Class 5: Data Viz with ggplot

Nicole (A18116280)

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

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

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

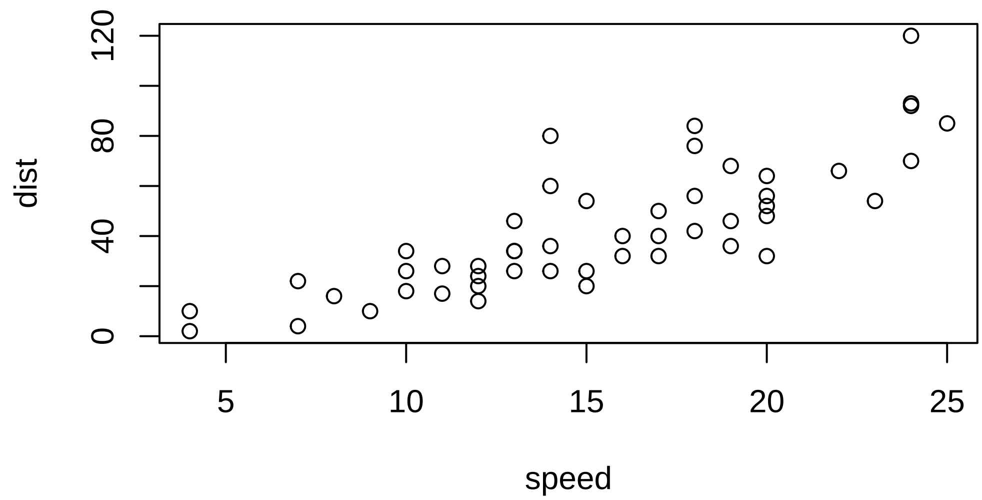
Here is a simple "base" R plot.

```
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 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.package()` function - **WE DO THIS IN THE CONSOLE, NOT our report**. This is a one time only deal.

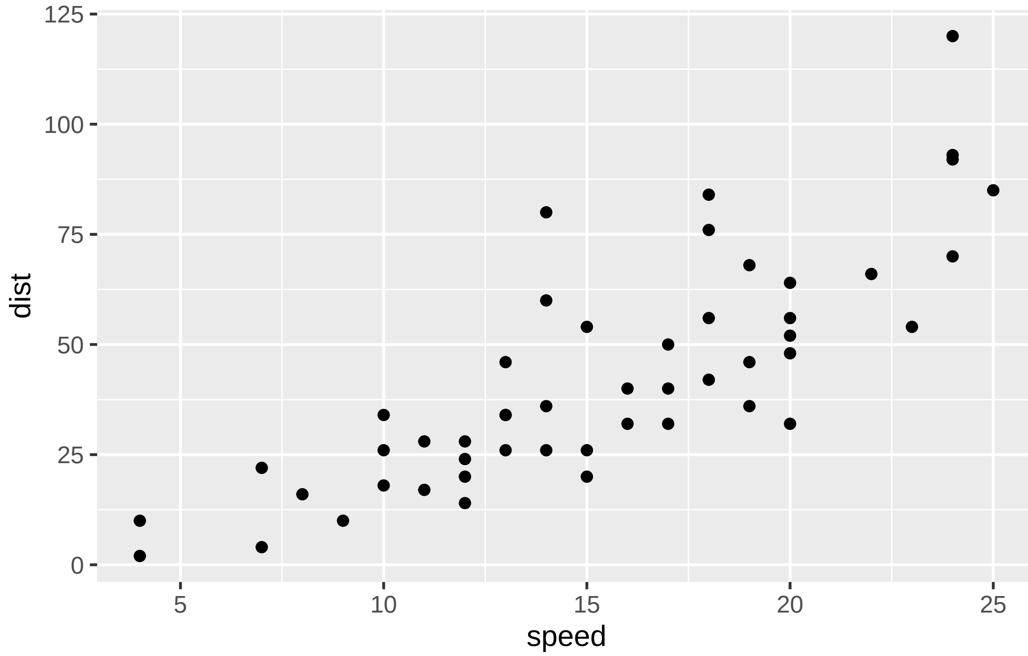
2nd we need to load the package with the `library()` functino every time we want to use it.

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

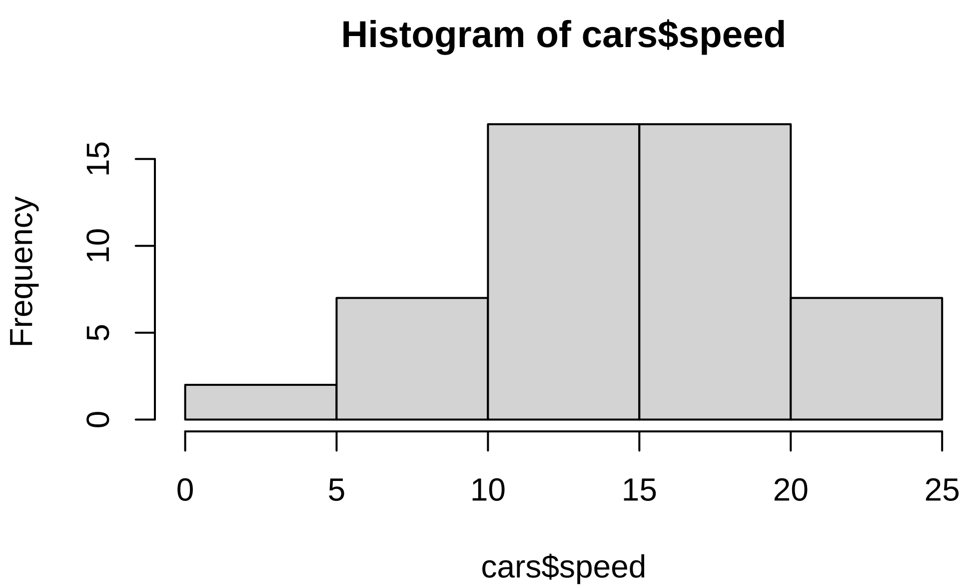
Every ggplot is composed of at least 3 layers:

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

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




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



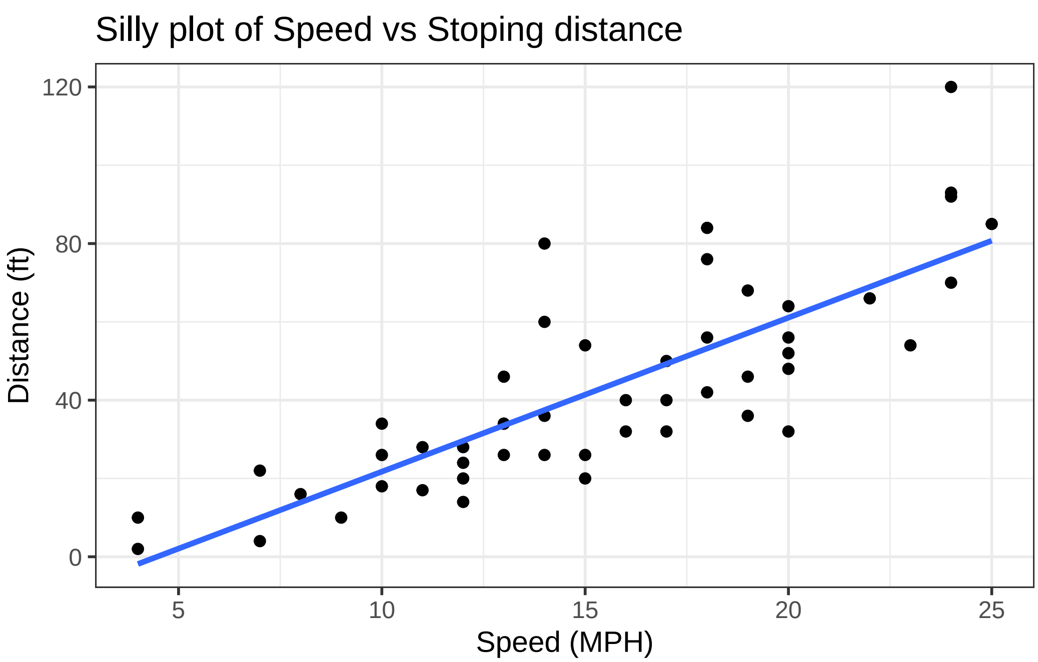
For simple “canned” graphs base R is quicker but as things get more custom and elaborate then ggplot wins out…

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 Stoping distance",
       x="Speed (MPH)",
       y="Distance (ft)") +
  theme_bw()
```

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



Going further

Read some gene expression data

```r
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?

```r
nrow(genes)
```

```
[1] 5196
```

> 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)
```

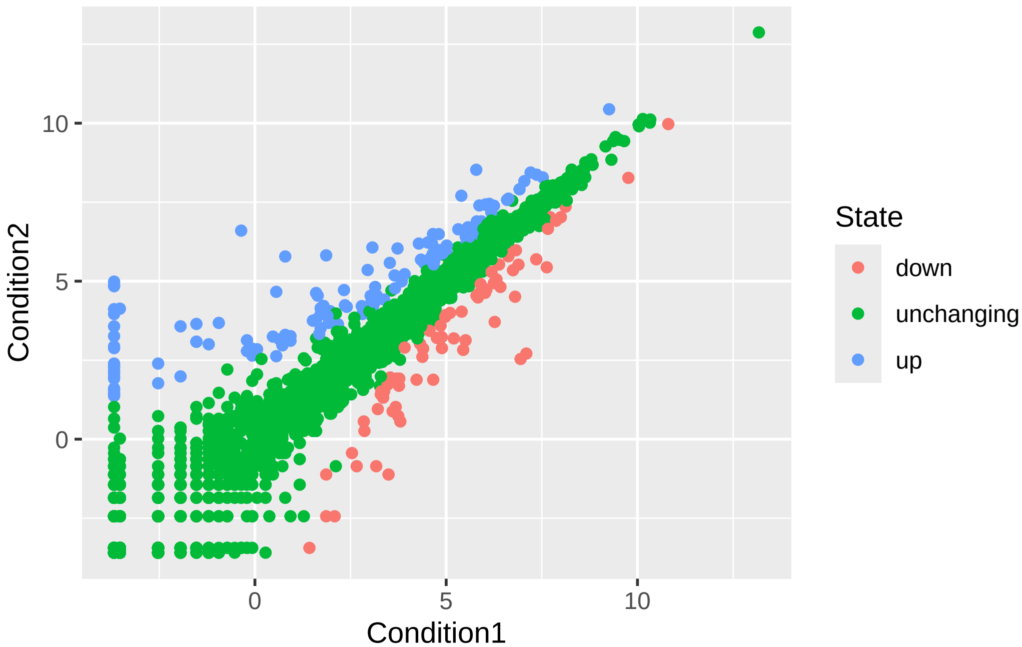
```

      down unchanging         up 
        72       4997        127 
```

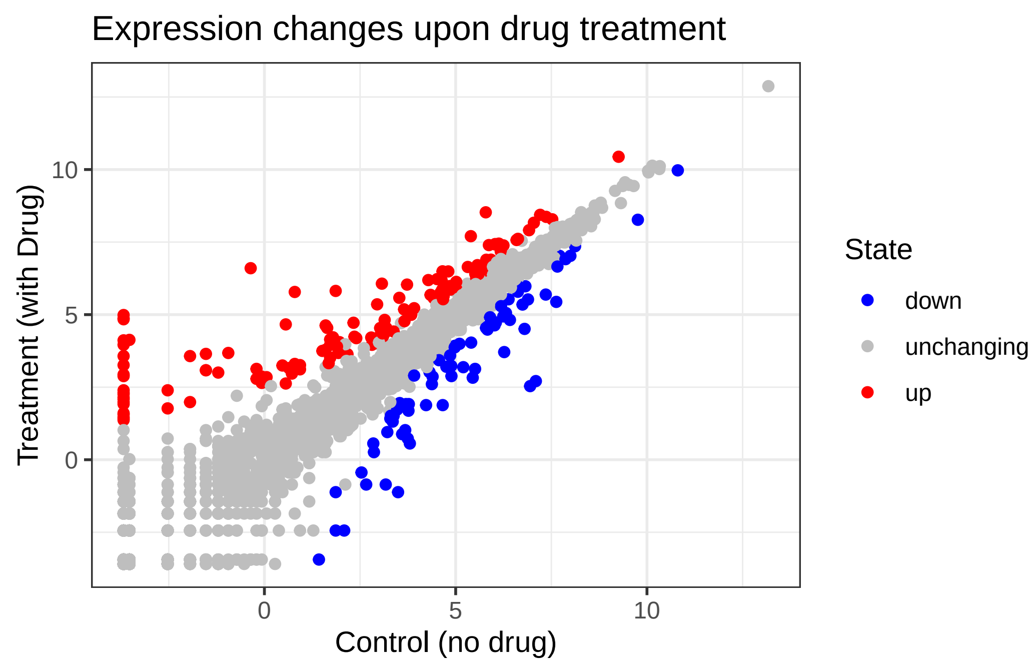
Make a v1 figure

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

p
```




```r
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)
```

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
```

```
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?

```r
nrow(gapminder)
```

```
[1] 1704
```

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

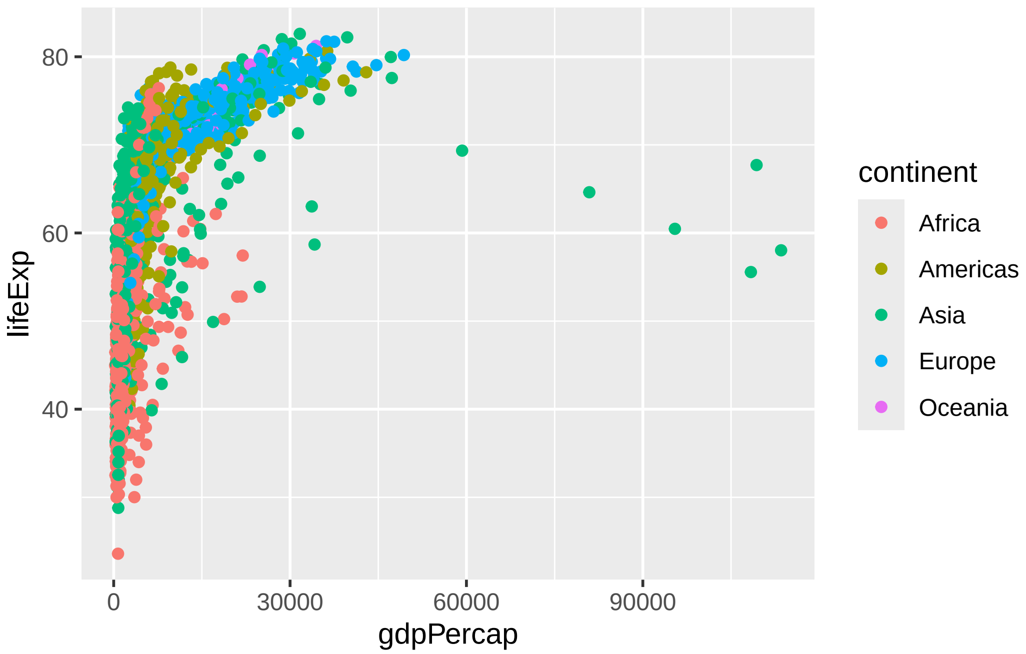
```
[1] 142
```

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

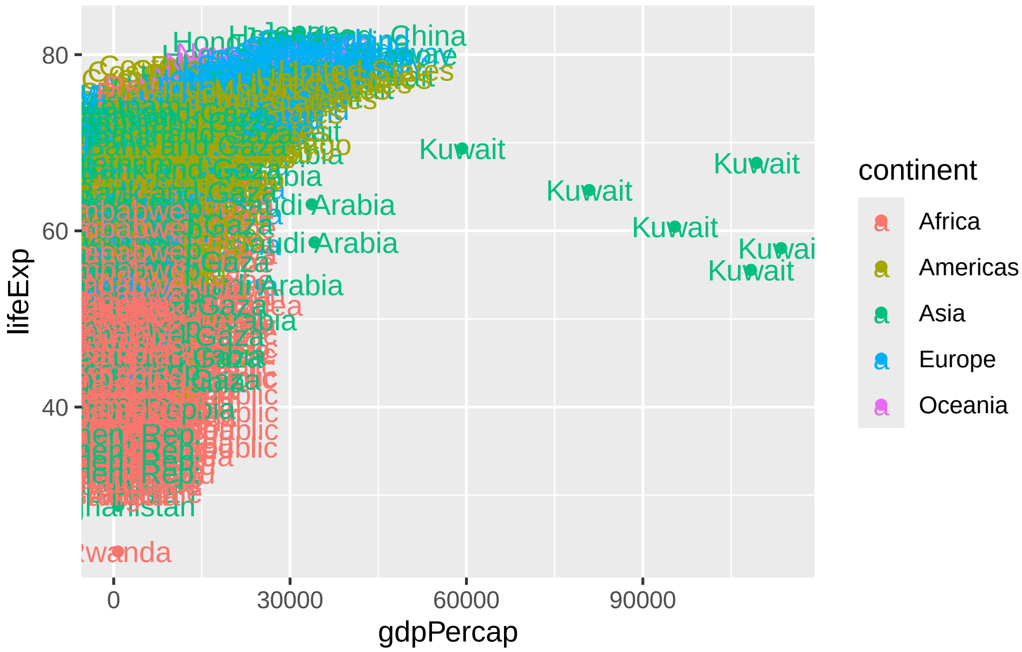
```r
unique(gapminder$continent)
```

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

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



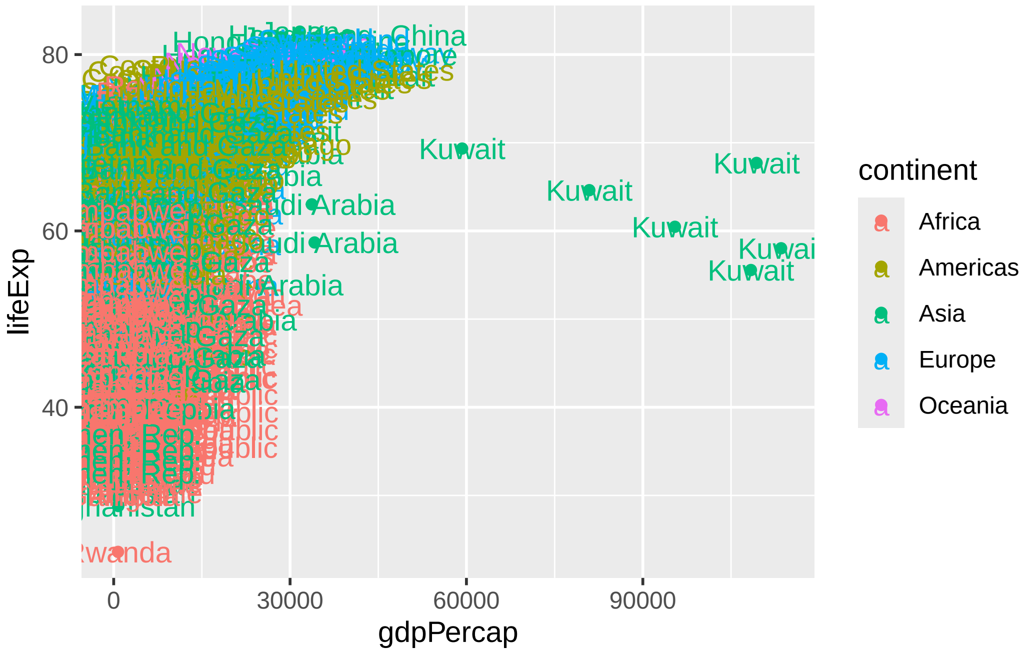
```
ggplot(gapminder) +
  aes(gdpPercap, lifeExp, col=continent, label=country) +
  geom_point() +
  geom_text()
```



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

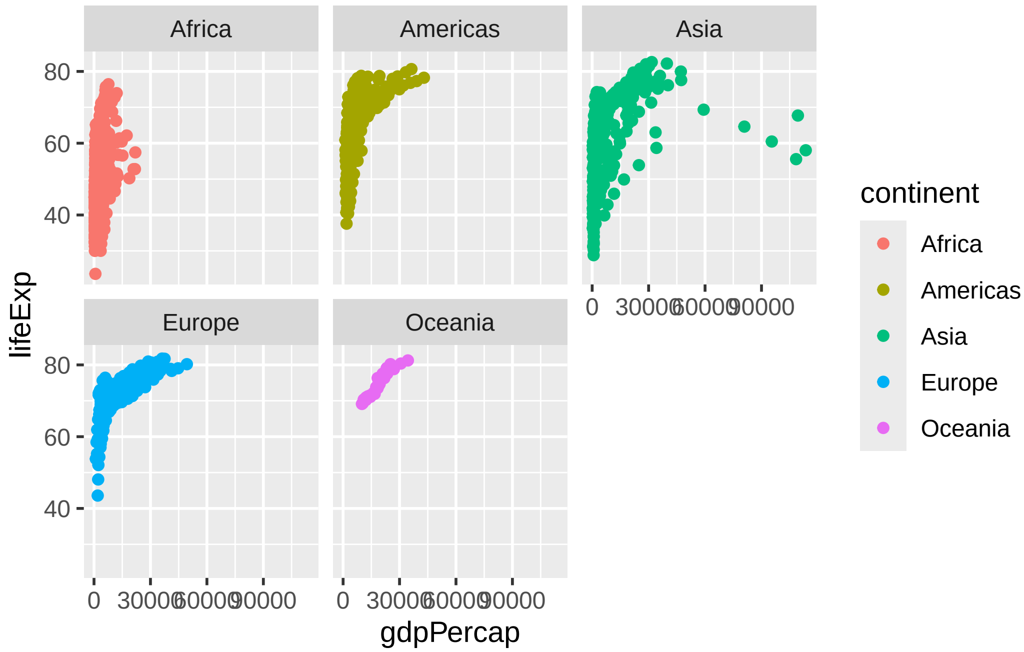
```
library(ggrepel)

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



I want a separate 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 are:

1. Layered Grammar: ggplot uses a consistent, layered approach—data, aesthetics, and geometry—making it easier to build and customize complex plots step by step, unlike base R which requires different functions and arguments for each plot type [1], [3], [5], [6], [4].
2. Publication Quality: ggplot produces attractive, publication-ready figures with sensible defaults, while base R plots often need more manual tweaking to look polished [1], [3], [5], [6], [4].
3. Reproducibility: ggplot code is modular and scriptable, making it easier to reproduce and update plots by changing data or layers [1], [5], [6].
4. Customization: Mapping data columns to visual features (color, size, shape) and adding legends, labels, and themes is straightforward in ggplot, but more cumbersome in base R [1], [3], [5], [6], [4].
5. Scalability: For simple plots, base R is quicker, but for complex, multi-layered figures, ggplot is more concise and manageable [1], [5].

Which of these advantages do you want to explore further?