# Class 5

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### Base R graphics vs ggplot2

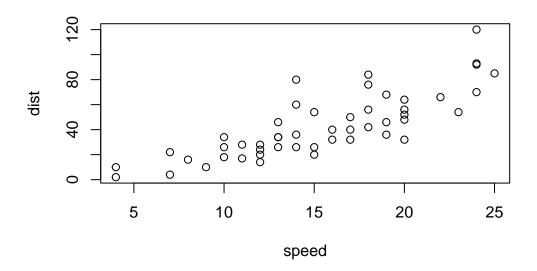
There are many graphics systems available in R, including so-called "base" R graphics and the very popular **ggplot2** package.

To compare these let's play with inbuilt cars dataset.

head(cars)

To use "base" R I can simply call the plot() function:

```
plot(cars)
```



To use  $\mathtt{ggplot2}$  package I first need to install it with the function  $\mathtt{install.packages}(\mathtt{"ggplot2"})$ 

I will run this in my R console (i.e the R brain) as I do not want to re-install it every time I render my report

The main function in this packge is called ggplot(). Can I just call it?

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

To manke a figure with ggplot I need always a least 3 things:

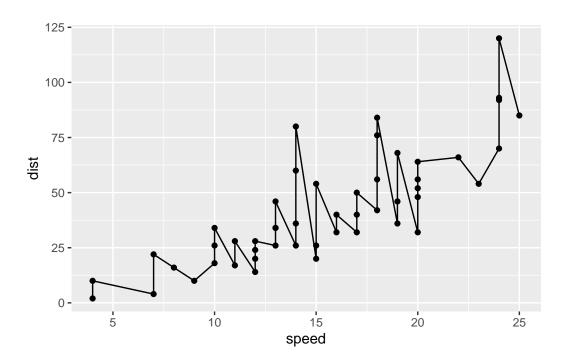
- data (i.e what I want to plot)
- ${\bf aesthetics}$  the aesthetic mapping of the data to the plot I want
- $\bullet~$  the geometries i.e how I want to plot the data with different geometries

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



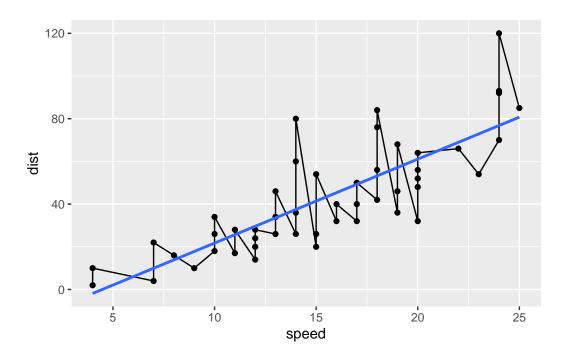
If I want to add more things I can just keep adding layers e.g.

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



```
ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_line() +
  geom_smooth(se = FALSE, method = "lm")
```

`geom\_smooth()` using formula = 'y ~ x'



#### \$title

[1] "stopping distance for old cars"

#### \$subtitle

[1] "This is really important data"

#### \$caption

[1] "dataset: 'cars'"

attr(,"class")

[1] "labels"

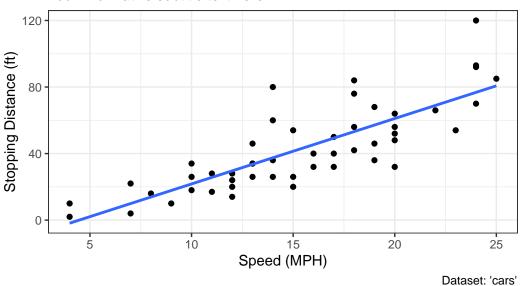
GGplot is much more verbose that base R plots but it has a consistent layer system that I cna use to make just about any plot.

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

`geom\_smooth()` using formula = 'y ~ x'

# Speed and Stopping Distances of Cars

Your informative subtitle text here



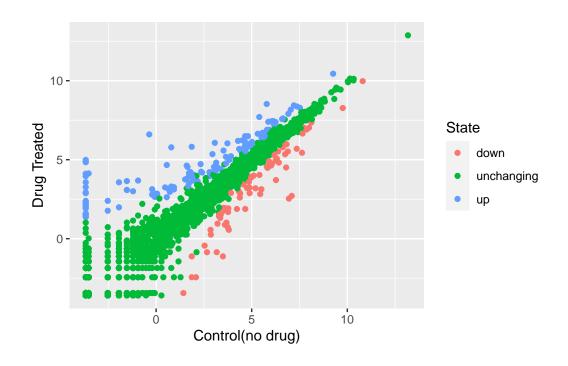
##A more complicated plot

Let's plot some gene expression data

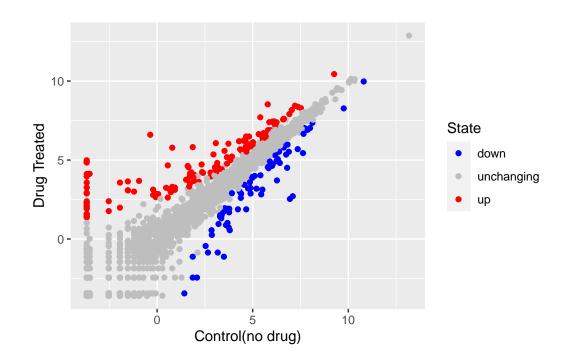
The code below reads the results of a differential expression analysis where a new anti-viral drug is being tested

```
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
              5.0784720
                         5.0151916 unchanging
        AATF
        AATK 0.4711421 0.5598642 unchanging
6 AB015752.4 -3.6808610 -3.5921390 unchanging
    Q. How many genes are in this dataset?
  nrow(genes)
[1] 5196
    Q. How can we summarize that last column - the "State column?"
  table(genes$State)
      down unchanging
        72
                 4997
                              127
  p <- ggplot(genes) +</pre>
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point() +
    labs(x="Control(no drug)", y="Drug Treated")
  p
```



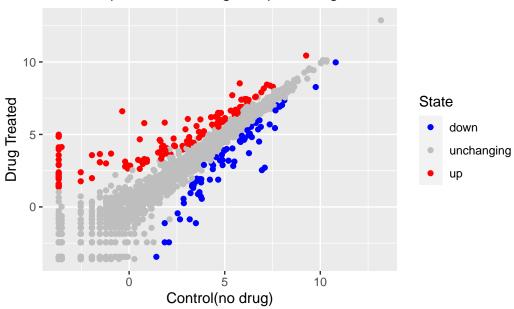
p + scale\_colour\_manual (values=c("blue","gray","red"))



I can now just call p when I want to plot or add to it.

```
p + scale_colour_manual (values=c("blue","gray","red")) +
    labs(title = "Gene Expression Changes Upon Drug Treatment")
```

# Gene Expression Changes Upon Drug Treatment



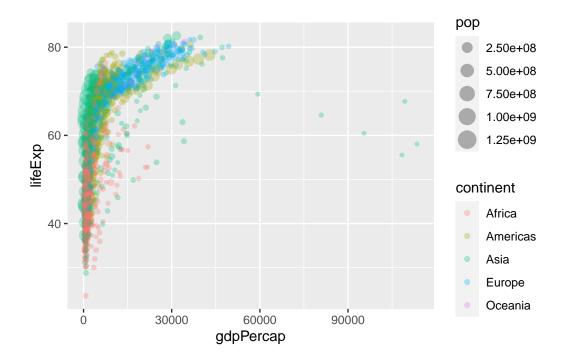
## **Going Further**

Here I read a slightly larger dataset

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

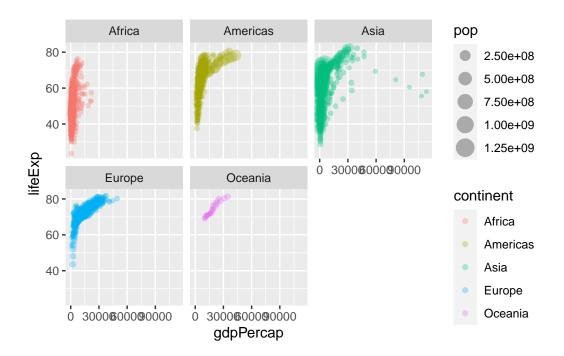
	country	${\tt continent}$	year	lifeExp	pop	${\tt gdpPercap}$
1	Afghanistan	Asia	1952	28.801	8425333	779.4453
2	Afghanistan	Asia	1957	30.332	9240934	820.8530
3	Afghanistan	Asia	1962	31.997	10267083	853.1007
4	Afghanistan	Asia	1967	34.020	11537966	836.1971
5	Afghanistan	Asia	1972	36.088	13079460	739.9811

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.3)
```



A very useful layer to add sometimes is for "facetting"

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.3) +
  facet_wrap(~continent)
```



```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color=pop) +
  geom_point(alpha=0.3)
```

