# BIMM 143, Class 5: Data Visualization

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# Base R graphics vs ggplot2

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

To compare these lets play with the inbuilt cars dataset

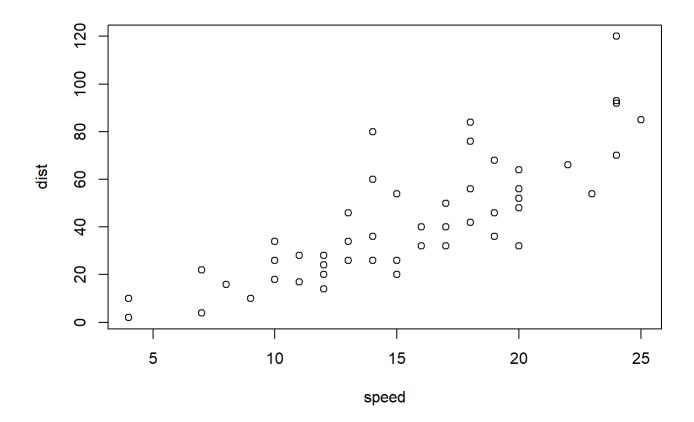
3 7 4

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, we first need to install it with the function install.packages("ggplot2").

I will rin 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...

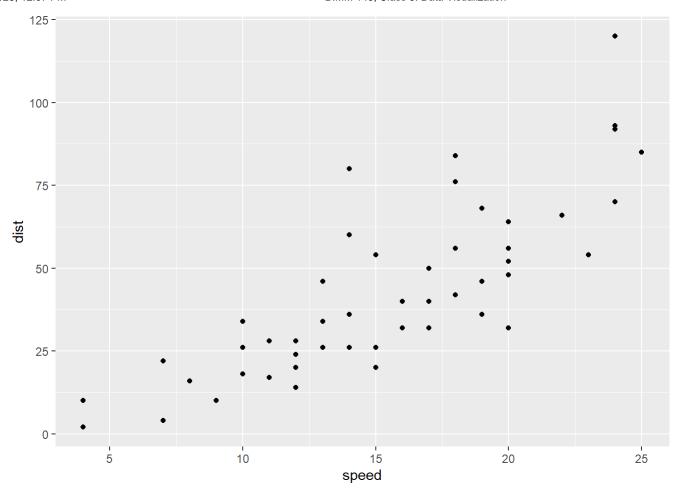
The main function in this package is called <code>ggplot()</code> , Can I just call it?

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

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

- data (what I want to plot)
- aesthetics (mapping of the data to the plot I want)
- the geoms (i.e. how I want to plot the data)

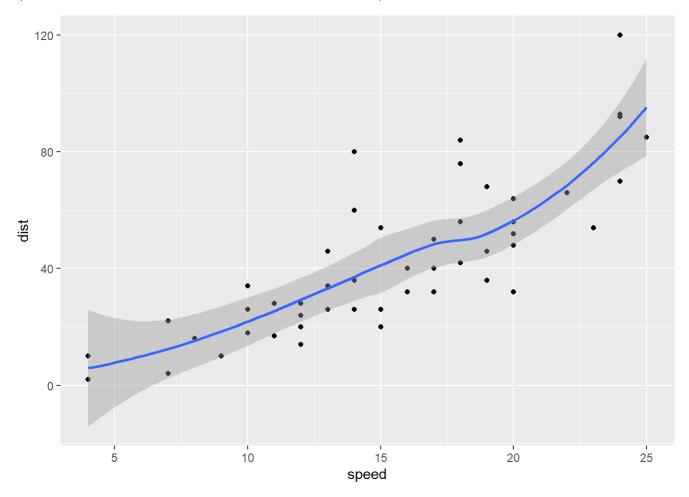
```
ggplot(data=cars) +
  aes(x=speed, y=dist) +
geom_point()
```



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

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

 $\ensuremath{\text{`geom\_smooth()`}}\ using method = 'loess' and formula = 'y \sim x'$ 



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.

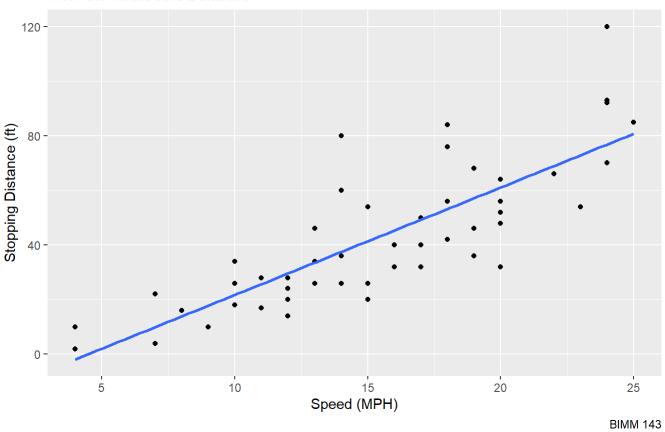
Lets make a plot with a striaght line fit - i.e. a linear model and no standard error shown

```
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 Database",
       caption = "BIMM 143",
       x= "Speed (MPH)", y= "Stopping Distance (ft)")
```

 $\ensuremath{\text{`geom\_smooth()`}}\$ using formula = 'y ~ x'

#### Stopping Distance for Old Cars

From the Inbuilt Cars Database



### A more complicated plot

Lets lot some gene expression data The code below reads the results of an artificial 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 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)
```

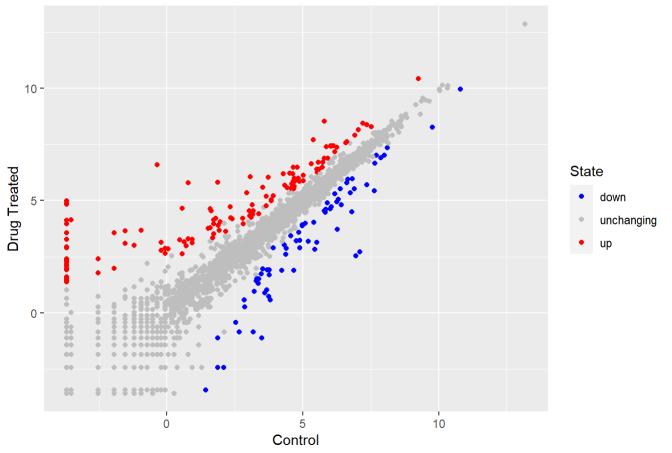
```
down unchanging up 72 4997 127
```

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

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

```
p + labs(title="Gene Expression Changes Upon Drug Treatment") + scale_color_manual(values=c("blue
```

#### Gene Expression Changes Upon Drug Treatment



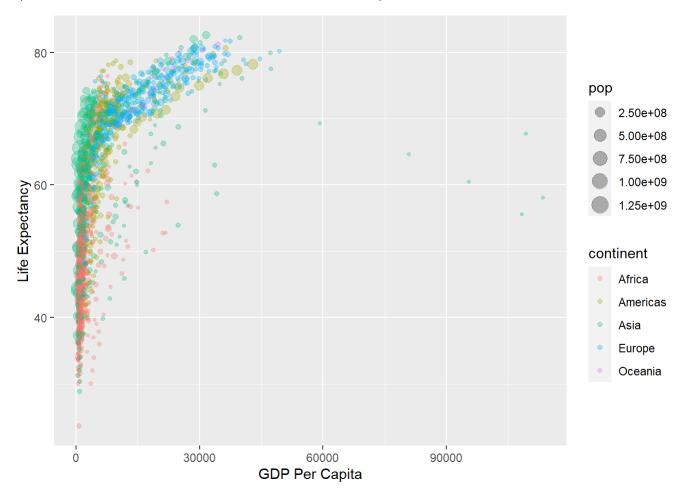
### **Going Further**

Here I read a slightly larger dataset

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

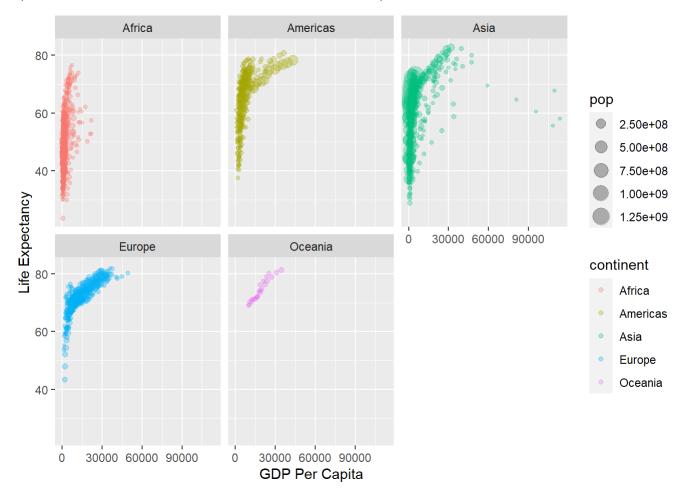
```
countrycontinentyearlifeExppopgdpPercap1 AfghanistanAsia195228.8018425333779.44532 AfghanistanAsia195730.3329240934820.85303 AfghanistanAsia196231.99710267083853.10074 AfghanistanAsia196734.02011537966836.19715 AfghanistanAsia197236.08813079460739.98116 AfghanistanAsia197738.43814880372786.1134
```

```
ggplot(gapminder) +
aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
geom_point(alpha=0.3)+
labs(x="GDP Per Capita", y="Life Expectancy")
```



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)+
labs(x="GDP Per Capita", y="Life Expectancy")+
facet_wrap(~continent)
```



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