Class05

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Install the package ggplot2

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

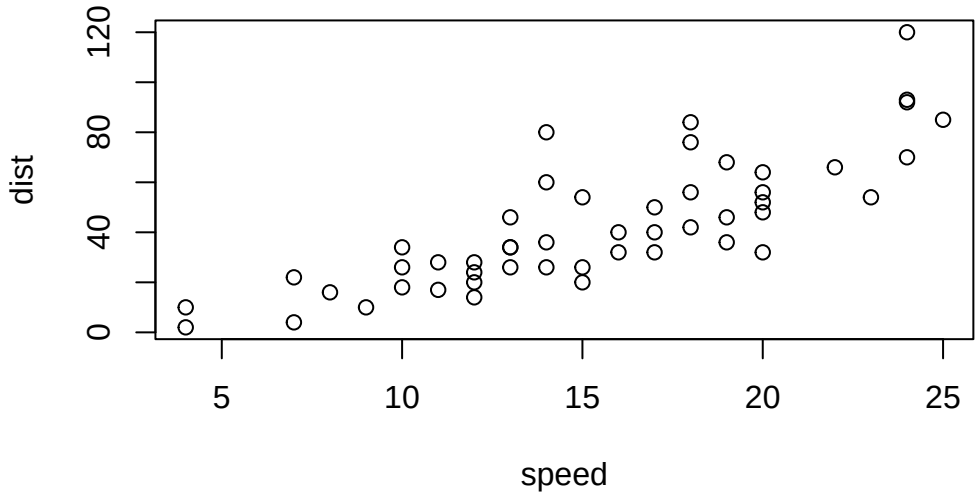
Any time I want to use this package I need to load it.

```
library(ggplot2)
```

```
View(cars)
```

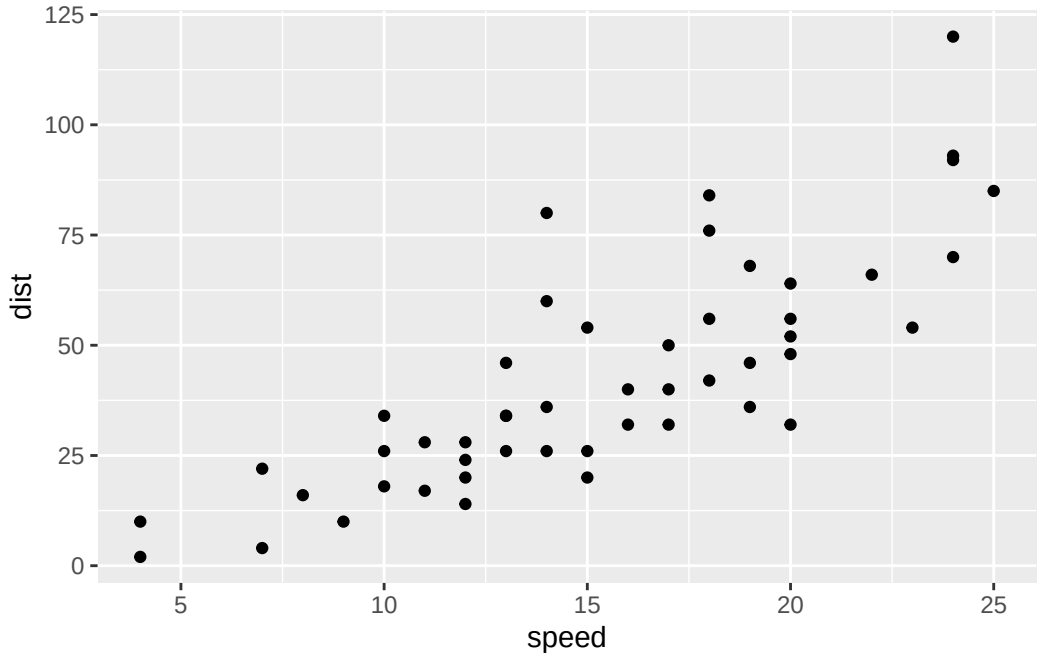
A quick base R plot - not in ggplot2

```
plot(cars)
```



Our First ggplot. We need data + aes + geoms

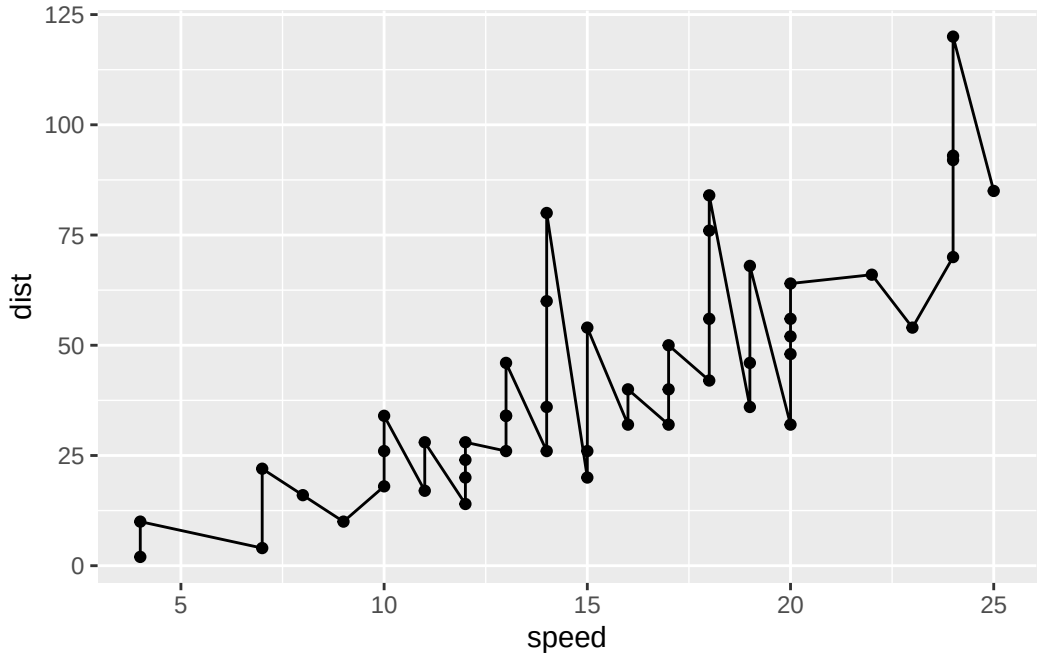
```
ggplot(data = cars) + aes(x = speed, y = dist) + geom_point()
```




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

Add a line geometry with line_geom()

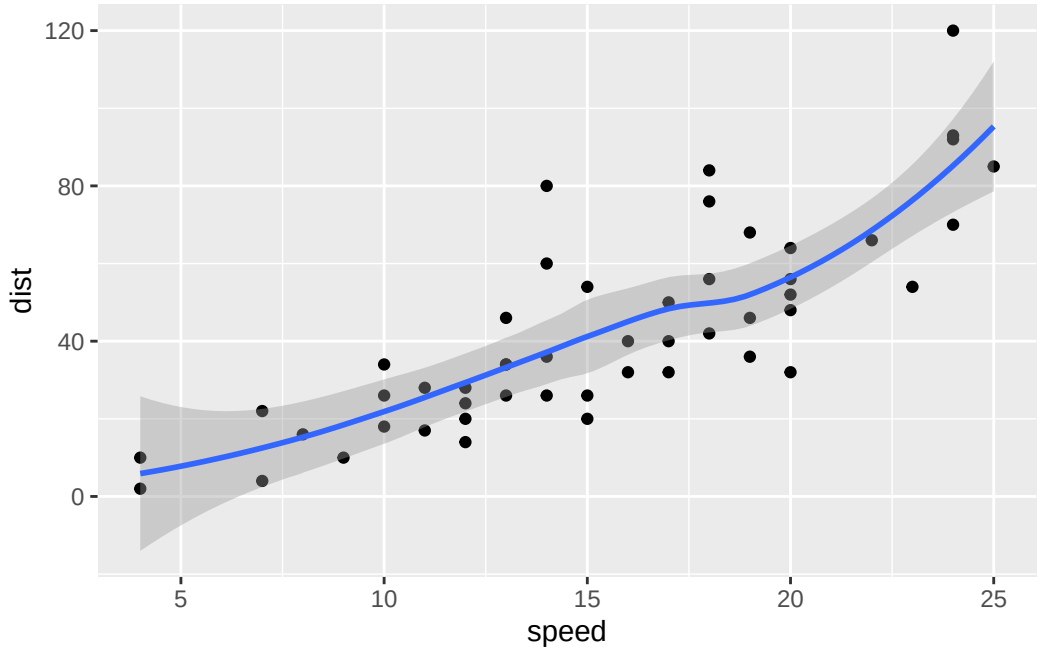
```
p + geom_line()
```



Add a trend line close to the data

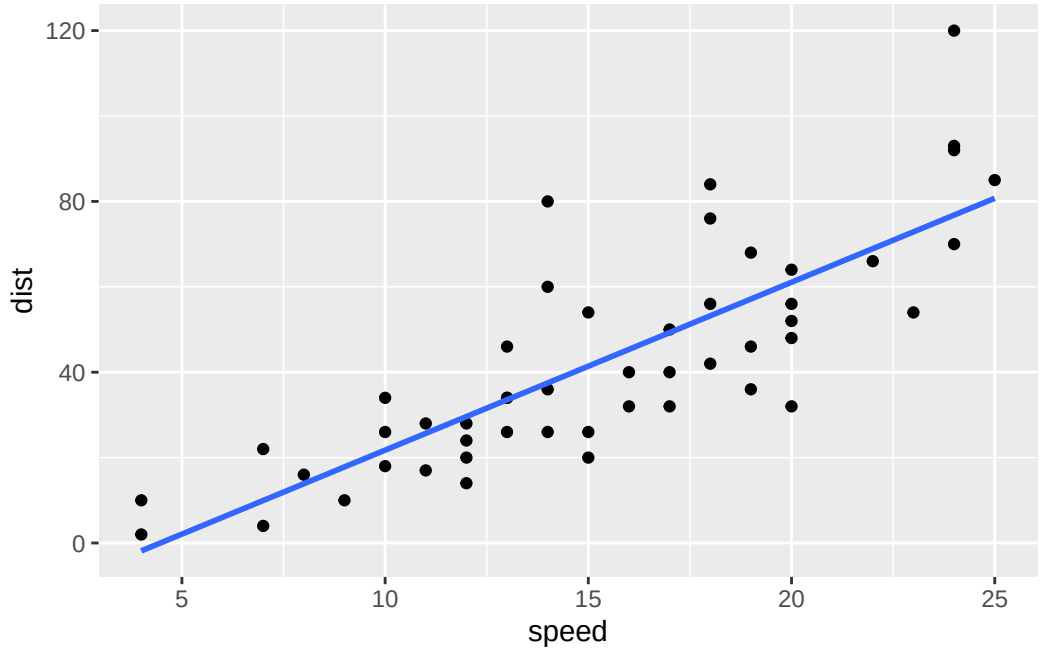
```
p + geom_smooth()
```

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



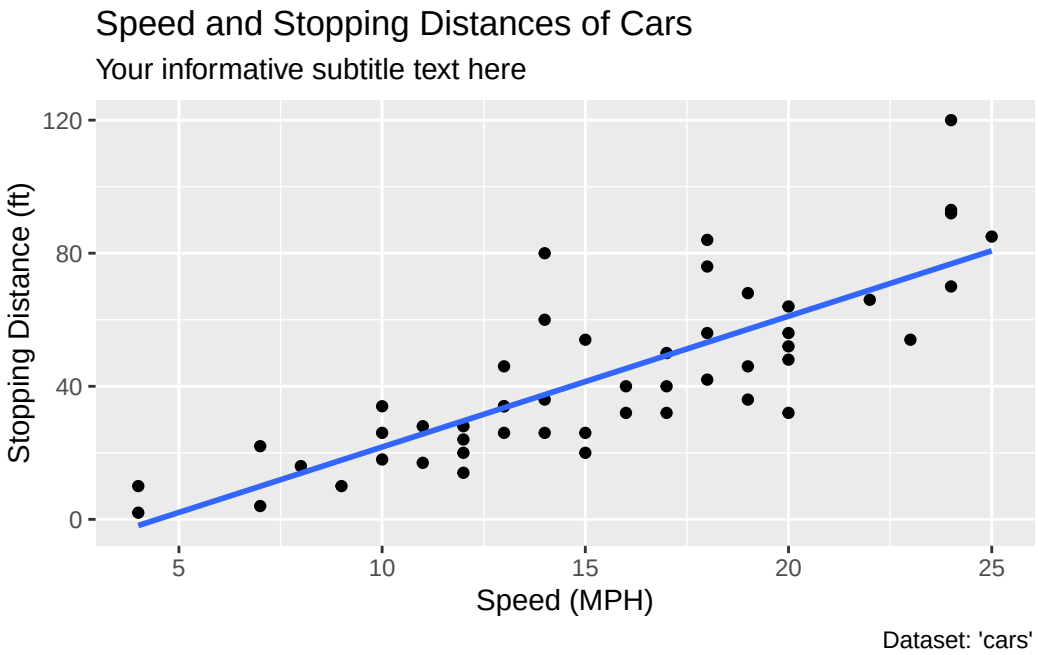

```
p + geom_smooth(method="lm", se = FALSE)
```

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




```
p + labs(title="Speed and Stopping Distances of Cars", x = "Speed (MPH)", y = "Stopping Di
```

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



Read in our drug expression data

```
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
```

Q. How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

How many Up regulated genes are there?

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

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

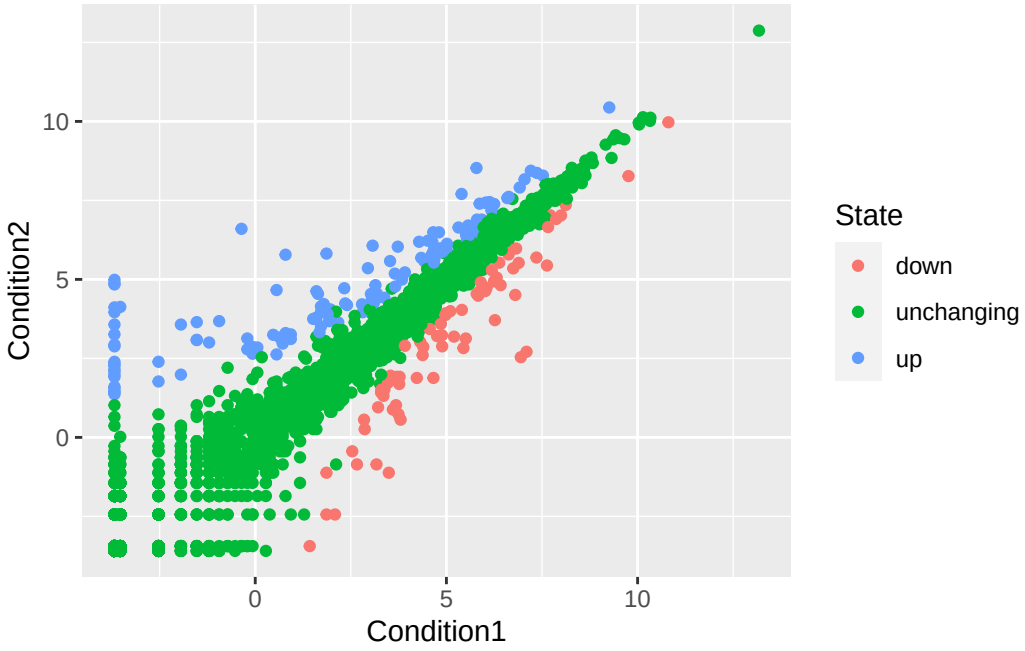
What fraction of genes are up regulated?

```
round(table(genes$State)/nrow(genes) * 100, 2)
```

```
      down unchanging         up
      1.39      96.17       2.44
```

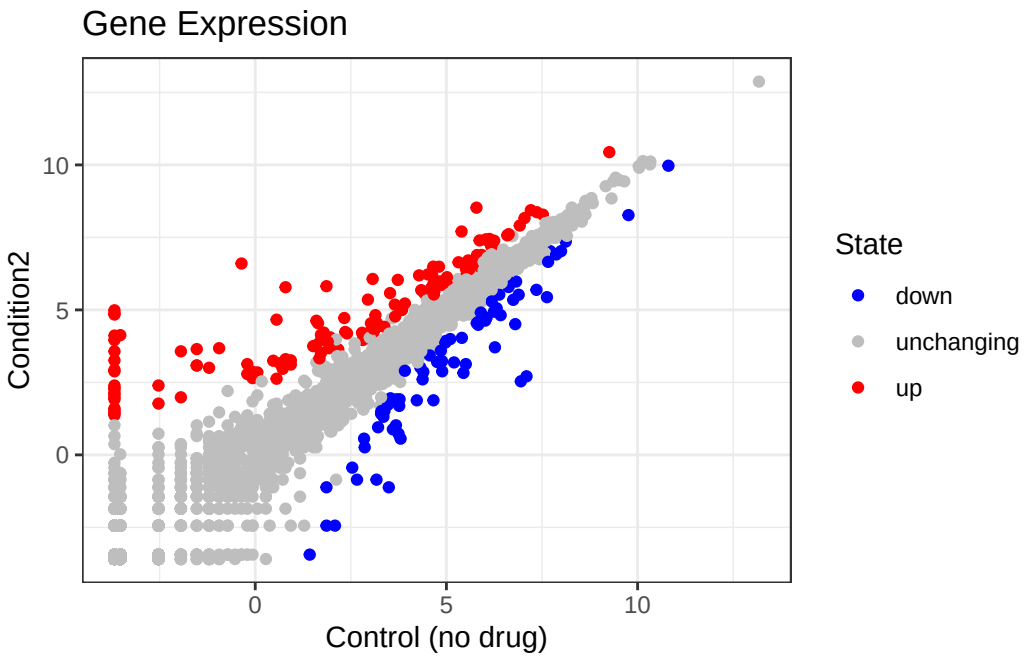
Lets make a first plot attempt

```
g <- ggplot(data = genes) + aes(x = Condition1, y = Condition2, col = State) +   geom_poin
g
```



Add some color

```
g + scale_color_manual(values=c("blue","gray","red")) + labs(title = "Gene Expression", x
```


Gene Expression
Condition2
10
5
0
0
5
10
Control (no drug)
State
down
unchanging
up