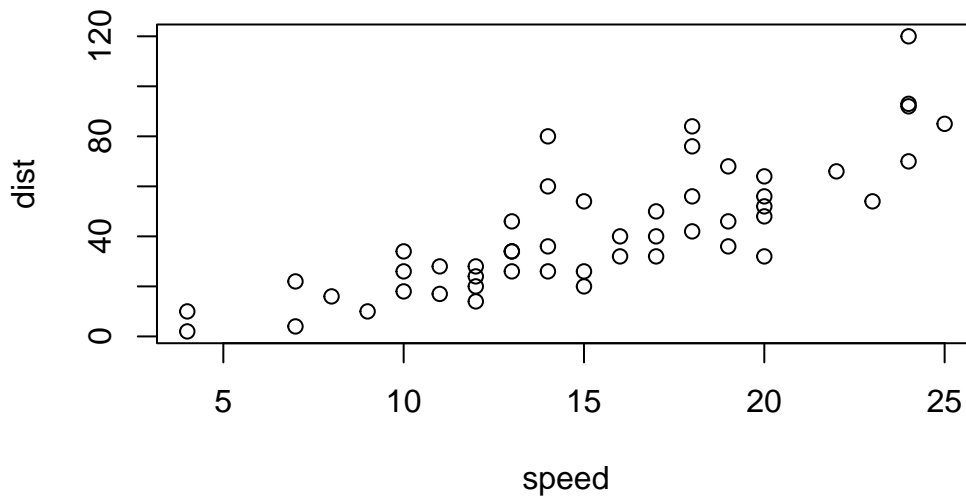


# Class 05

Abel

R has lot's of ways to make figures and graphs in particular. One that come with R out the box is called “**bas**” **R** - the ‘plot()’ function.

```
plot(cars)
```



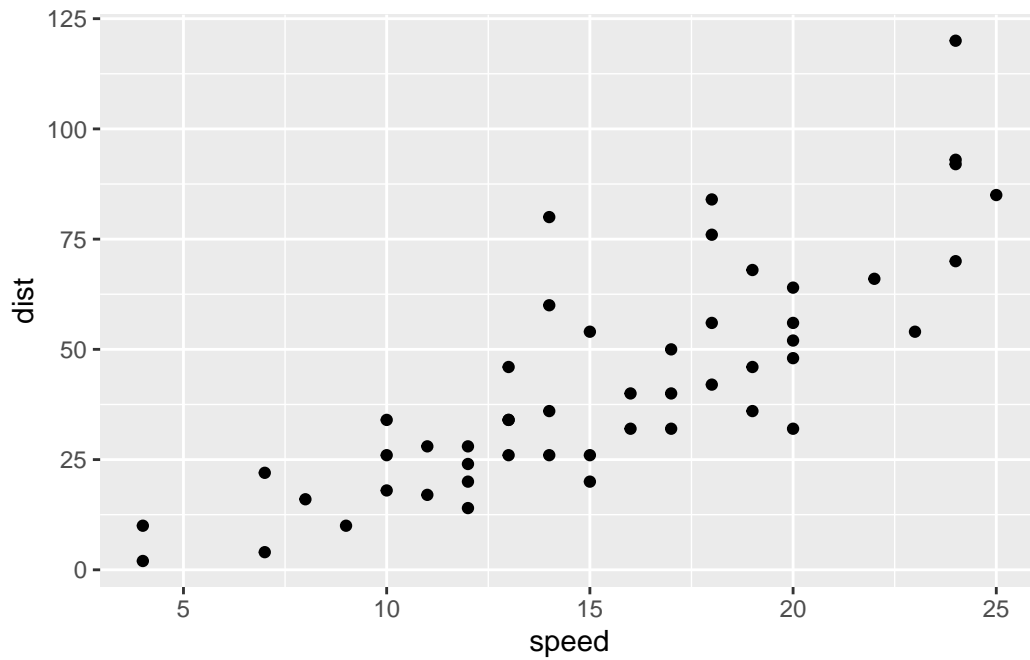
---

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")` command/function

Then to use hte package I need to load it with a ‘library(ggplot2)’ call.

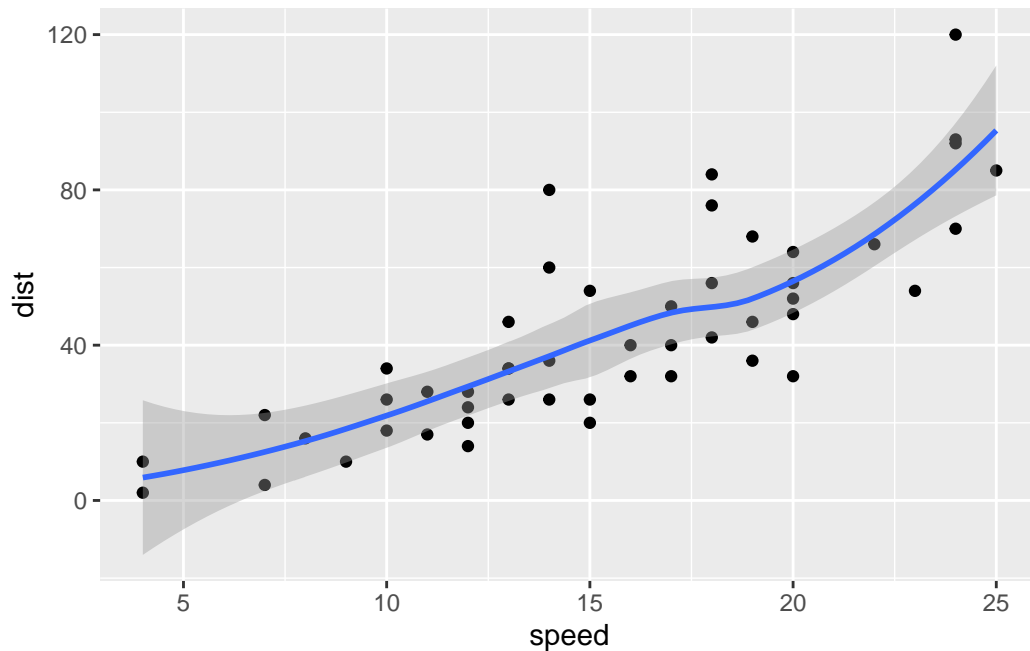
```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



For “simple” plots like this one base R code will be much shorter than ggplot code.

```
library(ggplot2)
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 three layers

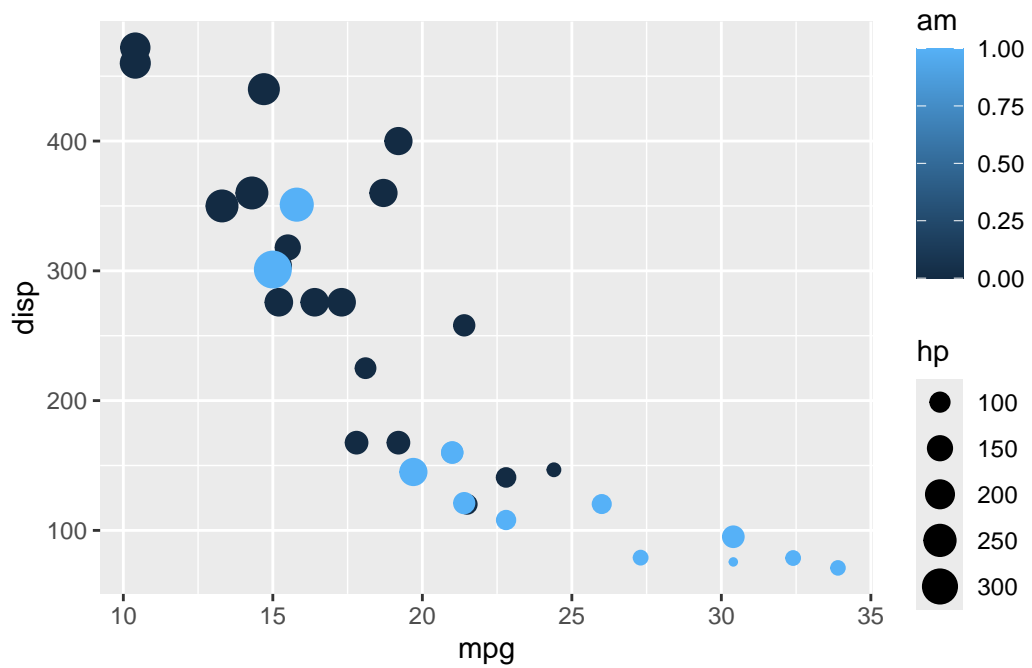
-**data** (data.frame with the number or stuff you want to plot) -**aesthetics** (mapping of your data cols to your plot) -**geoms** (there are tones of these, basics are `geom_point()`, `geom_line()`, `geom_col()`)

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

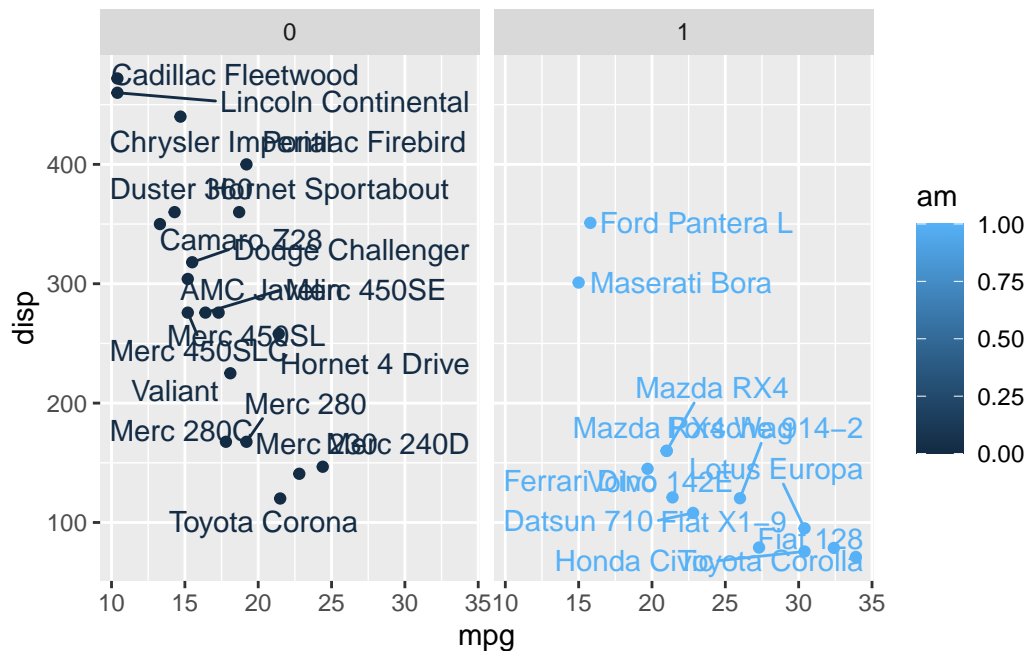
Make a ggplot of the `mtcars` data set using `mpg` vs `disp` and set the size for the points to the `hp` set the color to `am`

```
library(ggplot2)
ggplot(mtcars) +
  aes(x=mpg, y= disp, size=hp, color= am) +
  geom_point()
```



```
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

```
nrow(genes)
```

```
[1] 5196
```

There are 5196 genes in this dataset.

```
unique(genes$State)
```

```
[1] "unchanging" "up"          "down"
```

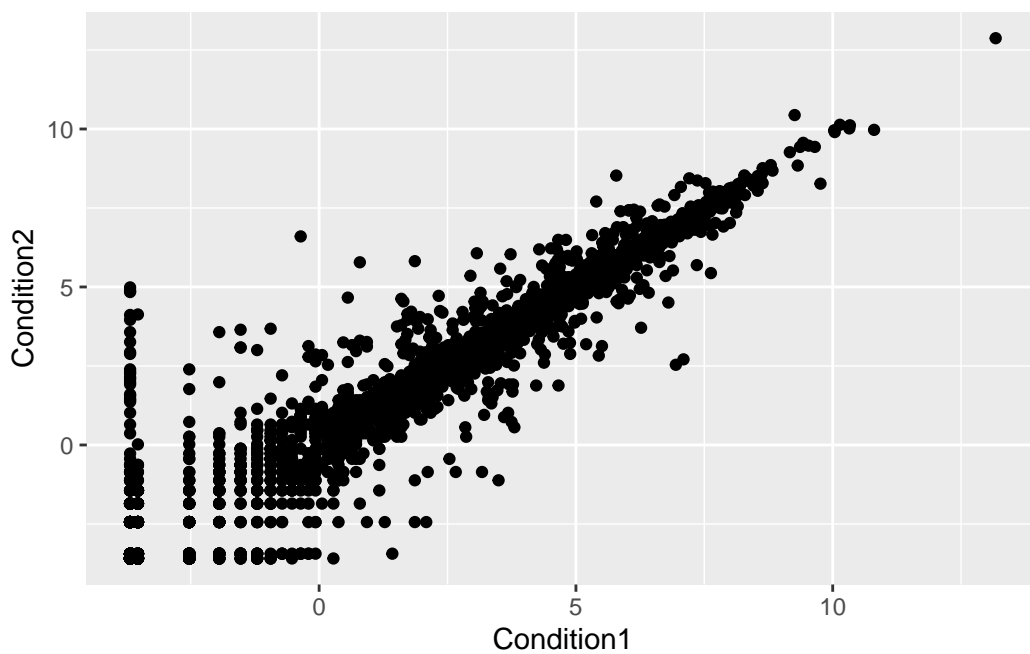
The `table()` function is super useful utility to tell me how many entries of each type there are.

```
table(genes$State) / nrow(genes)
```

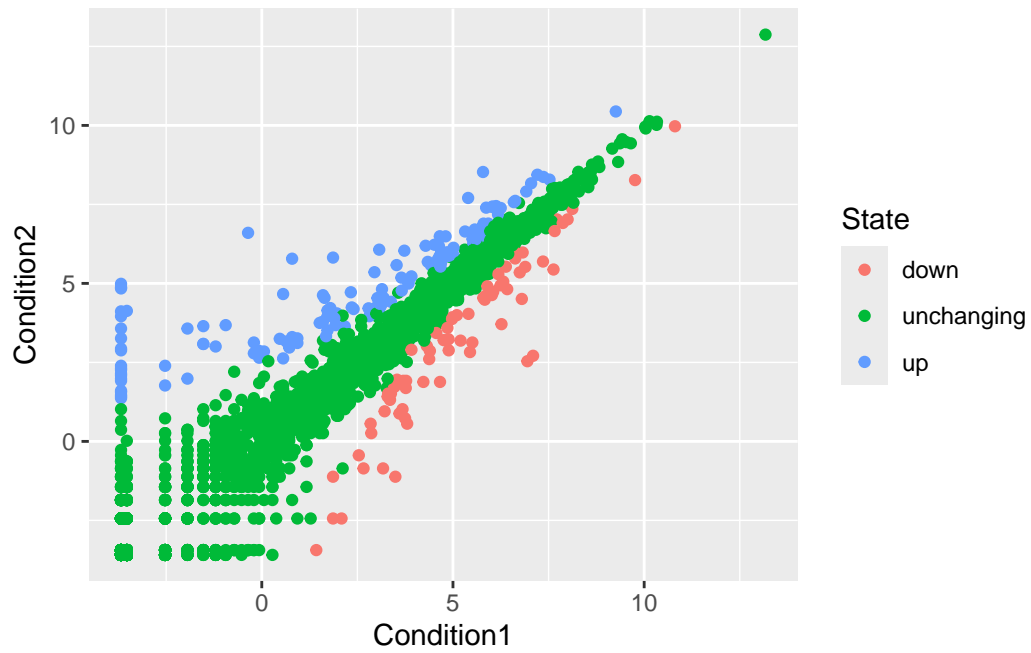
```
      down  unchanged      up  
0.01385681 0.96170131 0.02444188
```

The functions `nrow()`, and `table()` are ones I want you to know

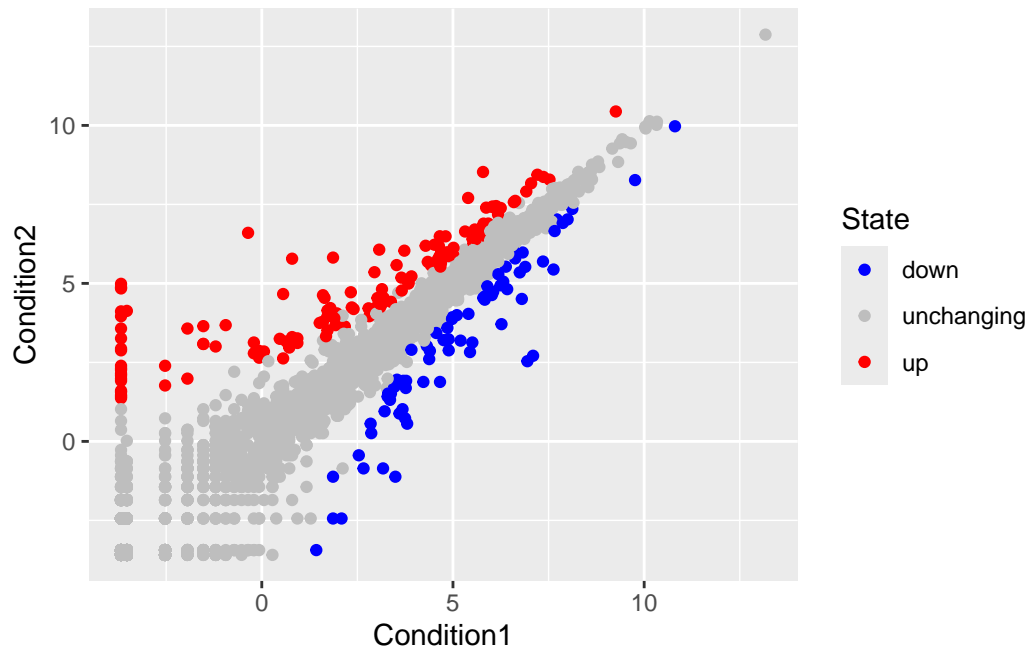
```
library(ggplot2)  
ggplot(genes) +  
aes(x=Condition1, y=Condition2) +  
geom_point()
```



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



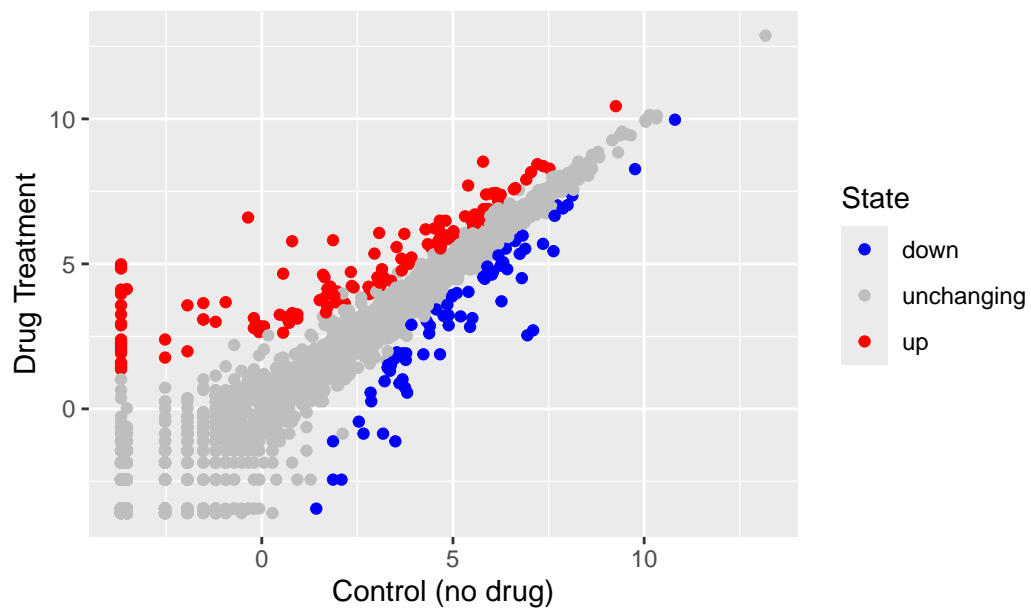
```
ggplot(genes) +  
  aes(x=Condition1, y=Condition2, col=State) +  
  geom_point() +  
  scale_colour_manual( values=c("blue","gray","red") )
```



```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  scale_colour_manual( values=c("blue","gray","red") ) +
  labs(title = "Gene Expression Changes Upton Drug Treatment", x = "Control (no drug)", y= "Drug Treatment")
```



## Gene Expression Changes Upton Drug Treatment



key points

```
p <-ggplot(mtcars)+  
  aes(mpg, disp) +  
  geom_point()  
  
ggsave("myplot.pdf")
```

Saving 5.5 x 3.5 in image

p

