Class 5: ggplot

Dhruv

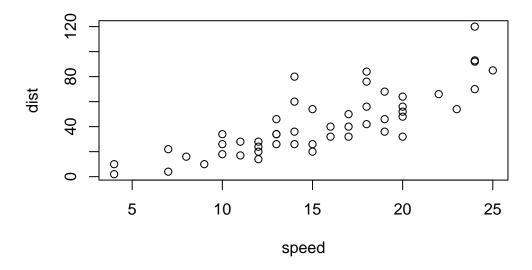
Making figures and graphs with R "base" $\bf R$ is the default program to make plots. This can be accessed using the plot() function.

cars

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10
7	10	18
8	10	26
9	10	34
10	11	17
11	11	28
12	12	14
13	12	20
14	12	24
15	12	28
16	13	26
17	13	34
18	13	34
19	13	46
20	14	26
21	14	36
22	14	60
23	14	80
24	15	20
25	15	26
26	15	54

```
27
      16
           32
      16
          40
28
29
      17
           32
30
      17
           40
31
      17
           50
32
      18
           42
          56
33
      18
34
      18
          76
35
      18
          84
36
      19
          36
37
      19
          46
38
      19
           68
          32
39
      20
40
      20
          48
41
      20
          52
42
      20
          56
43
      20
          64
44
      22
           66
45
      23
          54
46
      24
          70
47
      24
          92
48
      24
          93
49
      24 120
          85
50
      25
```

plot(cars)

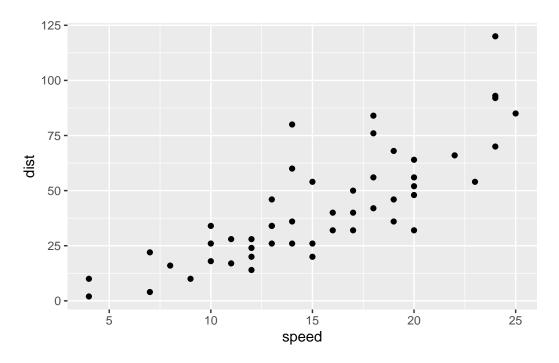


Popular package to do data visualization is ggplot2

 $\operatorname{ggplot}(\operatorname{cars})$ - this wont work

Before using an add-on package we must first install it: install.packages("ggplot2"). Next, this must be loaded.

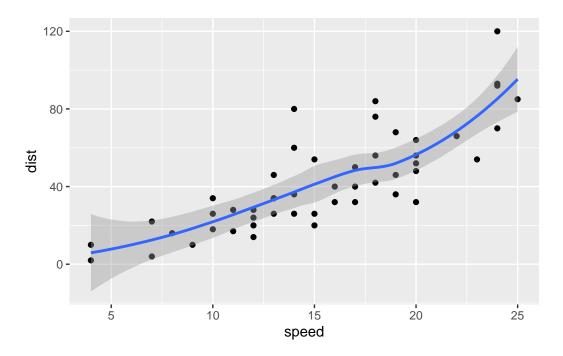
```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



"base" r is shorter for simpler graphs, and **ggplot** works better for complex graphs. Let's try to make the above plot more complex now

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

 $[\]ensuremath{\text{`geom_smooth()`}}\ using method = 'loess' and formula = 'y ~ x'$



Every ggplot has at minimum 3 layers

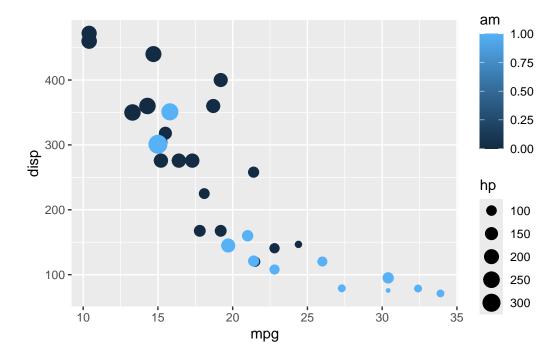
- data (data.frame with things you want to plot)
- aesthetics**
- geomss quite a few including geom_line(), geom_col(), geom_point()

head(mtcars)

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

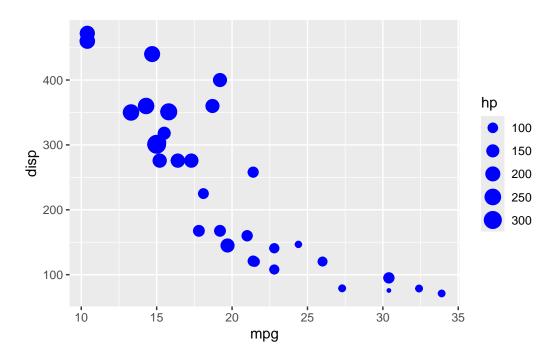
ggplot

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



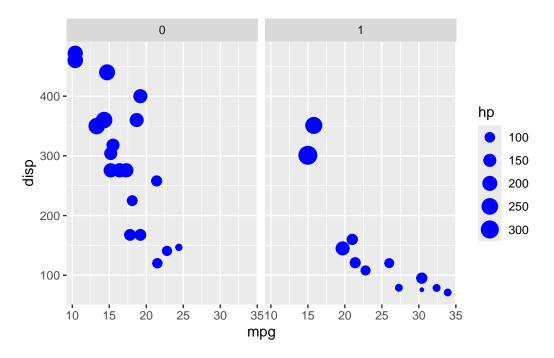
Now color all points blue

```
ggplot(mtcars) +
  aes(x = mpg, y = disp, size = hp) +
  geom_point(col = "blue")
```



can make the old plot faceted

```
ggplot(mtcars) +
  aes(x = mpg, y = disp, size = hp) +
  geom_point(col = "blue") +
  facet_wrap("am")
```



Now we will work through the lab sheet

1

Gene Condition1 Condition2

A4GNT -3.6808610 -3.4401355 unchanging

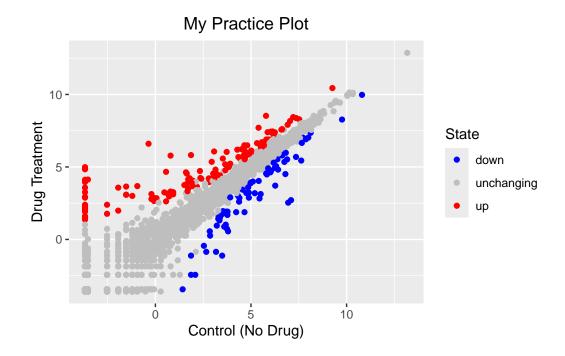
```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)</pre>
```

State

```
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

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

```
p + scale_color_manual(values = c("blue", "grey", "red")) + labs(title = "My Practice Plot", :
```



nrow(genes)

[1] 5196

There are 5196 genes in this dataset

The table() function is useful to look at how many of each entries are there. this is compared to unique() which tells you the actual unique variables but not how many of each.

table(genes\$State)

down	unchanging	up
72	4997	127

What fraction are up, down, or unchanging. Total genes = nrow(genes). Can divide table by this.

colnames(genes)

[1] "Gene" "Condition1" "Condition2" "State"

ncol(genes)

[1] 4

nrow(genes)

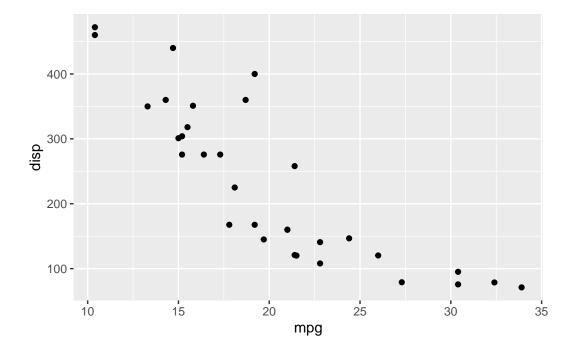
[1] 5196

round(table(genes\$State)/nrow(genes), 3)*100

down unchanging up 1.4 96.2 2.4

Key points: Saving plots with **ggsave()** "types" of plots with 'geoms_ Multi-plot layout with **patchwork** package

```
ggplot(mtcars) +
aes(mpg, disp) +
geom_point()
```



ggsave("myplot.pdf")

Saving 5.5×3.5 in image