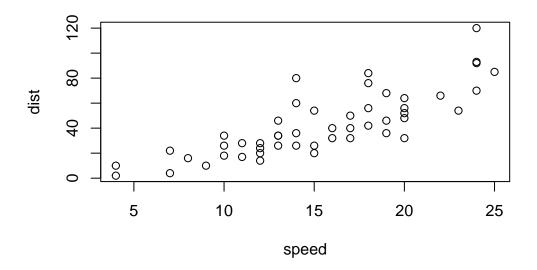
Class 5: Data Visualizations with GGPLOT

Olivia Chu

Plotting in R

R has multiple plotting and graphics systems. The most popular of which is **ggplot2**. We have already played with "base" R graphics. This comes along with R "out of the box".

plot(cars)



Compared to base R plots, ggplot is much more verbose - I need to write more code to get simple plots like the above.

To use ggplot, I need to first install the ggplot2 package. To install any package in R, I use the install.packages() command along with the package name.

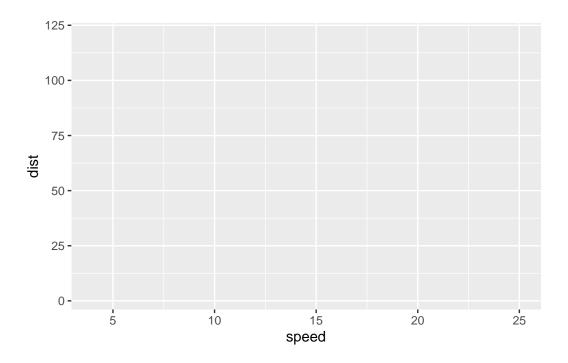
The install is a one-time only requirement. The package is now on our computer. I don't need to re-install it.

However, I can't just use it without loading it up with a library() call.

```
#install.packages("ggplot2")
library(ggplot2)

ggplot(cars)
```

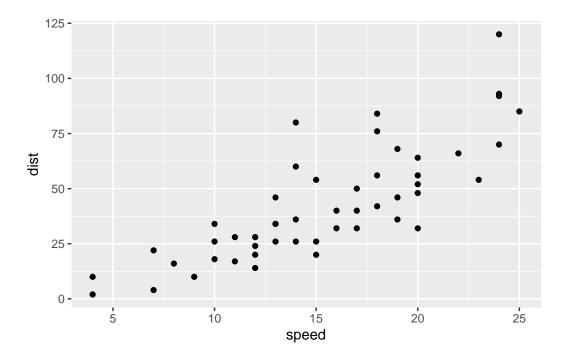
```
ggplot(cars) +
  aes(x=speed, y=dist)
```



All ggplot figures need at least 3 things:

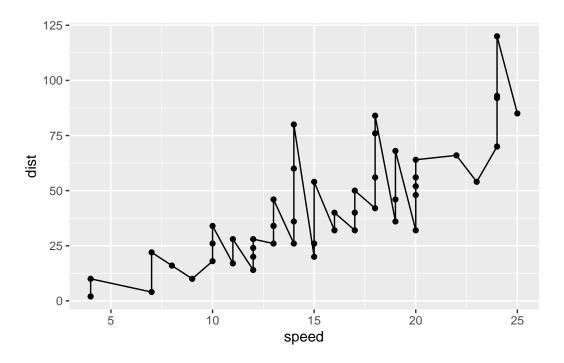
- data (this is the data.frame with our numbers)
- aesthetics ("aes", how our data maps to the plot)
- $\bullet\,$ geoms (do you want lines, points, columns, etc...)

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



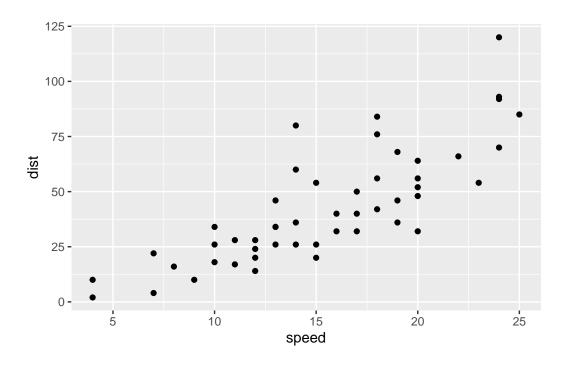
I want a trendline to show the relationship between speed and stopping distance...

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



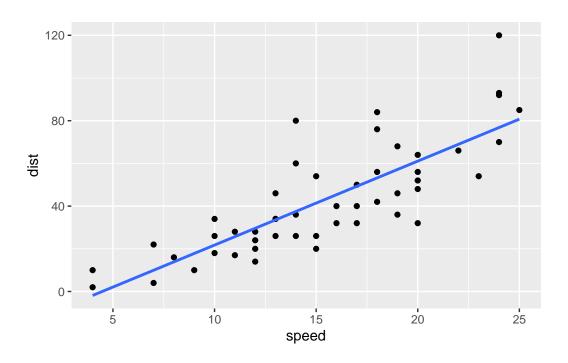
This is not what we want.

```
bb <- ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point()
bb</pre>
```



bb + geom_smooth(method = "lm", se=FALSE)

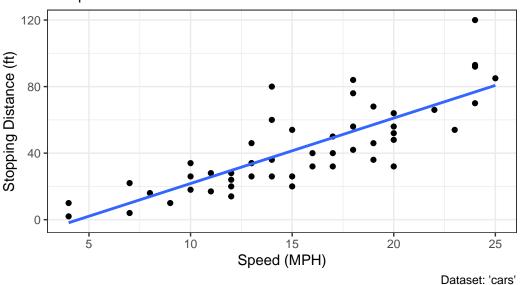
`geom_smooth()` using formula = 'y ~ x'



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

Speed and Stopping Distances of Cars

Comparison of different cars



Gene Expression Example

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

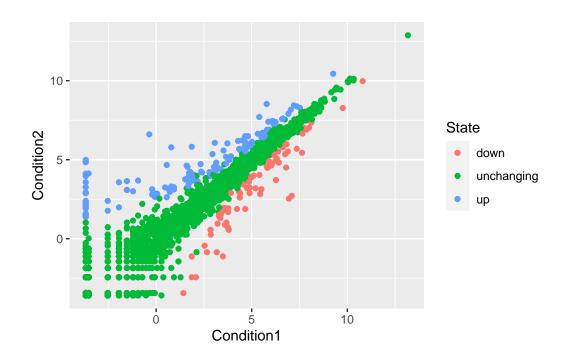
```
Gene Condition1 Condition2 State
1 A4GNT -3.6808610 -3.4401355 unchanging
2 AAAS 4.5479580 4.3864126 unchanging
3 AASDH 3.7190695 3.4787276 unchanging
4 AATF 5.0784720 5.0151916 unchanging
5 AATK 0.4711421 0.5598642 unchanging
6 AB015752.4 -3.6808610 -3.5921390 unchanging
```

The head() function will print out just the first few rows (by 6).

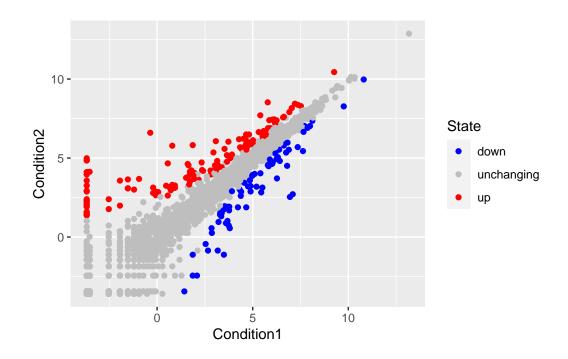
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2) +
  geom_point()
```

```
To-Supplied to the state of the
```

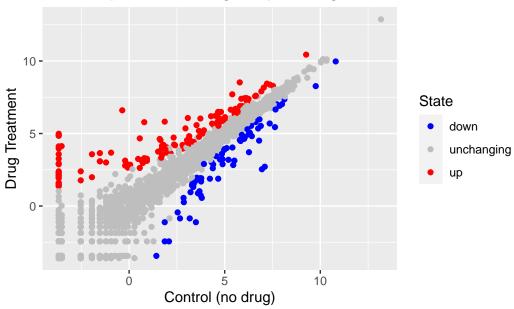
```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p</pre>
```



p + scale_colour_manual(values=c("blue", "gray", "red"))



Gene Expression Changes Upon Drug Treatment



...

Section 7 Gapminder Example

```
#install.packages("gapminder")
library(gapminder)

#Second method
#url2 <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder

#gapminder <- read.delim(url2)

#install.packages("dplyr")
library(dplyr)</pre>
```

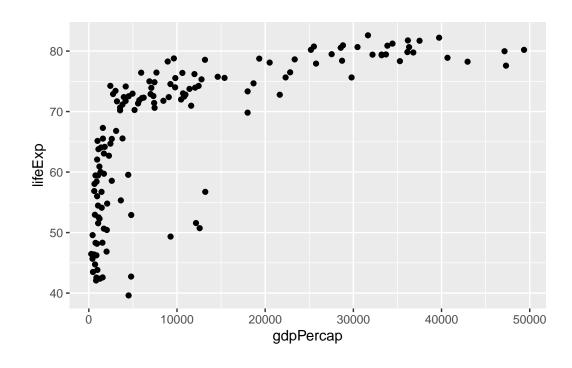
```
Attaching package: 'dplyr'
The following objects are masked from 'package:stats':
    filter, lag
The following objects are masked from 'package:base':
    intersect, setdiff, setequal, union

gapminder_2007 <- gapminder %>% filter(year==2007)

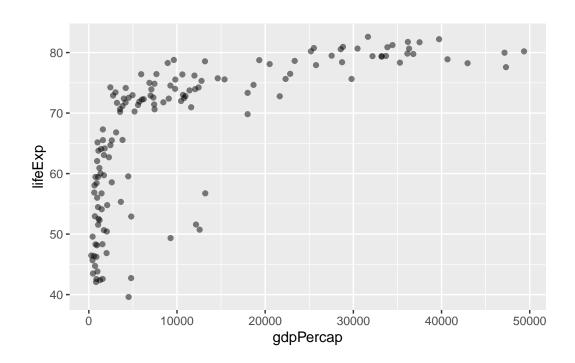
library(ggplot2)

ggplot(gapminder_2007) +
    aes(x=gdpPercap, y=lifeExp) +
```

geom_point()



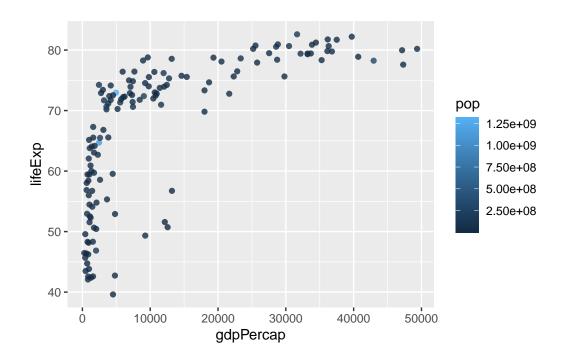
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.5)
```



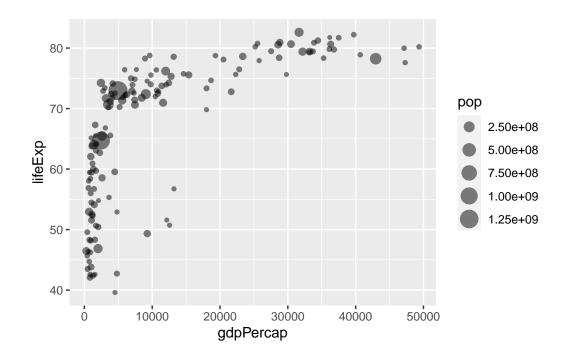
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```

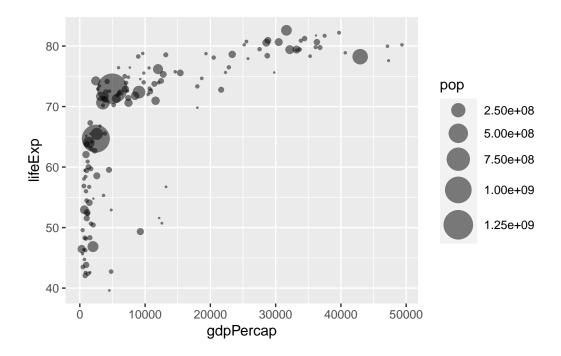


```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=pop) +
  geom_point(alpha=0.8)
```



```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, size=pop) +
  geom_point(alpha=0.5)
```





Producing for the year 1957:

