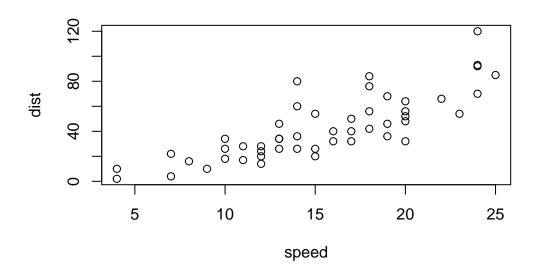
## class 5: Data Visulalization

## Nikan

## 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.

have to first install ggplts

the install is a onetime only requirement. package is now on our computer. no need to reinstall. does have to be loaded into the project tho by calling library().

```
library(ggplot2)
ggplot(cars)
```

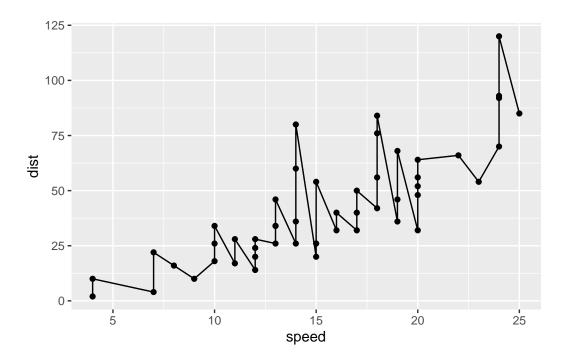
all ggplot figures need at least 3 things: - data (this is the data.frame with our numbers ) - aesthetics ("aes", how our data mp as to the plot) - geomes (do want lines, points, columns, etc... )

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



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

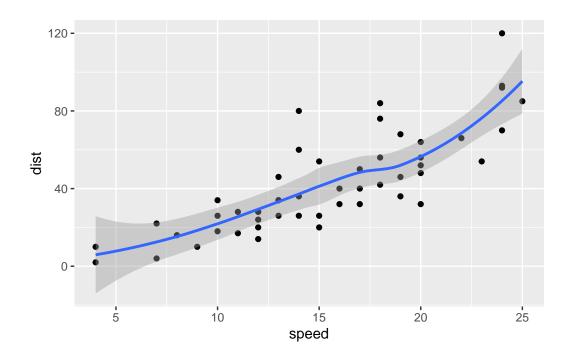
```
ggplot(data = cars) +
  aes(x=speed, y = dist) +
  geom_point() +
  geom_line()
```



thats not what we want

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

 $\ensuremath{\mbox{`geom\_smooth()`}}\ \mbox{using method} = \ensuremath{\mbox{'loess'}}\ \mbox{and formula} = \ensuremath{\mbox{'y}}\ \sim \ensuremath{\mbox{x'}}\ \mbox{'}$ 



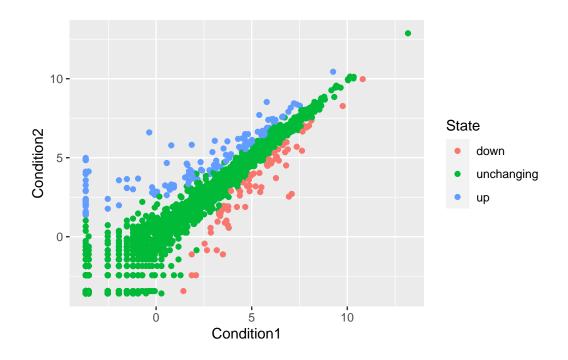
url <- "https://bioboot.github.io/bimm143\_S20/class-material/up\_down\_expression.txt"
genes <- read.delim(url)
head(genes)</pre>

```
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
```

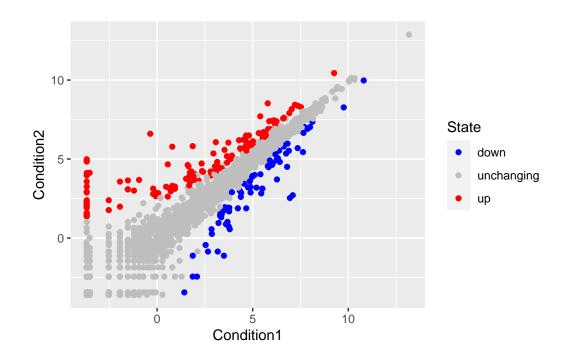
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2) +
  geom_point()
```

```
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 Expresion Changes Upon Drug Treatment

