Class05: Data Vis with ggplot

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Graphics systems in R

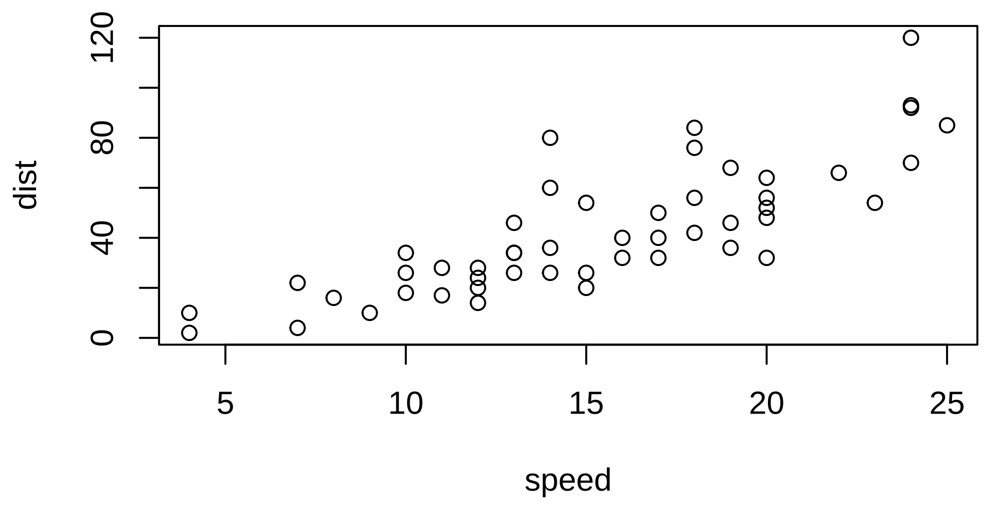
There are many graphics systems in R for making plots and figures.

We have already played a little with **"base R"** graphics and the `plot()` function

Today we will start learning about a popular graphics package called `ggplot2()`

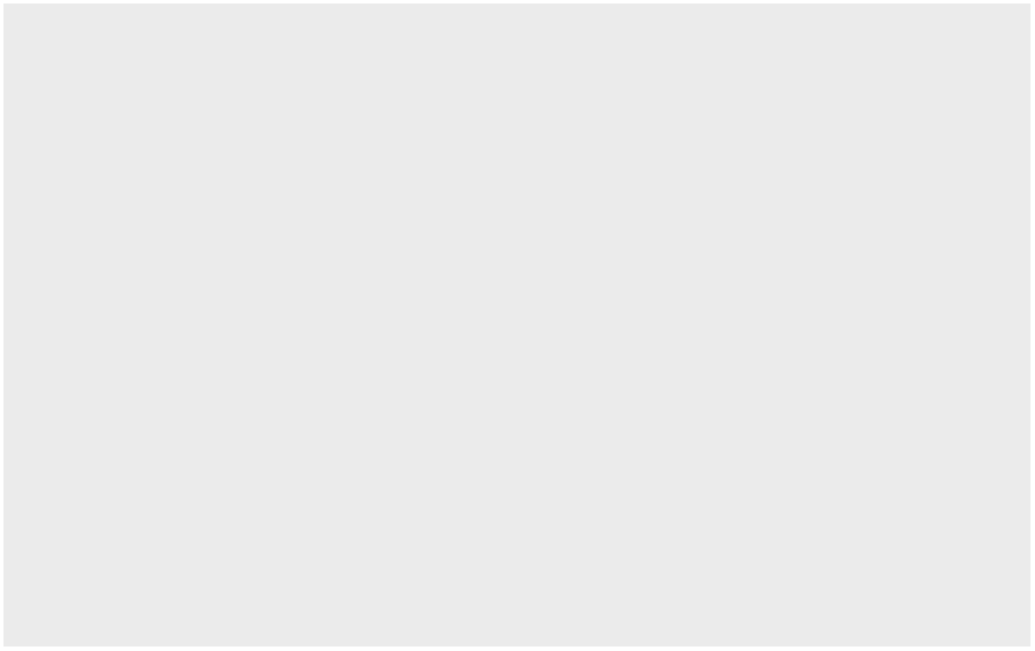
This is an add on package - i.e. we need to install it. I install it (like I install any package) with the `install.packages()` function.

```
plot(cars)
```



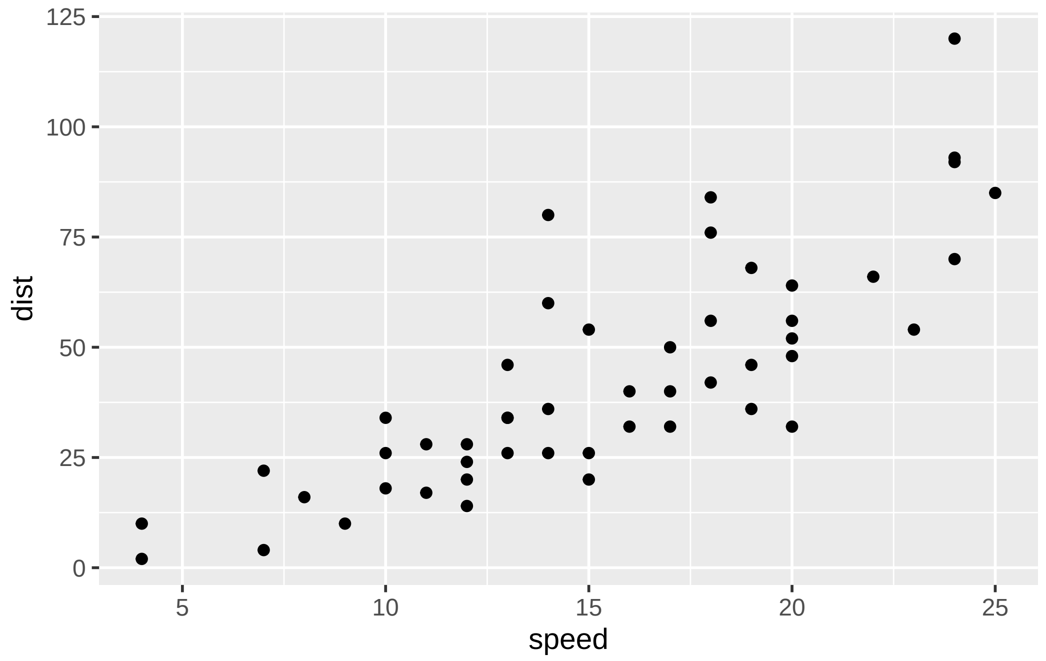
Before I can use the functions frmo a apackage I have to load up the package from my "library". We use the `library(ggplot2)` command to load it up.

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



Every ggplot is made up of at least 3 things: - data (the numbers etc. that will go into your plot) - aes (how the columns of data map to the plot aesthetics) - geoms (how the plot actually looks, points, bars, lines, etc.)

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

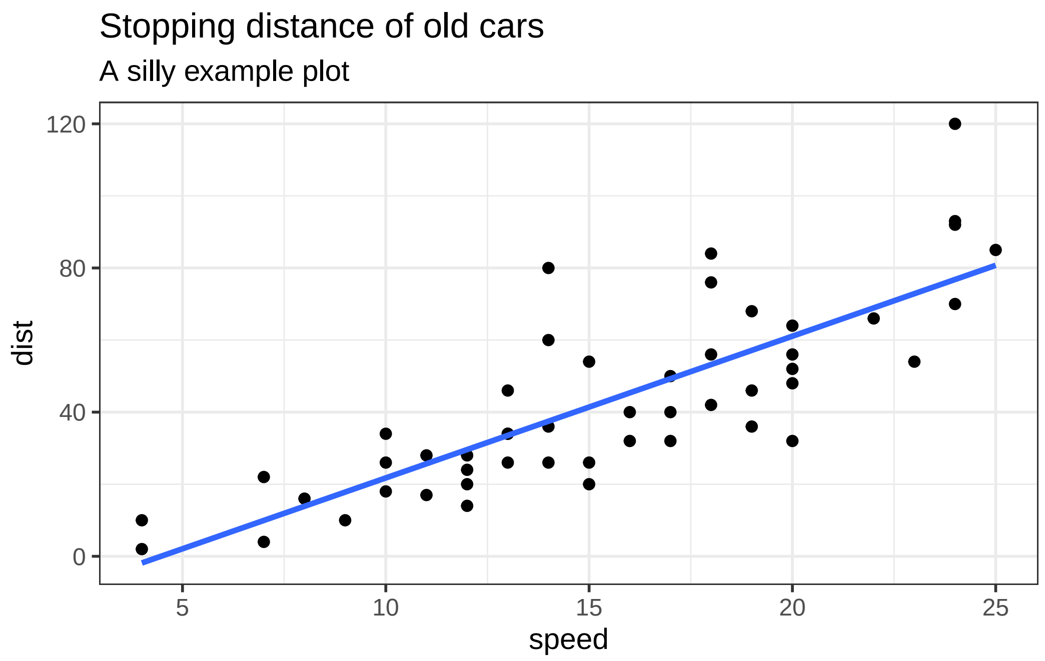


For simple plots ggplot is more verbose - it takes more code - than base R plots.

Add some layers to our ggplot.

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  labs(title="Stopping distance of old cars",
       subtitle="A silly example plot") +
  theme_bw()
```

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



The code below reads the results of a differential expression analysis where a new anti-viral drug is being tested. (lines 63-64)

Use the table() function on the State column of this data.frame to find out how many 'up' regulated genes there are. (line 69)

Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset? (line 70)

```
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
```

```
nrow(genes)
```

```
[1] 5196
```

```
colnames(genes)
```

```
[1] "Gene"       "Condition1" "Condition2" "State"
```

```
ncol(genes)
```

```
[1] 4
```

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

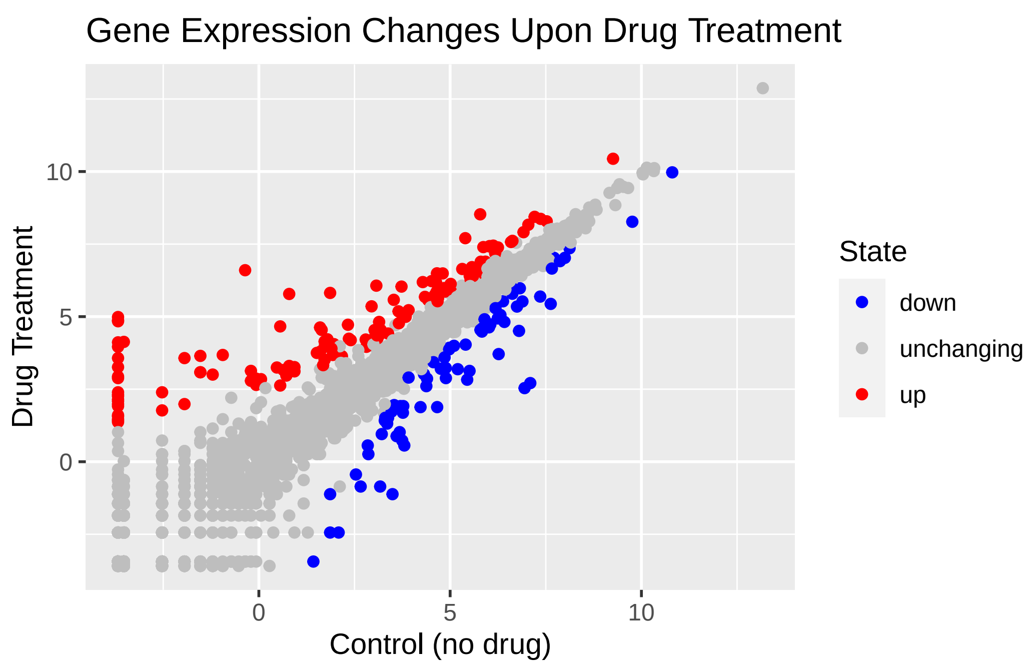
```

      down unchanging         up 
        72       4997        127 
```

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

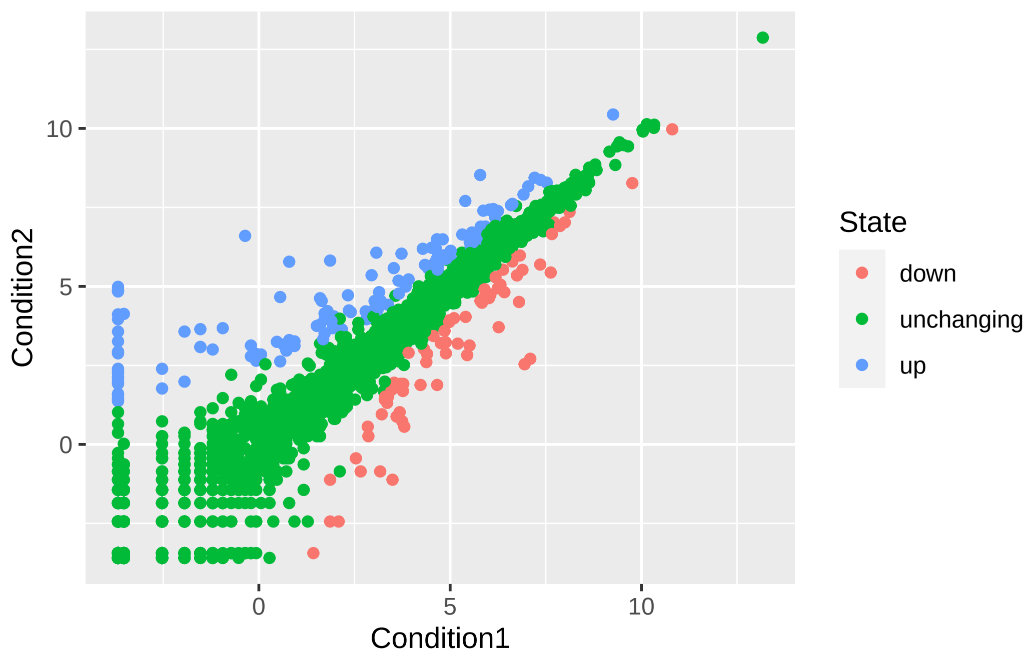
```

      down unchanging         up 
      1.39      96.17       2.44 
```

Make a scatterplot of genes

```
p <- ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
p + scale_color_manual(values=c("blue", "gray", "red")) +
  labs(title="Gene Expression Changes Upon Drug Treatment", x="Control (no drug)", y="Drug
```


Gene Expression Changes Upon Drug Treatment
Drug Treatment
Control (no drug)
0
5
10
State
down
unchanging
up

```
p
```


Condition2
Condition1
0
5
10
State
down
unchanging
up

Install and access gapminder dataset.

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

This dataset covers many years and many countries. Before we make some plots we will use some dplyr code to focus in on a single year. You can install the dplyr package with the command install.packages("dplyr").

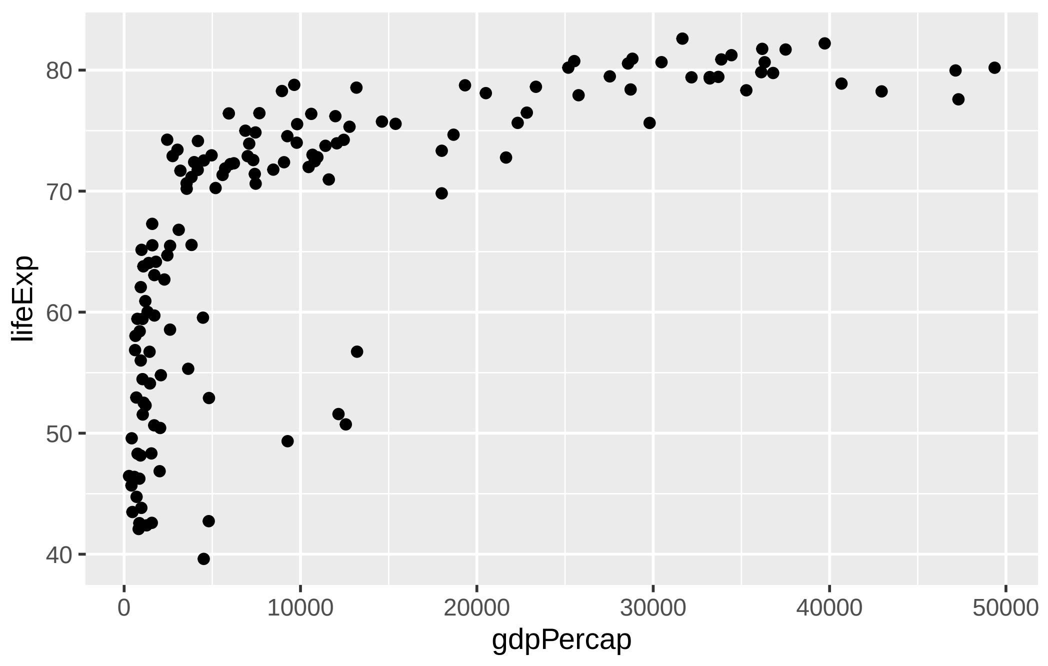
```
#install.packages("dplyr")
library(dplyr)
```

```


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)
```

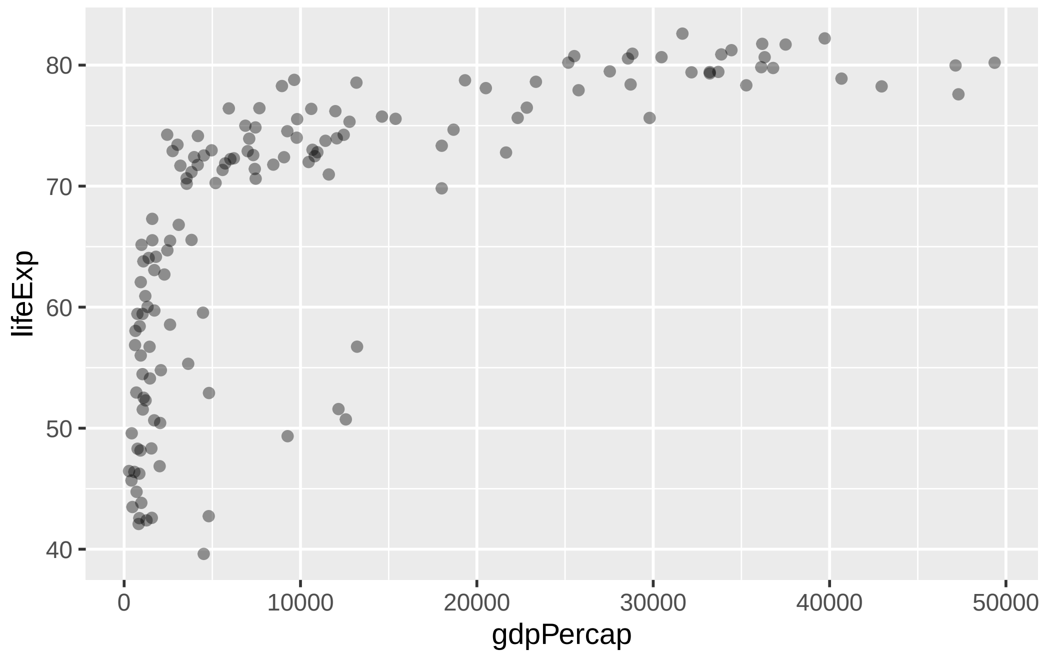
Q. Complete the code below to produce a first basic scater plot of this gapminder_2007 dataset

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



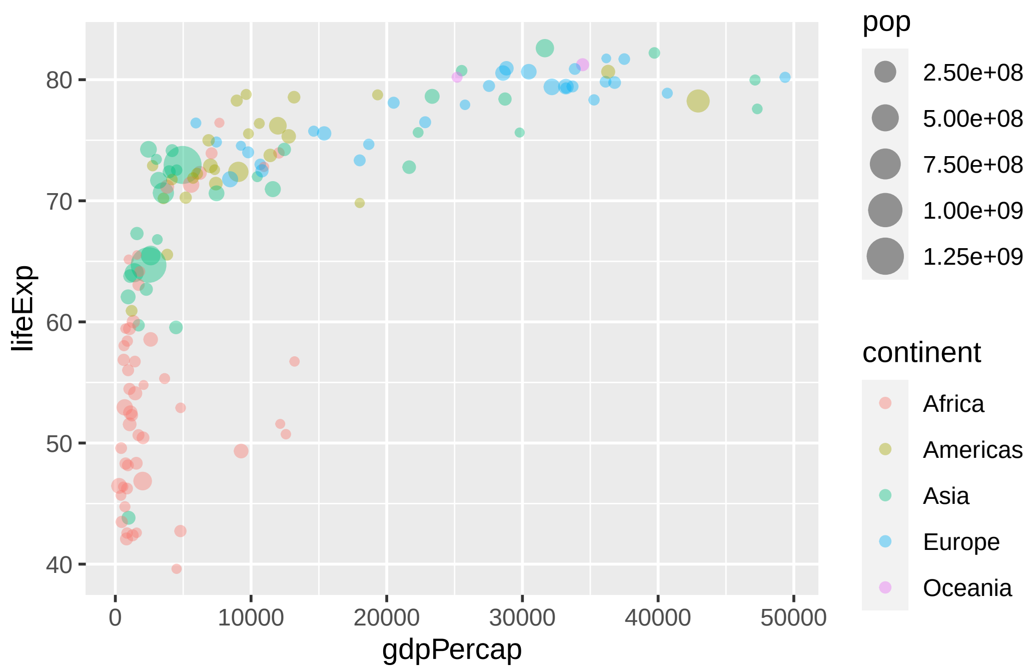
There are quite a few points that are nearly on top of each other in the above plot. One useful approach here is to add an alpha=0.4 argument to your geom_point() call to make the points slightly transparent. This will help us see things a little more clearly later on.

```
gdpAndLife <- ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.4)
gdpAndLife
```



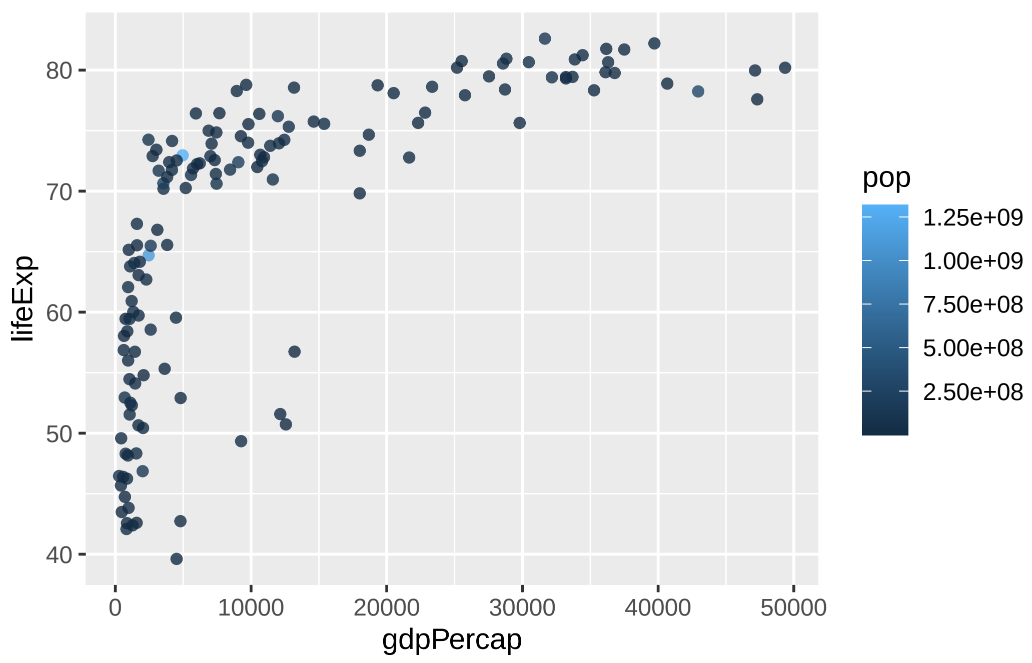
By mapping the continent variable to the point color aesthetic and the population pop (in millions) through the point size argument to aes() we can obtain a much richer plot that now includes 4 different variables from the data set:

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.4)
```



By contrast, let's see how the plot looks like if we color the points by the numeric variable population pop:

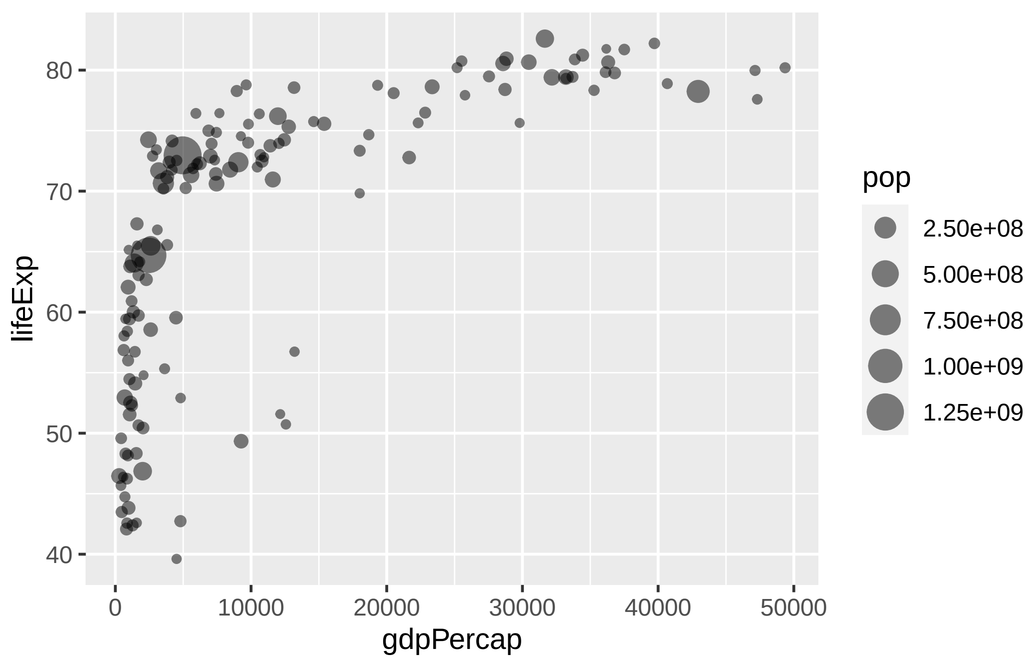
```
ggplot(gapminder_2007) +
  aes(x = gdpPercap, y = lifeExp, color = pop) +
  geom_point(alpha=0.8)
```



The scale immediately changes to continuous as can be seen in the legend and the light-blue points are now the countries with the highest population number (China and India).

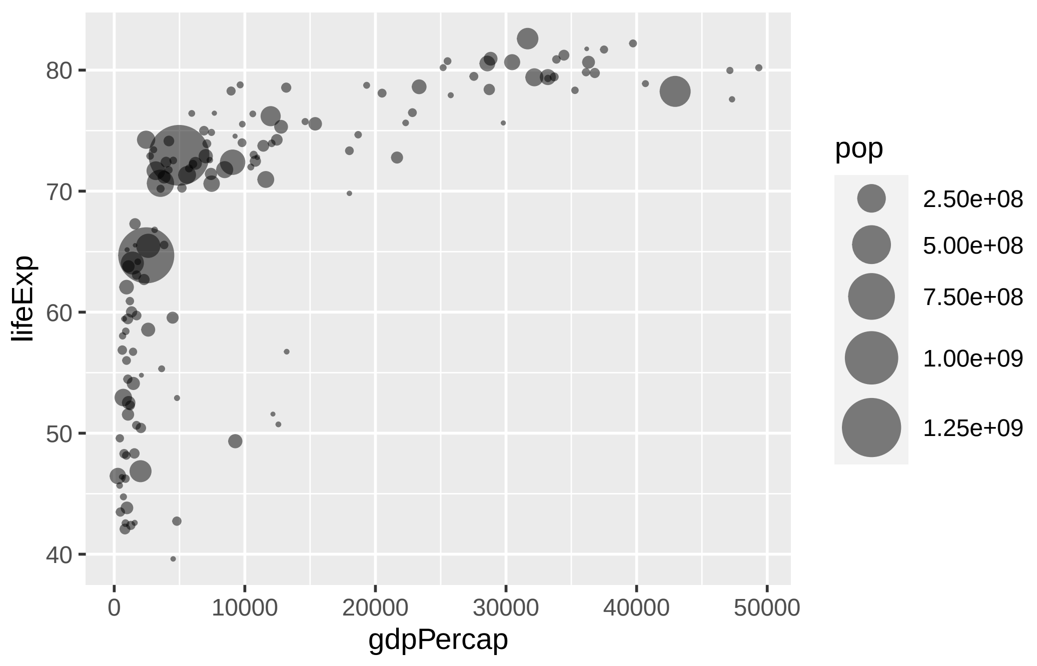
For the gapminder_2007 dataset we can plot the GDP per capita (x=gdpPercap) vs. the life expectancy (y=lifeExp) and set the point size based on the population (size=pop) of each country we can use:

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



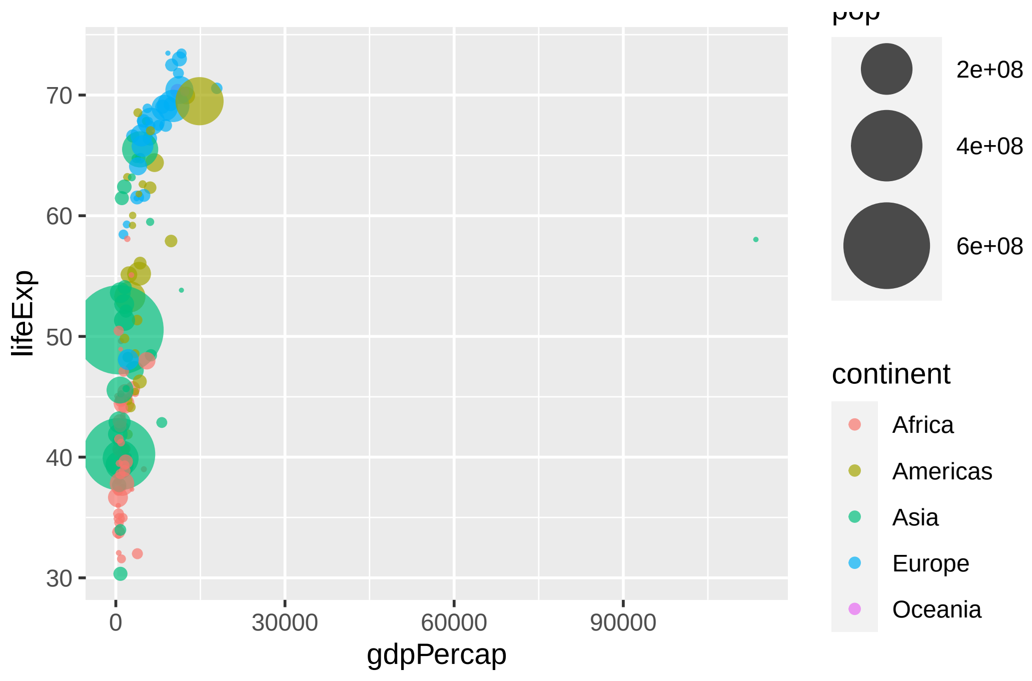
If we compare the point size representing a population of 250 million people with the one displaying 750 million, we can see, that their sizes are not proportional. Instead, the point sizes are binned by default. To reflect the actual population differences by the point size we can use the scale_size_area() function instead. The scaling information can be added like any other ggplot object with the + operator:

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



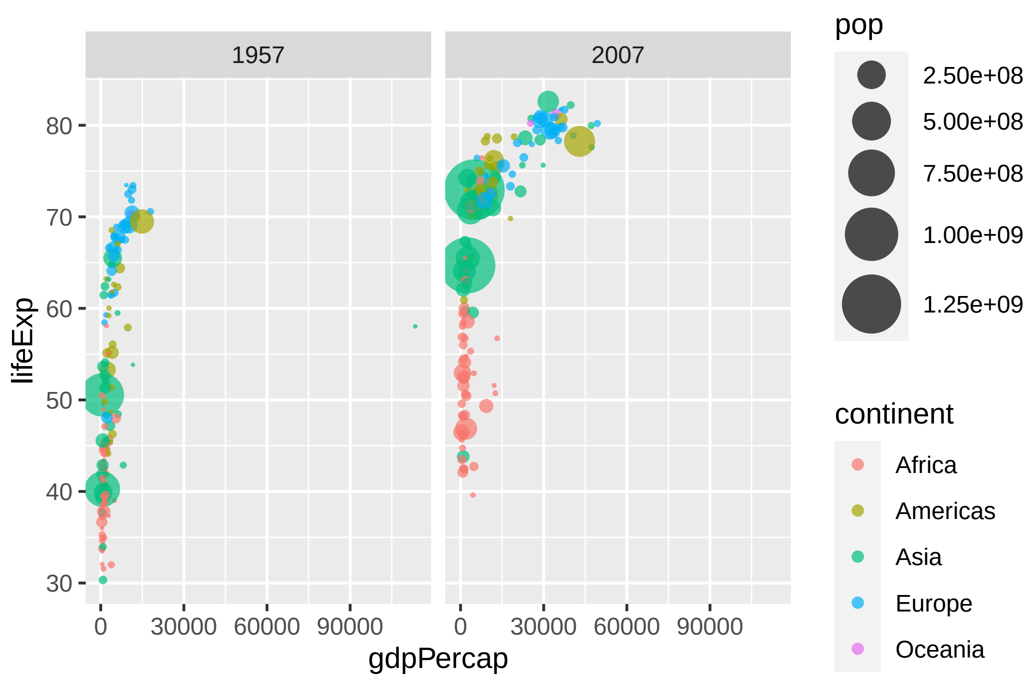
Q. Can you adapt the code you have learned thus far to reproduce our gapminder scatter plot for the year 1957? What do you notice about this plot is it easy to compare with the one for 2007?

```
gapminder_1957 <- gapminder %>% filter(year==1957)
ggplot(gapminder_1957) +
  geom_point(aes(x=gdpPercap, y=lifeExp, color=continent, size=pop), alpha=0.7) +
  scale_size_area(max_size = 15)
```



Do the same steps above but include 1957 and 2007 in your input dataset for ggplot(). You should now include the layer facet_wrap(~year) to produce the following plot:

```
gapminder_1957 <- gapminder %>% filter(year==1957 | year==2007)

ggplot(gapminder_1957) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,
                 size = pop), 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