Class 5: Data Visualization

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Plotting in R

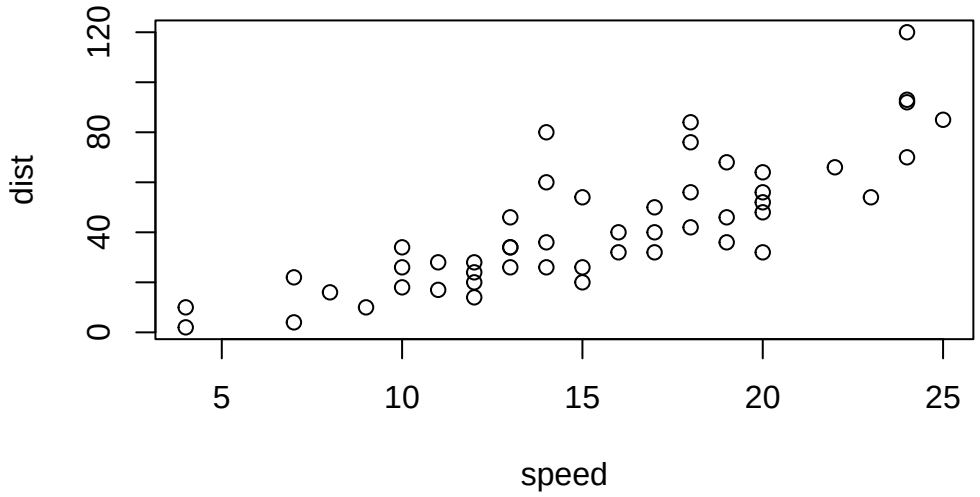
R has multiple plotting and graphics systems. The most popular of which is **ggplot2**

We have already played with "base" R graphics. This comes along with R "out of the box".

```
head(cars)
```

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

```
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 ggplot 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)
```

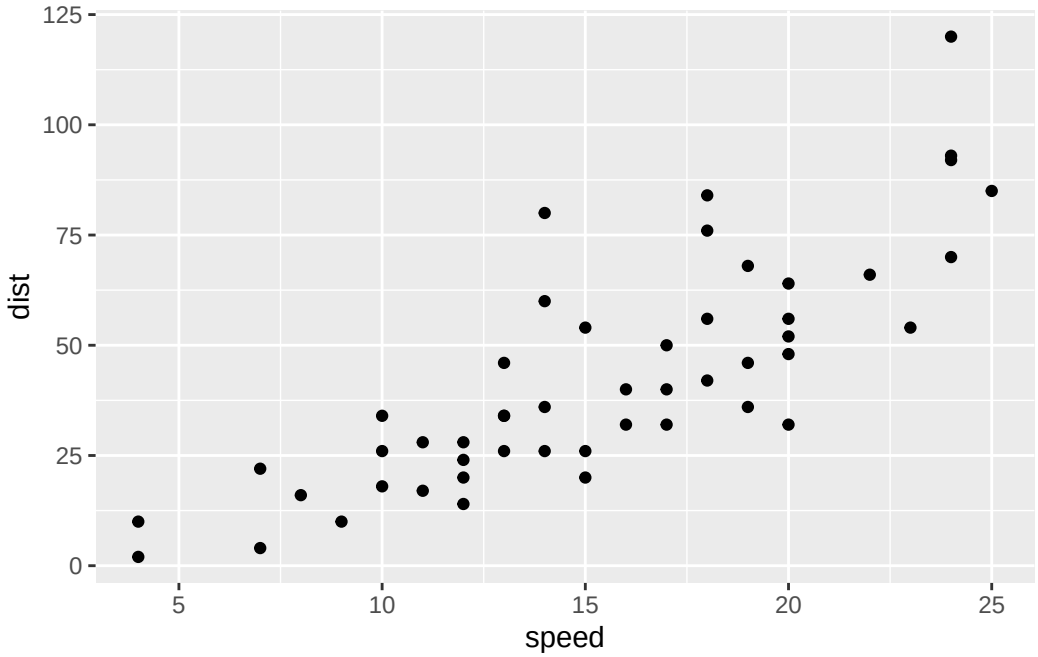
```
ggplot(cars)
```

All ggplot figures need at least 3 things:

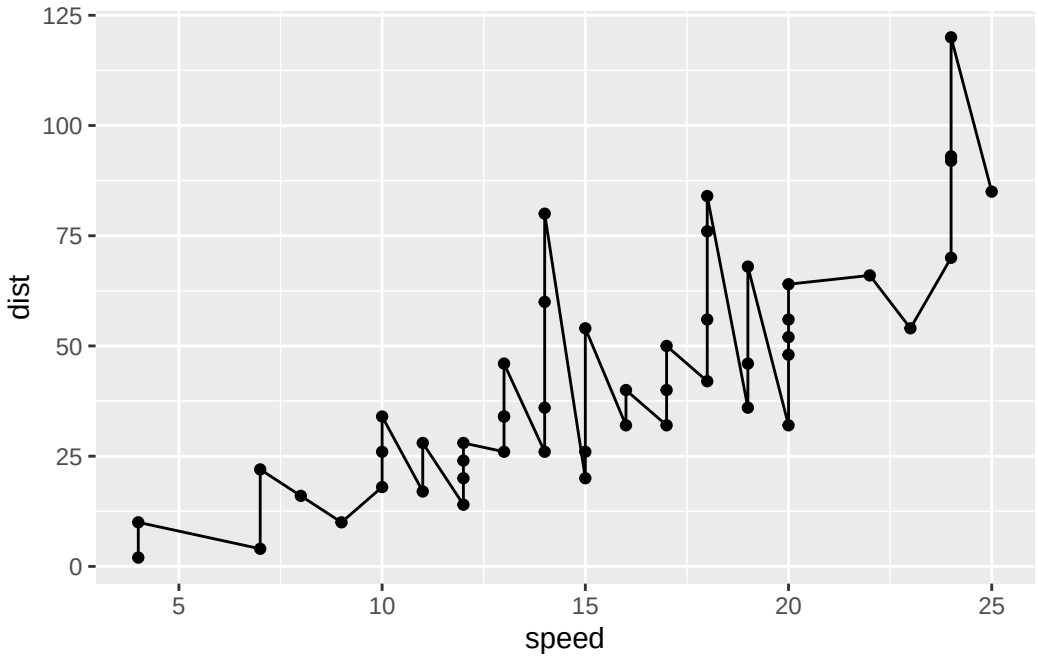
- data (this is the data.frame with our numbers)
- aesthetics ("aes", how our data maps to the plot)
- geoms (do want lines, points, columns, etc…)

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

```
bb
```

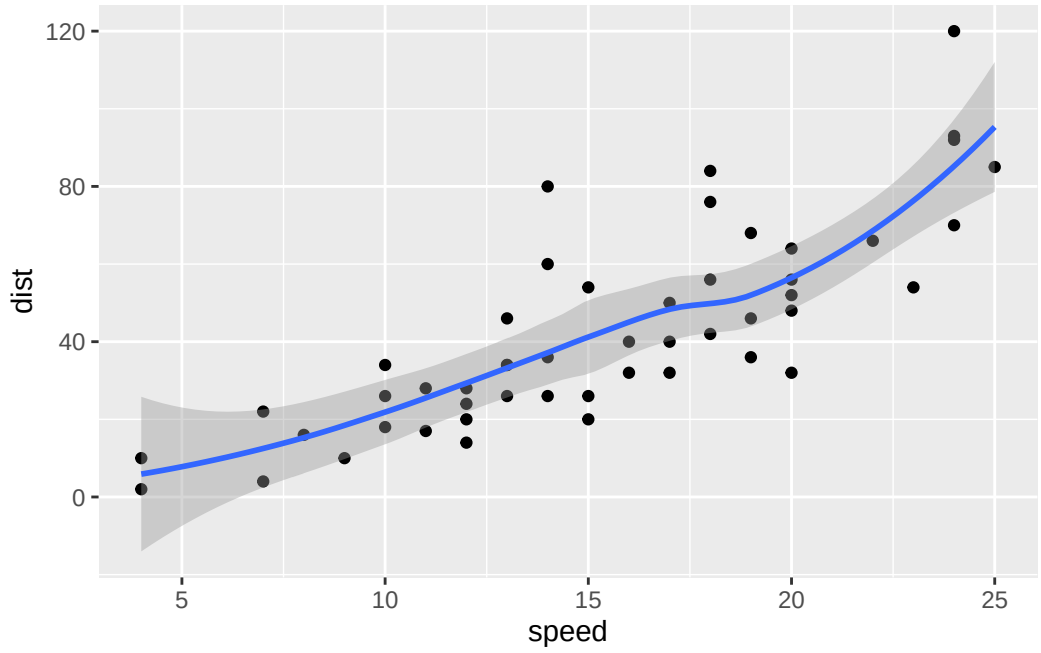

125
100
75
50
25
0
dist
5
10
15
20
25
speed

```
bb + geom_line()
```


125
100
75
50
25
0
dist
5
10
15
20
25
speed

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

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



Gene expression example

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes,10)
```

```
        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
7       ABCA7  3.4484220  3.8266509 unchanging
```

```
8   ABCA9-AS1 -3.6808610 -3.5921390 unchanging
9      ABCC11 -3.5288580 -1.8551732 unchanging
10      ABCC3  0.9305738  3.2603040         up
```

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
```

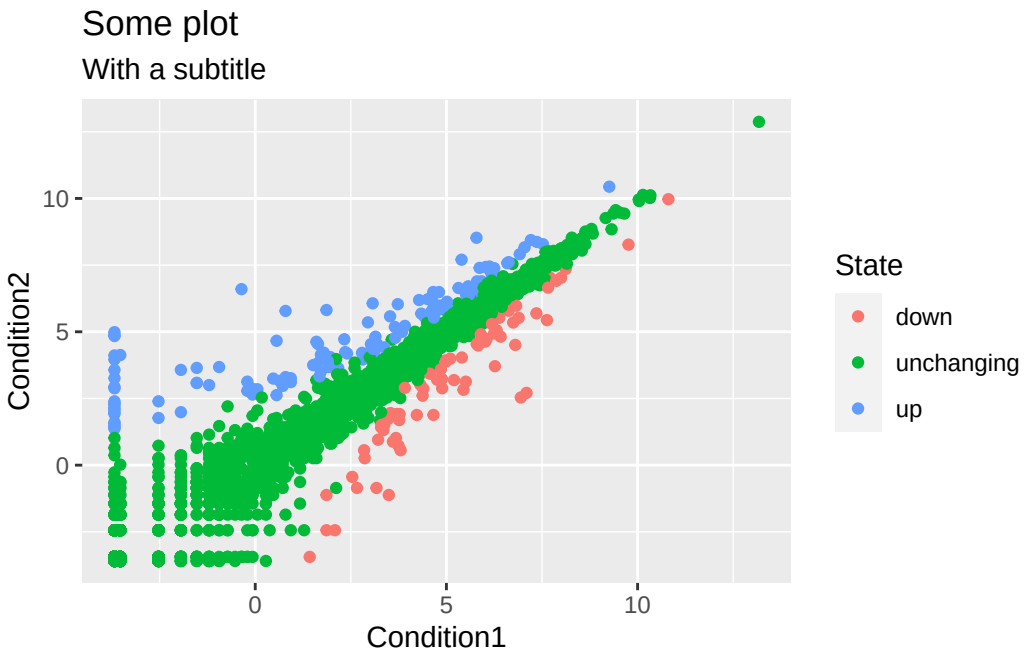
```
nrow(genes)
```

```
[1] 5196
```

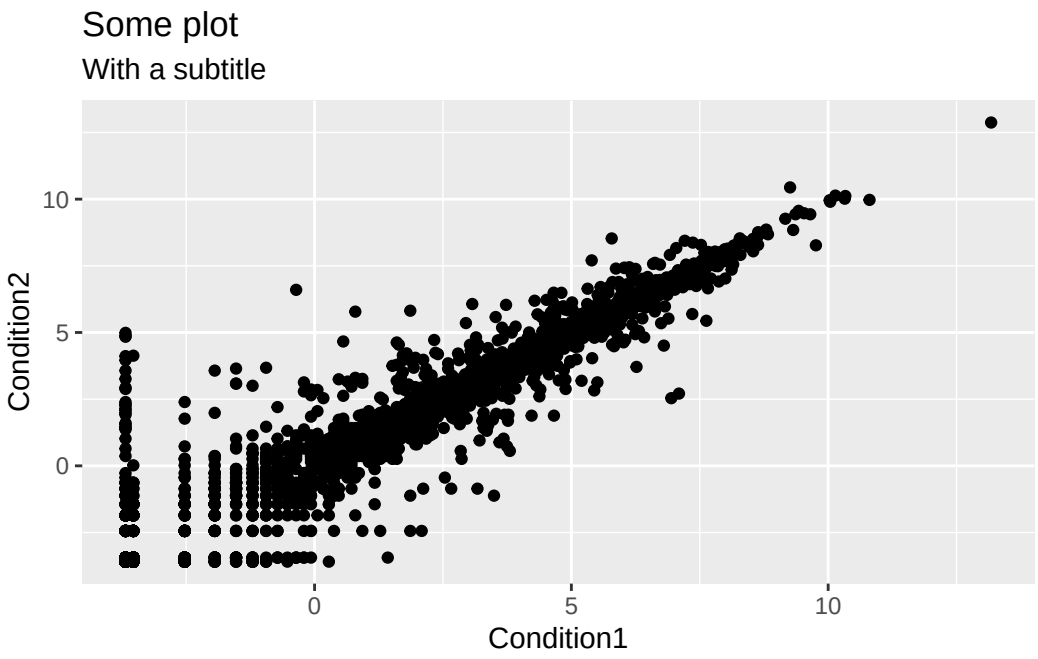
```
table(genes$State)
```

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

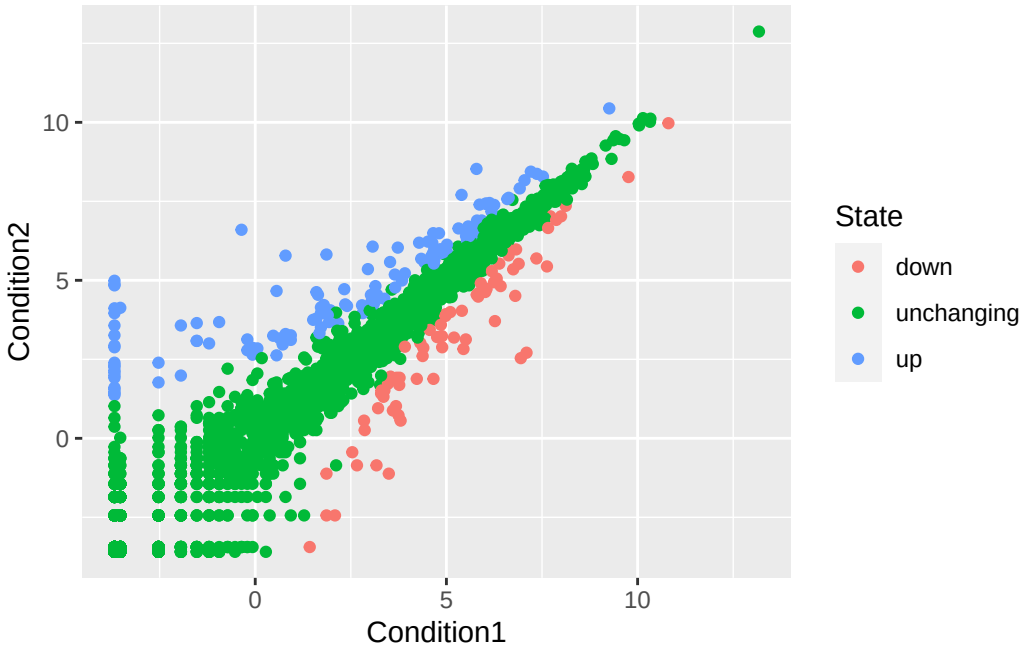
```
ggplot(genes) + aes(Condition1, Condition2, color=State) + geom_point() + labs(title= "Som
```



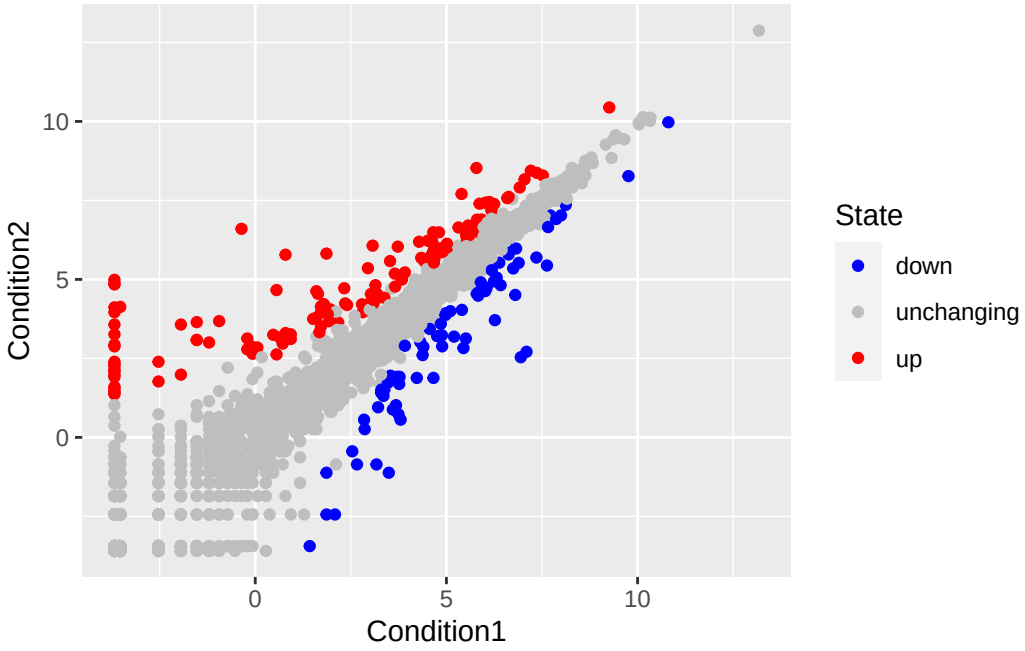

```
ggplot(genes) + aes(Condition1, Condition2) + geom_point() + labs(title= "Some plot", subt
```



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




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


10
5
0
Condition2
0
5
10
Condition1
State
down
unchanging
up