

# Class 5: Data Visualization

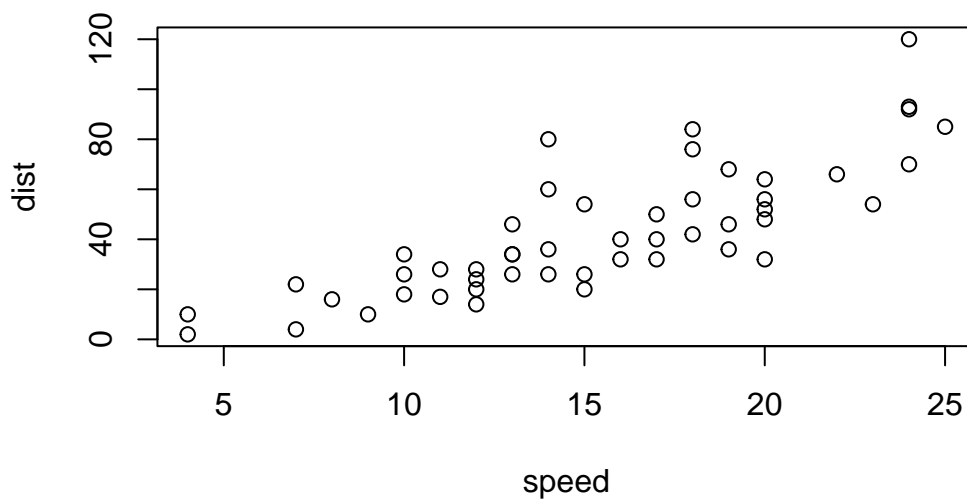
Patrick

## 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.

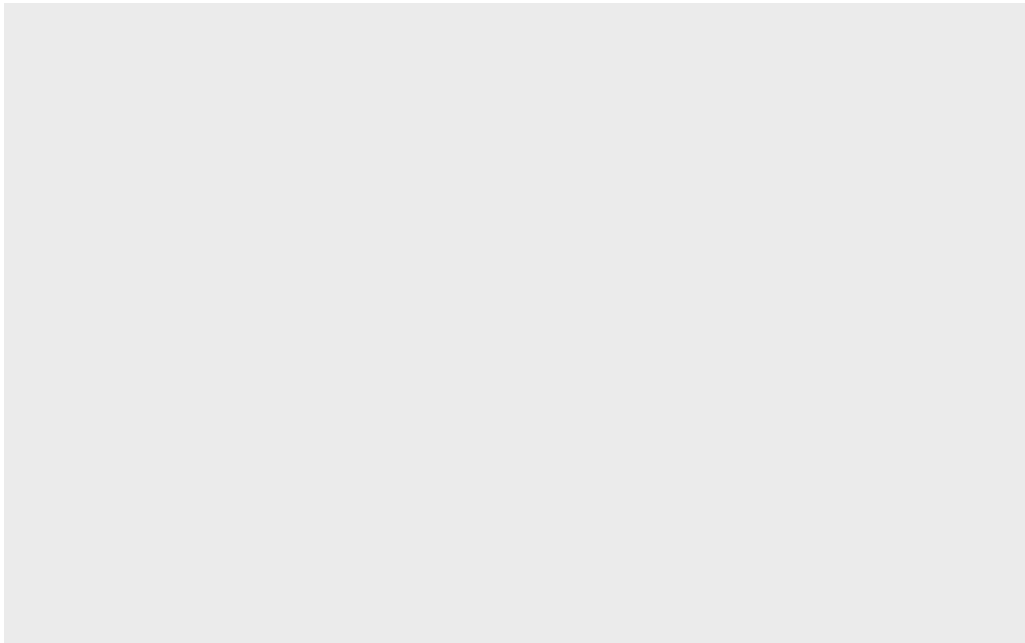
To use ggplot I need to first install the ggplot2 package. To install any package in R I use the `install.packages()` command along with the package name

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.

```
library(ggplot2)
```

```
ggplot(cars)
```



All ggplot figures need at least 3 things:

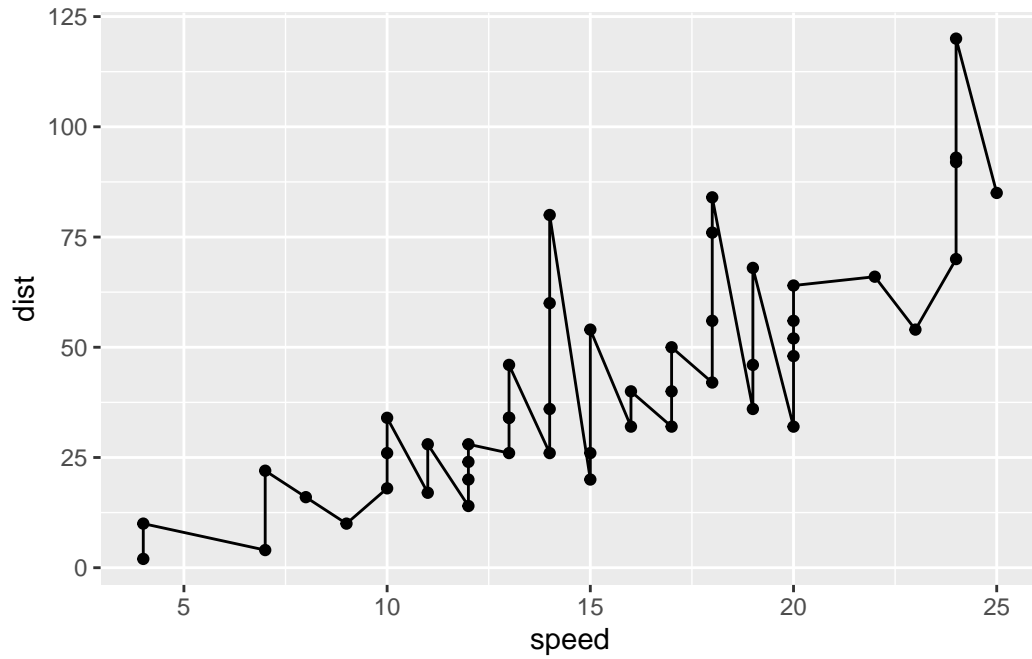
- data (this is the data.frame with our numbers)
- aesthetics ("aes", how our data maps to the plot)
- geoms (do want lines, points, columns, etc...)

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



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

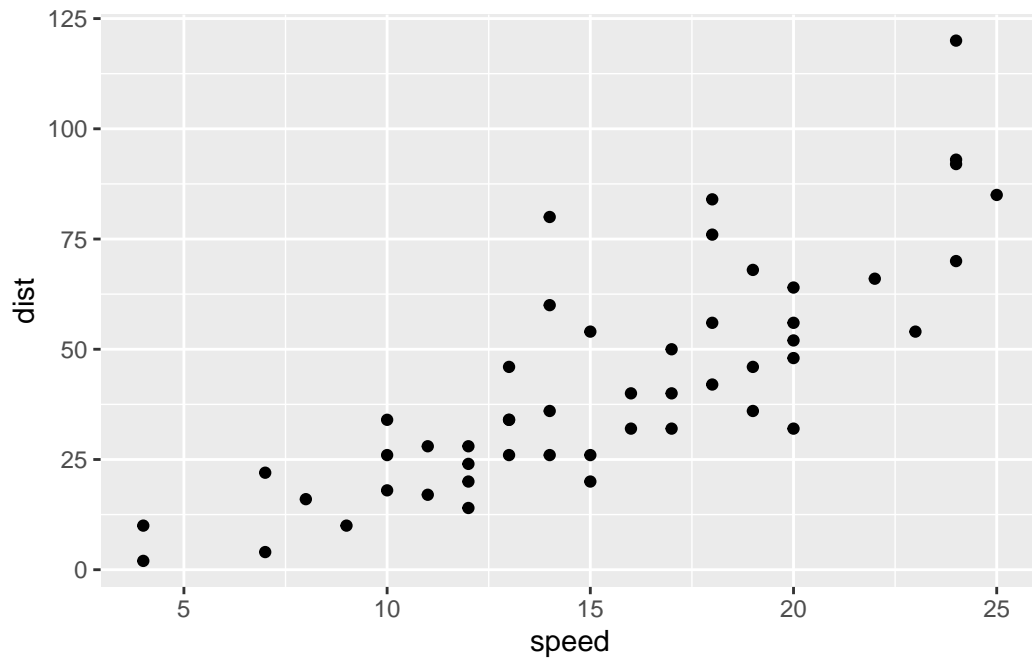
```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_line()
```



That is not what we want

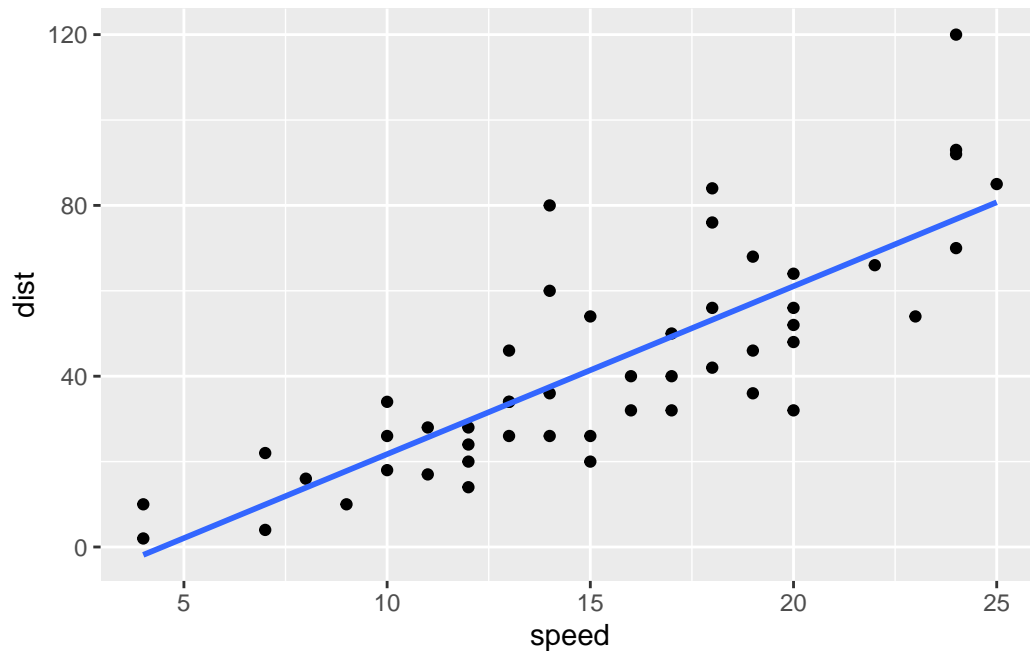
```
bb <- ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```

```
bb
```



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

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



```
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

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

```
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

```

```
nrow(genes)
```

```
[1] 5196
```

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

```

down unchanging      up
  72      4997      127

```

```

p<- ggplot(genes)+
  aes(Condition1, Condition2, color=State) +
  geom_point() +
  labs(title="Some Plot",
        subtitle="With a subtitle")

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

```

