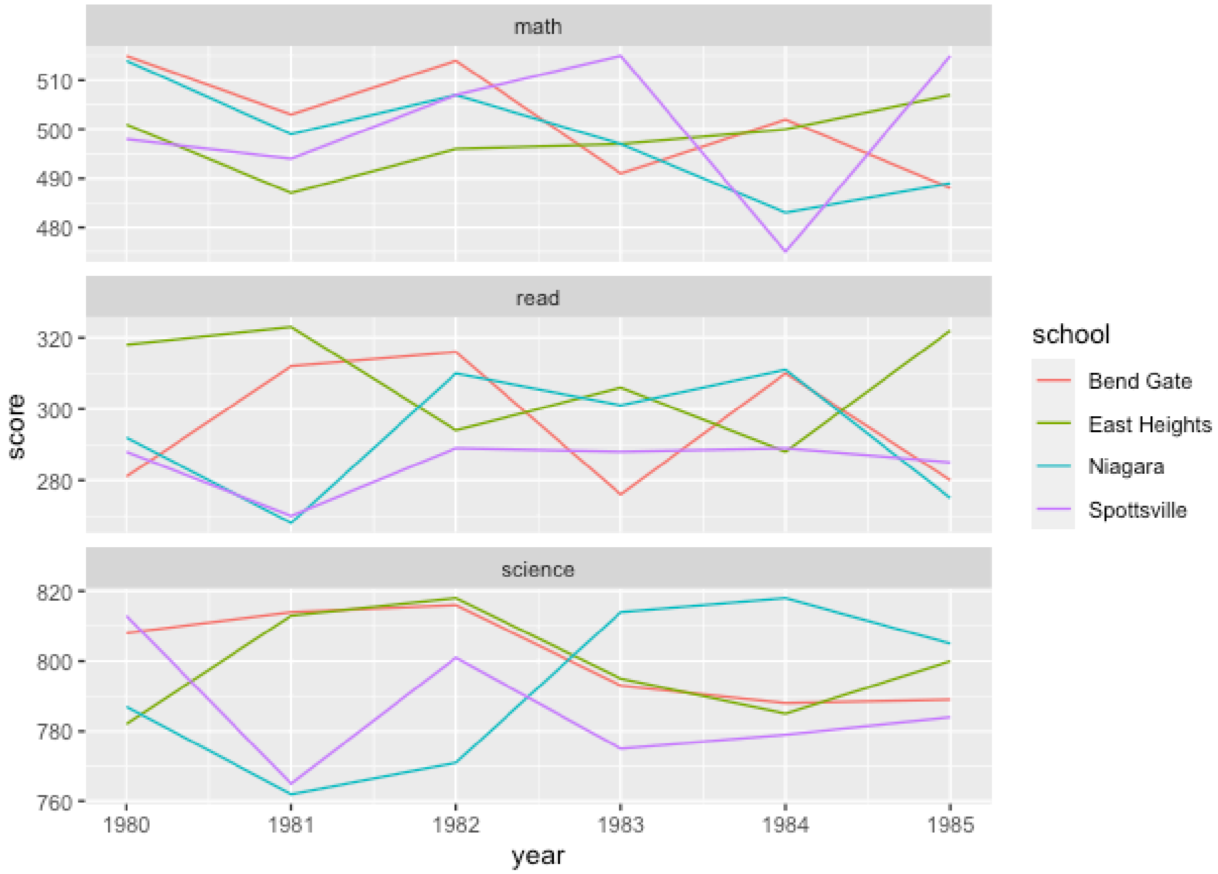
```
## facet line graph
p <- ggplot(data = df_ts_long,
            mapping = aes(x = year, y = score, colour = school)) +
    facet_wrap(~ test) +
    geom_line()
p
```



Okay. New problem. While it's maybe a *little* easier to see same-test differences across schools over time, the different scales of the tests still make the figure less useful. It's not that the students are *way* better at science than reading; it's just that the tests are scaled differently. Someone quickly reading this figure, however, might think that that was true.

One thing we can do is change the `y` axis for each facet. The default is to keep them the same. By adding `scales = "free_y"` to `facet_wrap()`, we'll let each test have it's own `y` axis scale. Because having different axis scales side-by-side can be confusing, we'll also add `ncol = 1` to `facet_wrap()`. This says our facets have to stick to one column, effectively meaning they will stack vertically rather than sit side-by-side.

```
## facet line graph, with one column so they stack
p <- ggplot(data = df_ts_long,
            mapping = aes(x = year, y = score, colour = school)) +
    facet_wrap(~ test, ncol = 1, scales = "free_y") +
    geom_line()
p
```



That looks better! But we can do even better…

Currently, each test score is on its own scale. While our new figure let's use make comparisons across schools over time *within* test, it's more difficult to make a good comparison *between* tests.

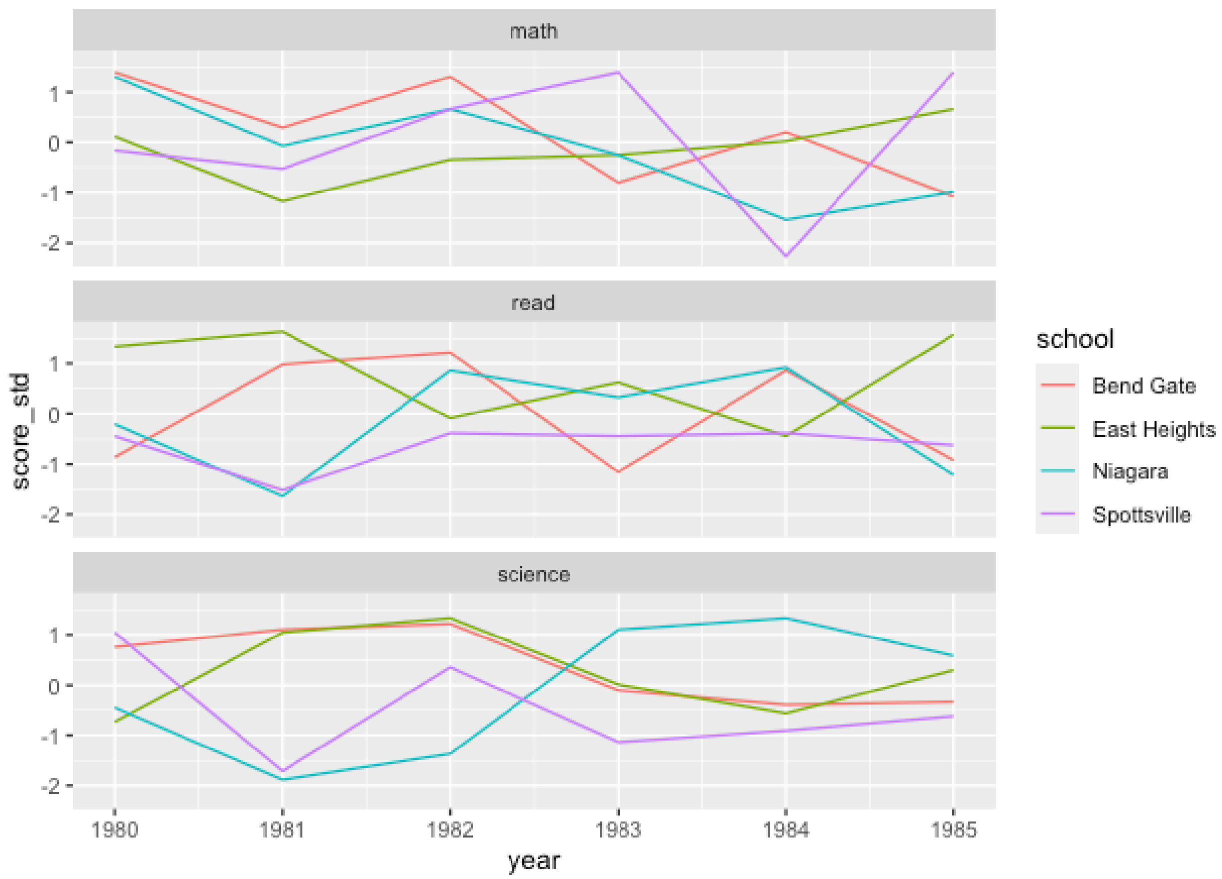
For example, East Heights has a little over 20 point drop in reading scores from 1981 to 1982 and about the same drop in science scores from 1982 to 1983.

How should we think about these drops? Are they about the same or does one drop mean more than another? To better answer this question, we could standardize each test score so that it's centered at 0 and a one unit change is equal to 1 standard deviation difference in score. We'll use the `scale()` function to `mutate()` a new variable `score_std`. Because we `group_by() test`, `score_std` will be standardized within test.

```
## rescale test scores
df_ts_long <- df_ts_long %>%
    group_by(test) %>%
    mutate(score_std = scale(score)) %>%
    ungroup
```

We'll repeat the same code as before, but this time substitute `y = score_std`. Because all tests are on the same standardized scale, we can also drop `scales = "free_y"`.

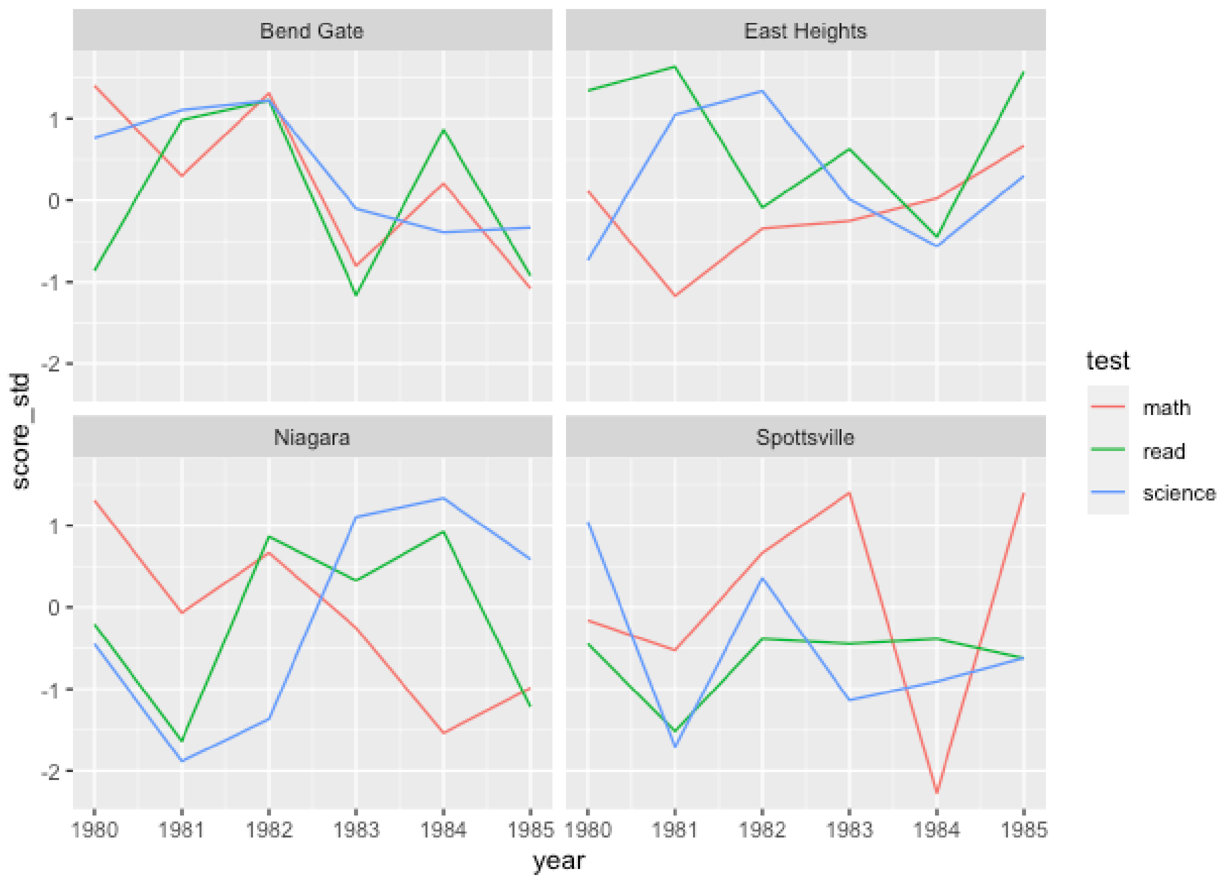
```
## facet line graph with standardized test scores
p <- ggplot(data = df_ts_long,
            mapping = aes(x = year, y = score_std, colour = school)) +
    facet_wrap(~ test, ncol = 1) +
    geom_line()
p
```



QUICK EXERCISE What happens if you use the argument `scales = "free_y"` in the last bit of code? Why might you not use that once we've scaled the test scores?

As a quick change, we can go back to having each school in its own facet and test scores within.

```
## facet line graph
p <- ggplot(data = df_ts_long,
            mapping = aes(x = year, y = score_std, colour = test)) +
    facet_wrap(~ school) +
    geom_line()
p
```



QUICK EXERCISE Why did we drop `ncol = 1` from `facet_wrap()`? What happens if you keep it?

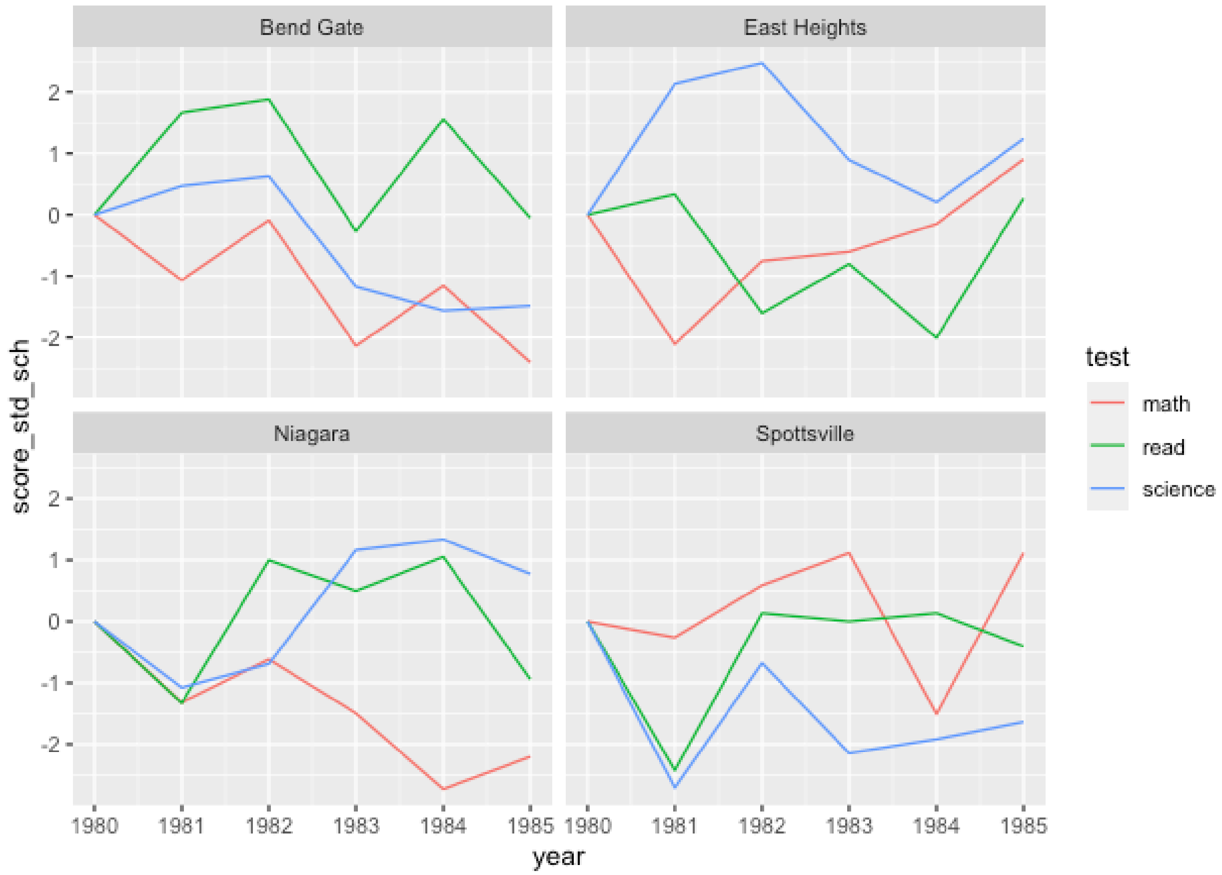
Our plot is looking better, but it still may not contain the information we want. We've standardized the test scores over this time window, but maybe what we really want to know is how they've *changed from the beginning of the sample period*. You can imagine a superindendent who took over in 1981 would be keen to know how scores have changed during their tenure.

This means that while we still want to standardize the scores, we should zero them not a the overall mean, but at the value in the first year. We can do that by grouping by `school` and `test`, arranging in year order, making a new variable that is the `first()` score (within test, within school) and using that rather than the mean test score to make our new variable, `score_std_sch`.

```
## standardize test scores within school to first year
df_ts_long <- df_ts_long %>%
    group_by(test, school) %>%
    arrange(year) %>%
    mutate(score_year_one = first(score),
           score_std_sch = (score - score_year_one) / sd(score)) %>%
    ungroup
```

```
## facet line graph
p <- ggplot(data = df_ts_long,
            mapping = aes(x = year, y = score_std_sch, colour = test)) +
    facet_wrap(~ school) +
```

```
    geom_line()
p
```



With this final graph, we can see relative changes across schools, across times, across tests. Is this the best version of this plot (minus making the axis and legend labels look nicer)? Again, it depends on what you want to show. Remember that figures don't speak for themselves: it's up to you to explain to your reader what they mean. That said, a well crafted figure will make that job much easier.