

Class 5: Data Viz with ggplot

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Today we are exploring the **ggplot** package and how to make nice figures in R.

There are lots of ways to make figures and plot in R. These include:

- so called “base”R
- and add on packages like **ggplot2**

Here is a simple “base” R plot

```
head(cars)
```

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

We can simply pass this to the ‘plot()’ function

```
plot(cars)
```



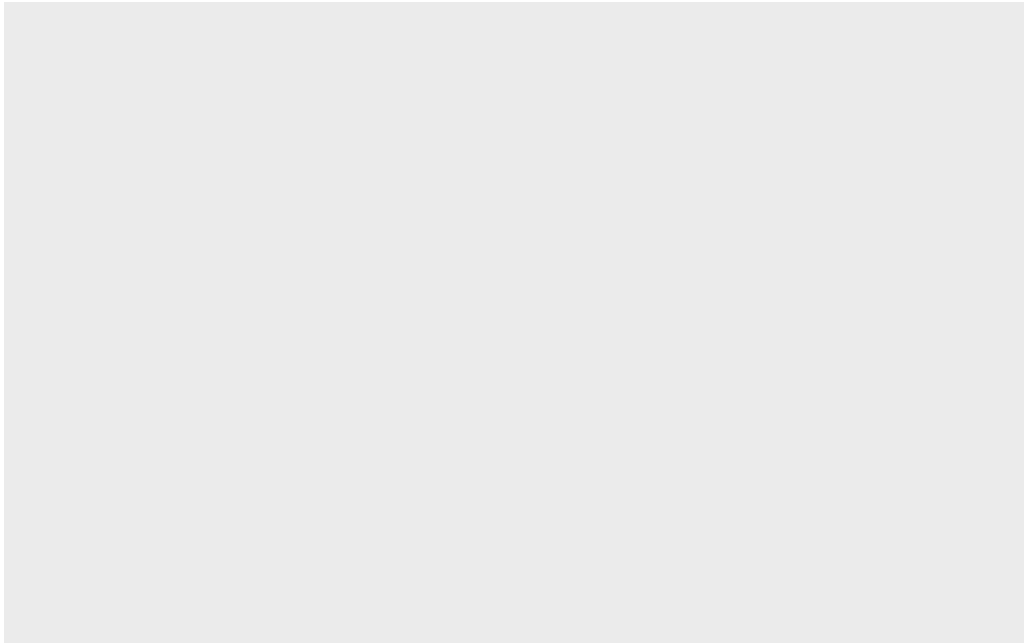
Key-point: Base R is quick but not so nice looking in some folks eyes.

let's see how we can plot this with **ggplot2**

1st I need to install this add-on package. For this we use the 'install.packages()' function - **WE DO THIS IN THE CONSOLE, NOT our report**

2nd We need to load the package with the 'library()' function every time we want to use it.

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



Every ggplot is composed of at least 3 layers:

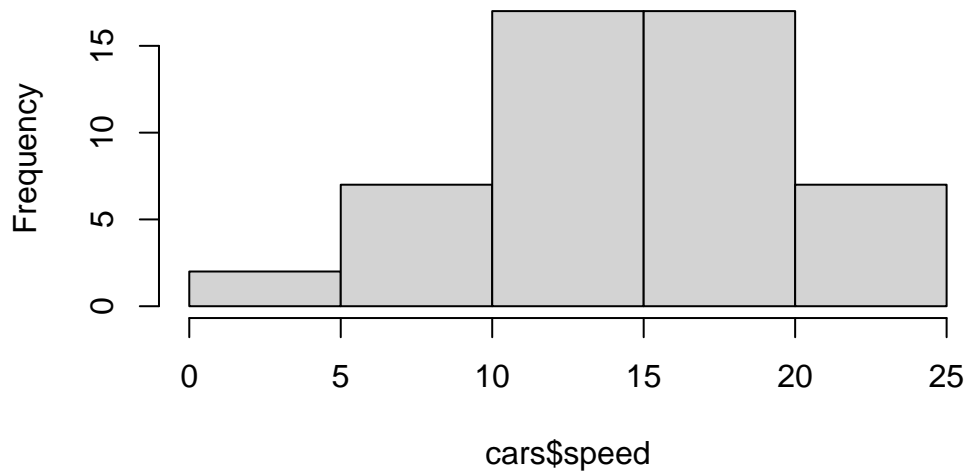
- **data** (i.e. a data.frame with the things you want to plot)
- aesthetics **aes()** that map the columns of data to your plot features (i.e. aesthetics)
- geoms like **geom_point()** that sort how the plot appears

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



```
hist(cars$speed)
```

Histogram of cars\$speed



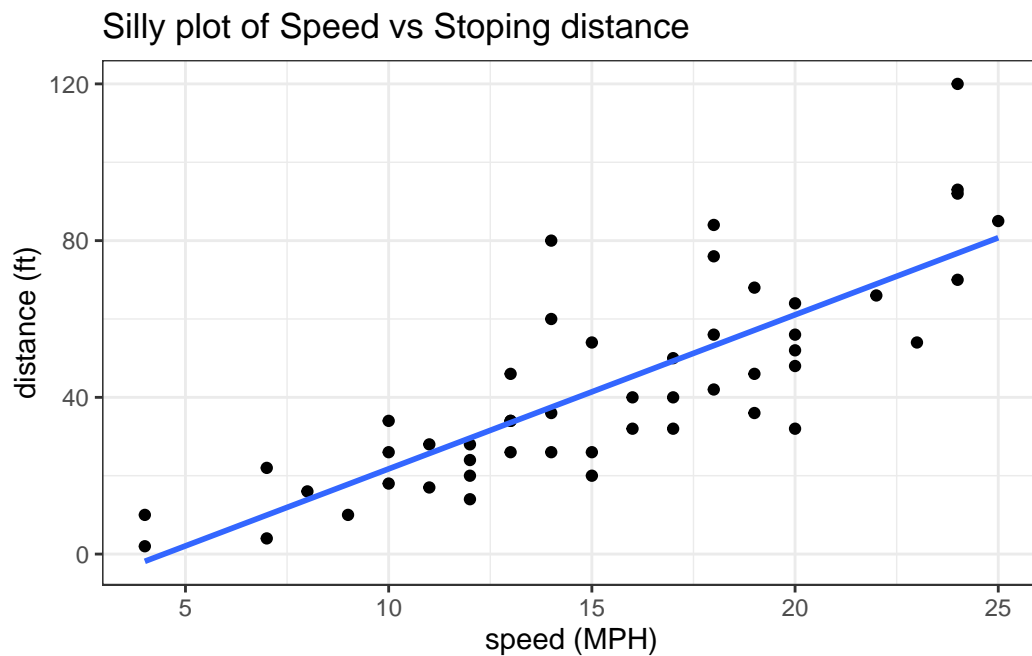
Key point: For simple “canned” graphs base R is quicker and more concise but as things get more custom the elaborate then ggplot wins out...

Let's add more layers to our ggplot

Add a line showing the relationship between x and y Add a title Add custom axis labels "Speed (MPH)" and "Distance (ft)" Change the theme...

```
ggplot(cars) +  
  aes(x=speed, y=dist) +  
  geom_point() +  
  geom_smooth(method="lm", se=FALSE) +  
  labs(title="Silly plot of Speed vs Stopping distance",  
        x="speed (MPH)",  
        y="distance (ft)") +  
  theme_bw()
```

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



##Going further

Read some gene expression data

```
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

Q1. How many genes are in this dataset

```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

Q2. How many “up” regulated genes are there?

```
sum(genes$State == "up")
```

```
[1] 127
```

A useful function for counting up occurrences of things in a vector is the ‘table()’ function

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

down	unchanging	up
72	4997	127

fraction

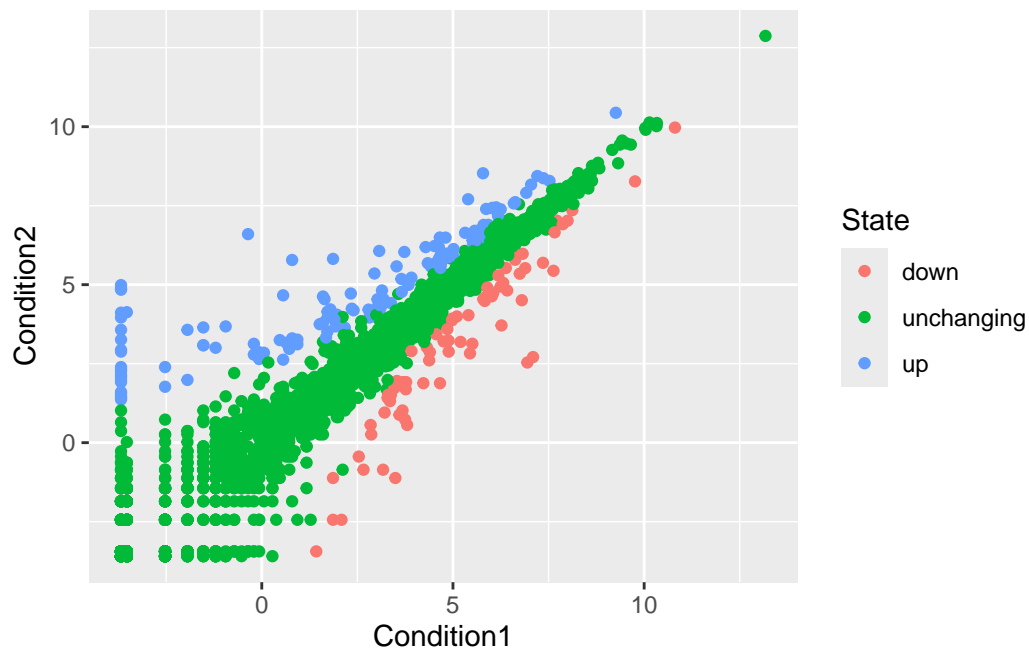
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

down	unchanging	up
1.39	96.17	2.44

Make a v1 figure

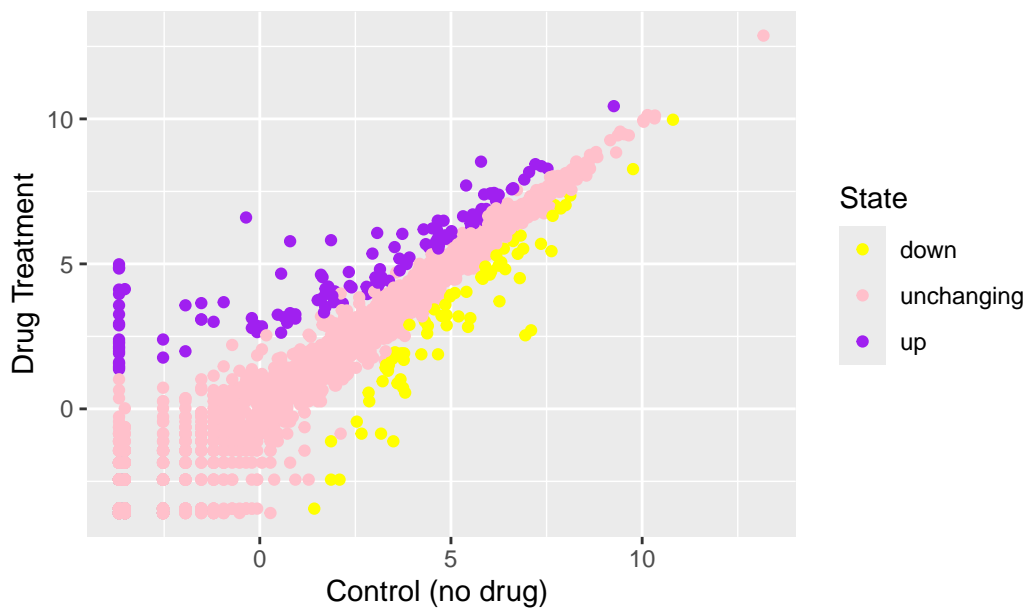
```
p <-ggplot(genes) +
  aes(x=Condition1,
      y=Condition2,
      col=State) +
  geom_point()
```

p



```
p + scale_colour_manual(values=c("yellow","pink","purple")) +
  labs(title="Gene Expression Changes Upon Drug Treatment",
       x="Control (no drug) ",
       y="Drug Treatment")
```

Gene Expression Changes Upon Drug Treatment



More Plotting

Read gapminder

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

Lets have a wee peak

```
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

Q4. How many different country values are in this dataset?


```
nrow(gapminder)
```

```
[1] 1704
```

```
table(gapminder$country)
```

Afghanistan	Albania	Algeria
12	12	12
Angola	Argentina	Australia
12	12	12
Austria	Bahrain	Bangladesh
12	12	12
Belgium	Benin	Bolivia
12	12	12
Bosnia and Herzegovina	Botswana	Brazil
12	12	12
Bulgaria	Burkina Faso	Burundi
12	12	12
Cambodia	Cameroon	Canada
12	12	12
Central African Republic	Chad	Chile
12	12	12
China	Colombia	Comoros
12	12	12
Congo, Dem. Rep.	Congo, Rep.	Costa Rica
12	12	12
Cote d'Ivoire	Croatia	Cuba
12	12	12
Czech Republic	Denmark	Djibouti
12	12	12
Dominican Republic	Ecuador	Egypt
12	12	12
El Salvador	Equatorial Guinea	Eritrea
12	12	12
Ethiopia	Finland	France
12	12	12
Gabon	Gambia	Germany
12	12	12
Ghana	Greece	Guatemala
12	12	12

Guinea	Guinea-Bissau	Haiti
12	12	12
Honduras	Hong Kong, China	Hungary
12	12	12
Iceland	India	Indonesia
12	12	12
Iran	Iraq	Ireland
12	12	12
Israel	Italy	Jamaica
12	12	12
Japan	Jordan	Kenya
12	12	12
Korea, Dem. Rep.	Korea, Rep.	Kuwait
12	12	12
Lebanon	Lesotho	Liberia
12	12	12
Libya	Madagascar	Malawi
12	12	12
Malaysia	Mali	Mauritania
12	12	12
Mauritius	Mexico	Mongolia
12	12	12
Montenegro	Morocco	Mozambique
12	12	12
Myanmar	Namibia	Nepal
12	12	12
Netherlands	New Zealand	Nicaragua
12	12	12
Niger	Nigeria	Norway
12	12	12
Oman	Pakistan	Panama
12	12	12
Paraguay	Peru	Philippines
12	12	12
Poland	Portugal	Puerto Rico
12	12	12
Reunion	Romania	Rwanda
12	12	12
Sao Tome and Principe	Saudi Arabia	Senegal
12	12	12
Serbia	Sierra Leone	Singapore
12	12	12
Slovak Republic	Slovenia	Somalia

12	12	12
South Africa	Spain	Sri Lanka
12	12	12
Sudan	Swaziland	Sweden
12	12	12
Switzerland	Syria	Taiwan
12	12	12
Tanzania	Thailand	Togo
12	12	12
Trinidad and Tobago	Tunisia	Turkey
12	12	12
Uganda	United Kingdom	United States
12	12	12
Uruguay	Venezuela	Vietnam
12	12	12
West Bank and Gaza	Yemen, Rep.	Zambia
12	12	12
Zimbabwe		
12		

```
length(table(gapminder$country))
```

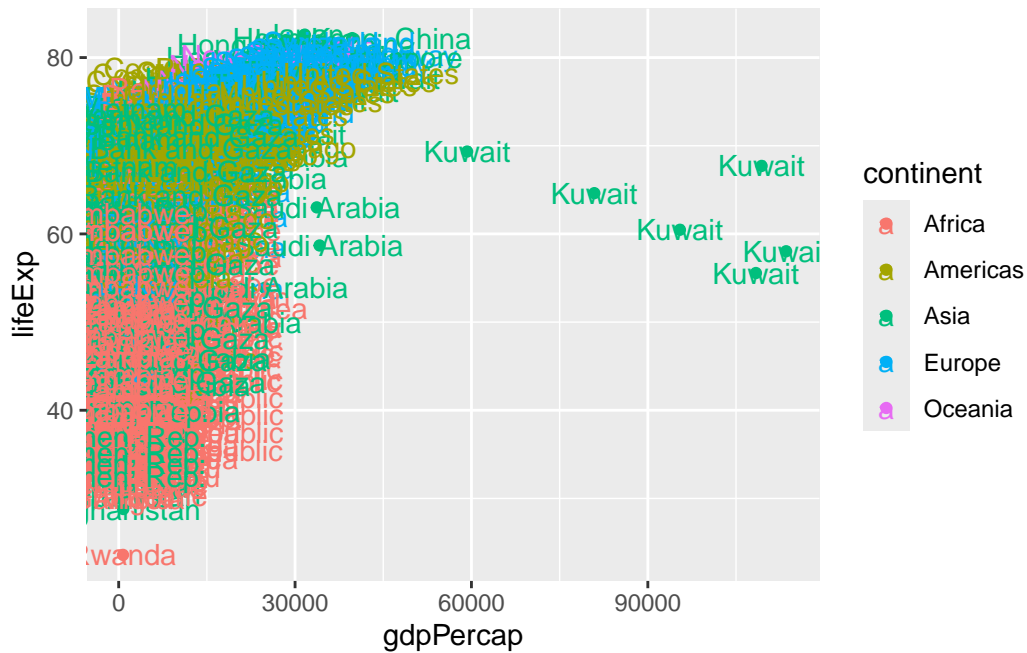
```
[1] 142
```

Q5.How many different continent values are in this dataset.

```
unique(gapminder$continent)
```

```
[1] "Asia"      "Europe"    "Africa"    "Americas" "Oceania"
```

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

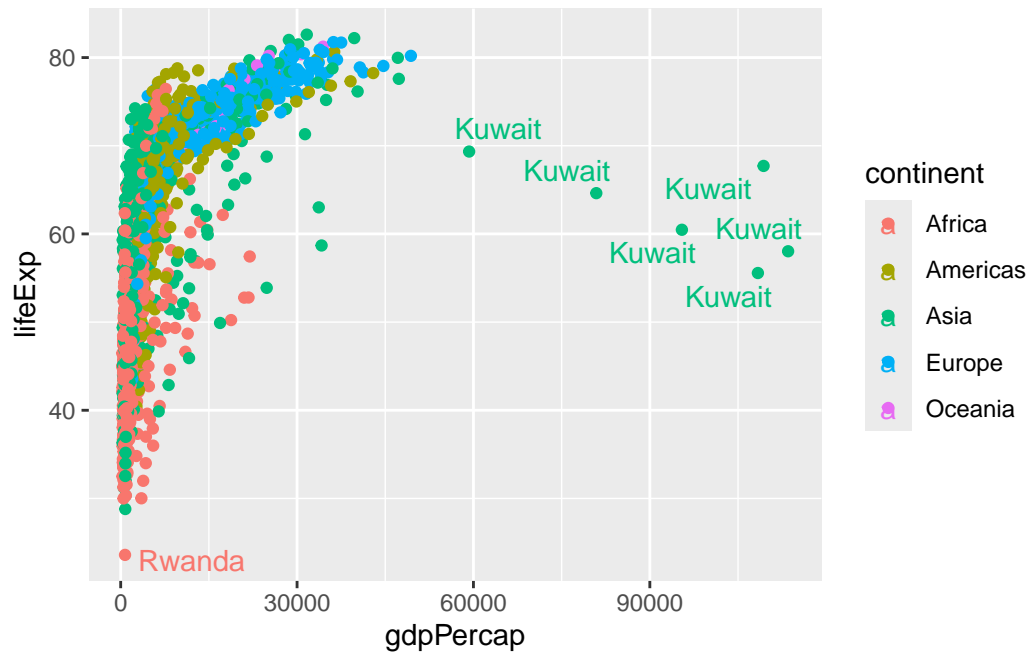


I can use **ggrepel** package to make more sensible labels here.

```
library(ggrepel)

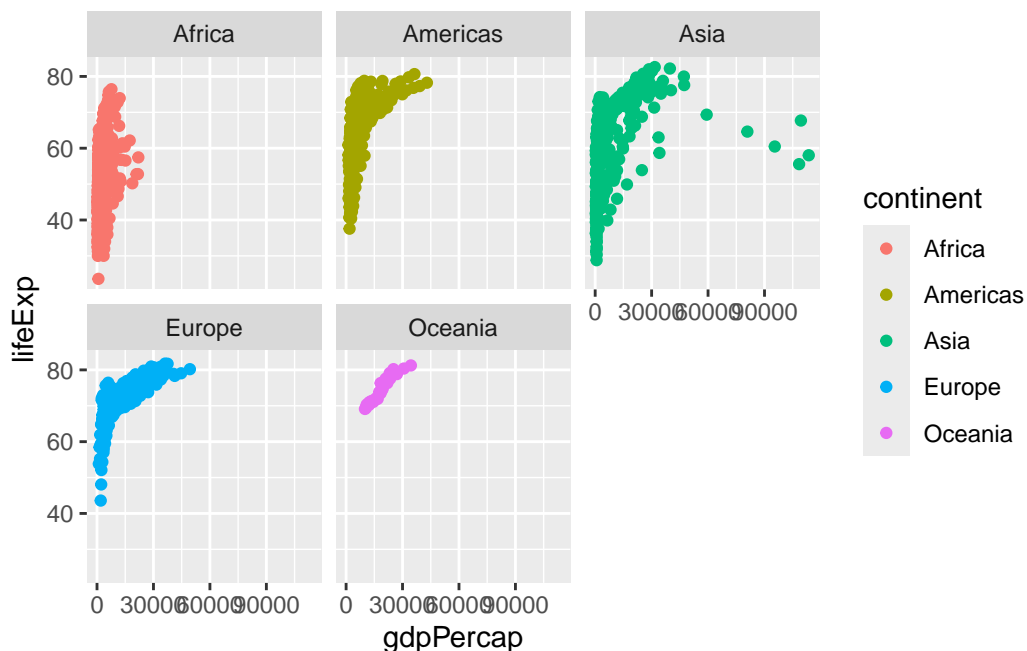
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, col=continent, label=country) +
  geom_point() +
  geom_text_repel()
```

Warning: ggrepel: 1697 unlabeled data points (too many overlaps). Consider increasing max.overlaps



I want a separate a pannel per continent

```
ggplot(gapminder) +
  aes(gdpPerCap, lifeExp, col=continent, label=country) +
  geom_point() +
  facet_wrap(~continent)
```



##Summary

The main advantages of ggplot over base R plotting are:

Let's focus on the main advantages of ggplot2 over base R plotting:

1. ggplot2 uses a layered approach (data, aesthetics, geometry), making it easier to build complex, publication-quality plots by adding layers step by step. Base R requires different functions and many arguments for each plot type, which can be fiddly and time-consuming to refine for publication-quality figures.
2. ggplot2 provides sensible defaults for aesthetics and themes, so plots look visually appealing with less manual tweaking. Base R gives full control but often needs more effort to polish.
3. ggplot2 code is more concise for complex plots, while base R is quicker for simple, exploratory plots but gets verbose and complicated for advanced visualizations.
4. ggplot2 makes it easier to automate and reproduce plots, especially for reports, since the same code structure applies to different datasets and plot types.