

# Class 5: Data Viz with ggplot

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## 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 `ggplot2`.

For example here we make the same plot with both:

```
head(cars)
```

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

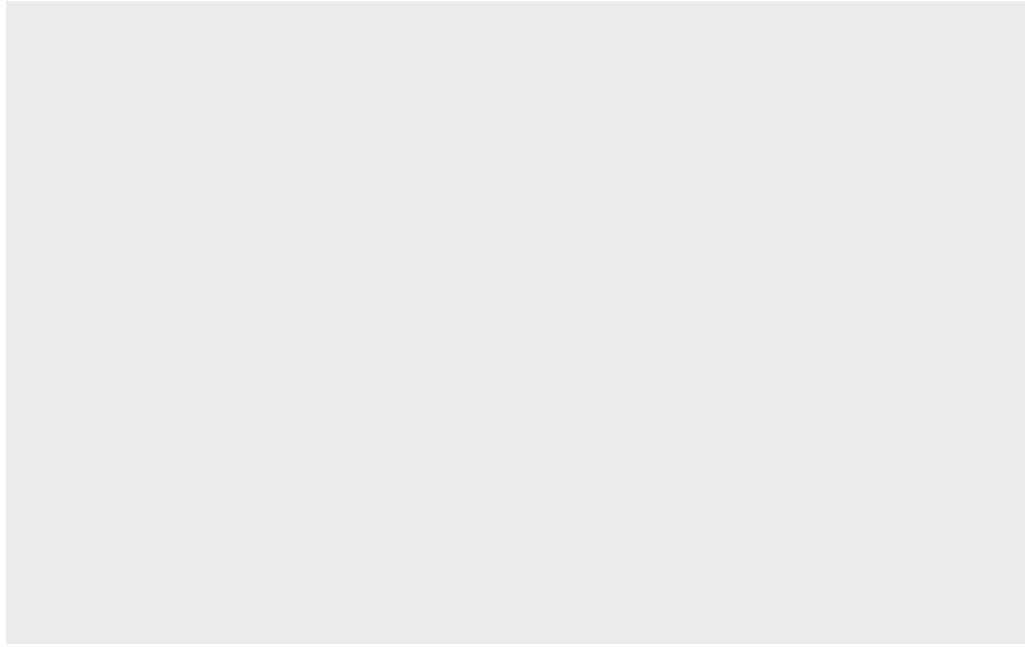
First I need to install the package with the command `install.package()`

**N.B.** We never run on 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 of these “add-on” 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 to the plot
- The **geometry**, the type of plot

```
p <- ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() + geom_smooth(method="lm", se=FALSE) + labs(title="Stopping distance of old cars")
```

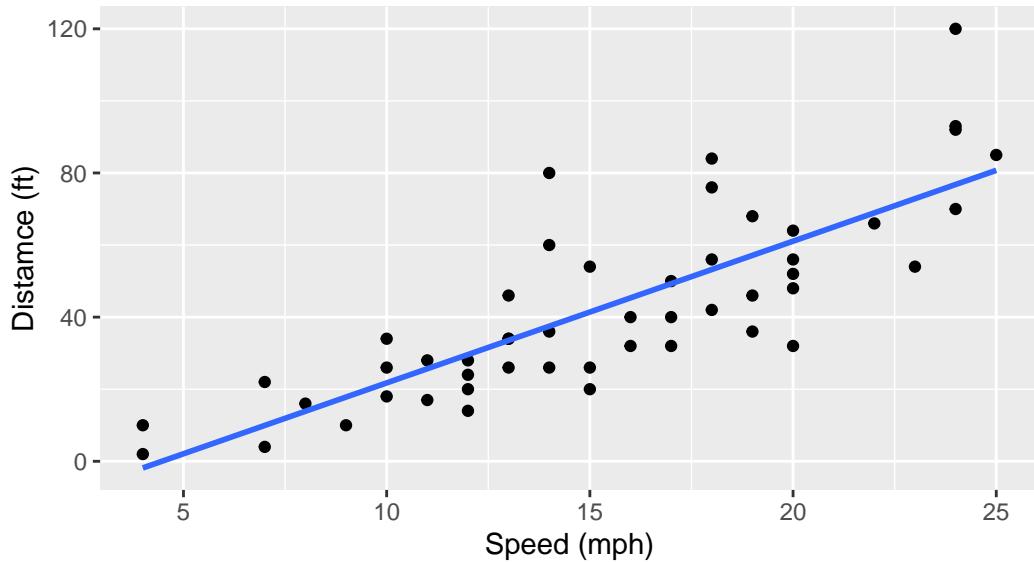
render it out

```
p
```

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

## Stopping distance of old cars

Data from the 'cars' object

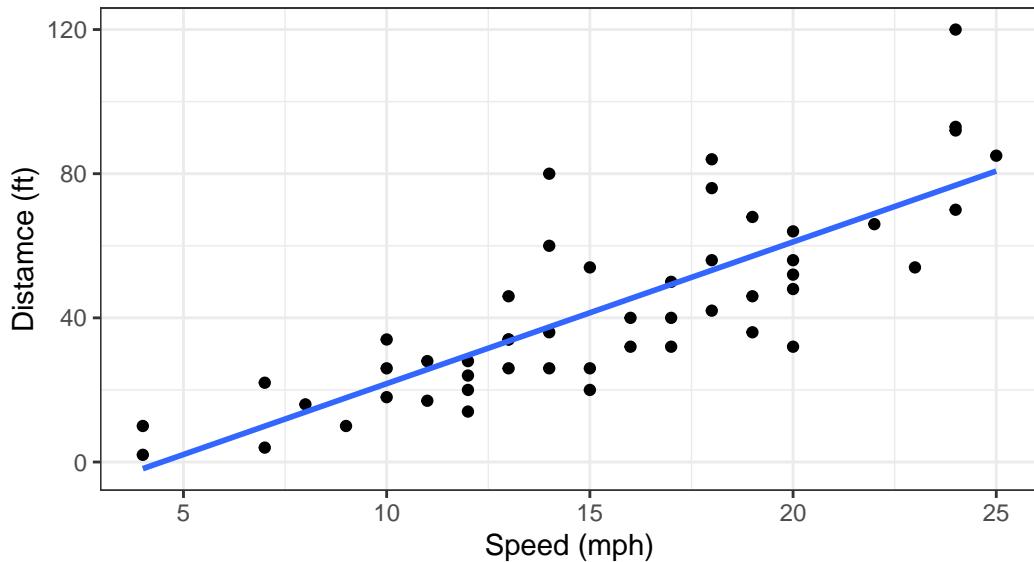


```
p+theme_bw()
```

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

## Stopping distance of old cars

Data from the 'cars' object



## Gene expression plot

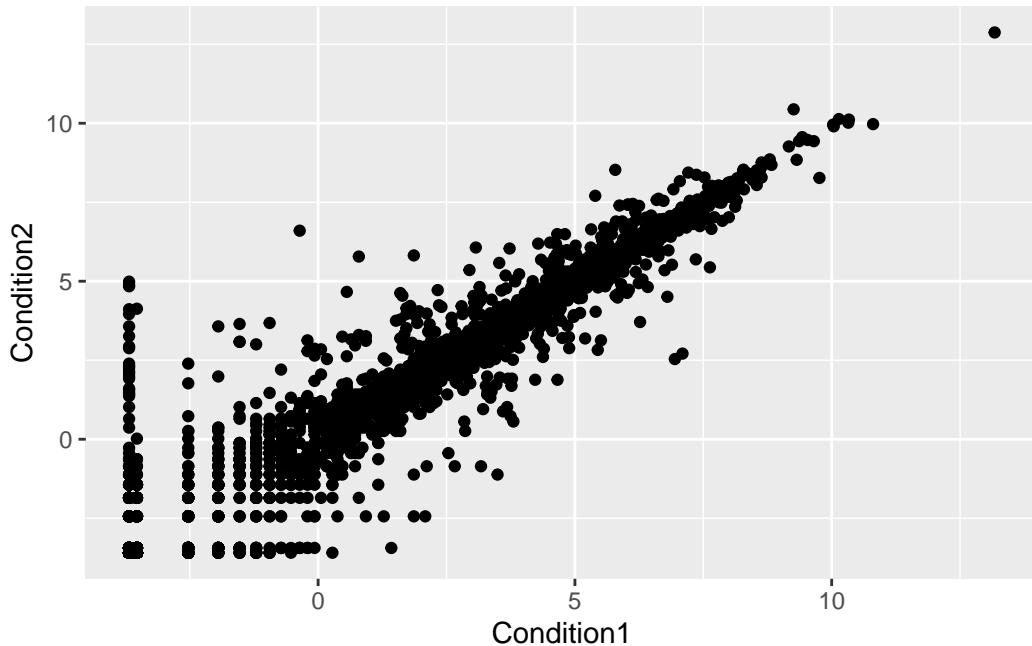
We can read the input data from the class website

```
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()
```

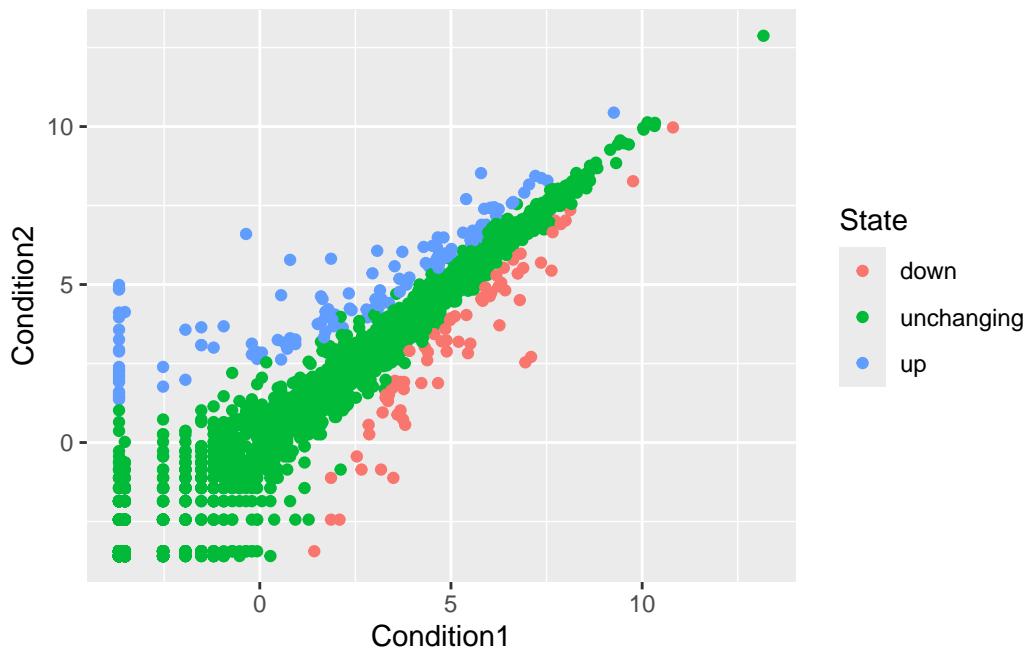


```
table(genes$State)
```

	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

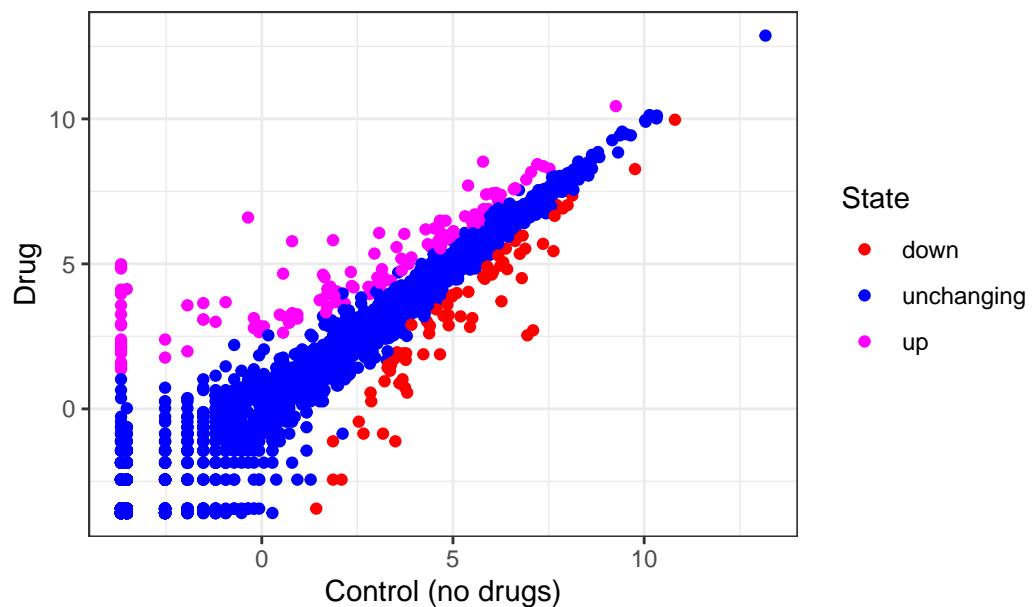
```
ggplot(genes)+ aes(Condition1, Condition2, col=State)+ geom_point()
```



Version 3 plots, let's modify the default colors to something we like

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

## Gene Expressin Changes upon GLP-1 drug



## Going Further

Let's have a look at the famous `gapminder` dataset

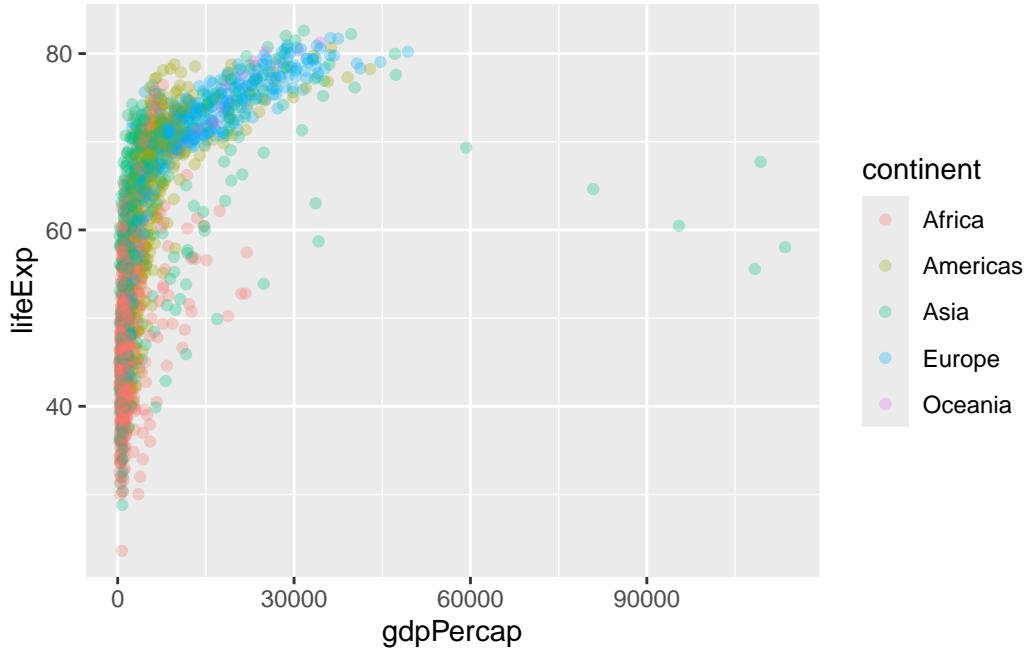
```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.csv"

gapminder <- read.delim(url)

head(gapminder, 3)
```

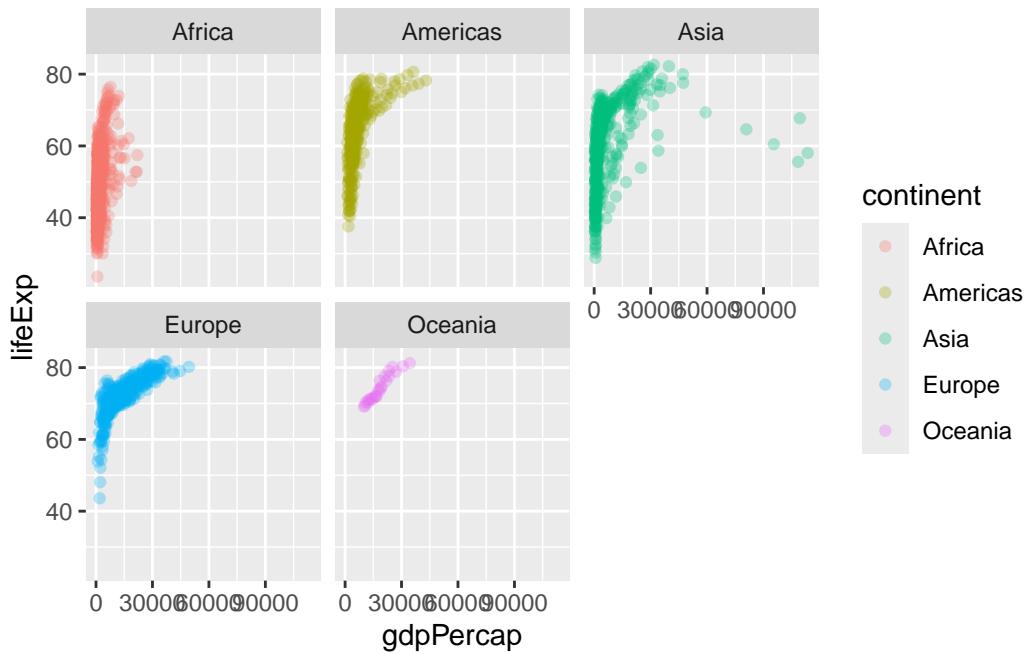
	country	continent	year	lifeExp	pop	gdpPerCap
1	Afghanistan	Asia	1952	28.801	8425333	779.4453
2	Afghanistan	Asia	1957	30.332	9240934	820.8530
3	Afghanistan	Asia	1962	31.997	10267083	853.1007

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



Let's "facet (i.e. make a separate plot) by continent rather than the big hot mess above.

```
ggplot(gapminder) + aes(gdpPercap, lifeExp, col=continent) + geom_point(alpha=0.3) + facet_w
```



## 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 me.

First I need to install it and then load it up... `install.packages("dplyr")` and then `library(dyplr)`

```
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
```

```
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=="United States")
```

```
country continent year lifeExp      pop gdpPercap
1 United States Americas 2007  78.242 301139947 42951.65
```

Q. Make a plot comparing 1997 and 2007 for all countries

```
input <- filter(gapminder, year %in% c(1977, 2007))
head (input)
```

```
country continent year lifeExp      pop gdpPercap
1 Afghanistan   Asia 1977  38.438 14880372  786.1134
2 Afghanistan   Asia 2007  43.828 31889923  974.5803
3    Albania     Europe 1977  68.930 2509048 3533.0039
4    Albania     Europe 2007  76.423 3600523  5937.0295
5    Algeria    Africa 1977  58.014 17152804 4910.4168
6    Algeria    Africa 2007  72.301 33333216 6223.3675
```

```
input <- filter(gapminder, year %in% c(1977,2007))
```

```
ggplot(data=input, aes(gdpPercap, lifeExp, col=continent)) + geom_point() + facet_wrap(~year)
```

