# Class 5: Data Viz with ggplot

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### Intro to ggplot

There are may graphics systems in R (ways to make plots and figures). These include "base" R plots. Today we will focus mostly on the **ggplot2** package.

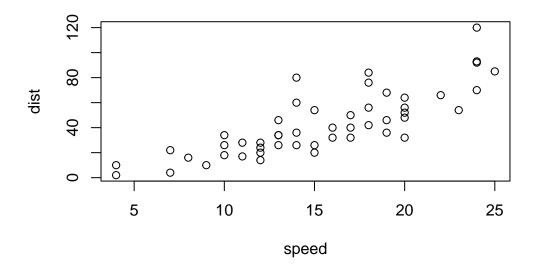
Let's start with a plot of a simple in-bulit dataset called cars.

#### 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
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           32
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45
      23
           54
46
      24
           70
47
      24
           92
48
      24
           93
49
      24 120
           85
50
      25
```

# plot(cars)



Let's see how we can make this figure using **ggplot**. First I need to install this package on my computer. To install any R package I use the function install.packages().

I will run 'install.packages("ggplot2") in my R console not this quarto document!

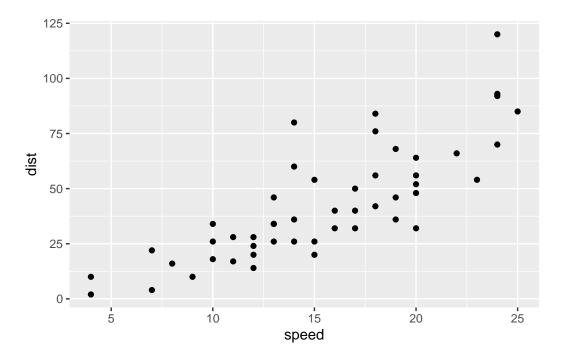
Before I can use any functions from add on packages I need to load the package from my "library()" with the library(ggplot2) call.

library(ggplot2)
ggplot(cars)

All ggplot figures have at least 3 things (called layers). These include:

- data (the input dataset I want to plot from),
- aes (the aesthetic mapping of the data to my plot),
- **geoms** (the geom\_point(), geom\_line() etc. that I want to draw).

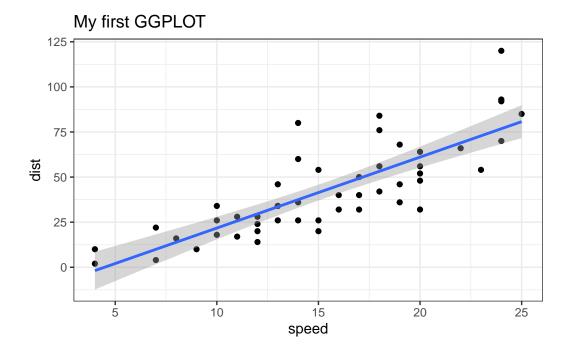
```
ggplot(cars) +
aes(x=speed, y=dist) +
geom_point()
```



Let's add a line to show the relationship here:

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm") +
  theme_bw() +
  labs(title="My first GGPLOT")
```

<sup>`</sup>geom\_smooth()` using formula = 'y ~ x'



Q1 Which geometric layer should be used to create scatter plots in ggplot2? geom\_point()

### Gene expresion figure

The code to read the dataset

```
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
```

How many genes are in this dataset?

```
nrow(genes)
```

#### [1] 5196

Q. Use the table() function on the State column of this data.frame to find out how many 'up' regulated genes there are. What is your answer?

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

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

Q. Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset?

```
round( table(genes$State)/nrow(genes), 4)
```

```
down unchanging up 0.0139 0.9617 0.0244
```

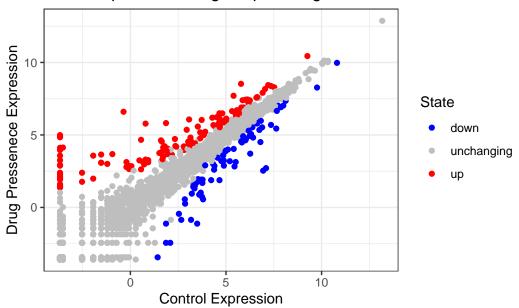
```
n.tot <- nrow(genes)
vals <- table(genes$State)

vals.percent <- vals/n.tot * 100
round(vals.percent, 2)</pre>
```

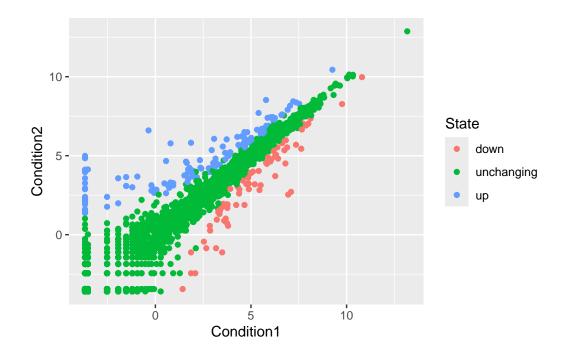
```
down unchanging up
1.39 96.17 2.44
```

A first plot of this dataset

# Gene Expresion changes upon drug treatement

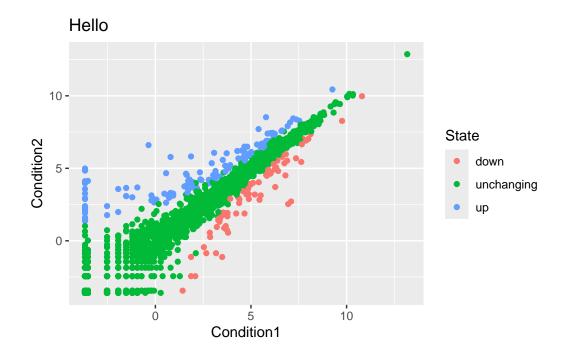


```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p</pre>
```

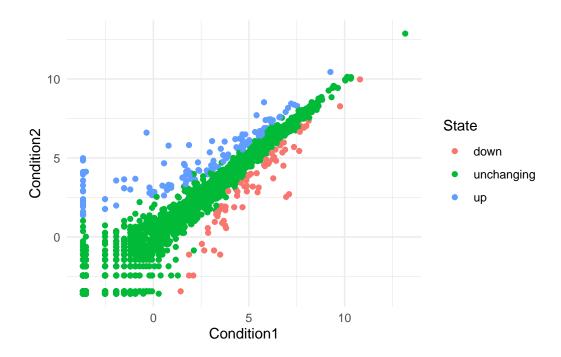


#p + scale\_colour\_manual( values=c("blue","gray","red") )

# p + labs(title="Hello")



### p + theme\_minimal()



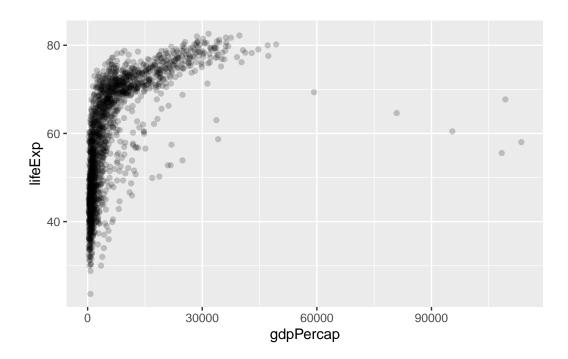
# **Exploring the gapmider dataset**

The gapminder dataset contains economic and demographic data about various countries since 1952.

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts
gapminder <- read.delim(url)
head(gapminder)</pre>
```

	country	continent	year	lifeExp	pop	gdpPercap
1	Afghanistan	Asia	1952	28.801	8425333	779.4453
2	Afghanistan	Asia	1957	30.332	9240934	820.8530
3	Afghanistan	Asia	1962	31.997	10267083	853.1007
4	Afghanistan	Asia	1967	34.020	11537966	836.1971
5	Afghanistan	Asia	1972	36.088	13079460	739.9811
6	Afghanistan	Asia	1977	38.438	14880372	786.1134

```
ggplot(gapminder) +
aes(x=gdpPercap, y=lifeExp) +
geom_point(alpha=0.2)
```



### Combining plots with patchwork

<sup>&#</sup>x27;geom\_smooth()' using method = 'loess' and formula = 'y ~ x'

