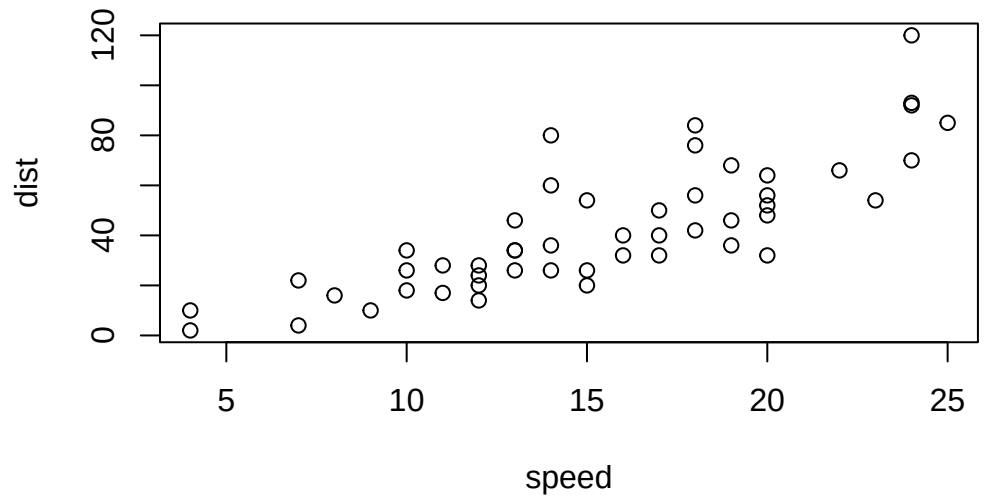
Class 5: Data Viz with ggplot

Tim

R has lot's of ways ti make figures and graphs in particular one that comes with R out of the box is called **"base" R** - the `plot()` function.

```
plot(cars)
```

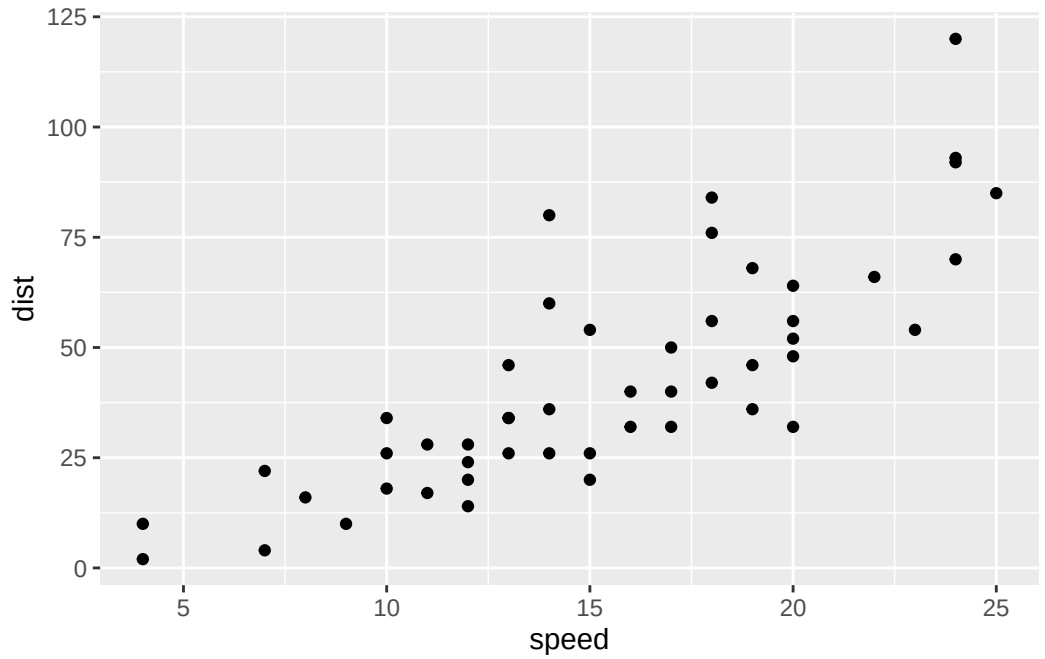


A very popular package in this area is called **ggplot2**

Before I can use any add-on package like this I must install it with the `install.packages("ggplot2")` then to use the package I need to load it with a `library(ggplot2)` call

```
library(ggplot2)

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



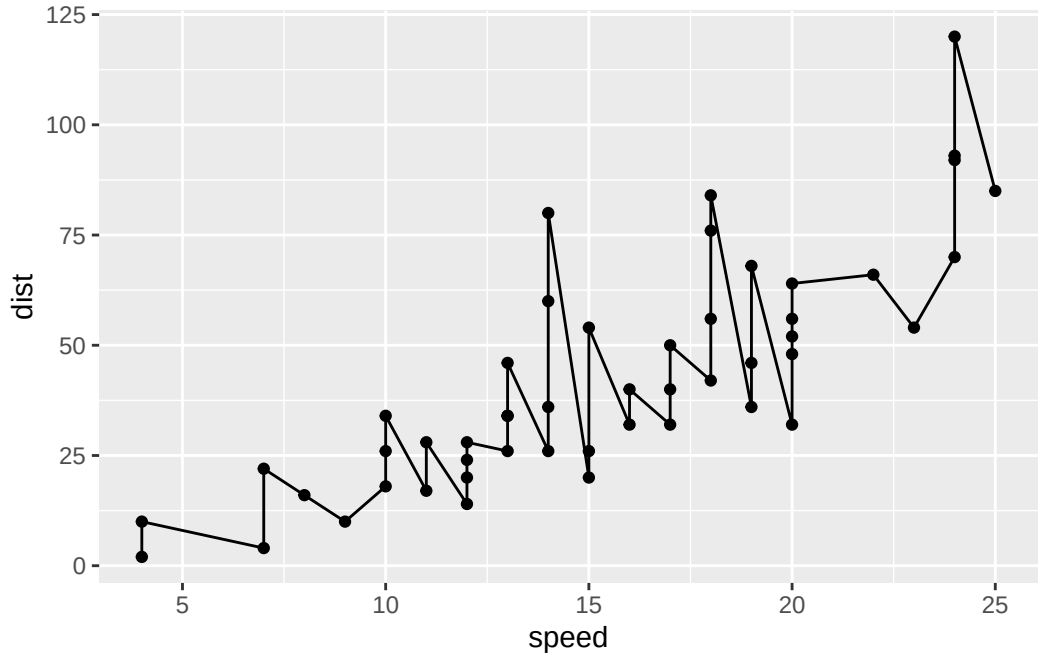

```
ggsave("myplot.png")
```

```
Saving 5.5 x 3.5 in image
```

for simple plots like this one base R code will be much easier to write than ggplot

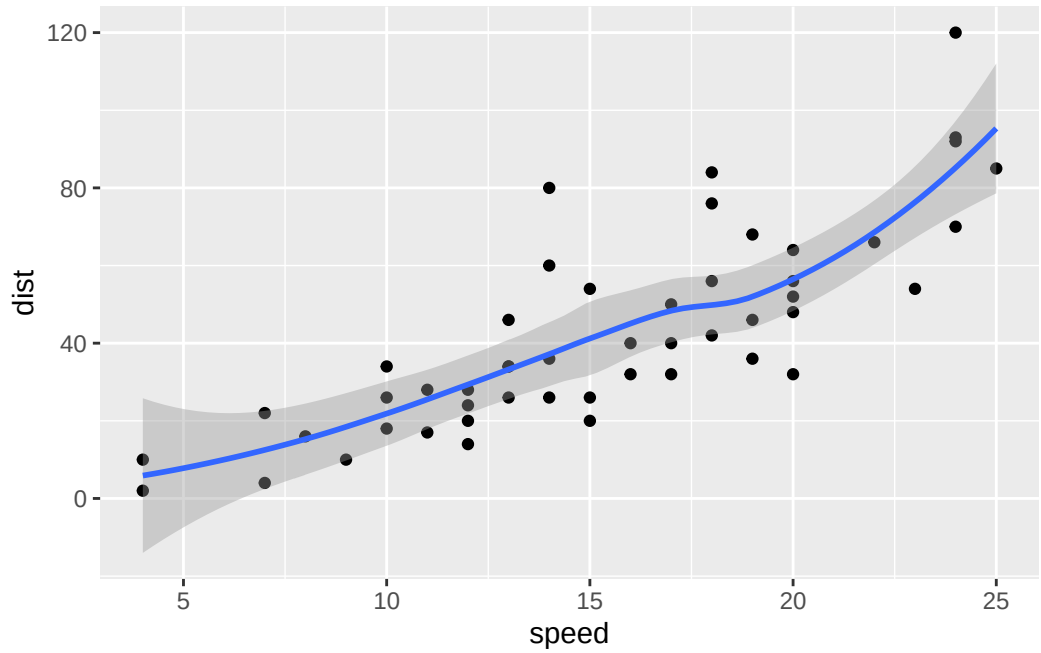
let first show it on my plot

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




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

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



every ggplot has at least 3 layers

- **data** (data.frame with the numbers or stuff you want to plot)
- aesthetics **aes** (maping of your data columns to your plot)
- **geoms** (geom_point, geom_line, geom_col)

```
mtcars
```

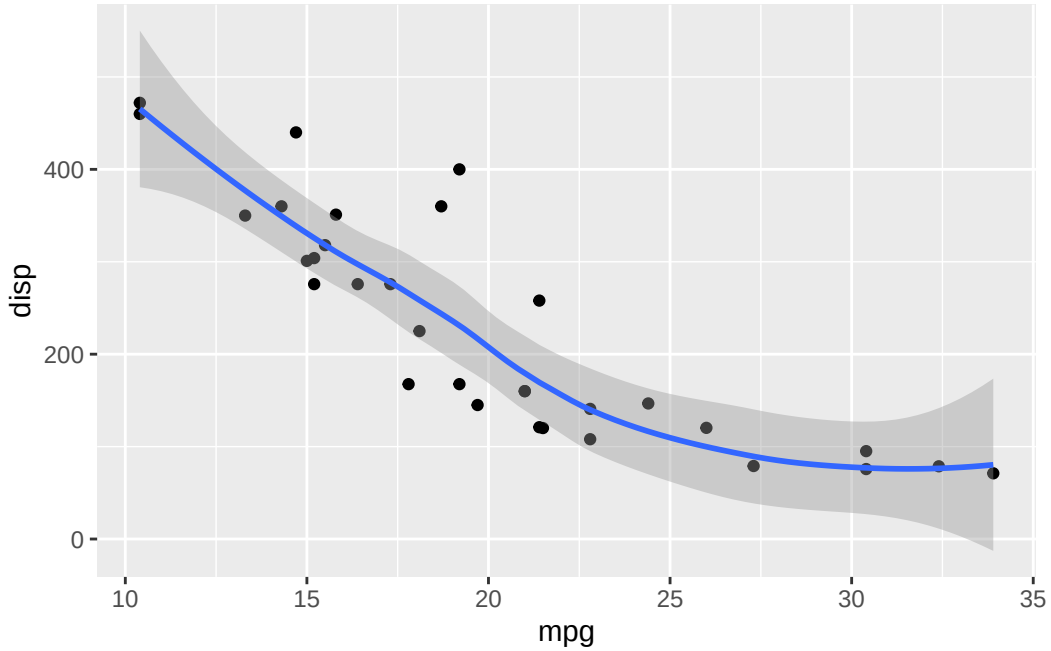
	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160.0	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160.0	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258.0	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360.0	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225.0	105	2.76	3.460	20.22	1	0	3	1
Duster 360	14.3	8	360.0	245	3.21	3.570	15.84	0	0	3	4
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Merc 280	19.2	6	167.6	123	3.92	3.440	18.30	1	0	4	4
Merc 280C	17.8	6	167.6	123	3.92	3.440	18.90	1	0	4	4
Merc 450SE	16.4	8	275.8	180	3.07	4.070	17.40	0	0	3	3
Merc 450SL	17.3	8	275.8	180	3.07	3.730	17.60	0	0	3	3
Merc 450SLC	15.2	8	275.8	180	3.07	3.780	18.00	0	0	3	3

```
Cadillac Fleetwood  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
Lincoln Continental 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4
Chrysler Imperial   14.7   8 440.0 230 3.23 5.345 17.42  0  0    3    4
Fiat 128            32.4   4  78.7  66 4.08 2.200 19.47  1  1    4    1
Honda Civic         30.4   4  75.7  52 4.93 1.615 18.52  1  1    4    2
Toyota Corolla      33.9   4  71.1  65 4.22 1.835 19.90  1  1    4    1
Toyota Corona       21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1
Dodge Challenger    15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2
AMC Javelin         15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2
Camaro Z28          13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4
Pontiac Firebird    19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2
Fiat X1-9           27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1
Porsche 914-2       26.0   4 120.3  91 4.43 2.140 16.70  0  1    5    2
Lotus Europa        30.4   4  95.1 113 3.77 1.513 16.90  1  1    5    2
Ford Pantera L      15.8   8 351.0 264 4.22 3.170 14.50  0  1    5    4
Ferrari Dino        19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
Maserati Bora       15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8
Volvo 142E          21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2
```

make a ggplot of the `mtcars` data set using `mpg` vs `disp`

```
ggplot(mtcars)+
  aes(x=mpg, y=disp)+
  geom_point()+
  geom_smooth()
```

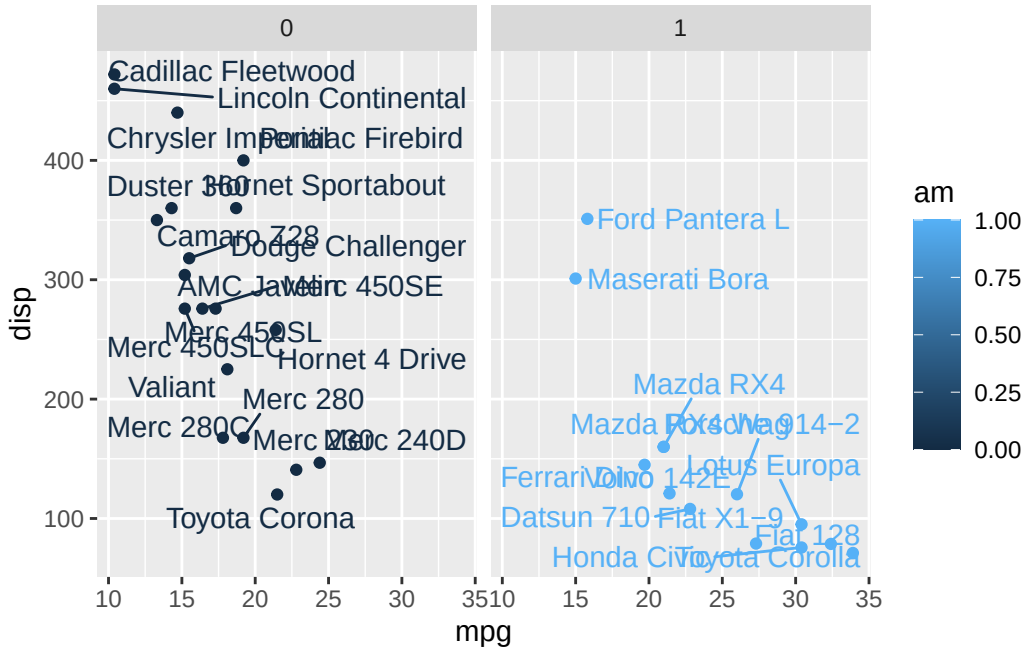
```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



make a ggplot of the `mtcars` data set using `mpg` vs `disp` and set the size of the points to the `hp`

```
library(ggrepel)

ggplot(mtcars)+
  aes(x=mpg, y=disp, col=am, label=rownames(mtcars))+
  geom_point() +
  facet_wrap(~am) +
  geom_text_repel()
```

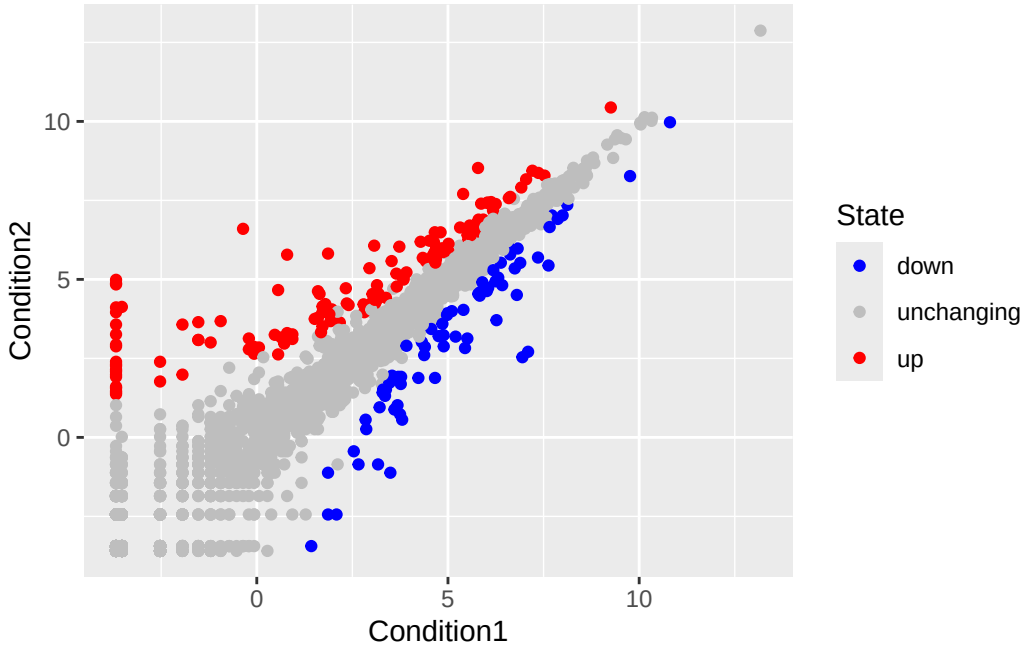



```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

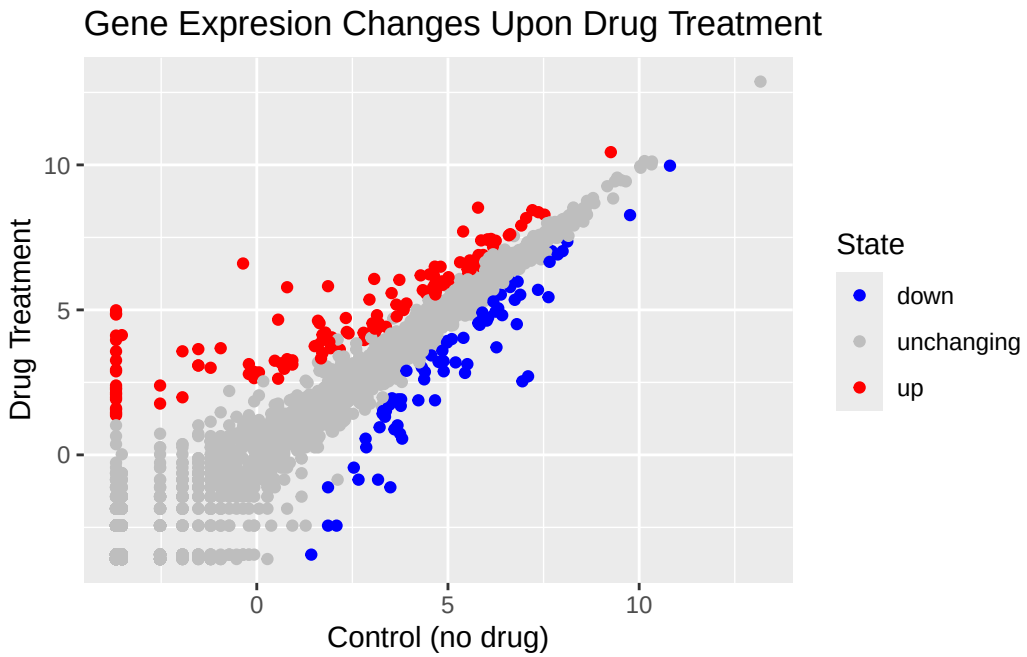
```
        Gene Condition1 Condition2      State
1      A4GNT -3.6808610 -3.4401355 unchanging
2       AAAS  4.5479580  4.3864126 unchanging
3      AASDH  3.7190695  3.4787276 unchanging
4       AATF  5.0784720  5.0151916 unchanging
5       AATK  0.4711421  0.5598642 unchanging
6 AB015752.4 -3.6808610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

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

```
tim1 <- tim + scale_color_manual( values = c("blue", "grey", "red"))
tim1
```




```
tim1 <- tim + scale_color_manual( values = c("blue", "grey", "red")) +
  labs(title = "Gene Expresion Changes Upon Drug Treatment",
       x="Control (no drug)",
       y="Drug Treatment")
tim1
```




```
ggsave("myplot.png")
```

```
Saving 5.5 x 3.5 in image
```

```
round(table(genes$State) / nrow(genes), 3)
```

```
      down unchanging         up
     0.014      0.962      0.024
```

#the function `nrow`, `ncol`, and `table()` are one I want you to know

```
library(gapminder)
```

key points: Saving plot with **ggsave()** Different plot "type" with different `geom_**()` Facting with `facet_wrap()` multi-plot layout with the **patchwork** package.

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts

gapminder <- read.delim(url)
```