

# Lab5: DataViz with ggplot

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## Background

There are lots of ways to make plots in R. These include so-called “base R” (like the `plot()`) and add on packages like `ggplot2`

Let’s make the same plot with these two graphics system. We can use 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
```

With “base R” we can simply:

```
plot(cars)
```

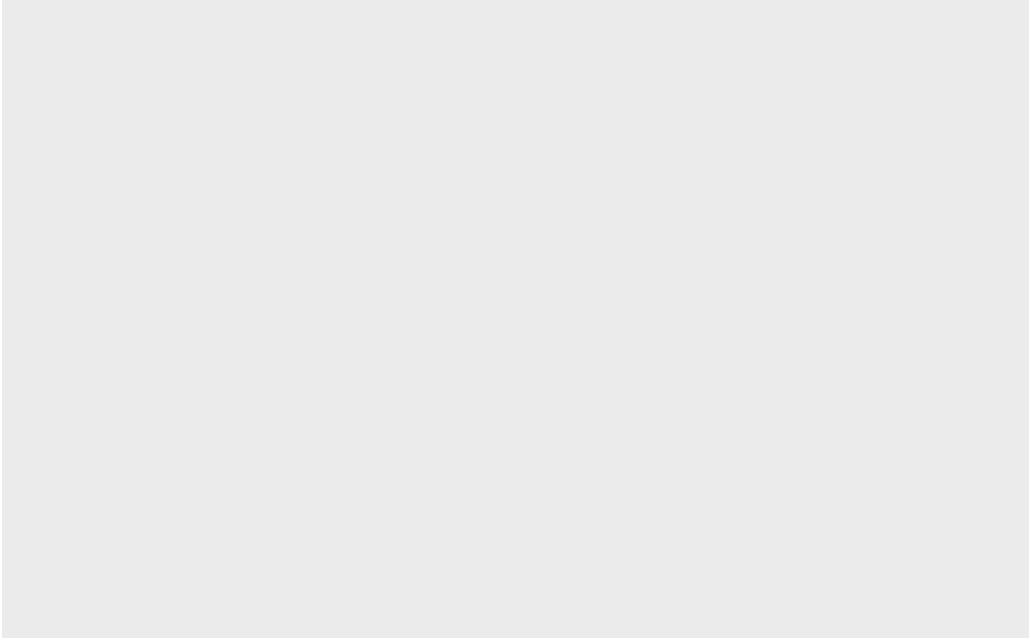


Now lets try ggplot. First ggplot needs to be installed with ‘install.packages(“ggplot2”)’.

**N.B.** we never run an *install.packages()* in a code chunk otherwise we will reinstall needlessly everytime the document is rendered

Everytime we want to use an addon package we must load it with a call to `library()`

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

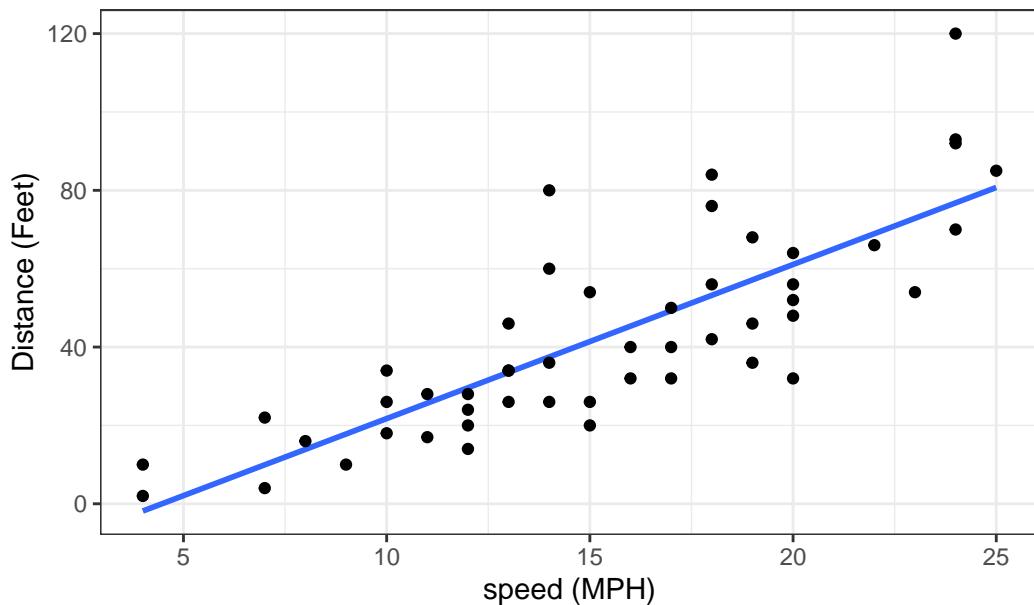


Every ggplot needs at least 3 things:

1. The **data** i.e. stuff to plot as a data.frame
2. The **aes** or aesthetics that map the ddata to the plot
3. The **geom\_** or geometry i.e. the plot type such as points, lines, etc

```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_smooth(method = "lm", se = FALSE) +  
  geom_point() +  
  labs(x="speed (MPH)",  
       y="Distance (Feet)",  
       title="Stopping Distance of Old Cars") +  
  theme_bw()  
  
`geom_smooth()` using formula = 'y ~ x'
```

## Stopping Distance of Old Cars



## Gene Expression Plot

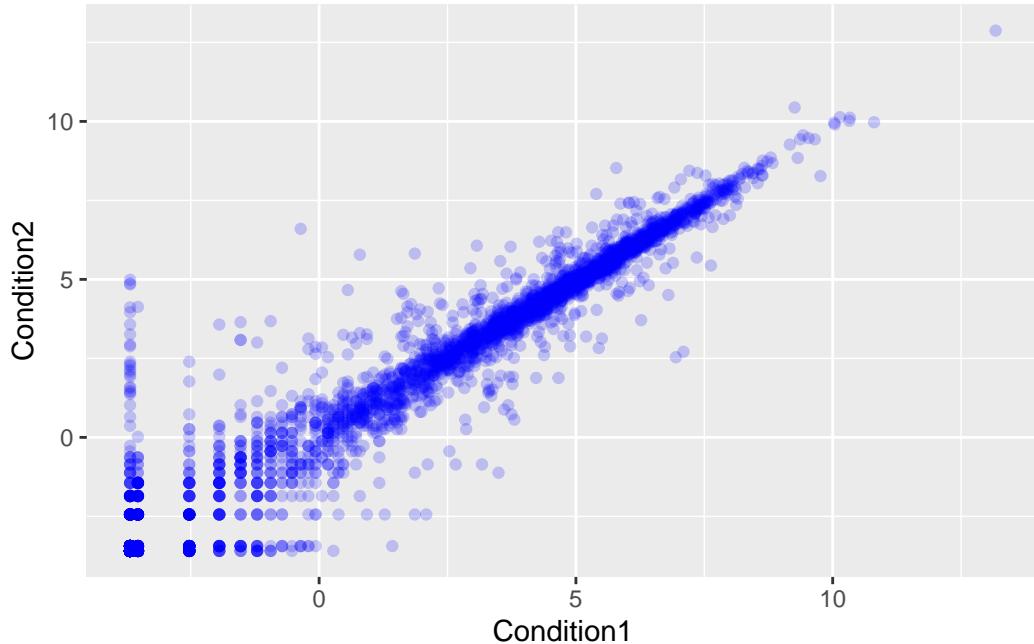
Read some data in the effects of GLP-1 inhibitor (drug) on gene expression values:

```
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

Version 1 plot - start simple by getting some ink on the page.

```
ggplot(genes) +
  aes(Condition1, Condition2) +
  geom_point(col = "blue", alpha = 0.2)
```



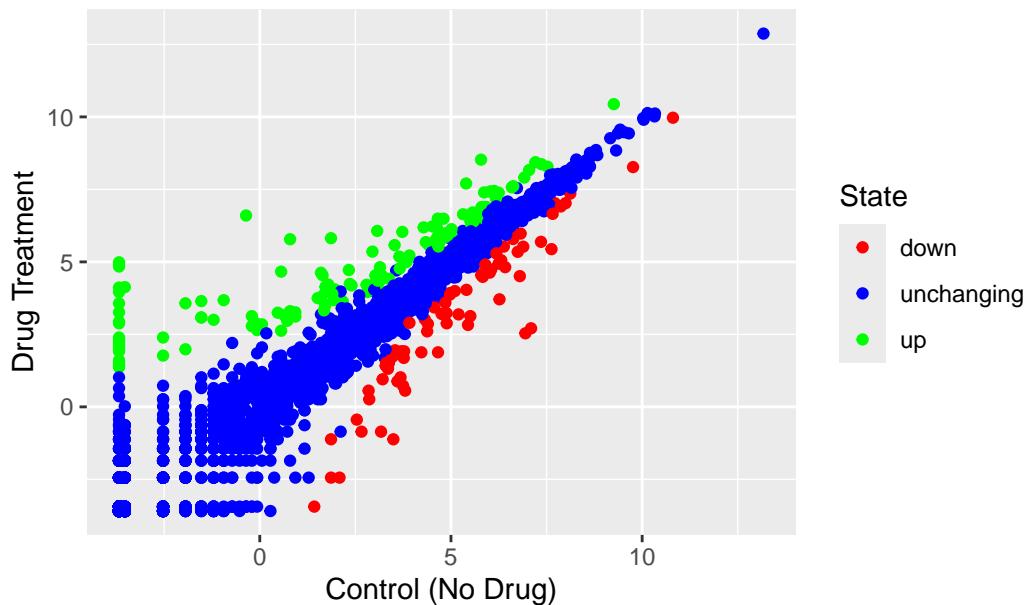
Lets color by state up, down or no change.

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

State	Count
down	72
unchanging	4997
up	127

```
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point() +
  scale_color_manual(values = c( "red", "blue", "green")) +
  labs(x="Control (No Drug)",
       y= "Drug Treatment",
       title = "Gene Expression Changes Upon Drug Treatment")
```

## Gene Expression Changes Upon Drug Treatment



## Going further with gapminder

Here we explore the famous `gapminder` dataset with some custom plots.

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

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

How many rows does this dataset have?

```
nrow(gapminder)
```

```
[1] 1704
```

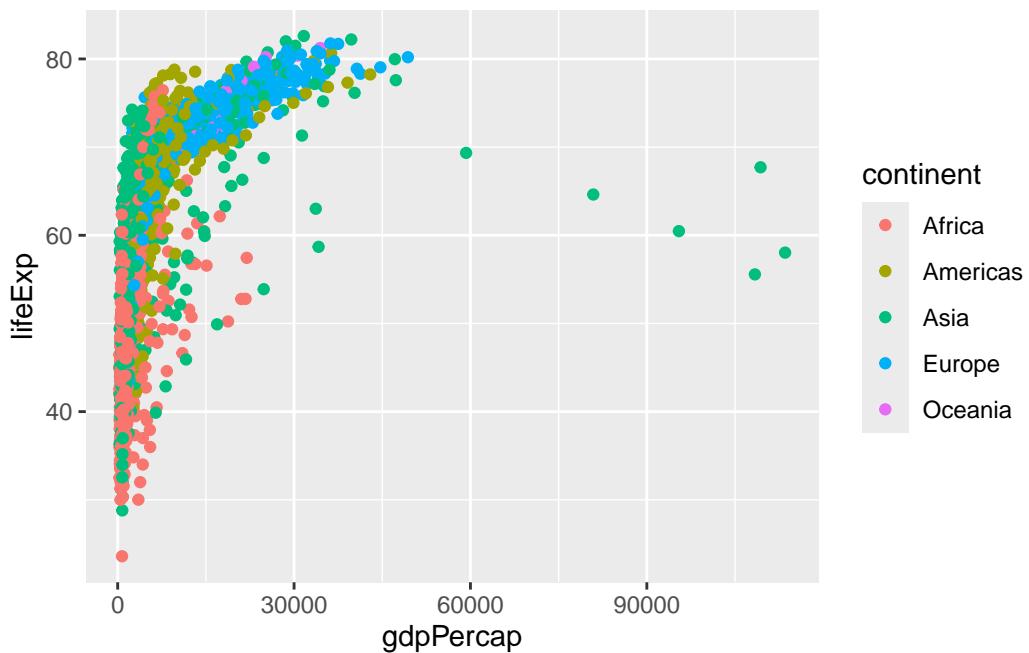
How many different continents are in this dataset?

```
table(gapminder$continent)
```

	Africa	Americas	Asia	Europe	Oceania
	624	300	396	360	24

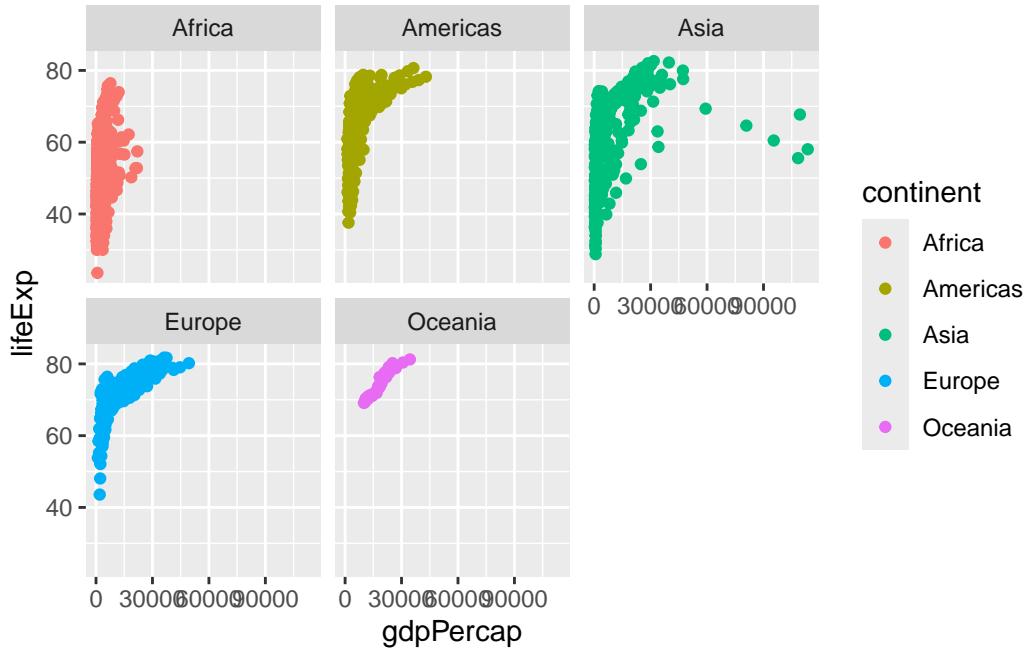
Version 1 plot gdpPercap vs LifeExp for all rows

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



I want to see a plot for each continent - in ggplot lingo this is called “faceting”

```
ggplot(gapminder) +  
  aes(gdpPercap, lifeExp, col = continent)+  
  geom_point() +  
  facet_wrap(~continent)
```



## First look at the dplyr package

Another add-on package with a function called `filter()` that we want to use install the dplyr code with “`install.packages("dplyr")`” call it with “`library(dplyr)`”

```
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`

```
filter(gapminder, year == 2007, country == "Ireland")
```

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

```
input <- filter (gapminder, year == 2007 | year == 1977)

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

