

class05: Data Viz with ggplot

Ethan Arevalo (A17393064)

Table of contents

Background	1
Gene expression plot	5
Going Further	8
Custom plots	10

Background

There are lot's of ways to make figures in R. These include so-called "base R" graphics (e.g. `plot()`) and tones of add-on packages like `ggplot2`

For example here we make the same plot with both:

```
plot(cars)
```



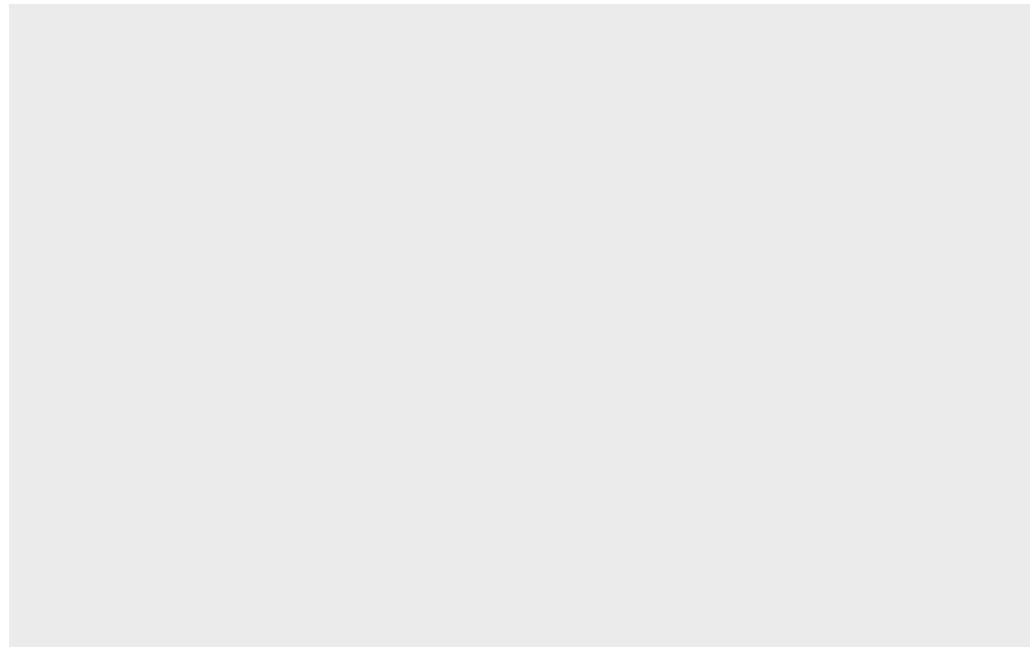
First I need to install the package with the command `install.packages()`.

N.B. We never run an install cmd in a quarto code chunk or we will end up re-installing packages many many times - which is not what we want!

Everytime we want to use one of these “add-on” packages we need to load it up in R with the packages we need to load it up in R with the `library()` function:

```
library(ggplot2)
```

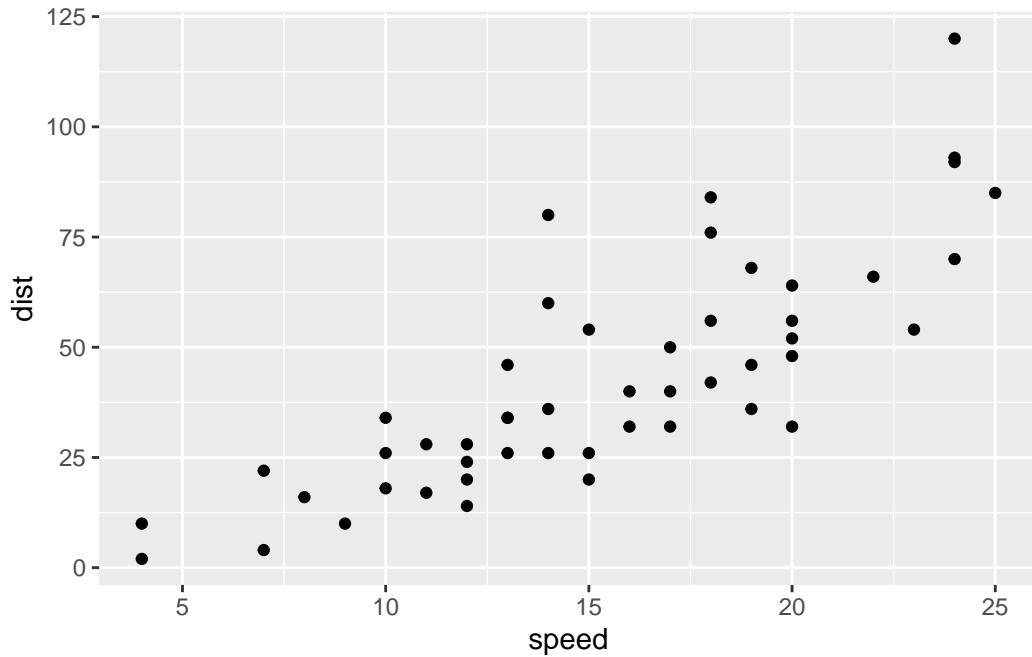
```
ggplot(cars)
```



Every ggplot needs at least 3 things:

- The **data**, the stuff you want plotted
- The **aesthetics**, how the data map on the plot
- The **geometry**, the type of plot

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



Add a line to better show relationship between speed and dist

```
p <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  labs(title="Stopping distance of old cars",
       subtitle="Data from the `cars` object",
       x="Speed (mph)",
       y="Distance (ft)")
```

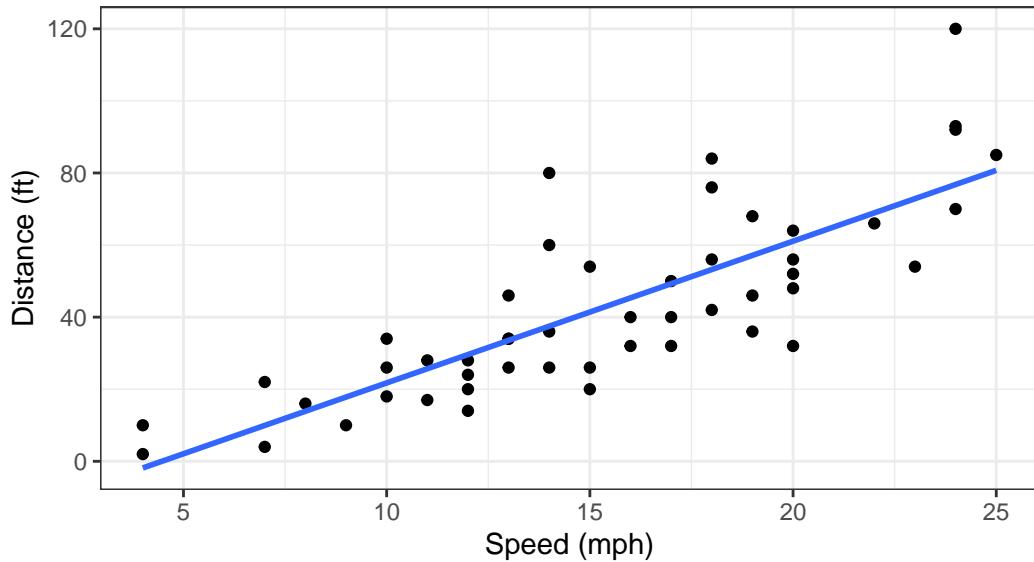
render it out

```
p + theme_bw()
```

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

Stopping distance of old cars

Data from the `cars` object



Gene expression plot

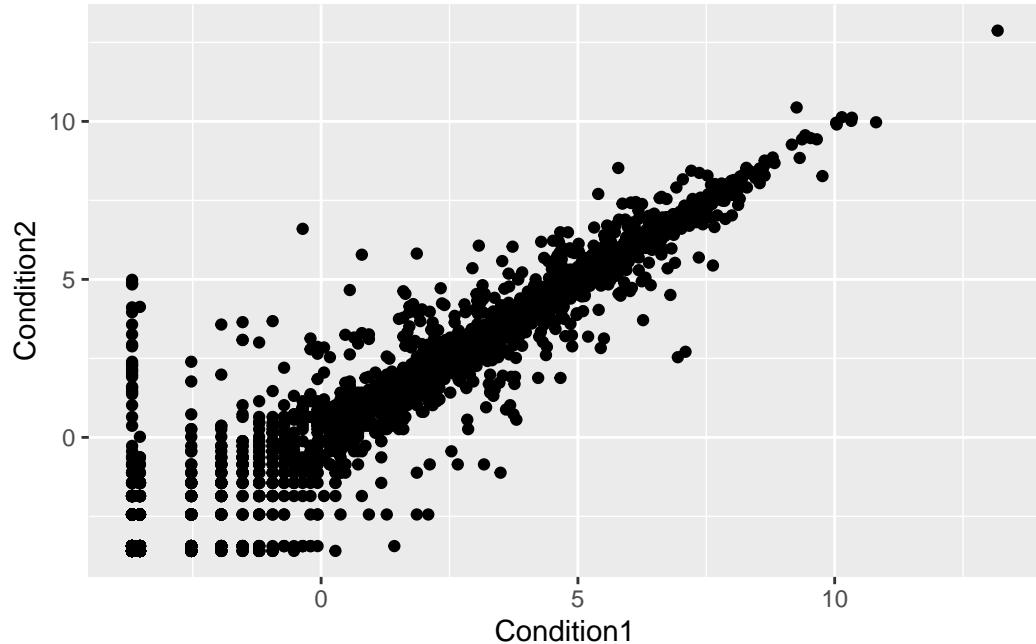
We can read the input data from the class website

```
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

A first version plot

```
ggplot(genes) +
  aes(Condition1, Condition2) +
  geom_point()
```

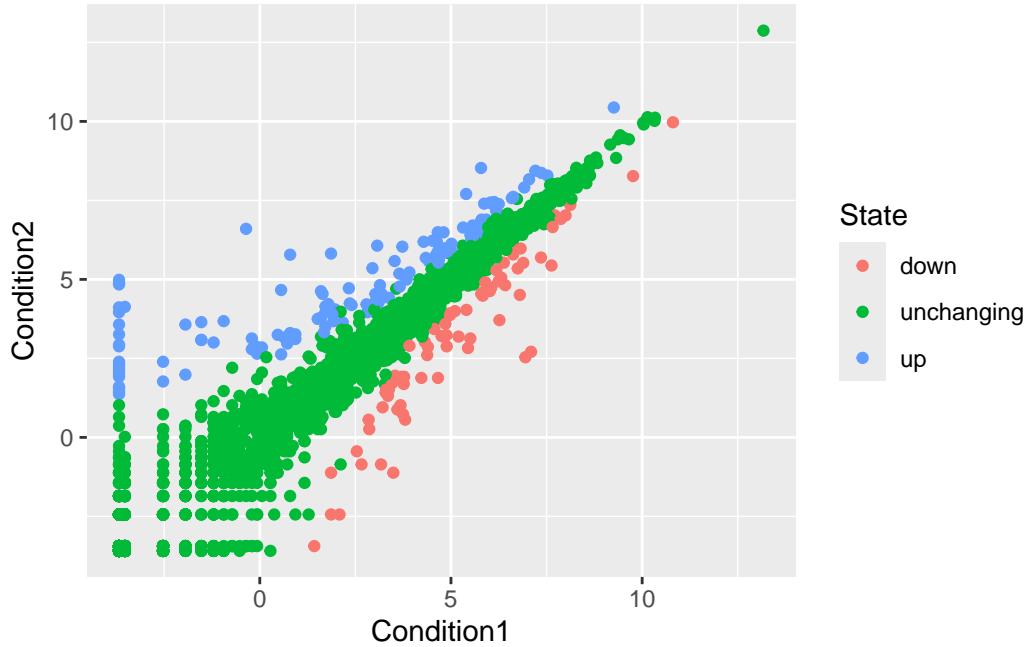


```
table(genes$State)
```

down	unchanging	up
72	4997	127

Version 2 let's color by `State` so we can see the up and down significant genes compared to all the "unchanging" genes

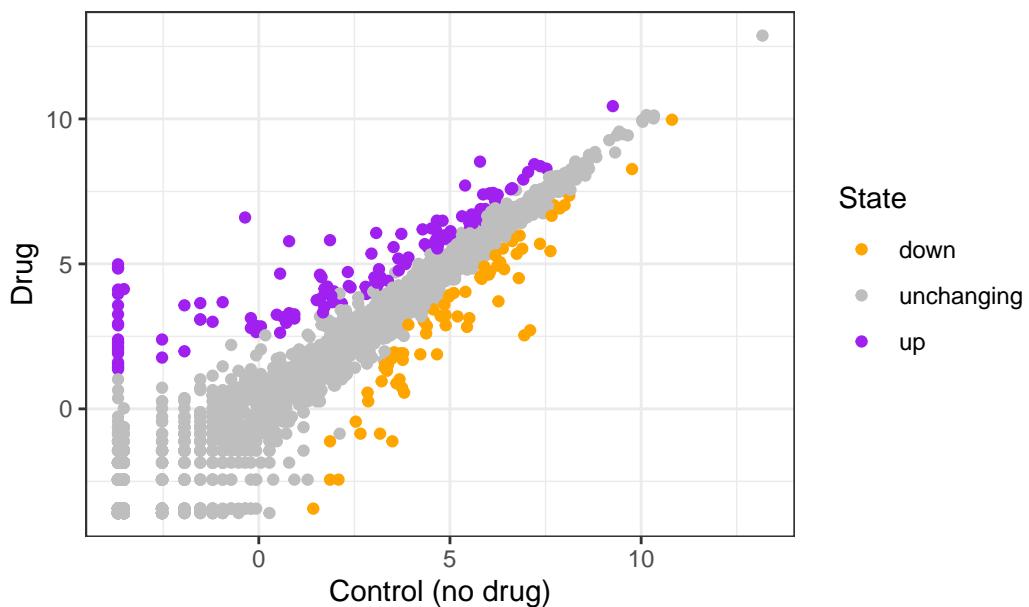
```
ggplot(genes) +
  aes(Condition1, Condition2, col=State) +
  geom_point()
```



Version 3 plot, lets modify the default colors to something we like

```
ggplot(genes) +
  aes(Condition1, Condition2, col=State) +
  geom_point() +
  scale_color_manual(values=c("orange",
                             "grey",
                             "purple")) +
  labs(x="Control (no drug)",
       y="Drug",
       title="Gene Expression Changes upon GLP-1 drug") +
  theme_bw()
```

Gene Expression Changes upon GLP-1 drug



Going Further

Lets have a look at the famous **gapminder**

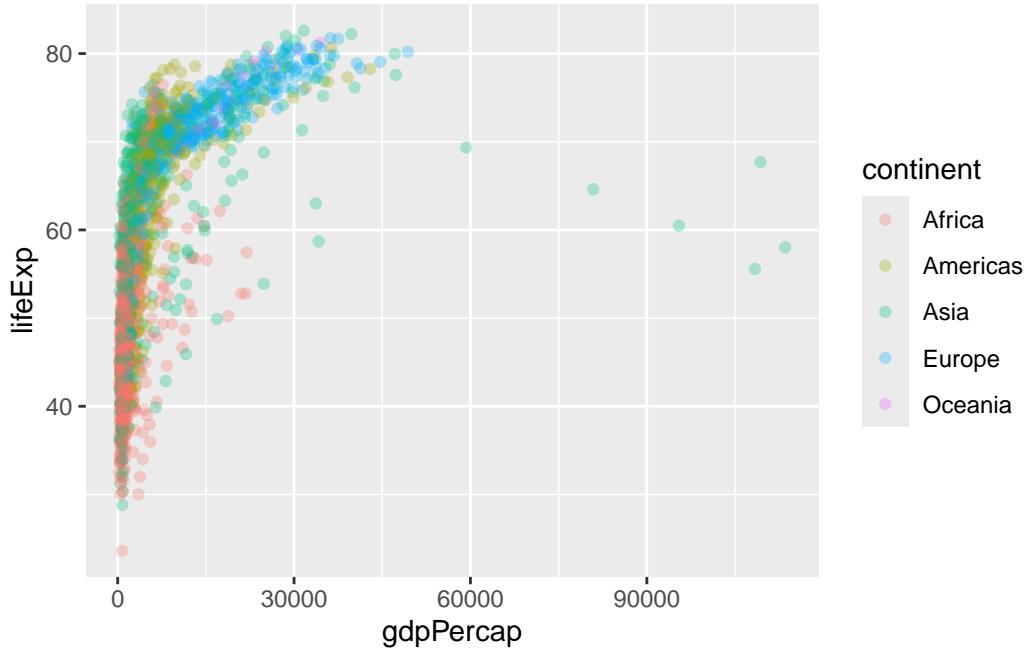
```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts"

gapminder <- read.delim(url)

head(gapminder, 3)
```

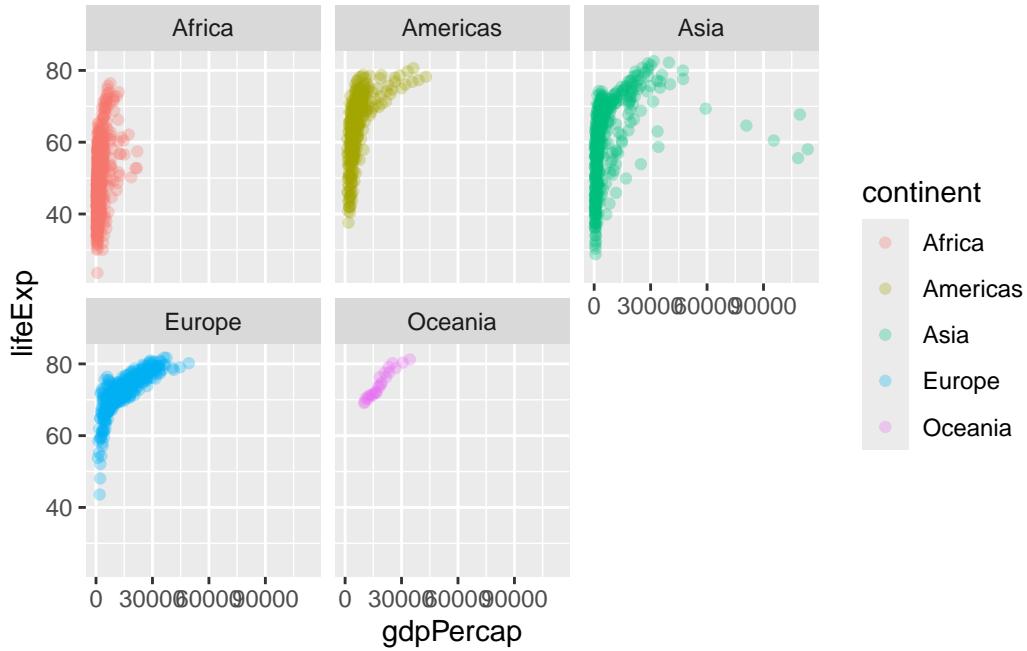
	country	continent	year	lifeExp	pop	gdpPerCap
1	Afghanistan	Asia	1952	28.801	8425333	779.4453
2	Afghanistan	Asia	1957	30.332	9240934	820.8530
3	Afghanistan	Asia	1962	31.997	10267083	853.1007

```
ggplot(data=gapminder) +
  aes(x=gdpPerCap, y=lifeExp, col=continent) +
  geom_point(alpha=0.3)
```



Lets “facet” (i.e. make a separate plot) by continent rather than the big hot mess above

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



Custom plots

How big is this gapminder dataset?

```
nrow(gapminder)
```

```
[1] 1704
```

I want to “filter” down to a subset of this data. I will use the **dplyr** package to help. First I need to install it and then load it up...

```
library(dplyr)
```

```
Attaching package: 'dplyr'
```

```
The following objects are masked from 'package:stats':
```

```
filter, lag
```

```
The following objects are masked from 'package:base':
```

```
intersect, setdiff, setequal, union
```

```
gapminder_2007 <- filter(gapminder, year==2007)  
head(gapminder_2007)
```

```
country continent year lifeExp      pop gdpPercap  
1 Afghanistan Asia 2007 43.828 31889923 974.5803  
2 Albania Europe 2007 76.423 3600523 5937.0295  
3 Algeria Africa 2007 72.301 33333216 6223.3675  
4 Angola Africa 2007 42.731 12420476 4797.2313  
5 Argentina Americas 2007 75.320 40301927 12779.3796  
6 Australia Oceania 2007 81.235 20434176 34435.3674
```

```
filter(gapminder_2007, country=="Ireland")
```

```
country continent year lifeExp      pop gdpPercap  
1 Ireland Europe 2007 78.885 4109086 40676
```

```
filter(gapminder, year==1997, country=="United States")
```

```
country continent year lifeExp      pop gdpPercap  
1 United States Americas 1997 76.81 272911760 35767.43
```

Q. Make a plot comparing 1977 and 2007 for all countries

```
ggplot(gapminder) +  
  aes(x=gdpPercap, y=lifeExp, col=continent) +  
  geom_point() +  
  filter(gapminder, year %in% c(1977, 2007)) +  
  facet_wrap(~year)
```

