

Class 5: Data visualization

Natalie (A15948318)

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.

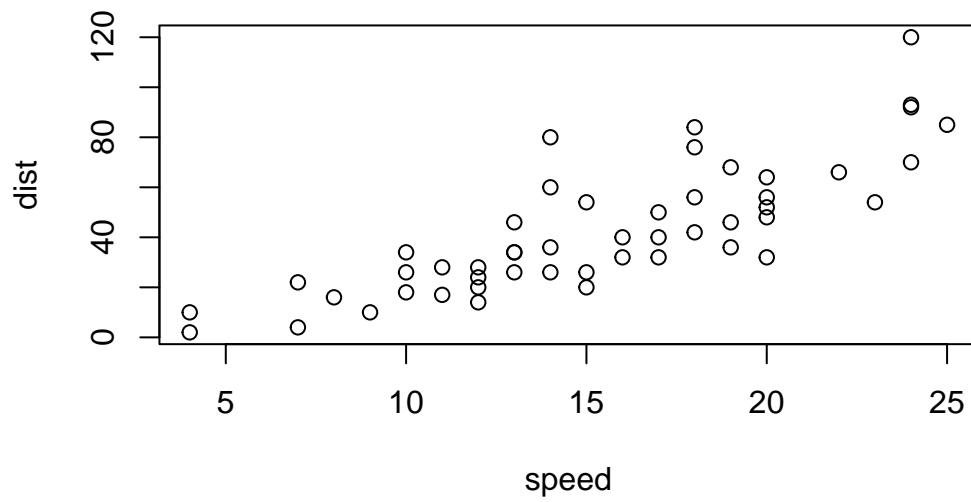
To compare these let's play with the inbuilt `cars` dataset.

```
head(cars, 10)
```

	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

To use “base” R I can simply call the `plot()` function:

```
plot(cars)
```

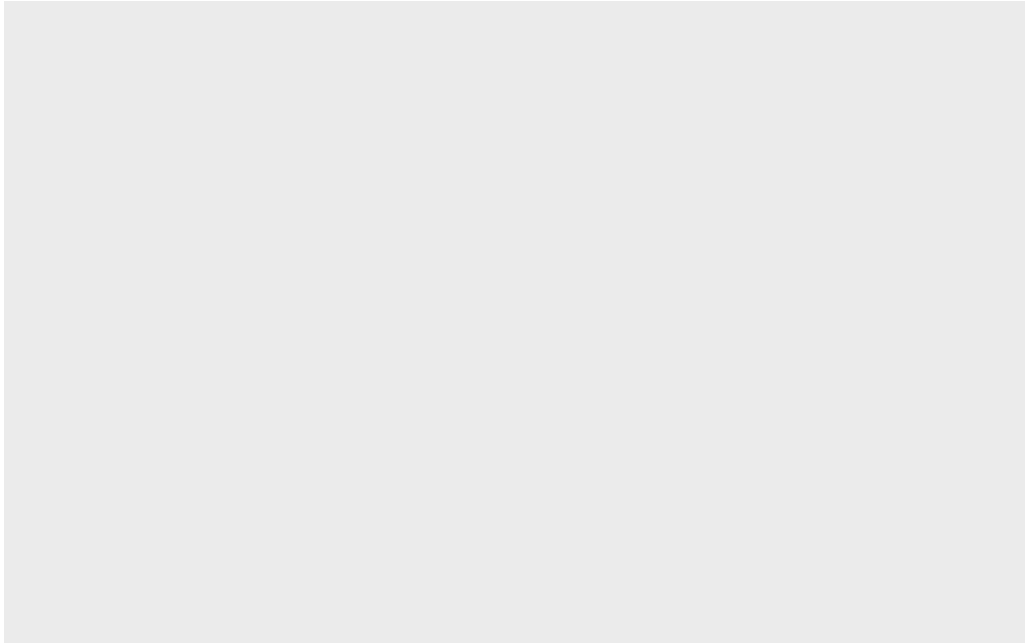


To use `ggplot2` package I first need to install it with the function `install.package("ggplot2")`.

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

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



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

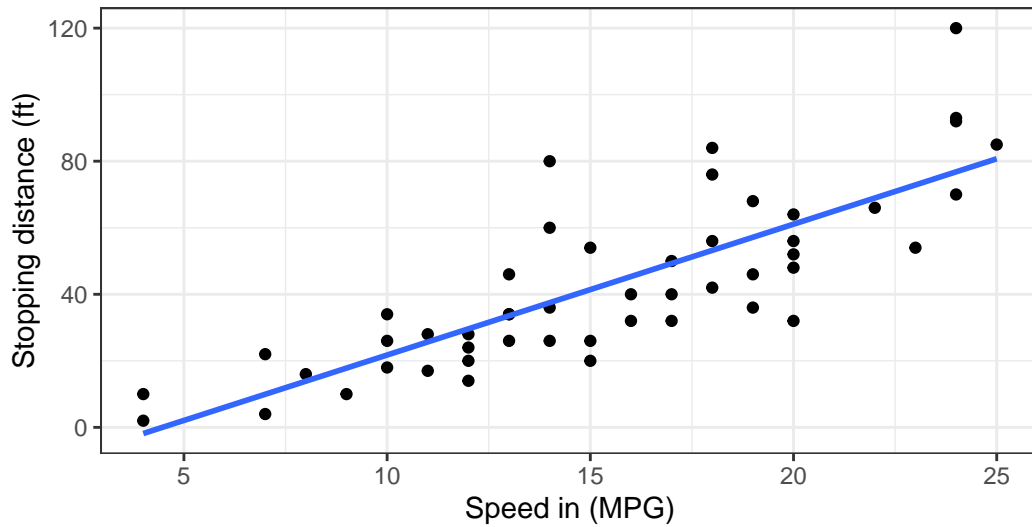
- **data** (i.e. what I want to plot)
- **aes** the aesthetic mapping of the data to the plot I want.
- the **geoms** i.e How I want to plot the data

```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(se=FALSE, method="lm") +  
  labs(title="Stopping distance for old cars",  
        subtitle = "From the inbuilt cars dataset",  
        caption = "BIMM143",  
        x= "Speed in (MPG)", y= "Stopping distance (ft)") +  
  theme_bw()
```

`geom_smooth()` using formula = 'y ~ x'

Stopping distance for old cars

From the inbuilt cars dataset



BIMM143

A more complicated plot

```
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

Q. How many genes are in this dataset?

```
nrow(genes)
```

```
[1] 5196
```

Q How can we summarize that last column - the "State" column?

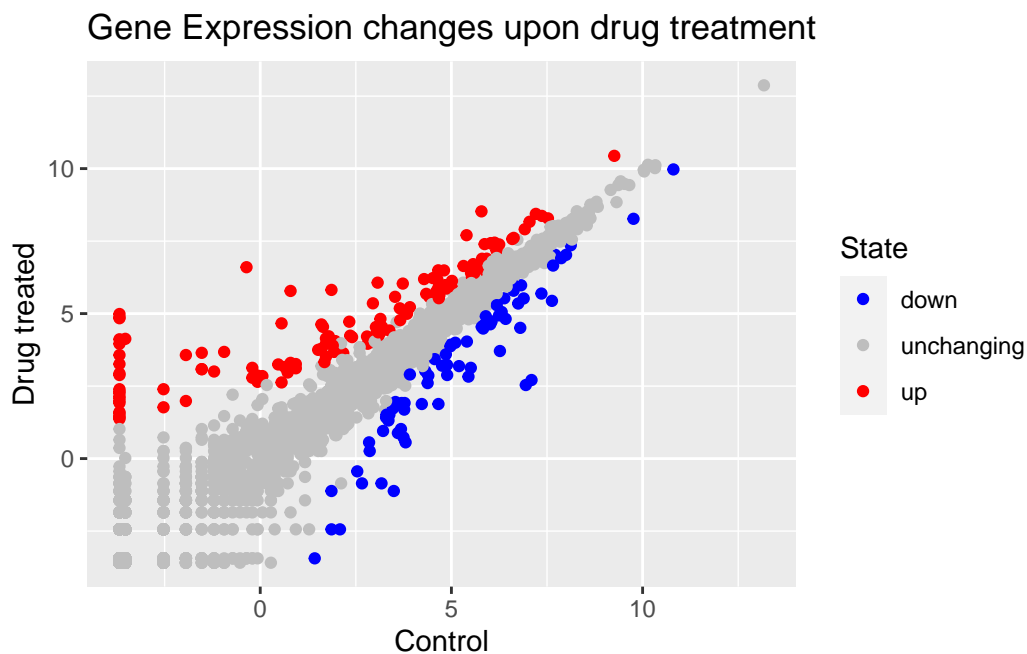
```
table(genes$State)
```

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

```
p <- ggplot(genes) +
  aes(x= Condition1, y=Condition2, color=State) +
  geom_point() +
  labs(x="Control", y="Drug treated")
```

Use p when I want to plot

```
p + labs(title = "Gene Expression changes upon drug treatment", x="Control", y="Drug treat") +
  scale_colour_manual( values=c("blue","gray","red") )
```



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

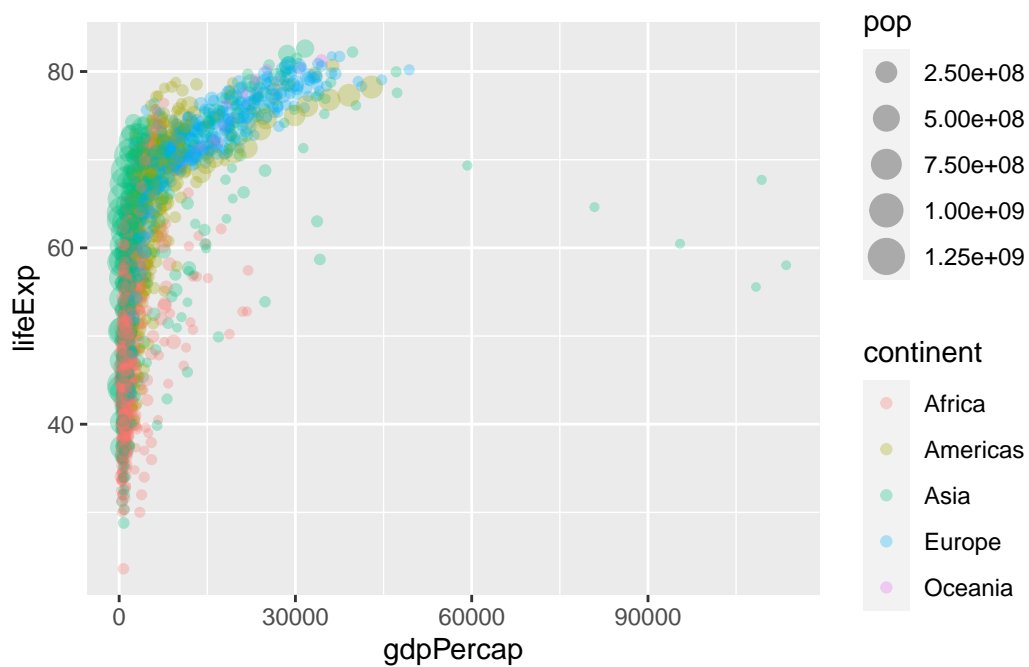
Here I read a slightly larger dataset

```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder."

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

	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, col=continent, size= pop) +
  geom_point(alpha=0.3)
```



A very useful layer to add sometimes if for “faceting”

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

