

Class 5: Data Visualization

Isabella Franco A16239546

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)
```

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10

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 the package is called `ggplot()`. Can I just call it

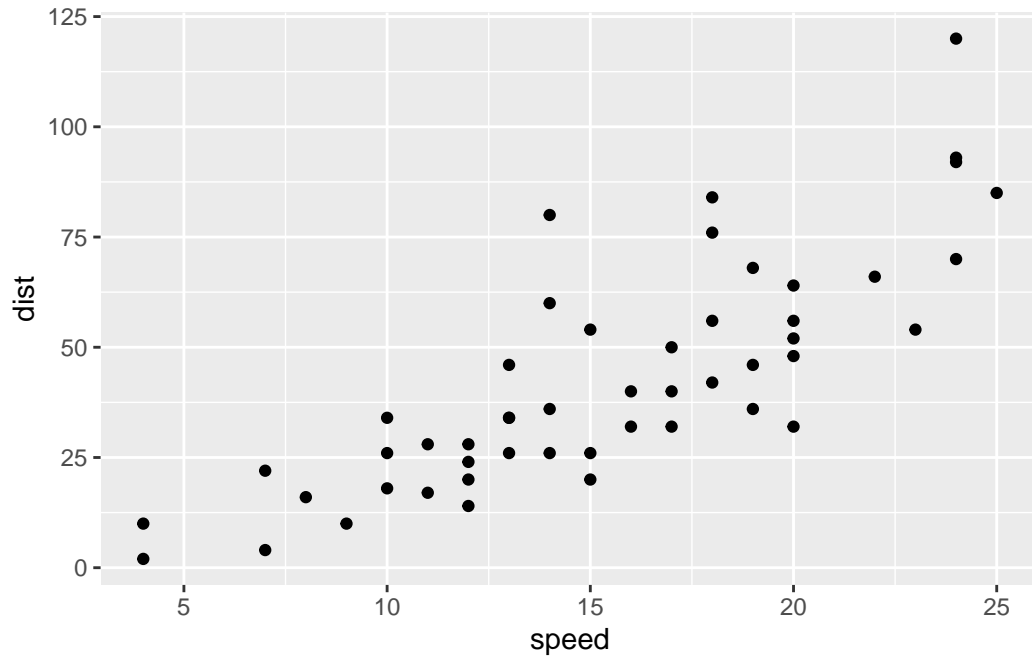
```
library(ggplot2)
ggplot()
```



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

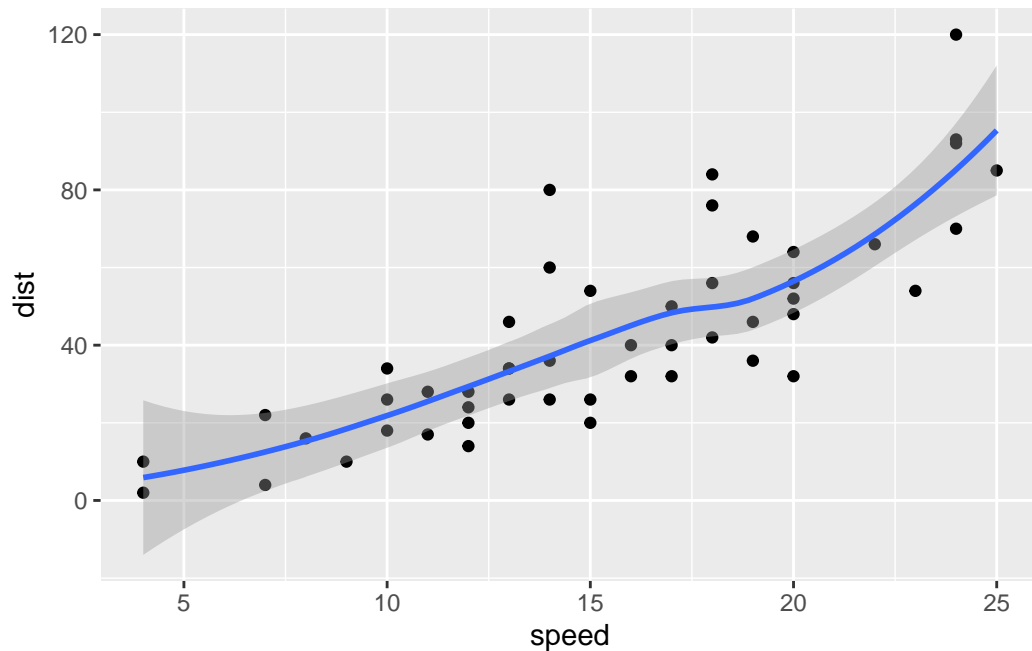
```
ggplot(data=cars) +  
  aes(x=speed, y=dist) +  
  geom_point()
```



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_smooth()
```

`geom_smooth()` using `method = 'loess'` and `formula = 'y ~ x'`



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

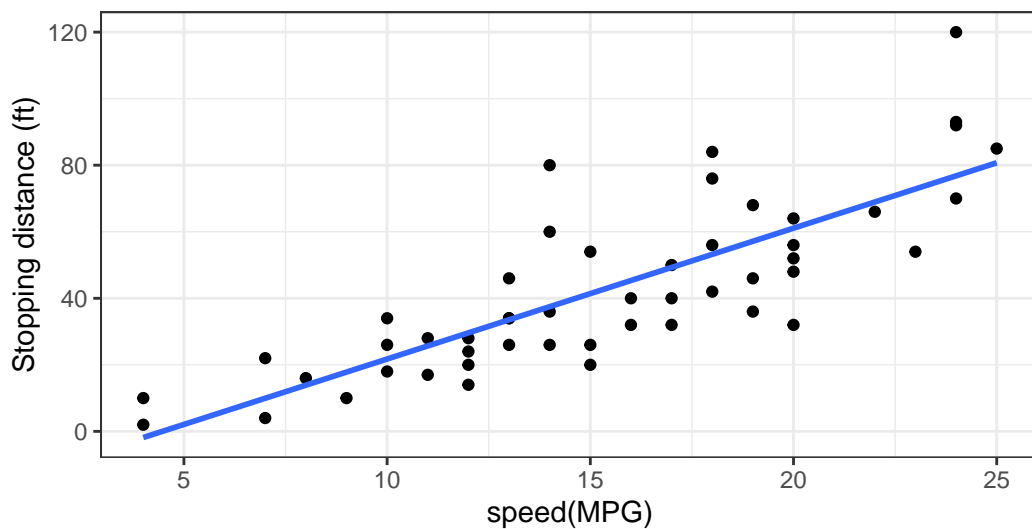
Let's make a plot with a straight line fit- i.e. a linear model and no standard error shown

```
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(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

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)
```

	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

```
ncol(genes)
```

[1] 4

Q. How can we summarize that last column- the “State” column?

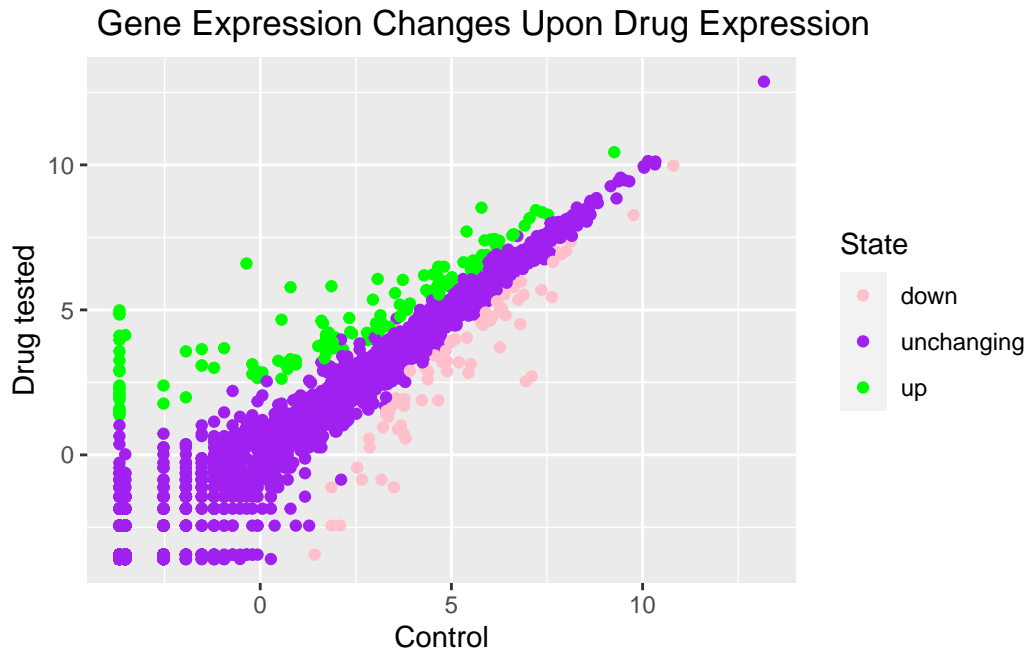
```
table(genes$State)
```

down	unchanging	up
72	4997	127

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

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

```
p+labs(title=" Gene Expression Changes Upon Drug Expression",  
x="Control", y= "Drug tested") +  
scale_colour_manual( values=c("pink","purple","green") )
```



##Going further

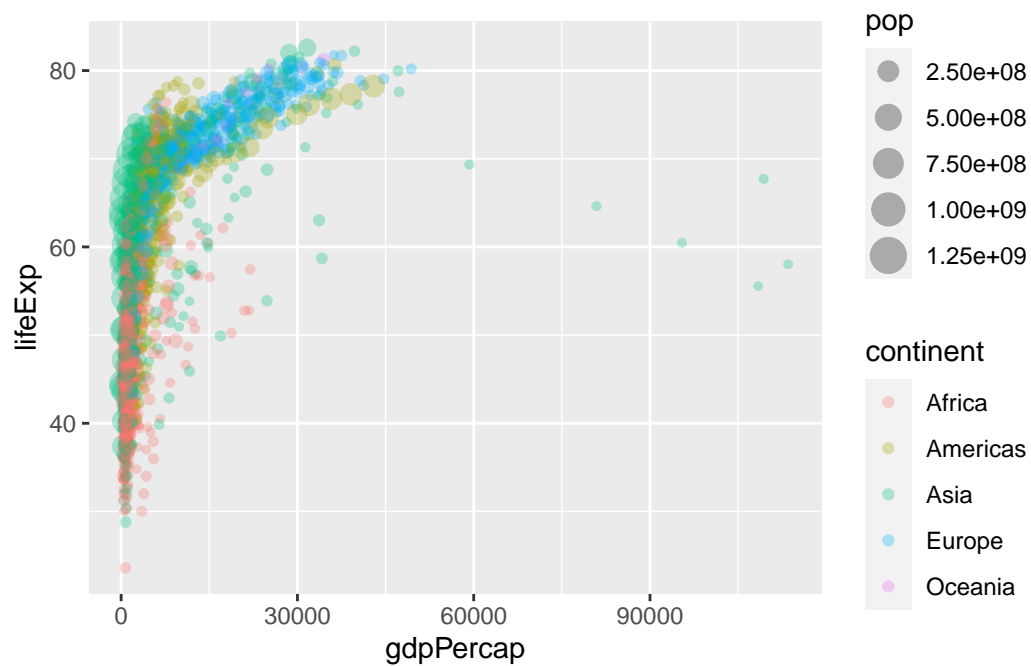
Here I read a slightly larger dataset

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

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

	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 is for “faceting”

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

