Lab 5: Data Visualization with ggplot

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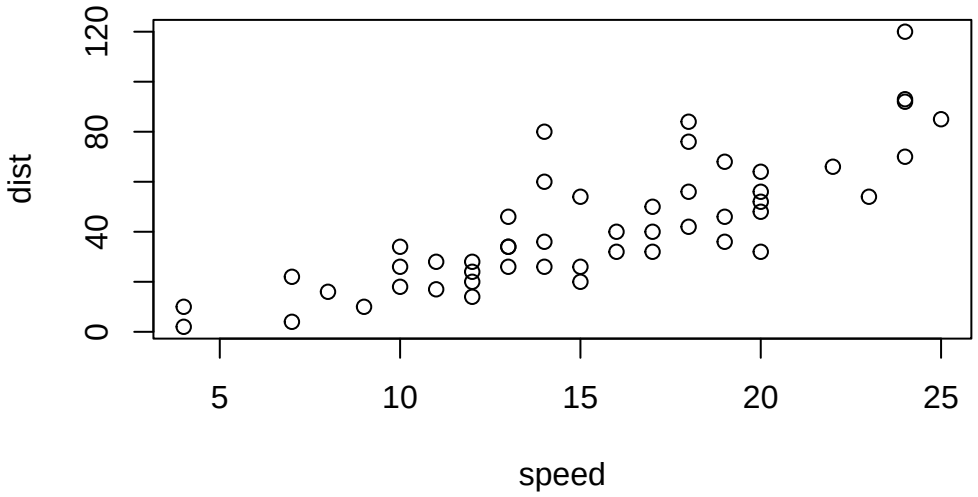
Today we will have fun with the **ggplot2** package - a popular data visualization package.

Other plotting systems in R include so-called *"base"* plotting/graphics.

```
plot(cars)
```



Base plot is generally rather short code and somewhat dull plots - but it is always there for you and is fast for big data sets.

Example 1: A basic scatter plot

Using **ggplot2** takes some more work

```
## ggplot(cars)
```

Writing `ggplot(cars)` will not work. I need to install the package first to my computer. To do this I can use the function `install.packages("ggplot2")` in the console.

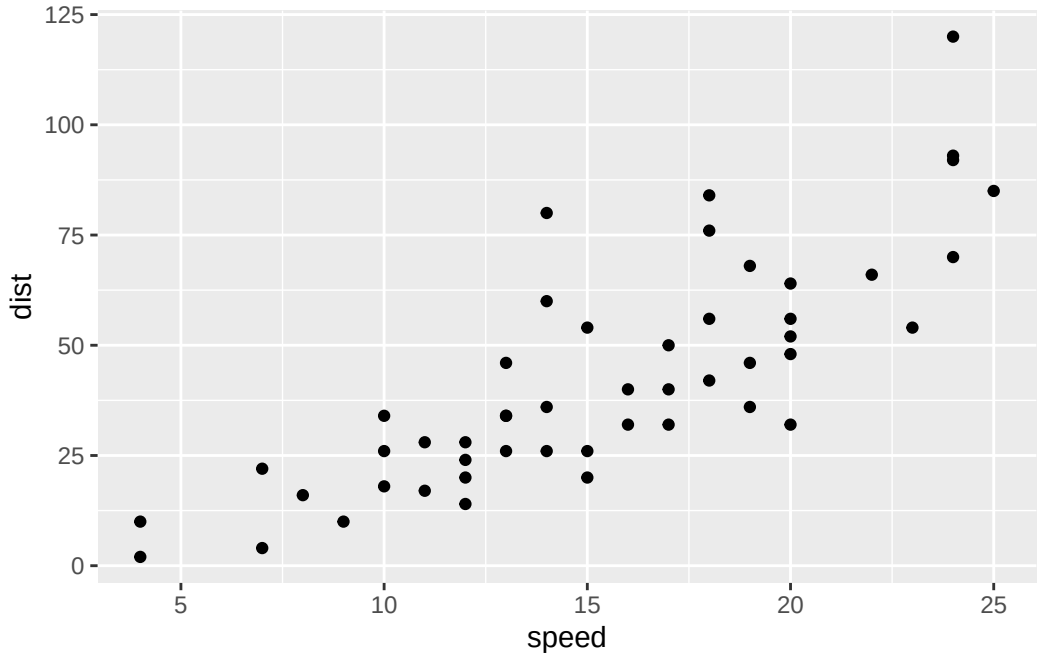
Then I will need to load the package I want to use with `library()` call.

```
## install.packages("ggplot2")
library(ggplot2)
```

Now to make my plot and use ggplot:

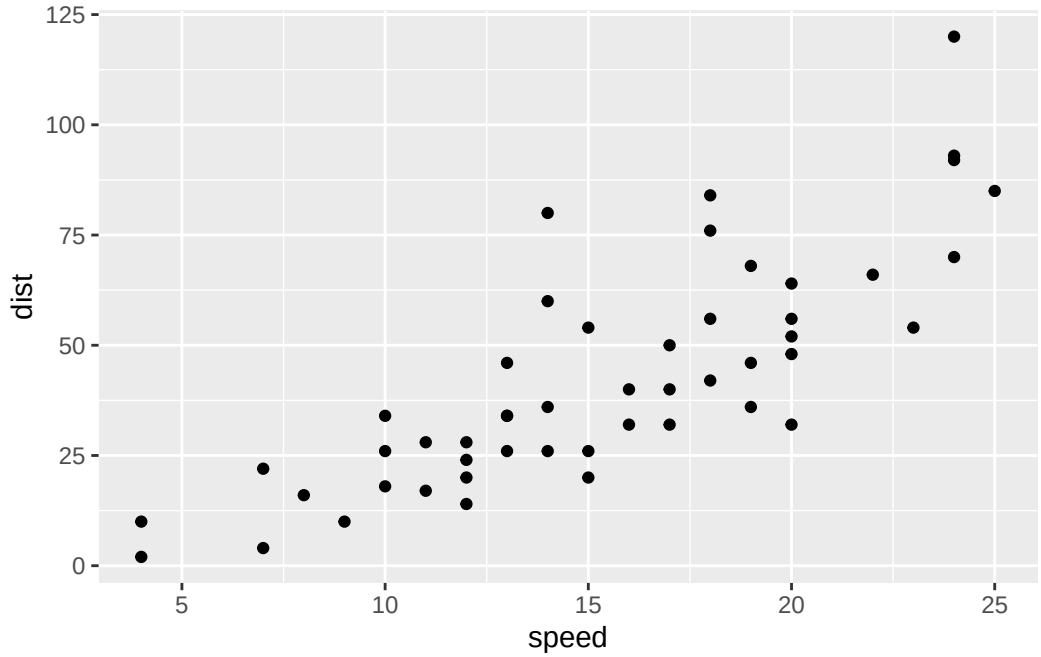
- I first must initialize the data set in ggplot using `ggplot()`.
- Using the + operator I can then add layers to the plot with `aes()` to map the dimensions of the data set to the plot aesthetics.
- Finally, `geom_point()` will plot a dot plot.

```
ggplot(cars) +
  aes(speed, dist) +
  geom_point()
```



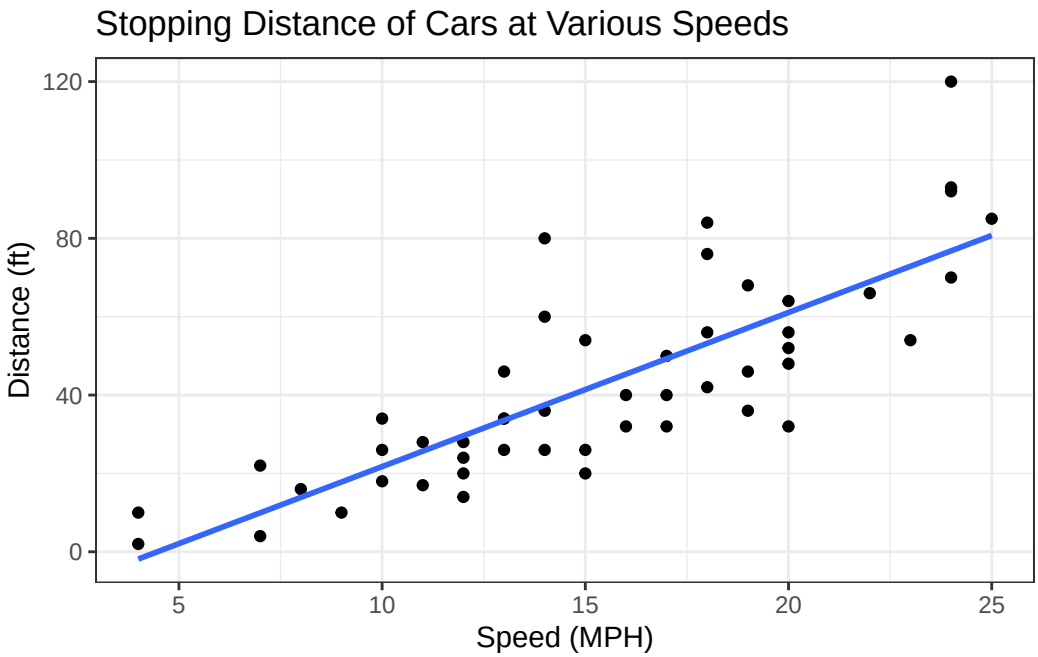
To add more layers, you can save the plot to an object and use it in later code chunks.

```
bp <- ggplot(cars) +
  aes(speed, dist) +
  geom_point()

bp
```




```
  bp + geom_smooth(method="lm", se=F) +
    theme_bw() +
    labs(title="Stopping Distance of Cars at Various Speeds", x = "Speed (MPH)",
         y="Distance (ft)")
```

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



Example 2: Getting more complicated

Now for a more realistic data set.

```
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
```

Some information about the dataset:

```
nrow(genes)
```

```
[1] 5196
```

```
ncol(genes)
```

```
[1] 4
```

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

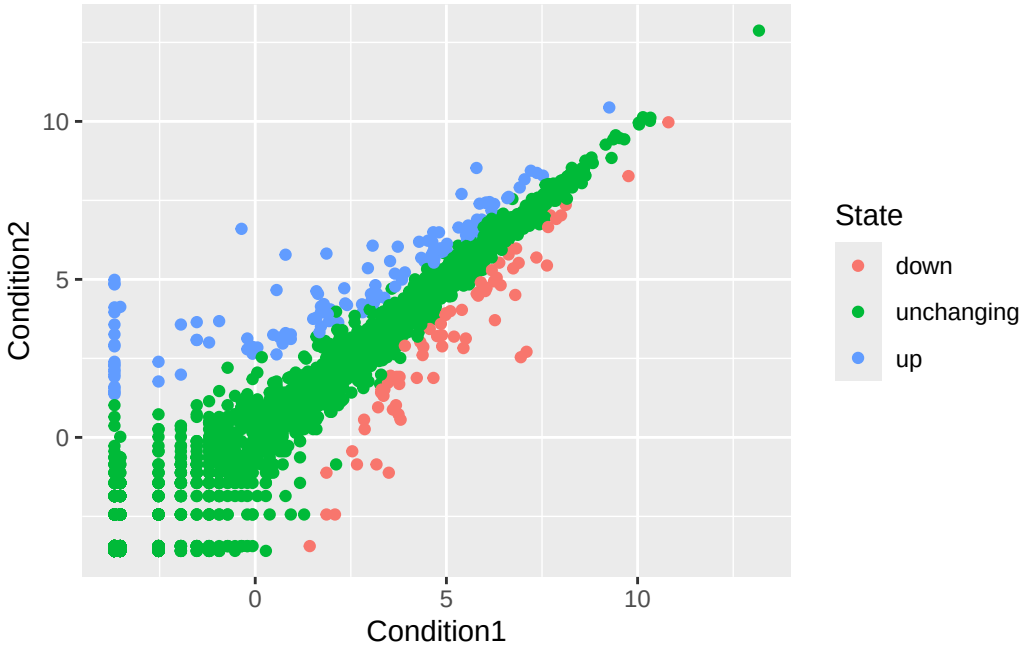
```
      down unchanging         up
        72       4997        127
```

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

```
      down unchanging         up
      1.39      96.17       2.44
```

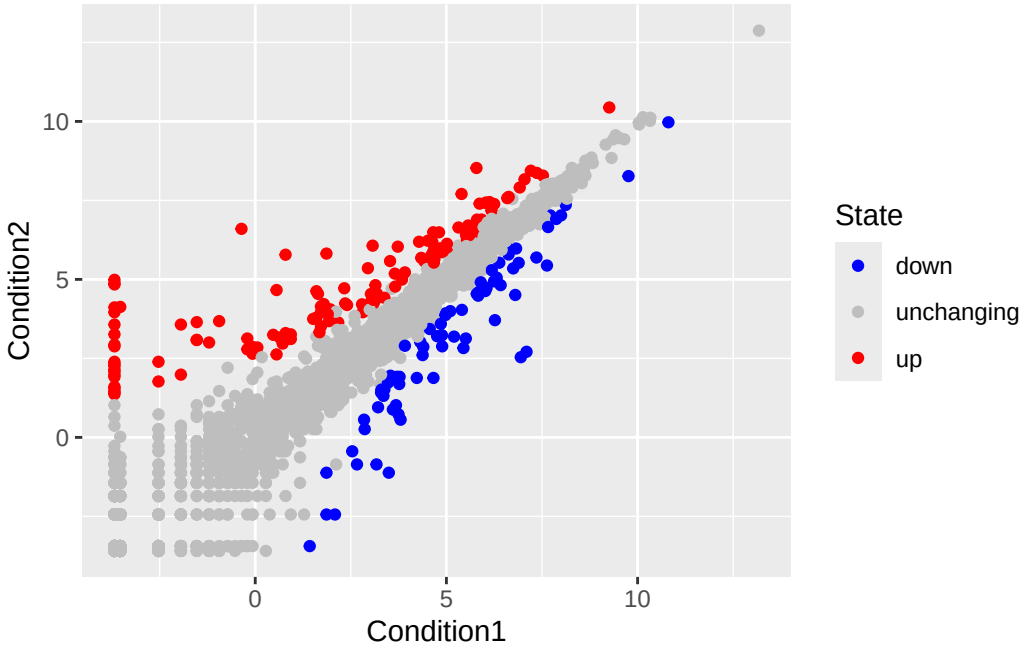
Plotting the data set

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

p
```



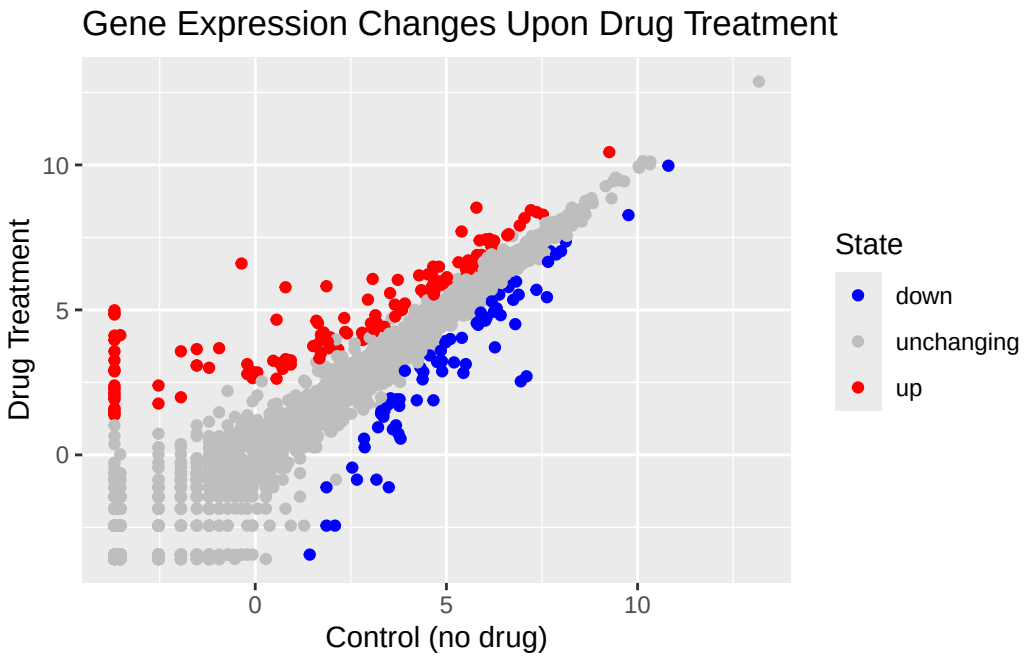
Now to adjust the color palette manually use `scale_color_manual()`

```
p <- p + scale_color_manual(values=c("blue","gray", "red"))

p
```



Adjusting the plot labels:

```
p <- p + labs(title="Gene Expression Changes Upon Drug Treatment",
              x="Control (no drug)",
              y="Drug Treatment")
p
```



Going Further: Optional Sections

Load in data set about economics and demographics about 142 countries across many years.
We focus on 2007 data only.

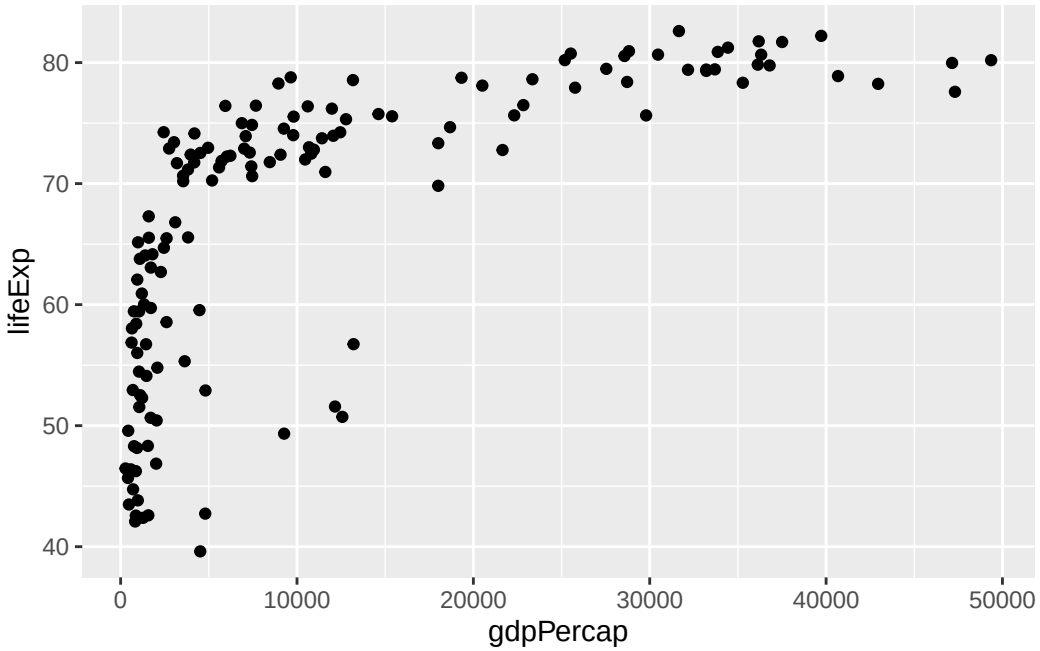
```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.

gapminder <- read.delim(url)

library(dplyr)
```

```
Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

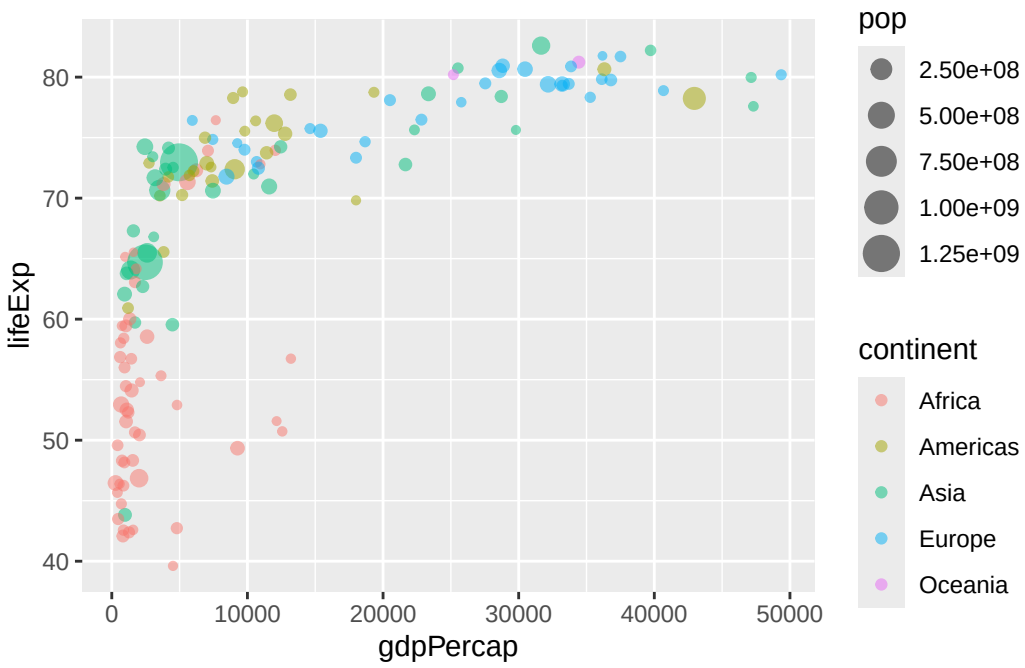
Create scatter plot mapping GDP to the average life expectancy of the countries.

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point()
```

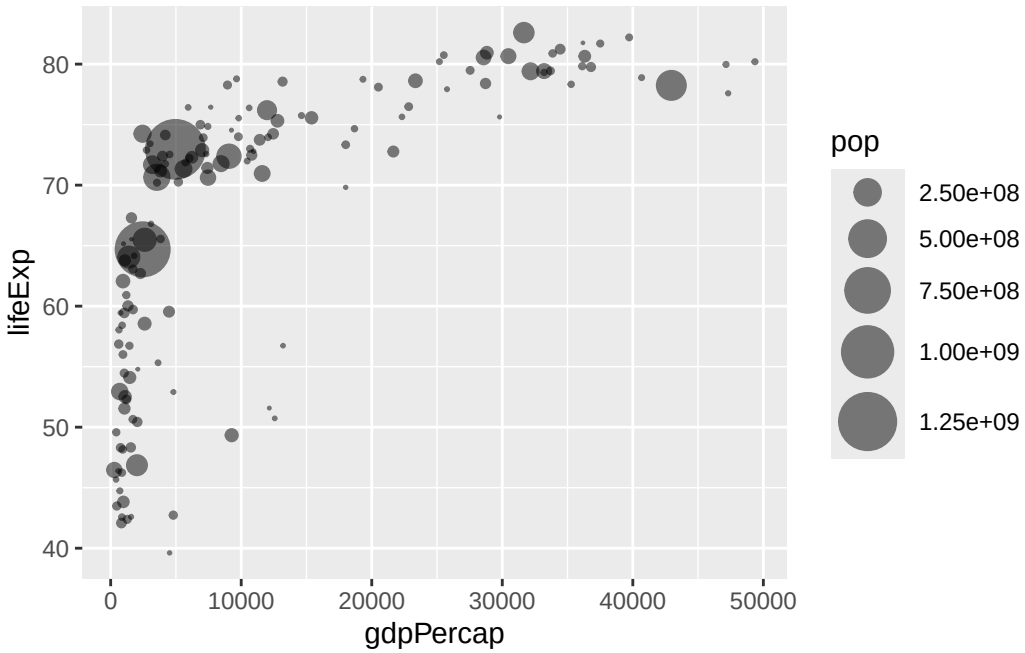


Adding more variables to aesthetics. We can distinguish the continents of the countries and add a size variable to the dot sizes to indicate population.

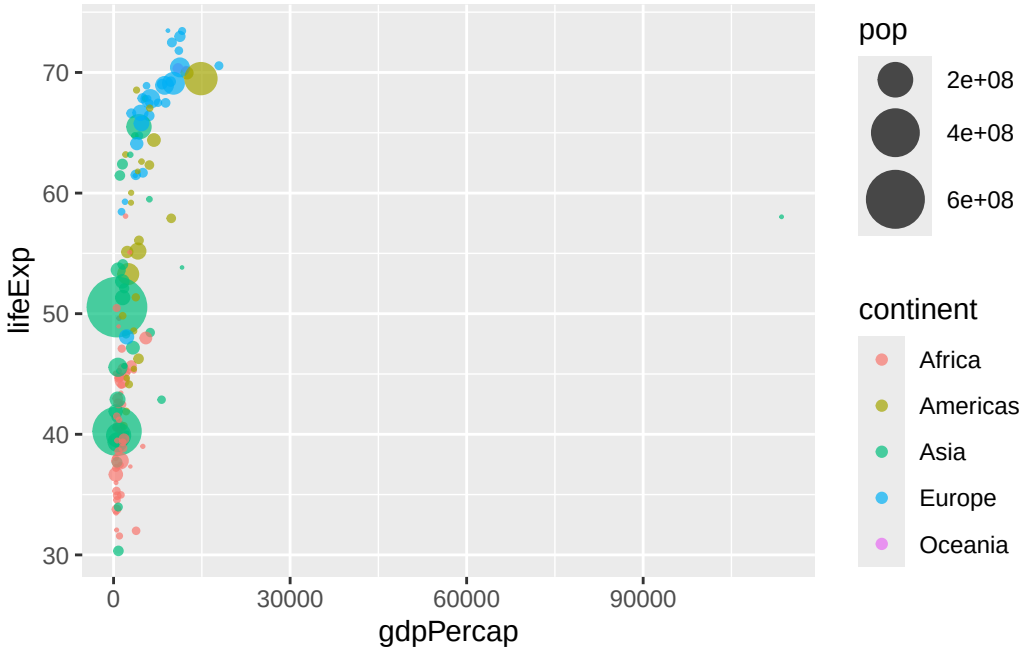
```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```



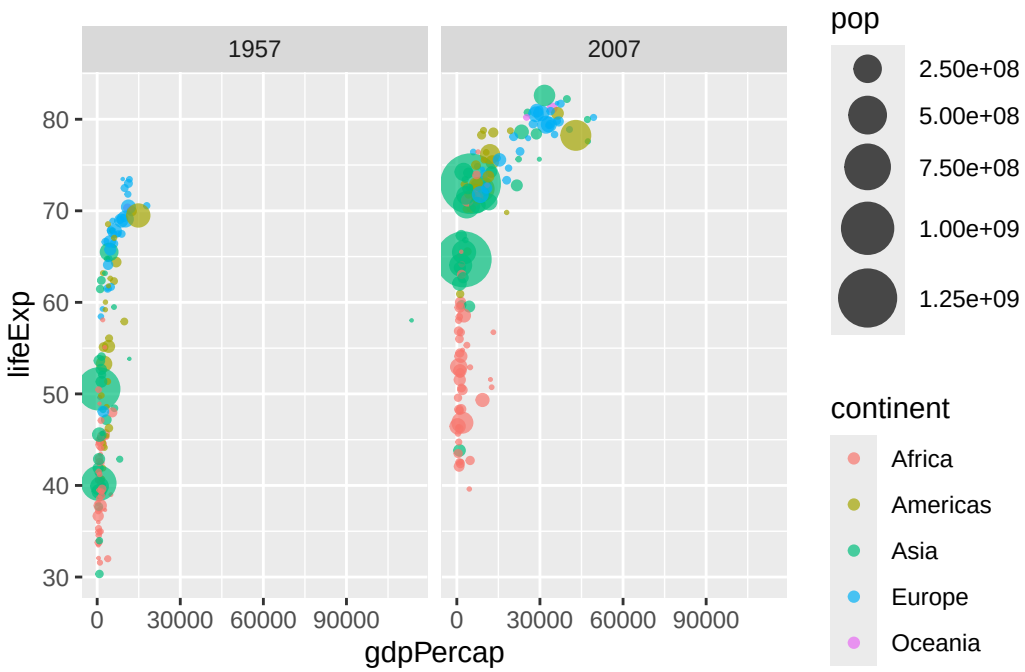

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, size=pop) +
  geom_point(alpha=0.5) +
  scale_size_area(max_size = 10)
```




```
gapminder_1957 <- gapminder %>% filter(year==1957)

ggplot(gapminder_1957) +
  aes(x=gdpPercap, y=lifeExp, size=pop, color=continent) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size=10)
```




```
gapminder_1957_2007 <- gapminder %>% filter(year==1957 | year == 2007)

ggplot(gapminder_1957_2007) +
  aes(x=gdpPercap, y=lifeExp, size=pop, color=continent) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size=10) +
  facet_wrap(~year)
```


1957
2007
lifeExp
80
70
60
50
40
30
0
30000
60000
90000
gdpPercap
pop
2.50e+08
5.00e+08
7.50e+08
1.00e+09
1.25e+09
continent
Africa
Americas
Asia
Europe
Oceania