Class 05: Data Visualization 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 plots in R. These include:

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

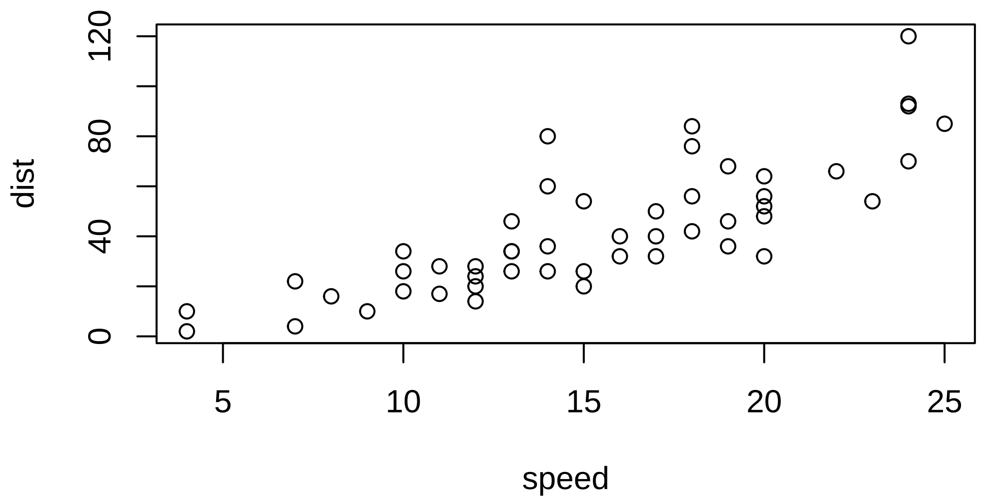
Below is a simple "base" R plot:

```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 this do the `plot()` function.

```r
plot(cars)
```



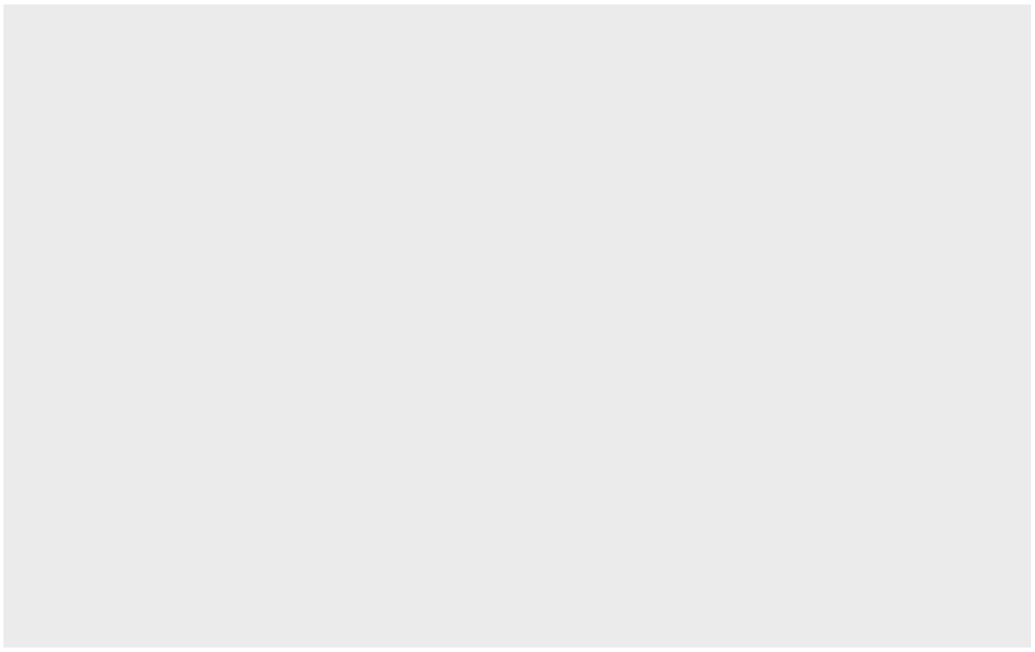
key-point: Base R is quick but not so nice-looking in some folks' eyes.

Now we are gonna make this plot with **ggplot2**

1st we need to install the **ggplot** package with the `install.packages()` function. - since we only need to install the package **once**, we do not want to install this package into the code chunk (as this will cause the code to run slowly because the package is getting installed over and over gain). **Instead** we are gonna install it in R brain (the console)

2nd we need to load the package with the `library()` function everytime we want to use it

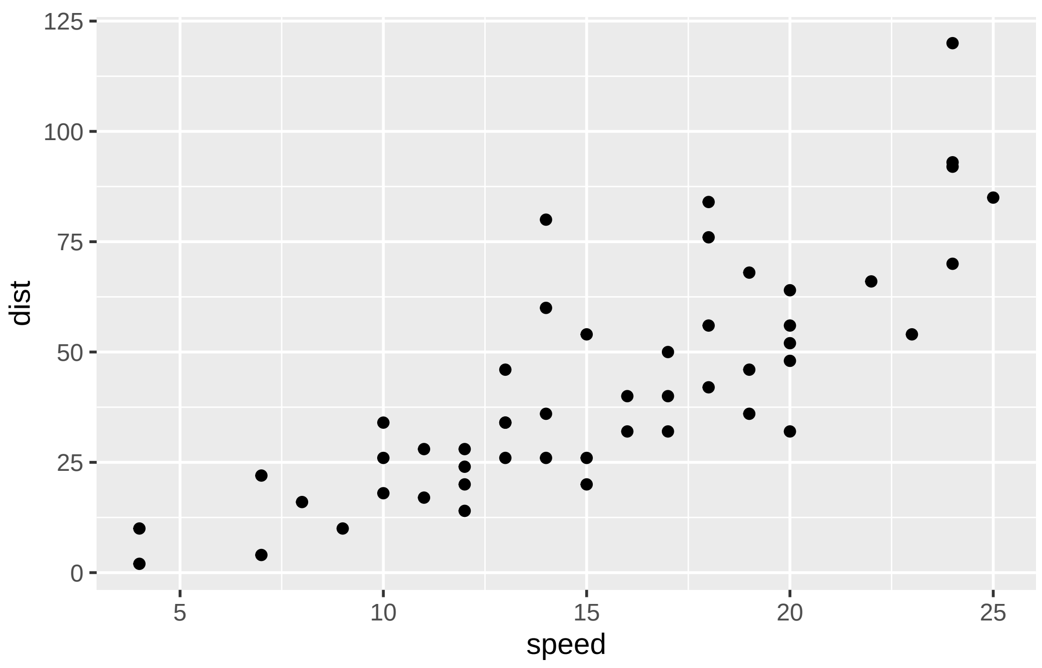
```
library(ggplot2)
ggplot(cars)
```



This did not work because every gg plot is composed of at least 3 layers

- data (i.e a data.frame with the things to plot)
- aesthetics **aes()** that map the columns of the data to your plot feature
- geoms like **geom_point()**

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



Compare base R plot with **ggplot**

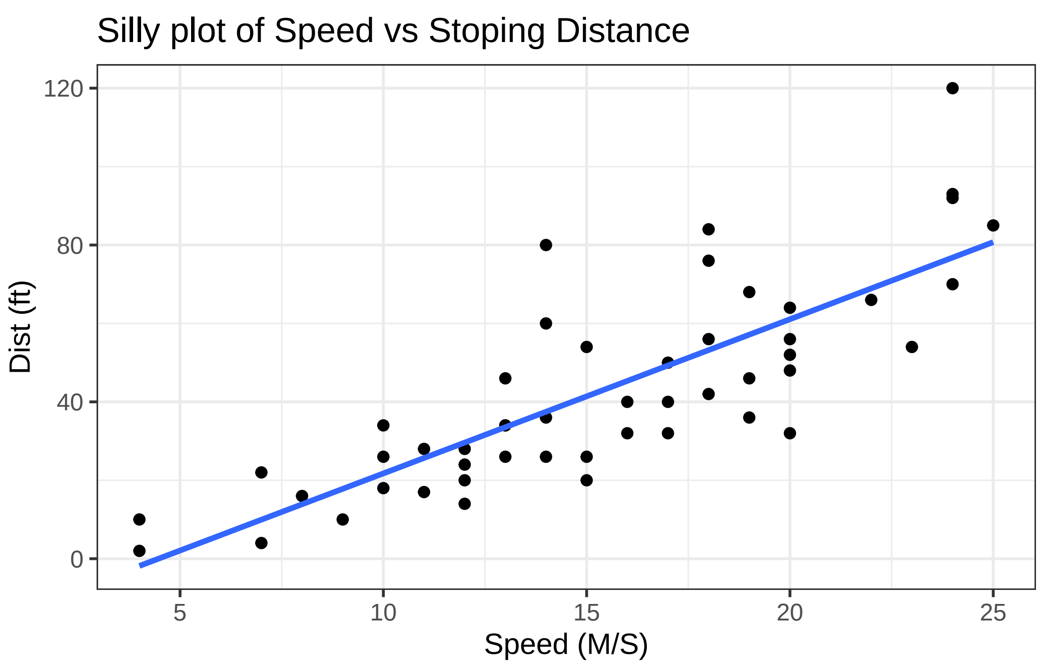
> key-point: For a simple "canned" plot, because R is quicker and more concise to write the code but as things get more customed and elaborate, the *ggplot* wins out.

Let's add more layers to our ggplot.

- Add a line showing the relationship between x and y (se=FALSE takes out the range around the linear fit)
- Add a title
- Add costume labels, x will be Speed (M/S), y will be dist (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 (M/S)",
       y = "Dist (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)
summary(genes)
```

```
     Gene              Condition1         Condition2           State          
 Length:5196        Min.   :-3.6809   Min.   :-3.5921   Length:5196       
 Class :character   1st Qu.:-3.6809   1st Qu.:-3.5921   Class :character  
 Mode  :character   Median :-0.9439   Median :-0.8552   Mode  :character  
                    Mean   : 0.1800   Mean   : 0.2796                     
                    3rd Qu.: 4.0859   3rd Qu.: 4.0437                     
                    Max.   :13.1733   Max.   :12.8731                     
```

```
summary(genes[,"State"] =="up")
```

```
   Mode   FALSE    TRUE 
logical    5069     127 
```

```
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? Anwer: 5196

```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

12. How many "up" regulated genes are there? Answer: 127

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

```
summary(genes[,"State"] =="up")
```

```
   Mode   FALSE    TRUE 
logical    5069     127 
```

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

```
[1] 127
```

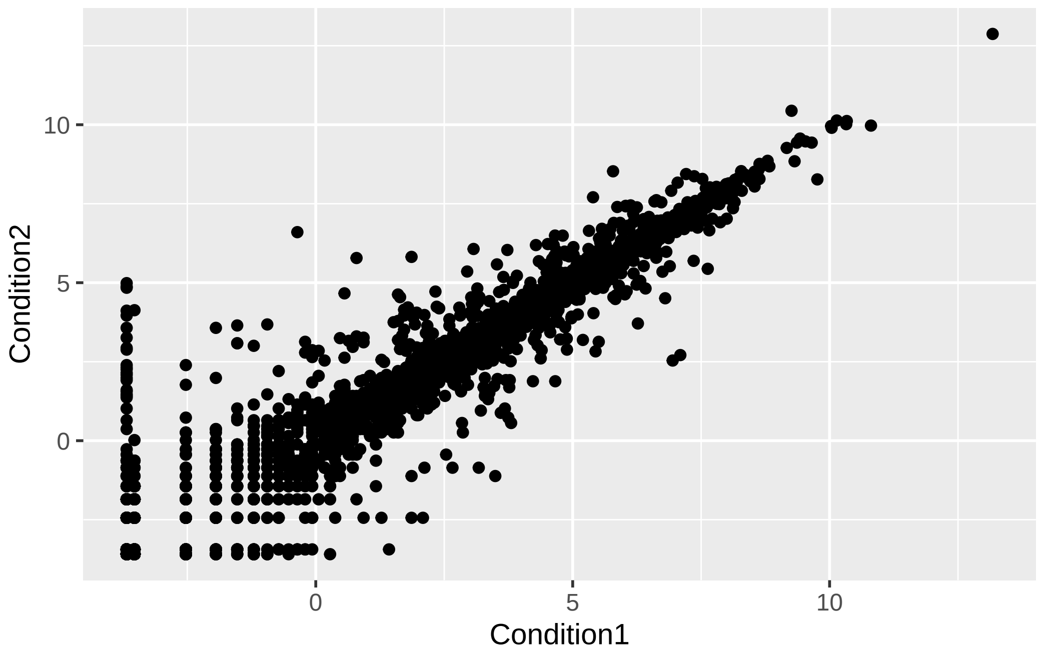
```
#or
table(genes$State)
```

```
      down unchanging         up
        72       4997        127
```

Now we are gonna make the first plot using the gene data.

Make a V1 figure

```r
library(ggplot2)
ggplot(genes)+
  aes(x=Condition1,
      y=Condition2)+
  geom_point()
```

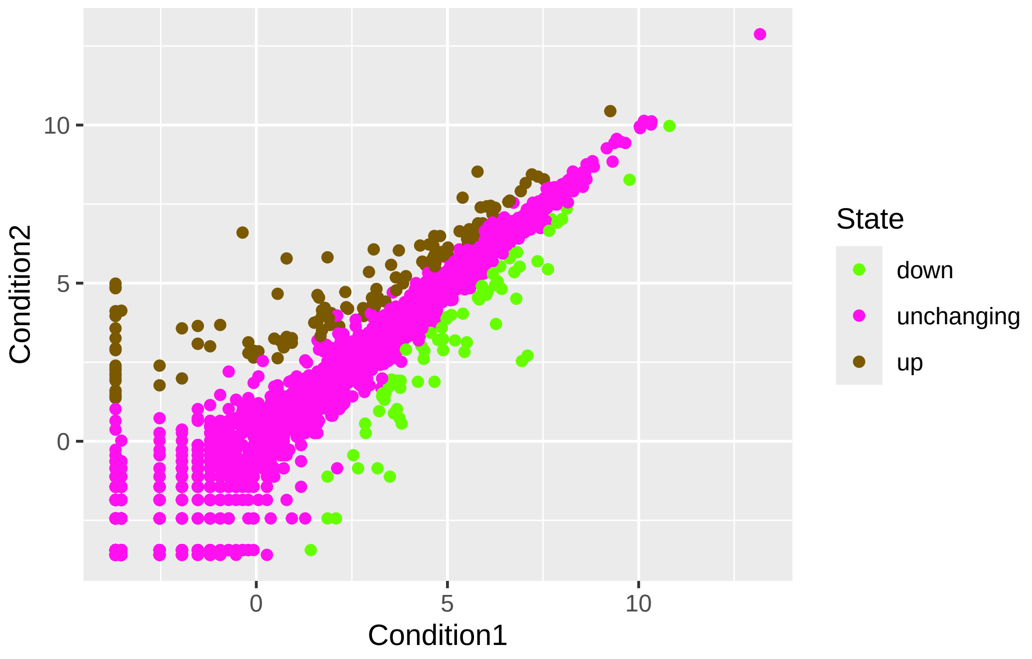


Now add colors to the graph to show up/down regulation

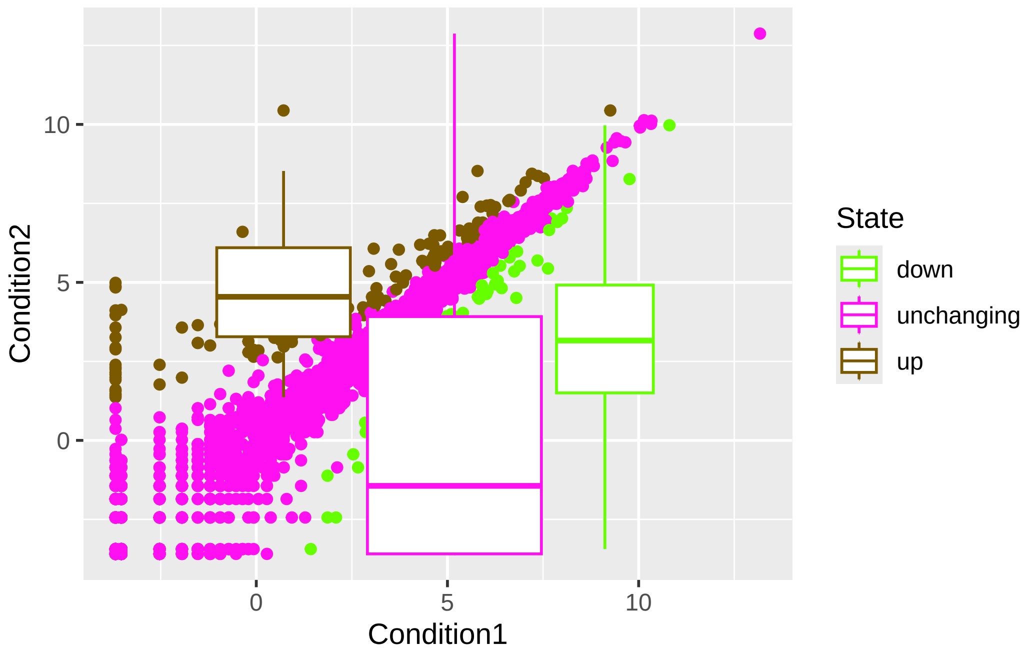
- use `col = variable` in aes() to color based on specific variable
- use `+scale_colour_manual(values = c( "#D79D00","#79797C", "#C5AECF"))` to add additional layer to define custom color scale
- we can also use `p<-` to save as a plot object, and use `p+additional layers` to build on the graph

```r
library(ggplot2)
p <- ggplot(genes)+
  aes(x=Condition1,
      y=Condition2,
      col = State)+
  scale_colour_manual(values = c( "#66ff00","#FF10F0", "#7A5901"))+
  geom_point()

p
```



```r
p +
  geom_boxplot()
```



Going Further

First, read the *gapminder* dataset

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

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

Now 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
```

```r
summary(gapminder)
```

```
   country           continent              year         lifeExp     
 Length:1704        Length:1704        Min.   :1952   Min.   :23.60  
 Class :character   Class :character   1st Qu.:1966   1st Qu.:48.20  
 Mode  :character   Mode  :character   Median :1980   Median :60.71  
                                       Mean   :1980   Mean   :59.47  
                                       3rd Qu.:1993   3rd Qu.:70.85  
                                       Max.   :2007   Max.   :82.60  
      pop              gdpPercap       
 Min.   :6.001e+04   Min.   :   241.2  
 1st Qu.:2.794e+06   1st Qu.:  1202.1  
 Median :7.024e+06   Median :  3531.8  
 Mean   :2.960e+07   Mean   :  7215.3  
 3rd Qu.:1.959e+07   3rd Qu.:  9325.5  
 Max.   :1.319e+09   Max.   :113523.1  
```

Q4. How many countries are in this dataset? Answer:142

```r
#Recall for
x <- c(1:5)
x
```

```
[1] 1 2 3 4 5
```

```r
#we can use
length(x)
```

```
[1] 5
```

```r
# this tells us how many elements are in X
length(table(gapminder$country))
```

```
[1] 142
```

```r
#or
length(unique(gapminder[,"country"]))
```

```
[1] 142
```

Q5. How many continents are in this dataset? Answer: 5

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

```

  Africa Americas     Asia   Europe  Oceania 
     624      300      396      360       24 
```

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

```
[1] 5
```

```r
#or
unique(gapminder[,"continent"])
```

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

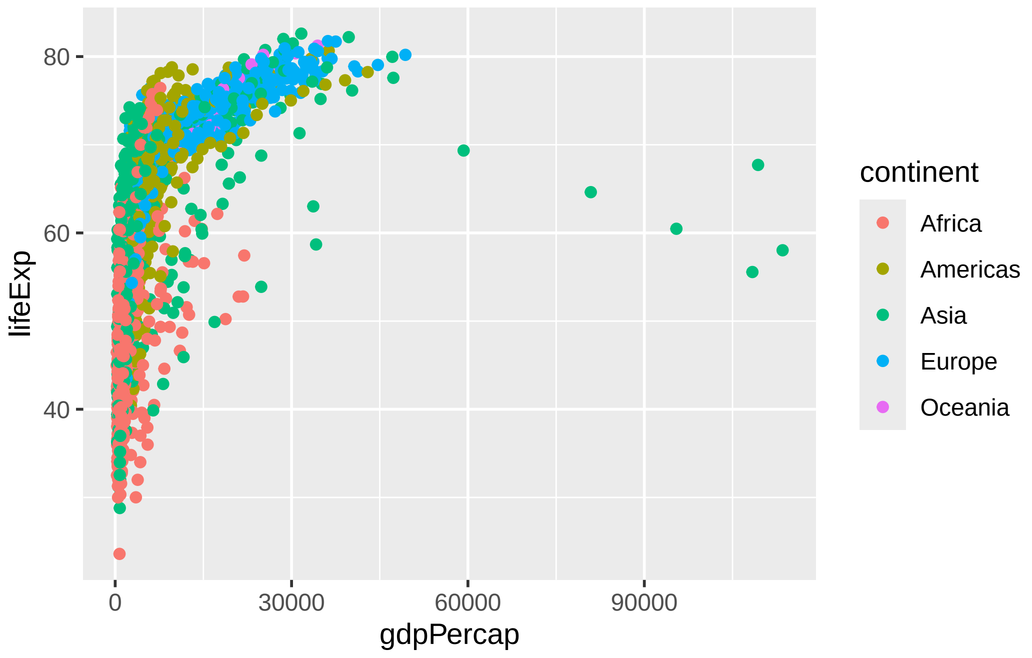
```r
length(unique(gapminder[,"continent"]))
```

```
[1] 5
```

Now we make a plot study the relationship between life expectancy and GDP

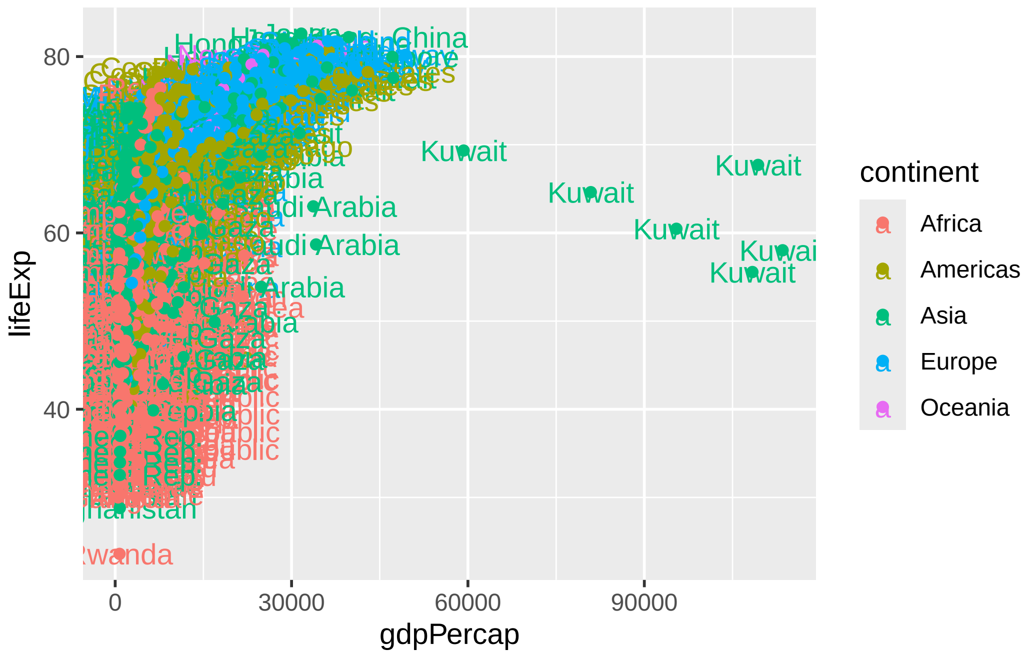
Make a v1 plot:

```r
ggplot(gapminder)+
  aes(x = gdpPercap, y = lifeExp, color = continent)+
  geom_point()
```



Make a v2 plot:

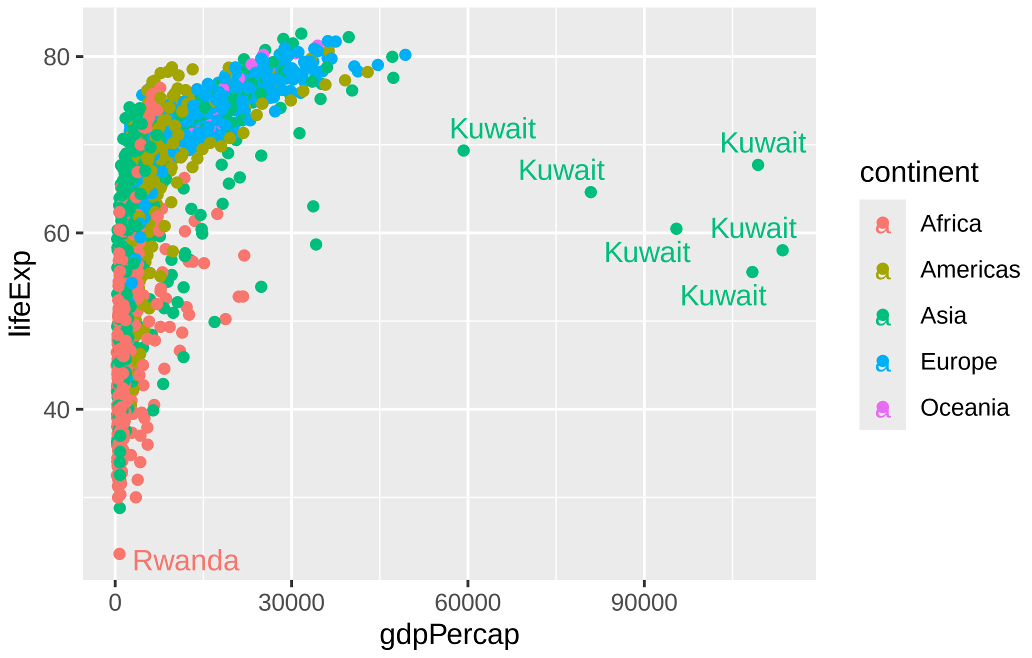
```
ggplot(gapminder)+
  aes(x = gdpPercap, y = lifeExp, color = continent,label = country)+
  geom_text()+
  geom_point()
```



we can use a package to adjust the labels: `ggrepl`, this will help us make more sensible, easier-to-read labels

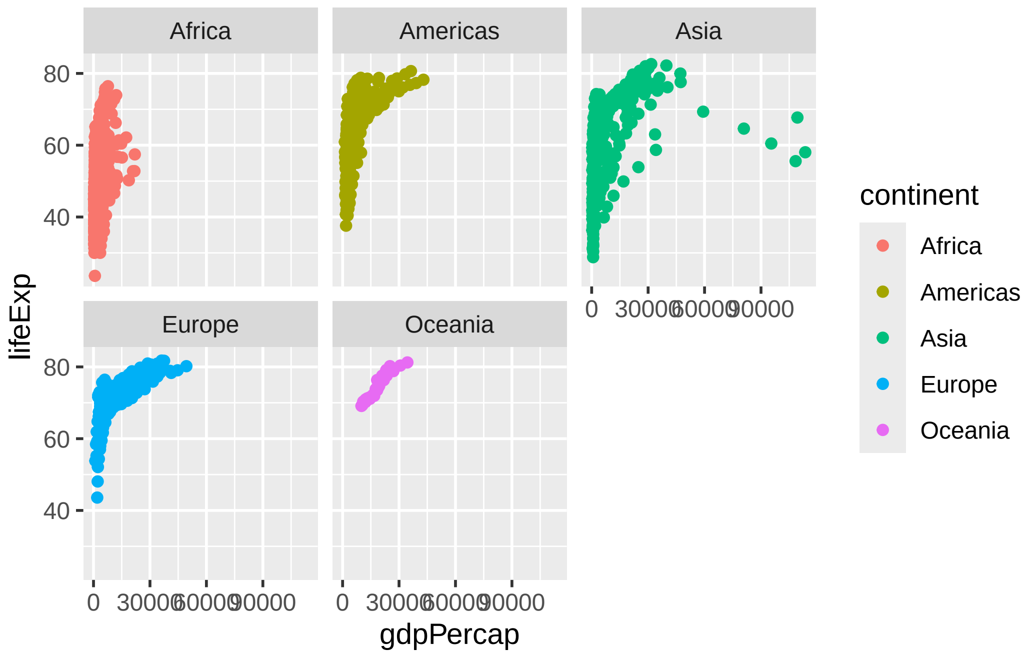
```
library(ggrepel)
ggplot(gapminder)+
  aes(x = gdpPercap, y = lifeExp, color = continent,label = country)+
  geom_point()+
  geom_text_repel()
```

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



Now we want to make this plot multi-paneled by continent

```r
ggplot(gapminder)+
  aes(x = gdpPercap, y = lifeExp, color = continent)+
  geom_point()+
  facet_wrap(~continent)
```



Summary: What are the advantages of ggplot over base R plot?

ggplot2 offers several advantages over base R plot:

- It produces more visually appealing, publication-quality figures with sensible defaults, making it easier to create beautiful and complex plots quickly [1], [3], [2], [5].
- Plots are built using a consistent, layered grammar (data, aesthetics, geometry), which makes code more readable and modular [1], [3], [5].
- Customizing and refining plots is easier and less "fiddly" than with base R, which often requires many arguments and manual adjustments [1], [3], [2].
- ggplot2 enables declarative specification of plots, mapping data to visual features in a clear way [1], [3].
- Adding layers (e.g., points, lines, labels) and combining plots is straightforward, while base R often requires more complex code for advanced visualizations [1], [3], [5].
- ggplot2 is widely used and supported, with extensive documentation and community resources [1], [3], [2].

What aspect of ggplot2 are you most interested in using?