Class 5: Data Vis with Ggplot

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

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

- "base" R
- add on packages like **ggplot2**

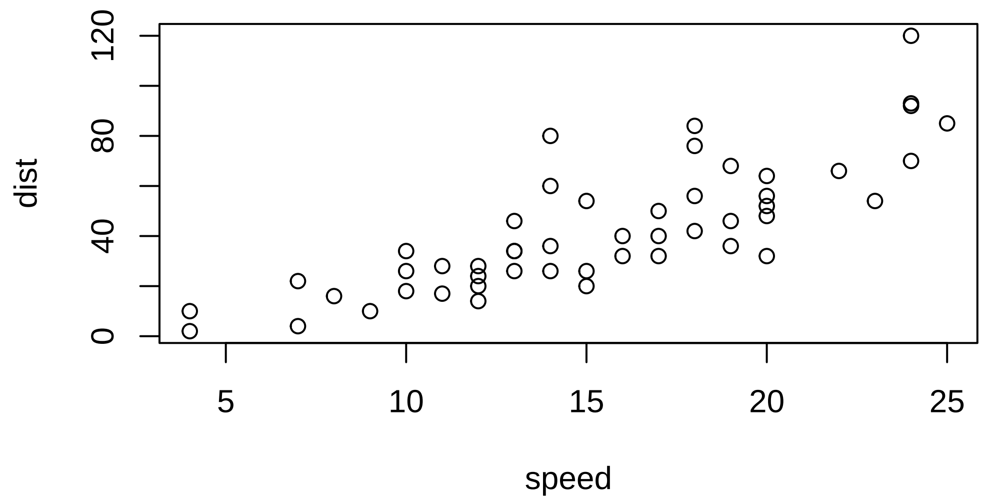
Here is a simple "base" R plot. Add code chunk by +C then R.

```
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 it 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**…

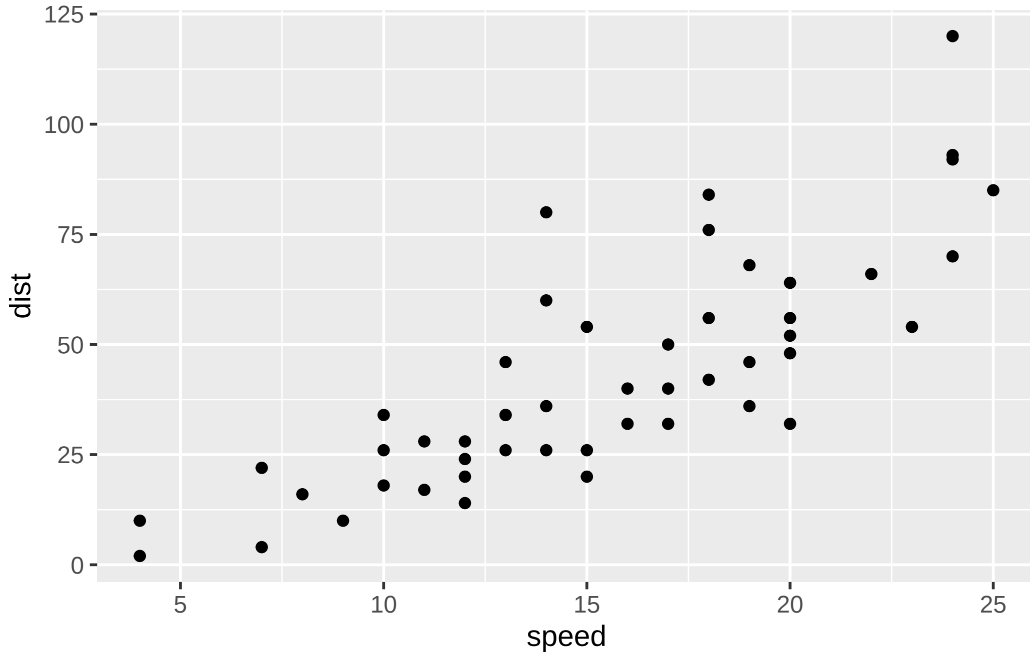
First, instal this add-on package. For this we use the `install.packages()` function. **We do this in the console to save time, not our report** This is one time only.

Second, load the package with the `library()` function every time we want to use it.

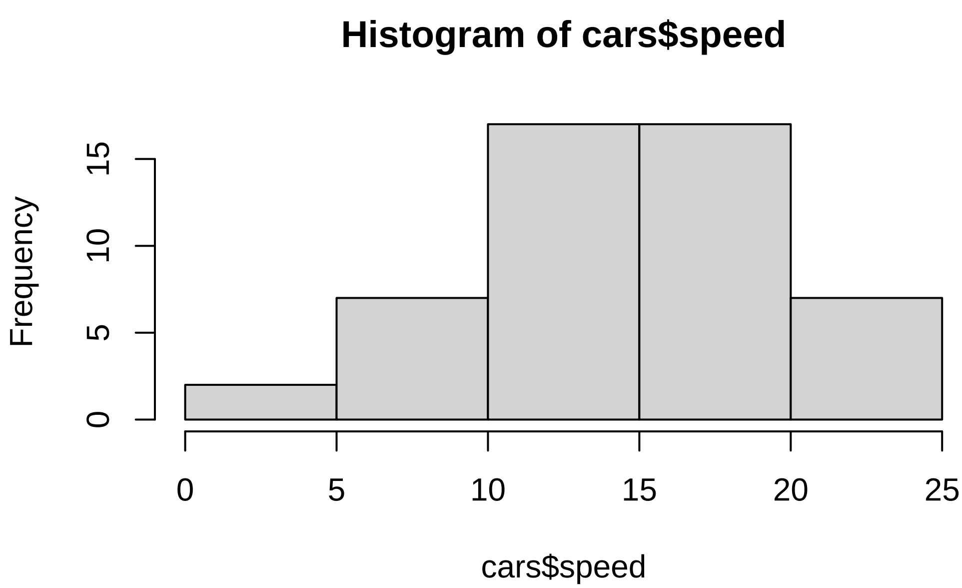
```
library(ggplot2)
ggplot(cars)
```

Every ggplot is composed of at least 3 layers: _ **Data** (e.g. a dataframe with the things you want to do) - Data aesthetics **aes()** maps the columns of data to your plot features _ geoms like **geom_point()** that srt how the plot appears

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




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



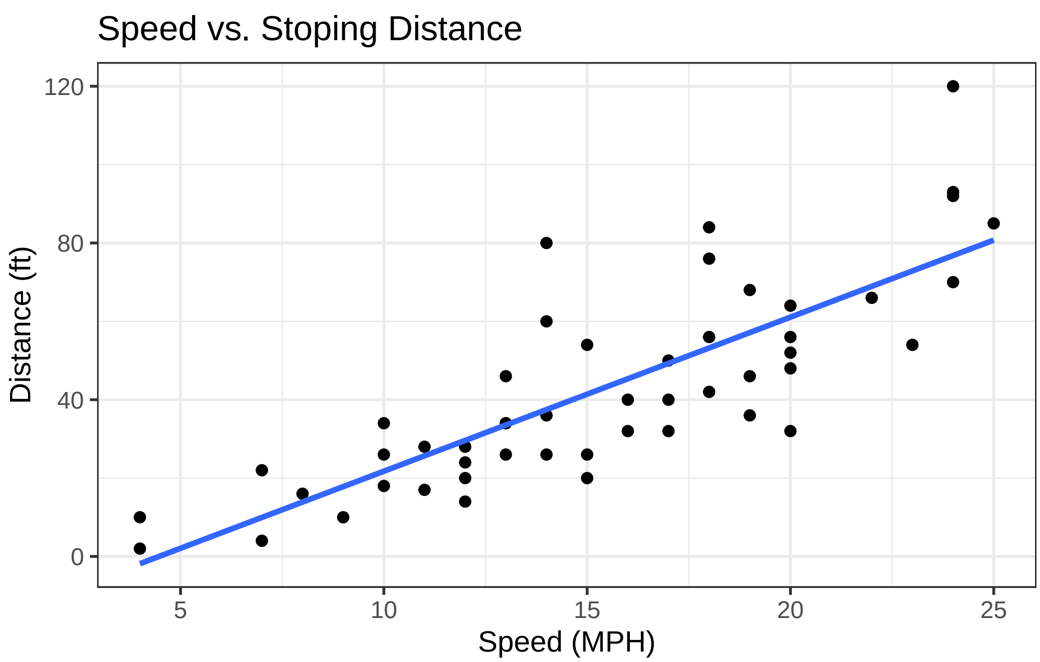
key_point: or simple “canned” graphs base R is quick and more concise. As things get more custom and elaborate them theen ggplot will win.

Add more layers!

Add a line to show relationship between X and Y. Add a title Add custom axis labels "Speed (MPH)" and "Distance (ft)"

```
ggplot(cars) + aes(x=speed, y=dist) + geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  labs(title = "Speed vs. Stoping 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 data set?

```r
nrow(genes)
```

```
[1] 5196
```

```r
ncol(genes)
```

```
[1] 4
```

Q2: How many "up" related genes are there?

nrow(genes$State=="up") gives Null. nrow expects a matrix, not a logical vector.

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

```
[1] 127
```

A useful function for counting up occurrences of things in a vector is the `tables()` function.

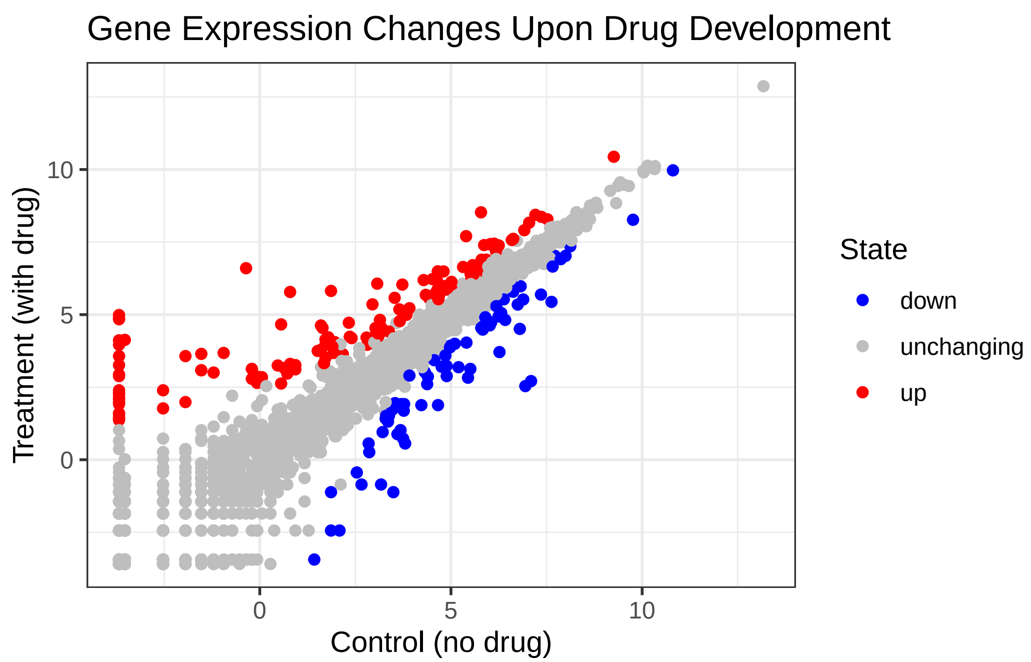
```r
table(genes$State)
```

```

      down unchanging         up 
        72       4997        127 
```

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

p + scale_color_manual(values=c("blue", "grey", "red")) +
  labs(title="Gene Expression Changes Upon Drug Development",
       x="Control (no drug)", y="Treatment (with drug)") +
  theme_bw()
```



More Plotting

Read in the gap minder data set.

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

gapminder <- read.delim(url)
```

Let's have a peak.

```
tail(gapminder,3)
```

```
      country continent year lifeExp      pop gdpPercap
1702 Zimbabwe    Africa 1997  46.809 11404948  792.4500
1703 Zimbabwe    Africa 2002  39.989 11926563  672.0386
1704 Zimbabwe    Africa 2007  43.487 12311143  469.7093
```

Q4: How many different countries are in this data set?

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

```
[1] 142
```

Q5: How many different continents are in this data set?

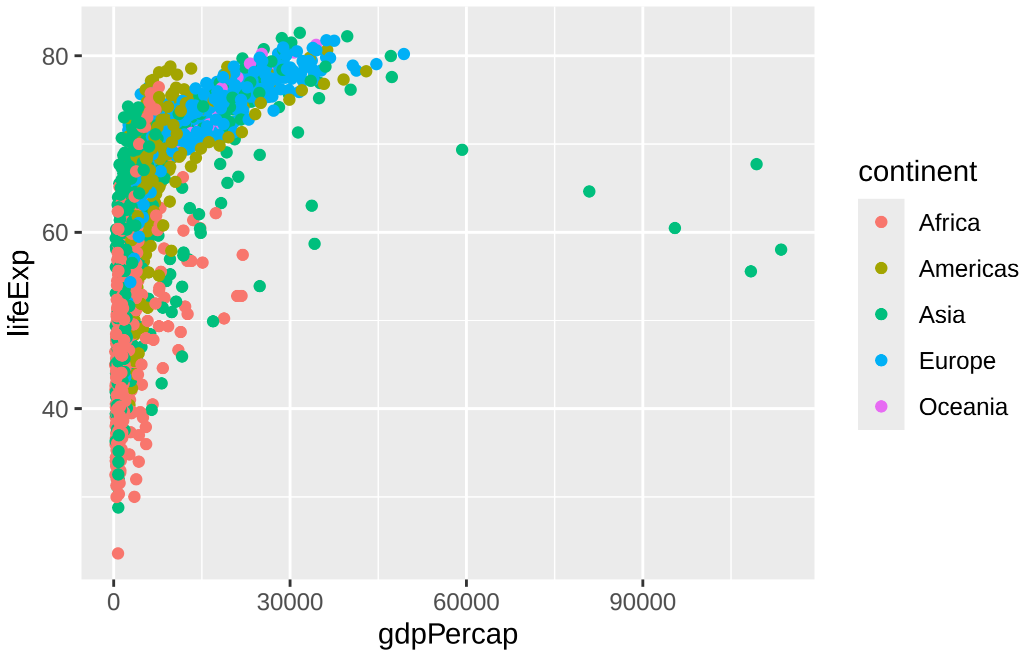
```
length(table(gapminder$continent))
```

```
[1] 5
```

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

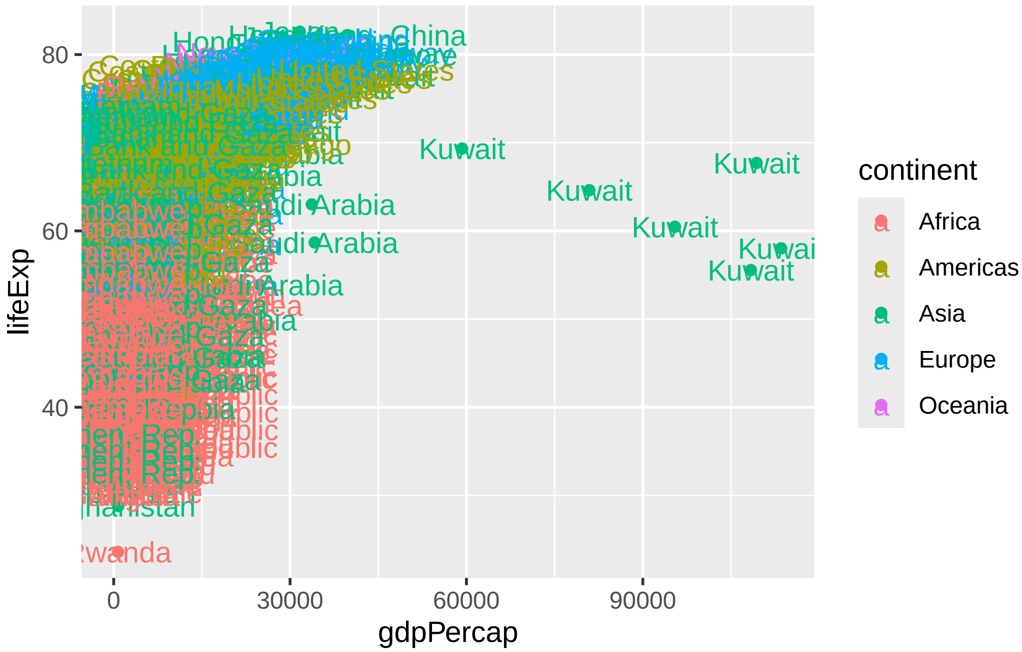
```
[1] "Asia"     "Europe"   "Africa"   "Americas" "Oceania"
```

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



To add the names...

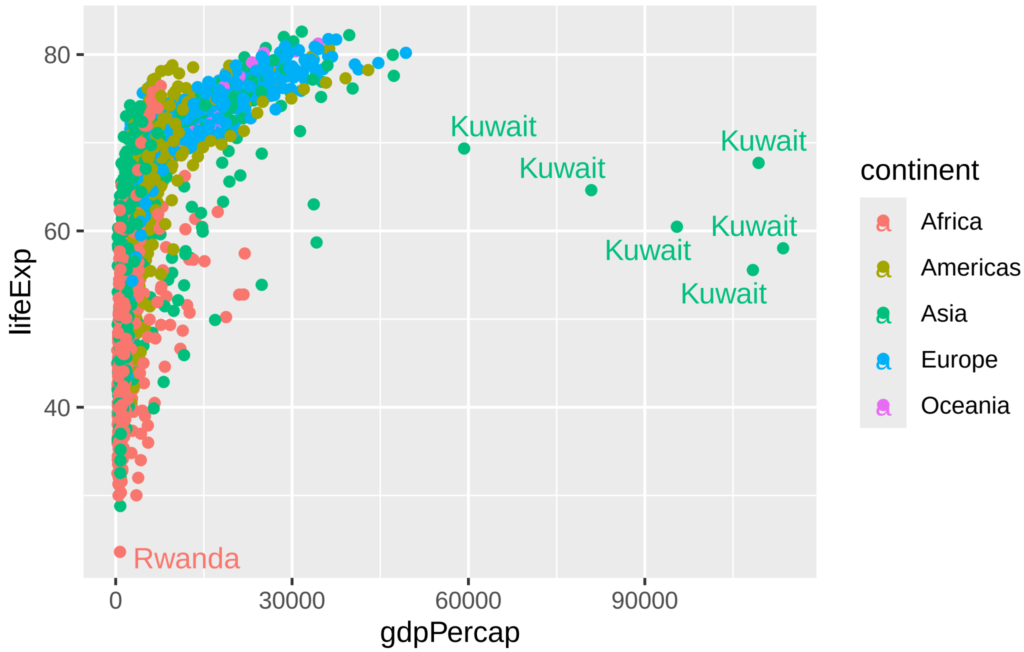
```
ggplot(data=gapminder) + aes(x=gdpPercap, y=lifeExp, col=continent, label=country) + geom_poi
```



Use **ggrepel** to make more sensible labels here. Add on package install.packages("ggrepel") in the console.

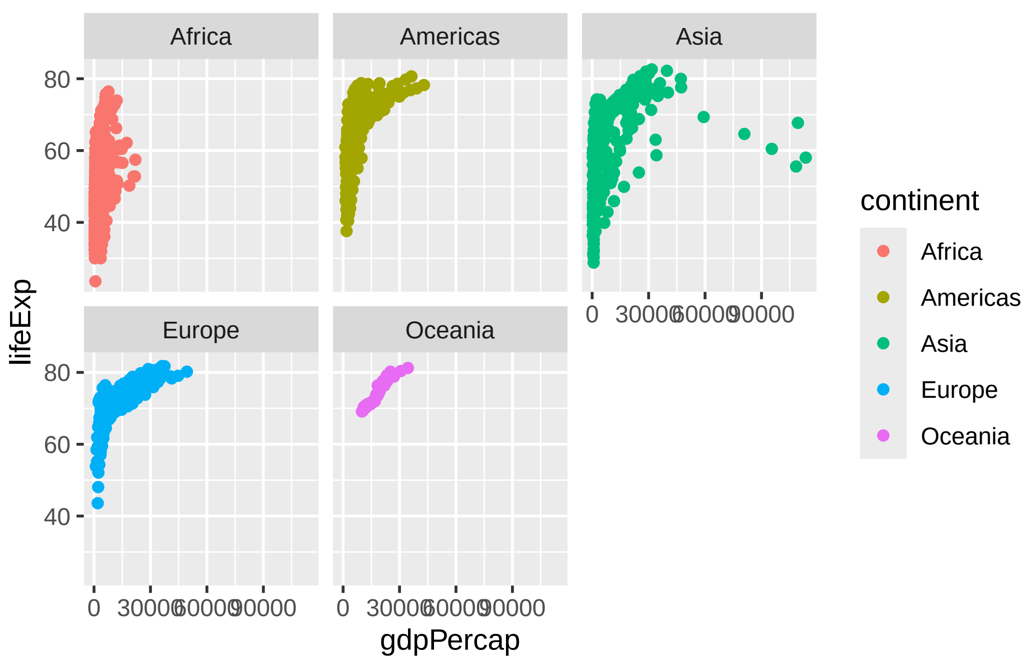
```
library(ggrepel)
ggplot(data=gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent, label=country) +
  geom_point() + geom_text_repel()
```

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



I want a separate panel for each continent.

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



Summary

ggplot2 offers several main advantages over base R graphics:

1. Layered grammar: ggplot2 uses a consistent, layered approach (data + aesthetics + geometry) for building plots, making it easier to create complex, publication-quality figures by adding layers step-by-step [5], [6].
2. Declarative syntax: You specify what you want to see (mapping data to aesthetics), rather than how to draw each element, which is more intuitive and less fiddly than base R [1], [3], [6].
3. Sensible defaults: ggplot2 provides attractive default themes and legends, so plots look good with minimal effort, while base R often requires more manual tweaking for aesthetics [1], [3].
4. Customization: It is easier to customize and extend plots in ggplot2, especially for adding color, labels, themes, and other features [3], [6].
5. Consistency: The same building blocks are used for all plot types, reducing the need to learn many different functions as in base R [5], [6].
6. Reproducibility: ggplot2 code is more modular and scriptable, making it easier to reproduce and update figures [1], [3].

Do you have questions about any of these advantages?