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**

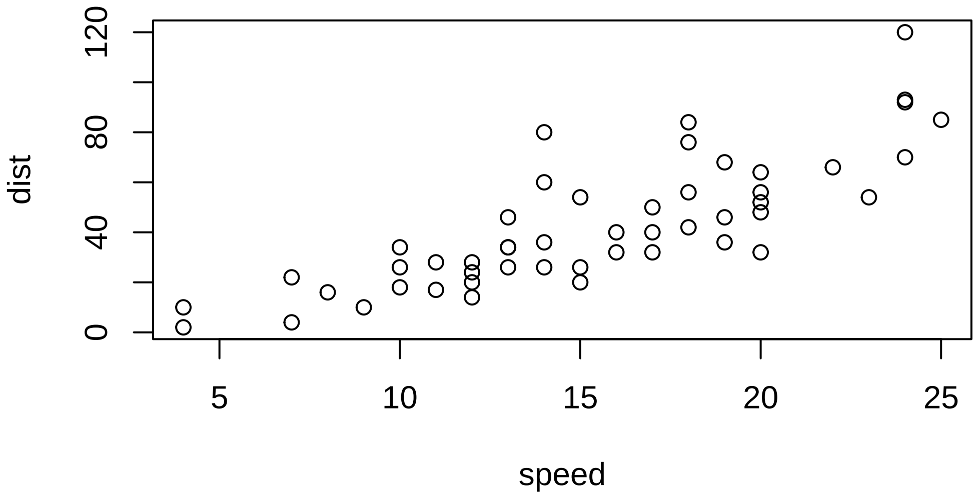
Here is a simple "base" R plot.

```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 to the `plot()` function.

```r
plot(cars)
```



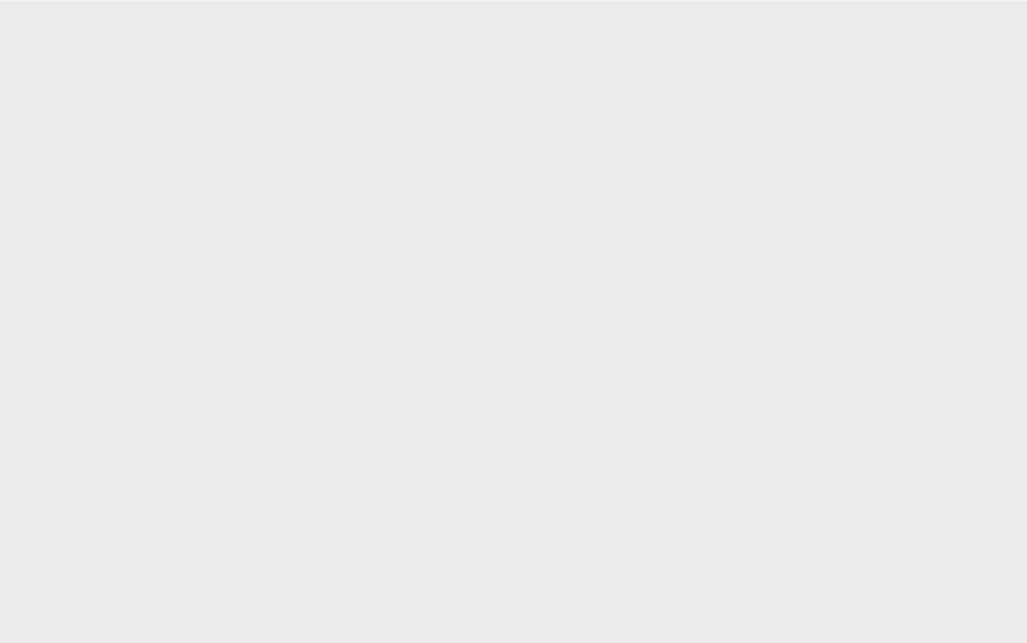
Key-point: Base R is quick but not so nice looking in some folks eyes

Let's see how we can plot this with **glotplot2**…

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**. This is a one time only deal.

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

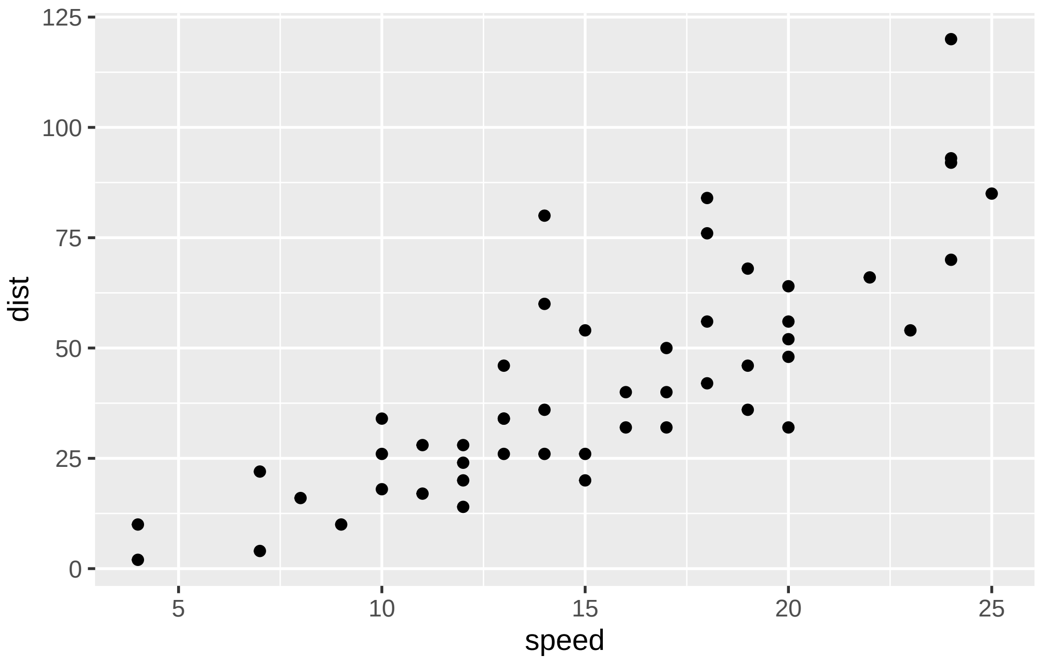
```
library(ggplot2)
ggplot(cars)
```



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 srt how the plot appears

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



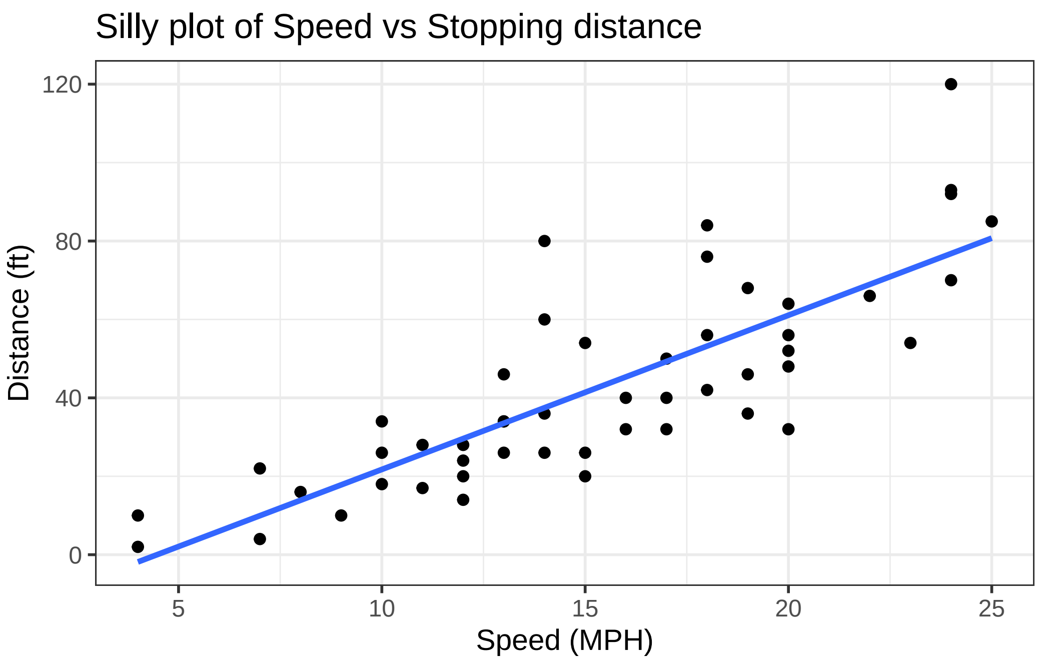
> Key point: For simple "canned" graphs, base R is quicker, but as things get more custom and elaborate, then ggplot wins out…

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 wee dataset?

```
nrow(genes)
```

```
[1] 5196
```

```r
ncol(genes)
```

```
[1] 4
```

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

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

```
[1] 127
```

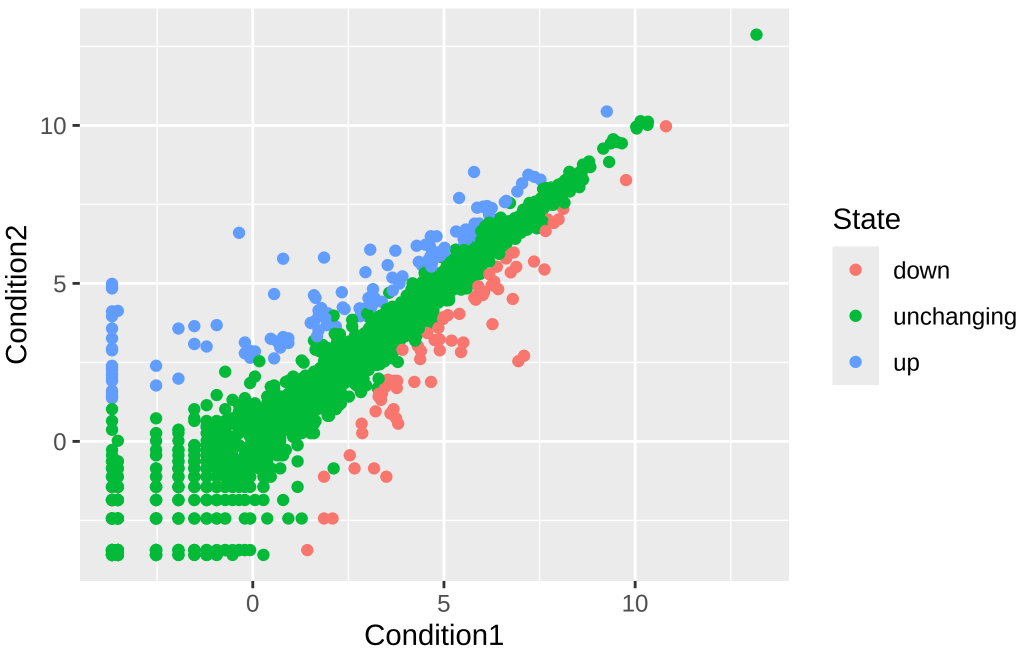
A useful function for counting up occurrences of things in a vector is the `table()` function.

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

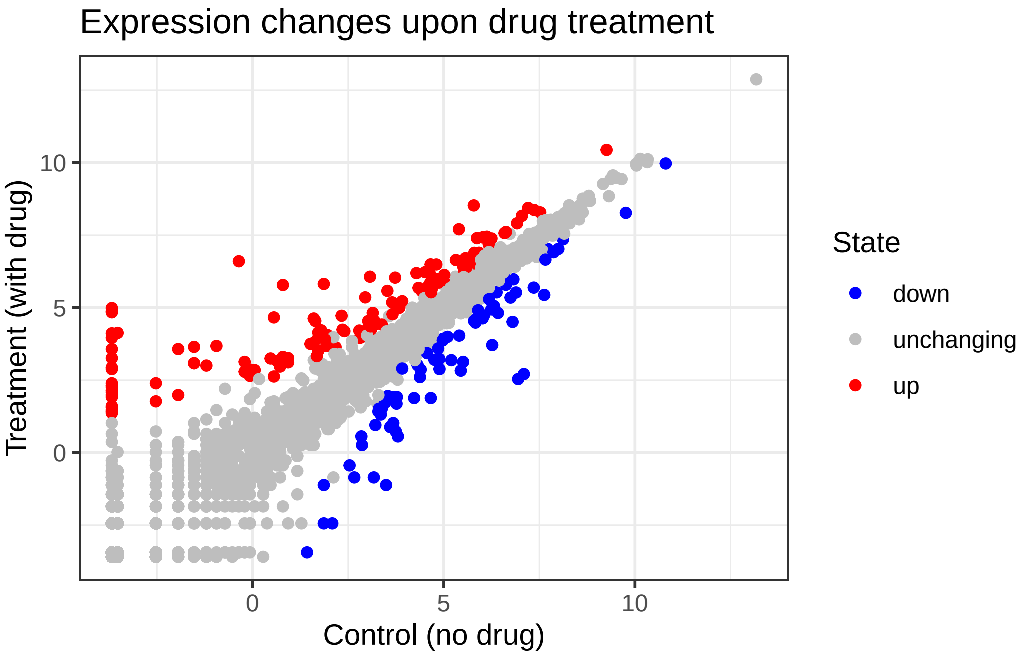
```

      down unchanging         up 
        72       4997        127 
```

Make a v1 figure

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

p
```



```
p + scale_colour_manual(values =c("blue", "gray", "red")) +
  labs(title="Expression changes upon drug treatment",
       x= "Control (no drug)",
       y= "Treatment (with drug)") +
  theme_bw()
```



More Plotting

Read in the gapminder dataset

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

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

Let's 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
```

```
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 country values are in this dataset?

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

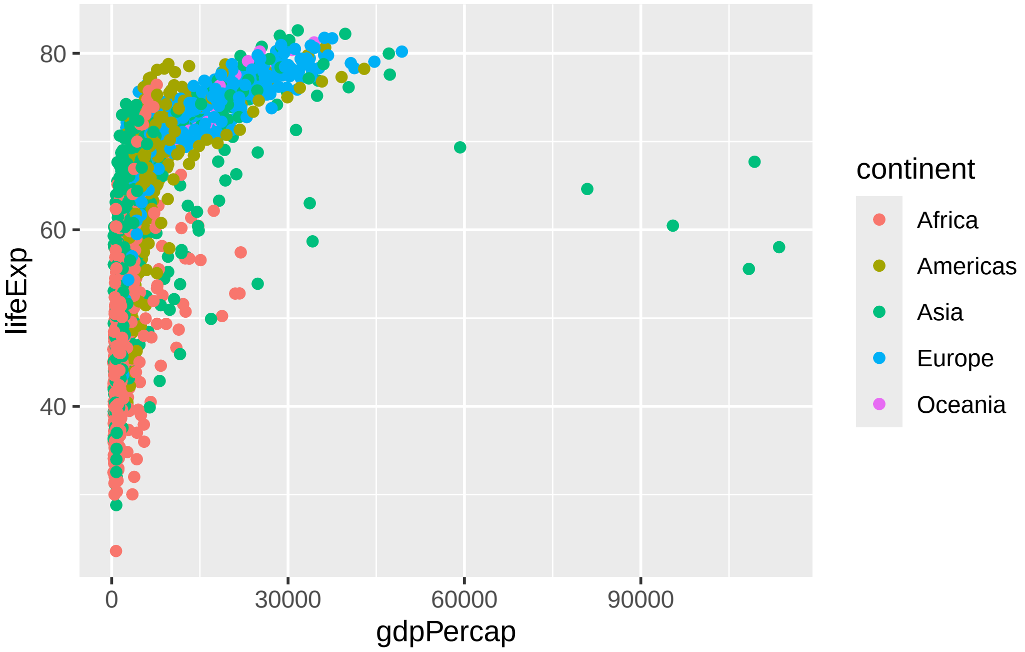
```
[1] 142
```

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

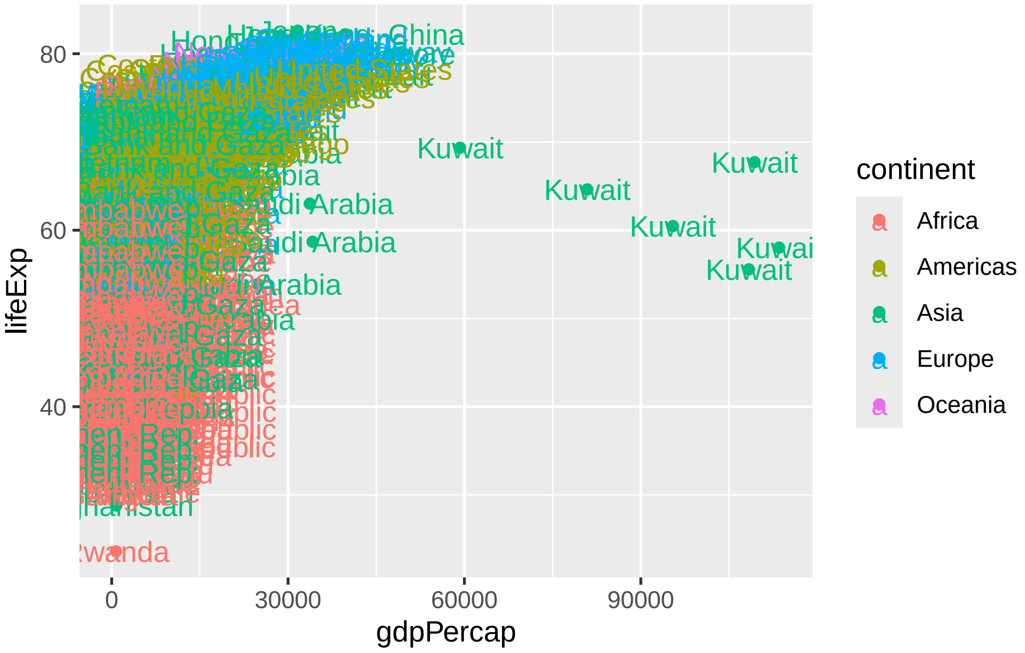
```
length( unique(gapminder$continent) )
```

```
[1] 5
```

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



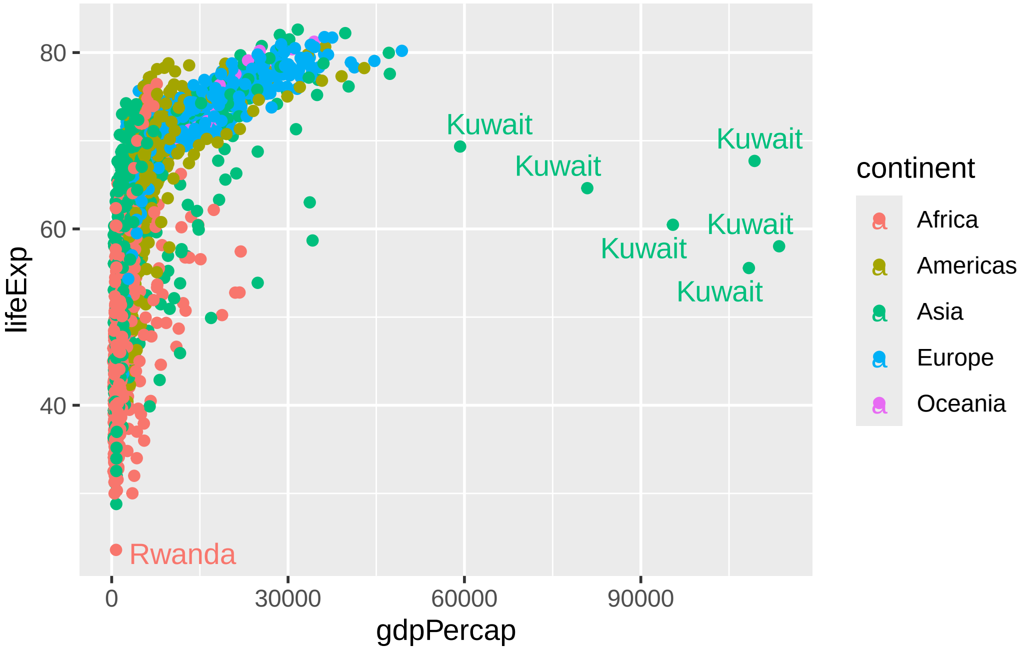
```r
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, col= continent, label= country) +
  geom_point() +
  geom_text()
```



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

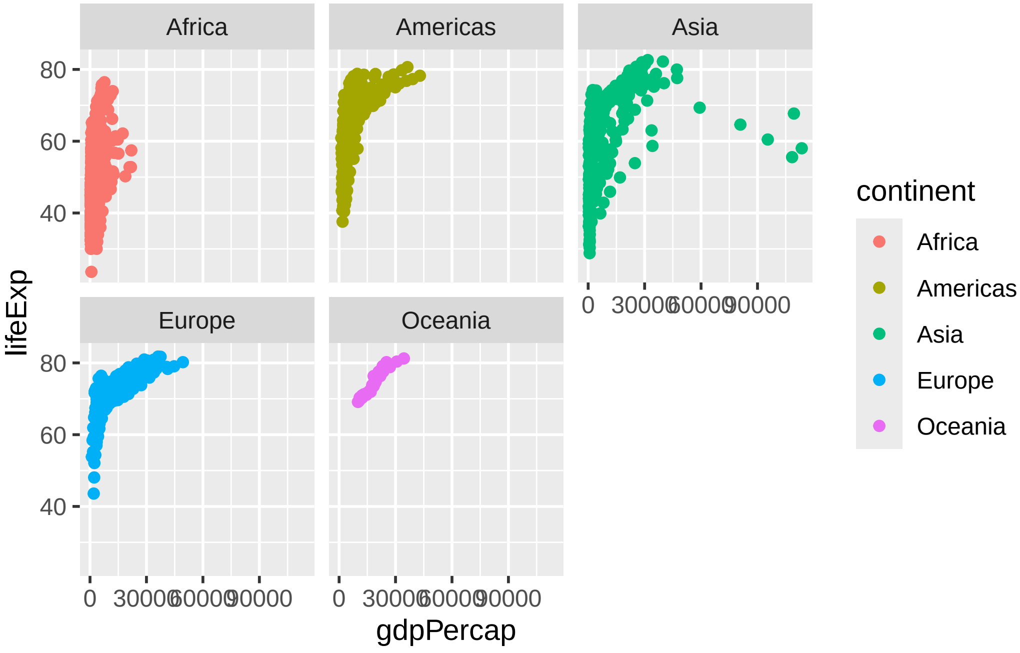
```r
library(ggrepel)

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 panel per continent

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



ggplot2 offers several advantages over base R plots:

The main advantages of ggplot over base R plot are:

1. **Layered grammar**: ggplot2 builds plots by adding layers (data, aesthetics, geoms, themes), making complex plots easier to construct and modify step-by-step [1], [2], [3].
2. **Consistency**: The same syntax and logic apply across different plot types, reducing the need to learn new functions for each visualization [1], [2], [3].
3. **Publication-quality visuals**: ggplot2 produces attractive, polished figures suitable for scientific publications with sensible defaults [1], [2], [3].
4. **Customization**: It is easier to customize legends, colors, themes, and annotations, and to combine multiple plots [1].
5. **Data mapping**: Direct mapping of data columns to visual aesthetics (color, size, shape) is built-in and intuitive [2], [3].
6. **Reproducibility**: ggplot2 code is scriptable and reproducible, making it easy to regenerate or update figures [1], [2].

Base R plots are quick for simple, exploratory graphics, but become fiddly and time-consuming for refined, complex, or publication-ready figures [1], [2], [3], [5], [4].

Which of these advantages do you think is most important for your work?