Class 5: Data Visualization with ggplot

Grace Wang (A16968688)

Table of contents

Background

R has many graphics systems, including "base R" and additional packages such as **ggplot2**.

Let's compare base R and **ggplot2** briefly:

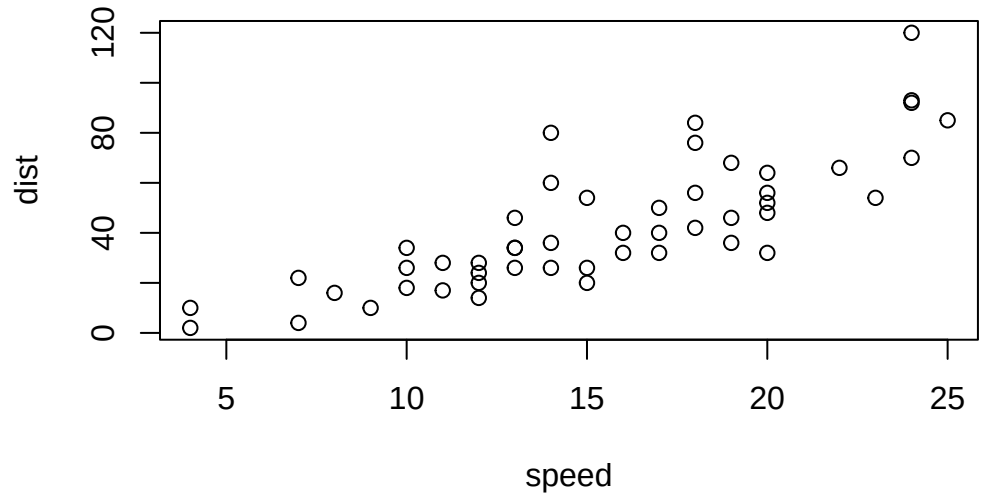
Use built-in example data called `cars`.

```
head(cars)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

In base R we can call `plot()`:

```
plot(cars)
```



How can we do this with **ggplot2**?

First, we need to install the package using `install.packages("ggplot2")`. This only needs to be done once.

> Key point: only install packages in the R console

Now, before any add-on package can be used, it must be loaded with a call to `library()`.

```
library(ggplot2)
```

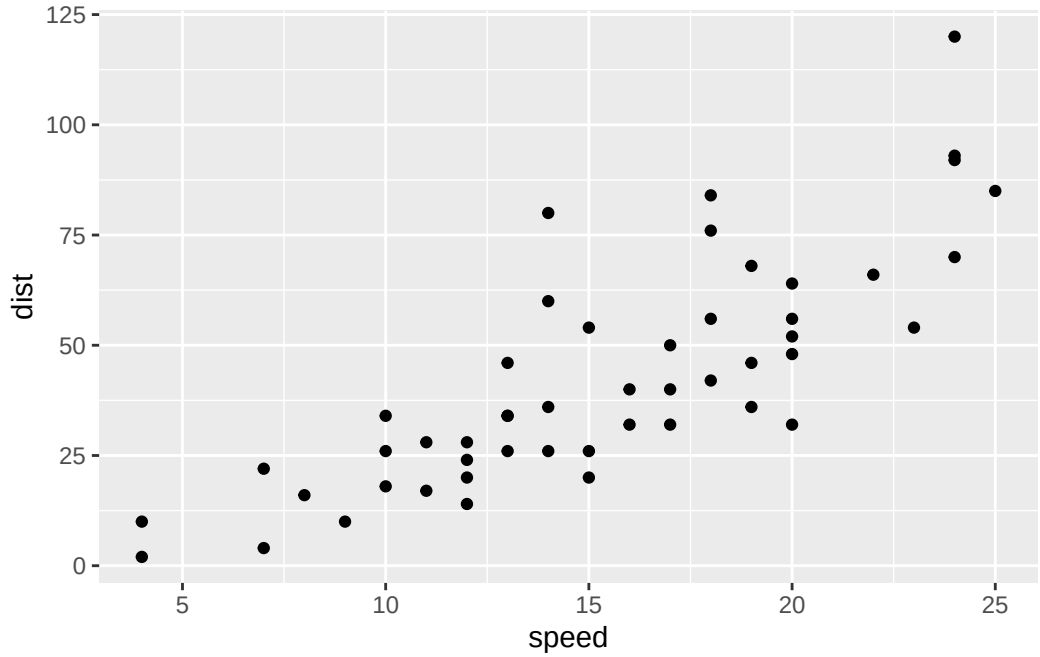
```
Warning: package 'ggplot2' was built under R version 4.4.3
```

```
ggplot(cars)
```

Every ggplot needs at least 3 layers:

- the **data** (e.g., `cars`)
- the **aes**thetics (how the data map to the plot)
- the **geom**etries (how the plot is drawn - e.g., lines, points, columns, etc)

```
ggplot(cars) +
  aes(x = speed, y = dist) +
  geom_point()
```

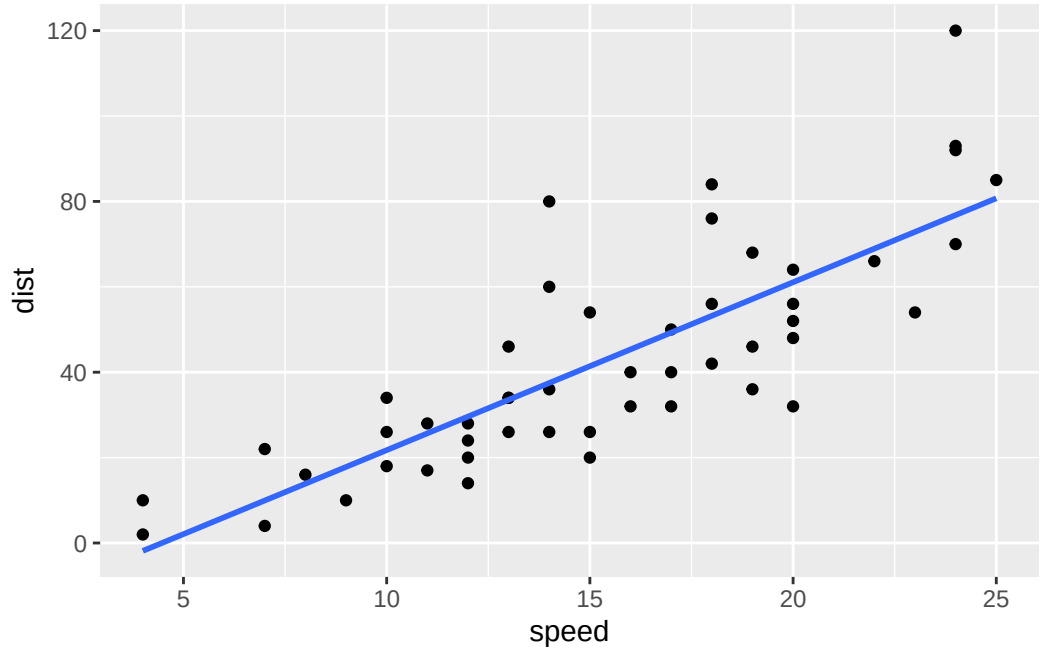


For "simple" plots ggplot is more verbose than base R, but the defaults are nicer. For complicated plots it becomes much more efficient and structured.

> Add a line to show the relationship between speed and stopping distance in another layer:

```
p <- ggplot(cars) +
  aes(x = speed, y = dist) +
  geom_point() +
  geom_smooth(se = F, method = "lm")
p
```

```
`geom_smooth()` using formula = 'y ~ x'
```

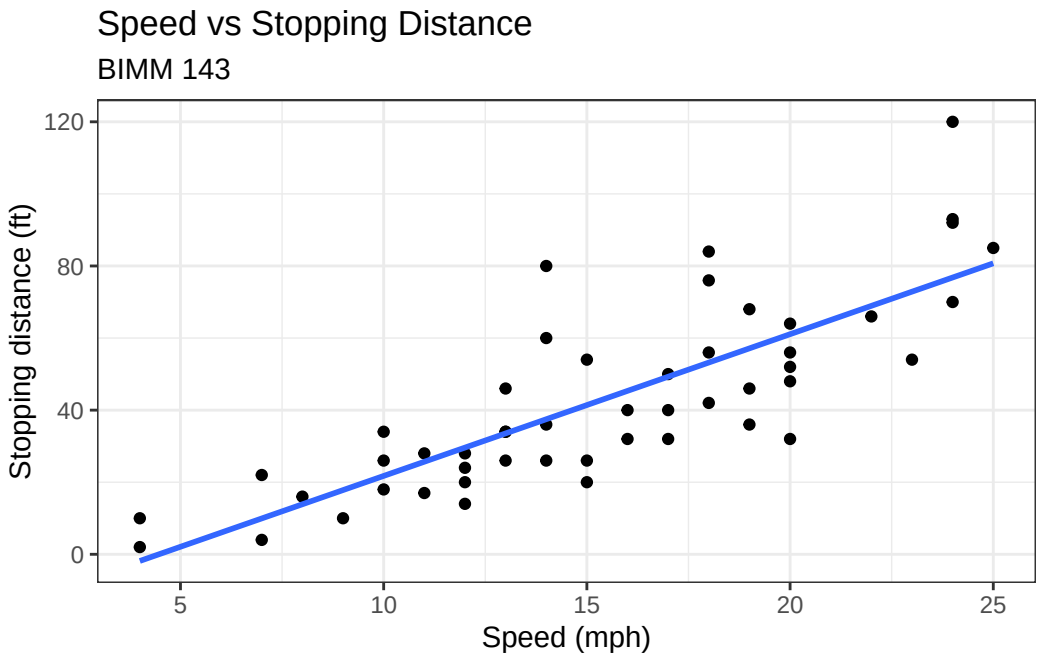


I can always save any ggplot object and use it later.

Add a title and subtitle to the plot:

```
p + labs(title = "Speed vs Stopping Distance",
         subtitle = "BIMM 143",
         x = "Speed (mph)",
         y = "Stopping distance (ft)") +
  theme_bw()
```

```
`geom_smooth()` using formula = 'y ~ x'
```



Gene expression plot

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```
        Gene Condition1 Condition2      State
1      A4GNT -3.6808610 -3.4401355 unchanging
2       AAAS  4.5479580  4.3864126 unchanging
3      AASDH  3.7190695  3.4787276 unchanging
4       AATF  5.0784720  5.0151916 unchanging
5       AATK  0.4711421  0.5598642 unchanging
6 AB015752.4 -3.6808610 -3.5921390 unchanging
```

How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

How many columns are there?

```
ncol(genes)
```

```
[1] 4
```

What are the column names?

```
colnames(genes)
```

```
[1] "Gene"       "Condition1" "Condition2" "State"
```

How many up- and down-regulated genes are there?

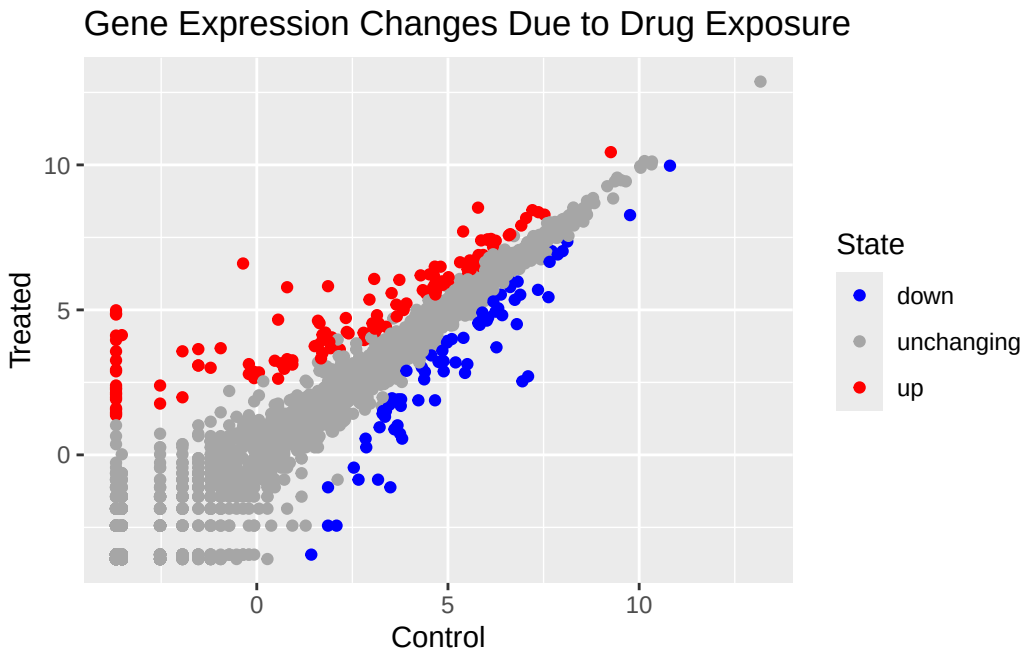
```
table(genes$State)
```

```
      down unchanging         up
        72       4997        127
```

Custom color plot

Make a first plot of the data

```
ggplot(genes) +
  aes(x = Condition1, y = Condition2, col = State) +
  geom_point() +
  scale_color_manual(values = c("blue", "gray65", "red")) +
  labs(title = "Gene Expression Changes Due to Drug Exposure",
       x = "Control",
       y = "Treated") +
  theme_gray()
```



Using different geoms

Use `mtcars`.

```
head(mtcars)
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

Scatter plot of `mpg` vs `disp`

```
p1 <- ggplot(mtcars) +
  aes(x = mpg, y = disp) +
  geom_point()
```

Boxplot of `gear` vs `disp`

```
p2 <- ggplot(mtcars) +
  aes(x = factor(gear), y = disp) +
  geom_boxplot() +
  labs(x = "gear")
```

Barplot of `carb`

```
p3 <- ggplot(mtcars) +
  aes(carb) +
  geom_bar()
```

Smooth of `disp` vs `qsec`

```
p4 <- ggplot(mtcars) +
  aes(x = disp, y = qsec) +
  geom_smooth()
```

Goal: combine all four plots into one multipanel figure.

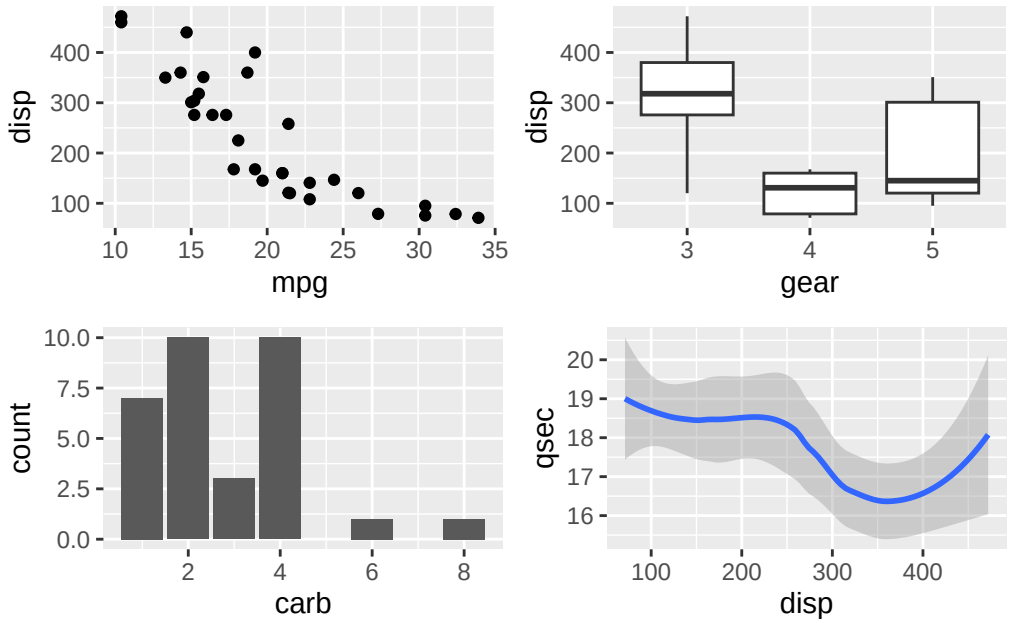
We can use the **patchwork** package to do this.

```
library(patchwork)
```

```
Warning: package 'patchwork' was built under R version 4.4.3
```

```
((p1 | p2) / (p3 | p4))
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



Save the figure.

```
ggsave(filename = "mtcars_plot.png", width = 5, height = 3)
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

Gapminder

Read in `gapminder` data.

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts

gapminder <- read.delim(url)
head(gapminder)
```

```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1952  28.801  8425333  779.4453
2 Afghanistan      Asia 1957  30.332  9240934  820.8530
3 Afghanistan      Asia 1962  31.997 10267083  853.1007
4 Afghanistan      Asia 1967  34.020 11537966  836.1971
5 Afghanistan      Asia 1972  36.088 13079460  739.9811
6 Afghanistan      Asia 1977  38.438 14880372  786.1134
```

How many countries are in the dataset?

```
length(table(gapminder$country))
```

```
[1] 142
```

Plot GDP vs life expectancy, colored by continent

```
ggplot(gapminder) +
  aes(x = gdpPercap, y = lifeExp, col = continent) +
  geom_point(alpha = 0.3) +
  labs(x = "GDP per capita", y = "life expectancy") +
  facet_wrap(~continent) +
  theme_bw()
```