Class 5: Data Visualization

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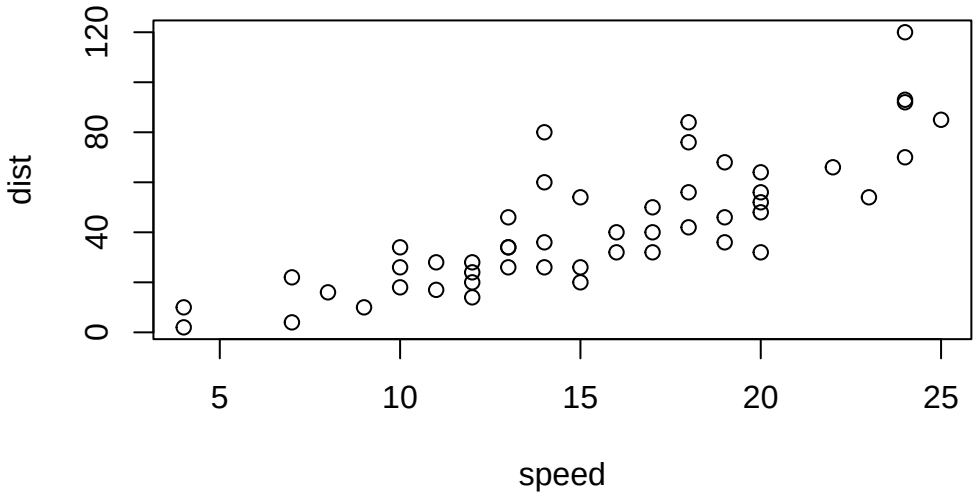
Plotting in R

R has multiple plotting and graphics systems. The most popular of which is **ggplot2**.

We have already played with "base" R graphics. This comes along with R "out of the box".

```
plot(cars)
```



Compared to base R plots ggplot is much more verbose - I need to write more code to get simple plots like the one above.

To use ggplot I need to first install the ggplot2 package. To install any package in R I use the `install.packages()` command along with the package name.

The install is a one time only requirement. The package is now on our computer. I don't need to re-install it.

However, I can't just use it without loading it up with a `library()` call.

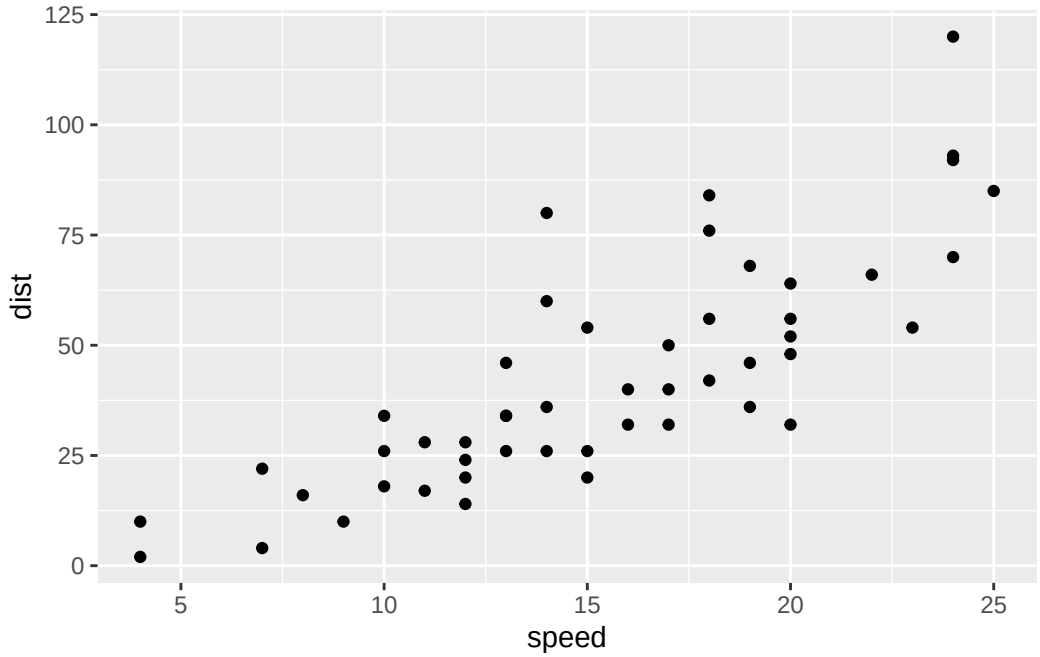
```
library(ggplot2)
```

```
ggplot(cars)
```


All ggplot figures need at least 3 things:

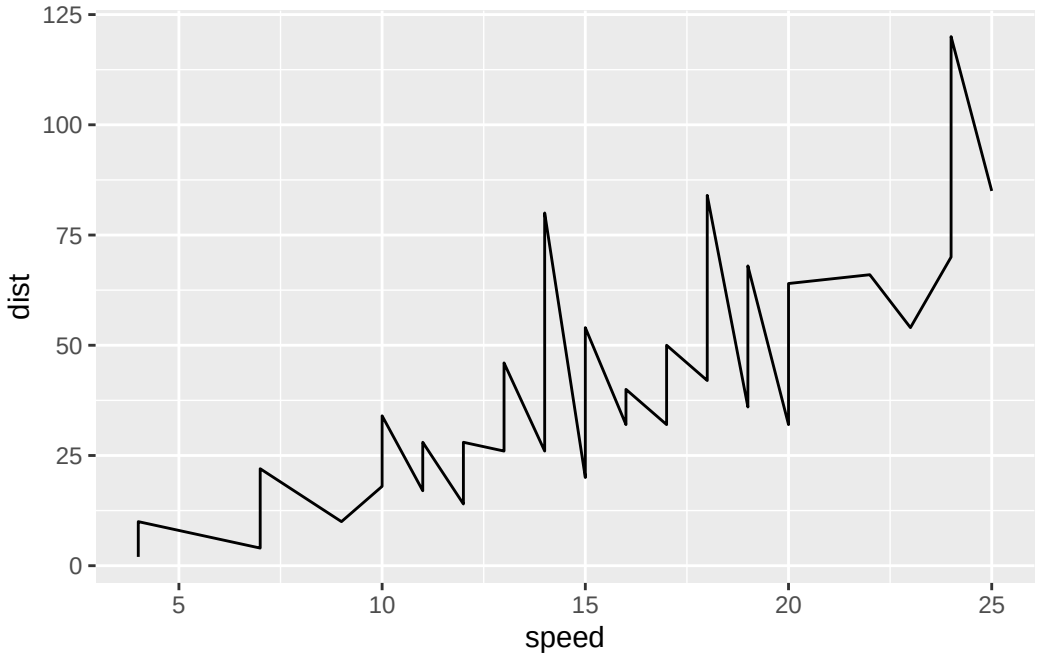
- data (this is the data.frame with our numbers)
- aesthetics ("aes", how our data maps to the plot)
- geoms (do want lines, points, columns, etc…)

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



I want a trend line to show the relationship between speed and stopping distance…

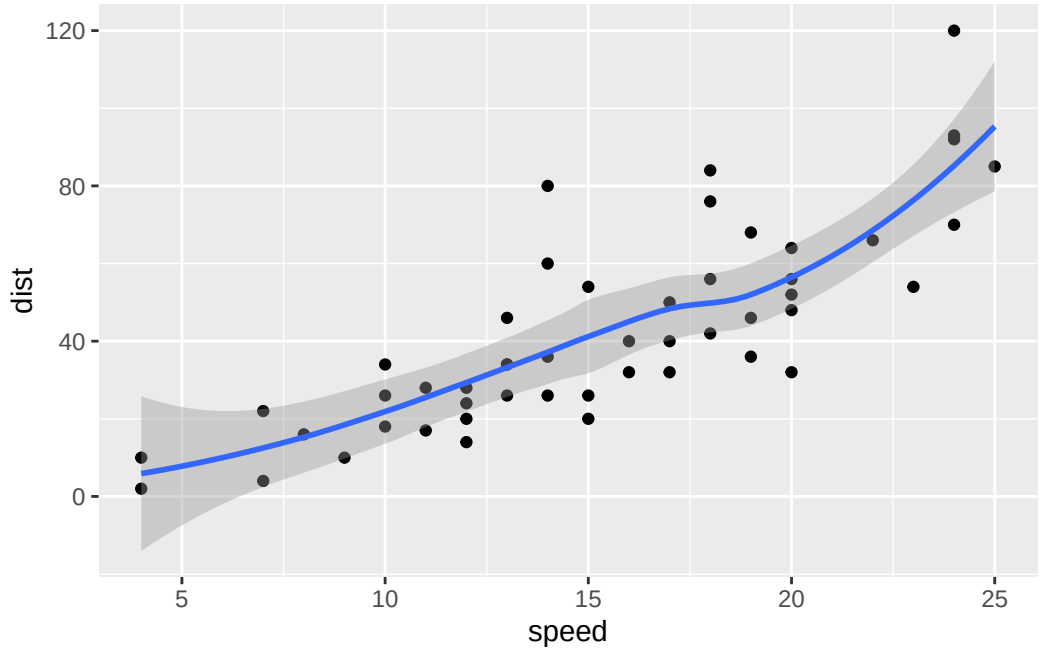
```
ggplot(cars)+
  aes(x=speed, y=dist)+
  geom_line()
```



That is not what we want

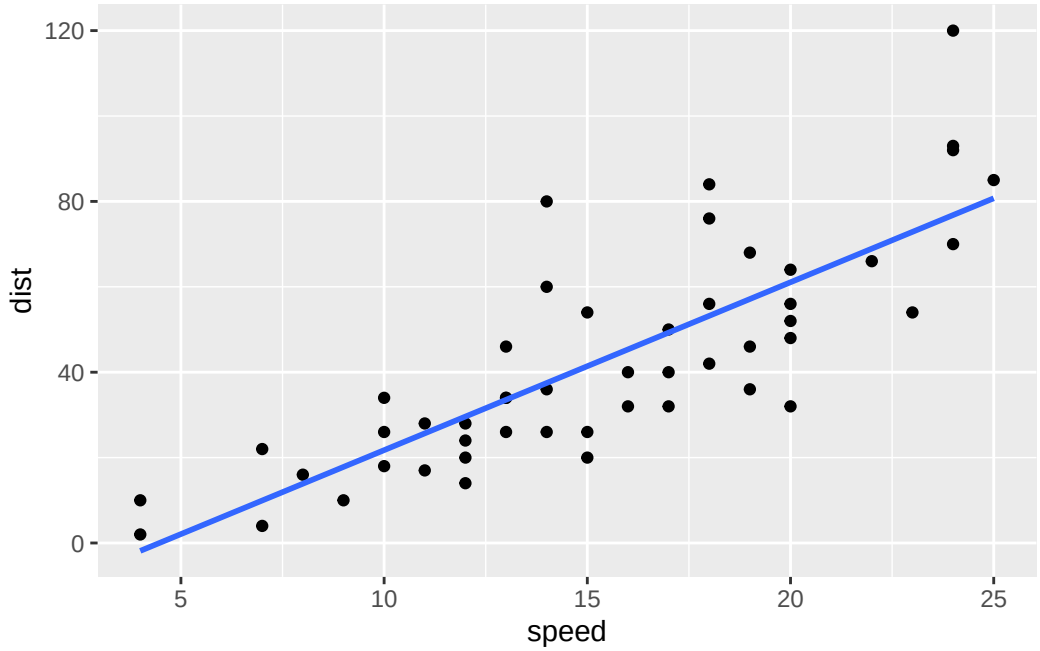
```
bb+geom_smooth()
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```




```
bb+
  geom_smooth(method="lm", se=FALSE)
```

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



text in **bold** and text in *italics* are important

Gene Expression Example

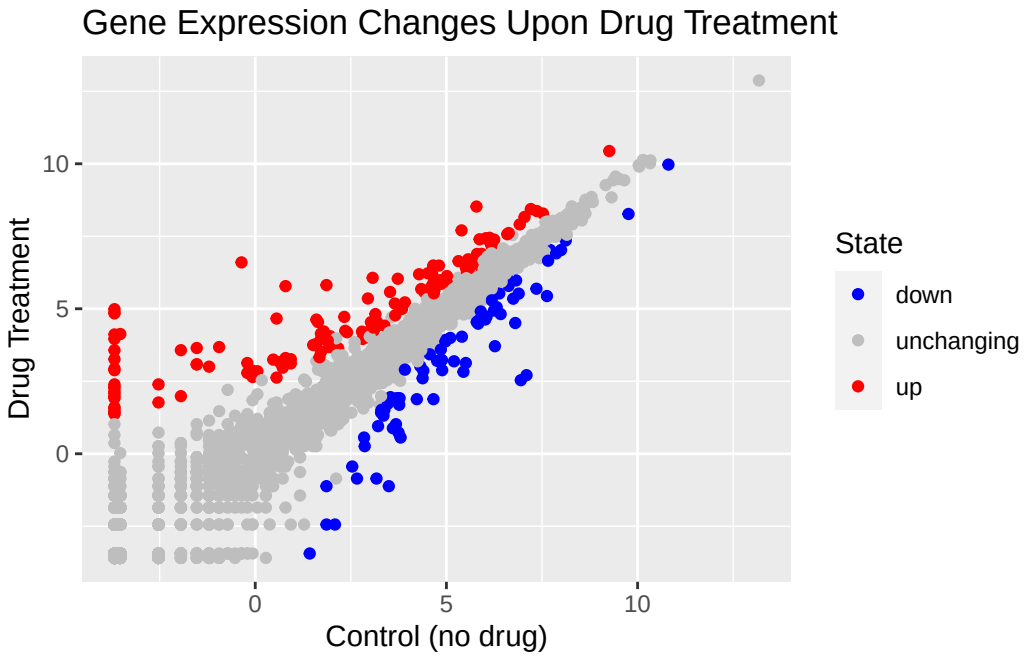
Open Genes

```
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
```

Graph

```
p <- ggplot(genes)+aes(x=Condition1, y=Condition2, col=State)+geom_point()
p+scale_colour_manual(values=c("blue", "gray", "red")) + labs(title="Gene Expression Chang
```



Gapminder Example

Gapminder contains economic and demographic data about various countries since 1952. To install use the `install.packages("gapminder")` and access it again with `library(gapminder)` Must also download dplyr, using `install.packages("dplyr")`, and run with `library(dplyr)`

```
library(gapminder)
library(dplyr)
```

```
Attaching package: 'dplyr'
```

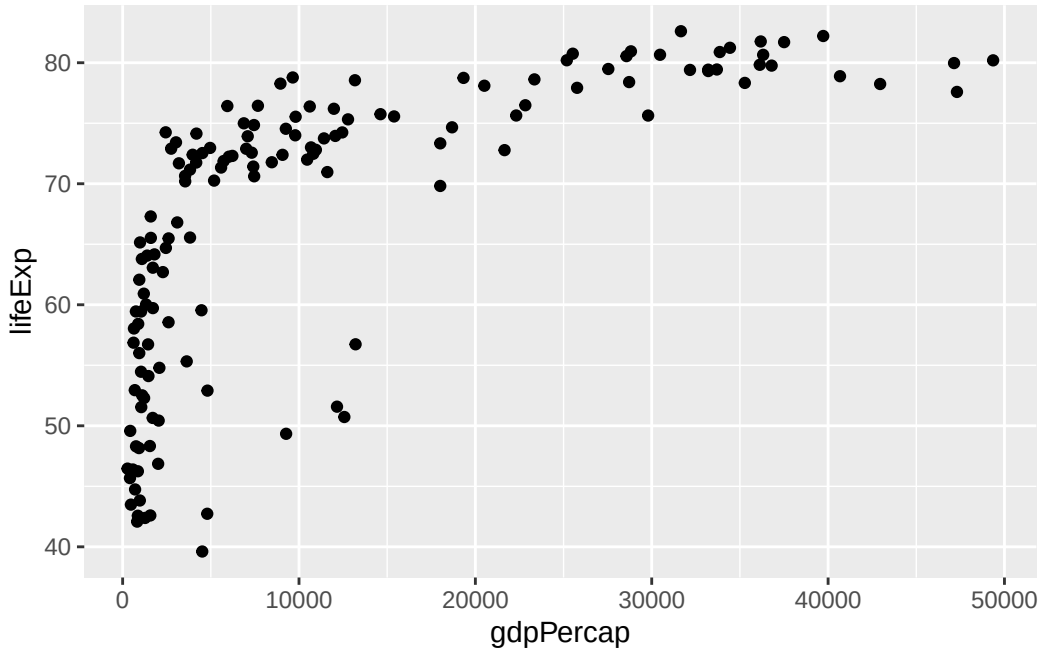
```
The following objects are masked from 'package:stats':
```

```
    filter, lag
```

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

    intersect, setdiff, setequal, union
```

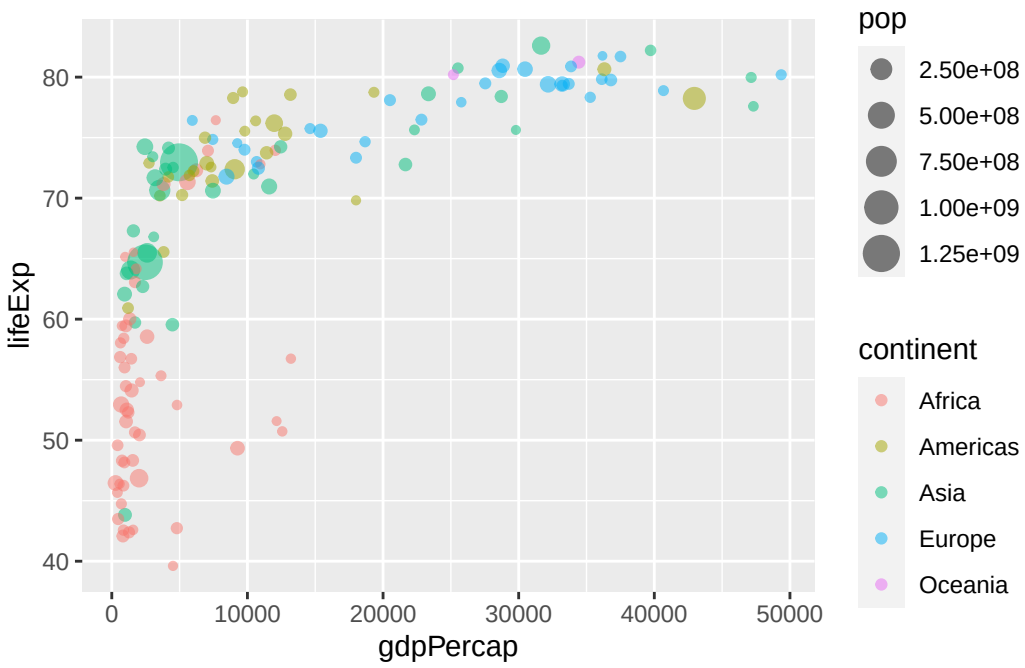
Set data for 2007 only and then open the plot

```
gapminder_2007 <- gapminder %>% filter(year==2007)
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point()
```



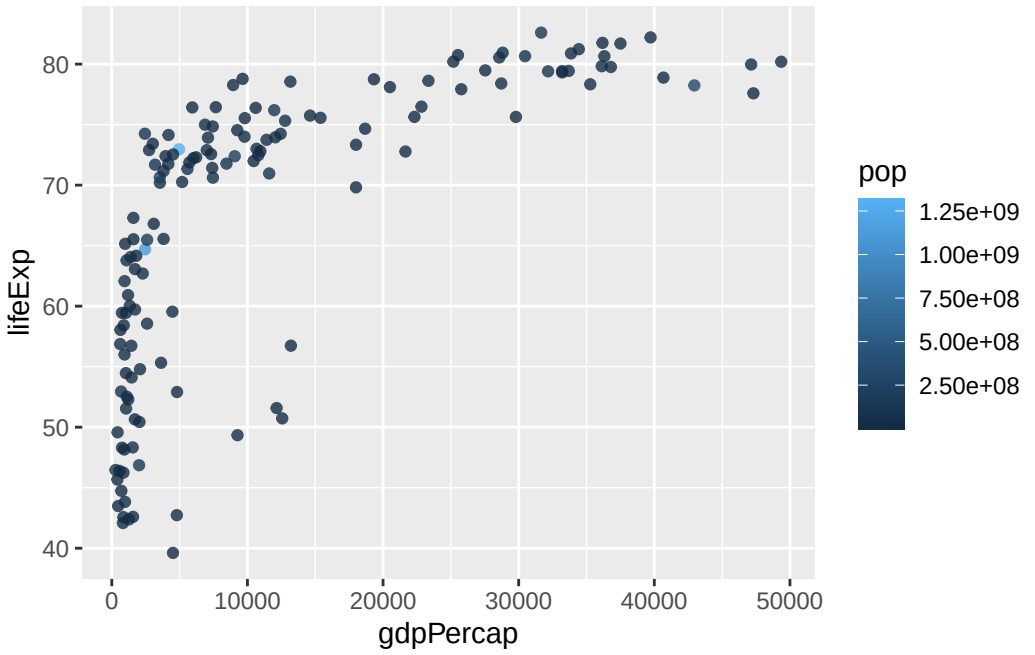
By mapping the variable "continent" to the aesthetic "color" and the population pop (in millions) through the argument to aes() we can obtain a richer plot that includes 4 different variables from the data set:

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



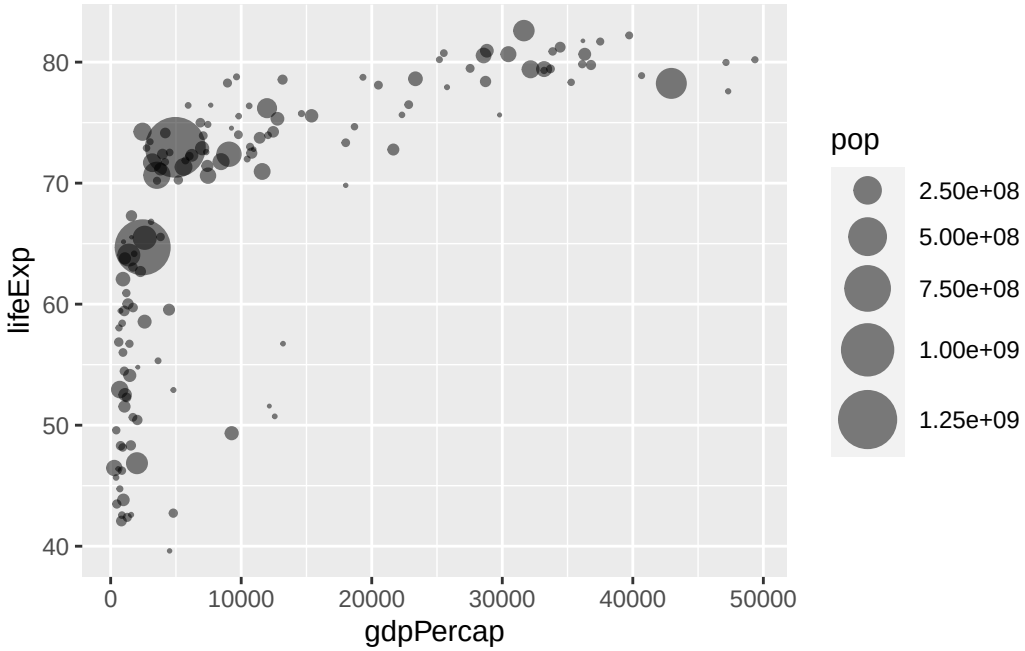
If we were to color by numeric population

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



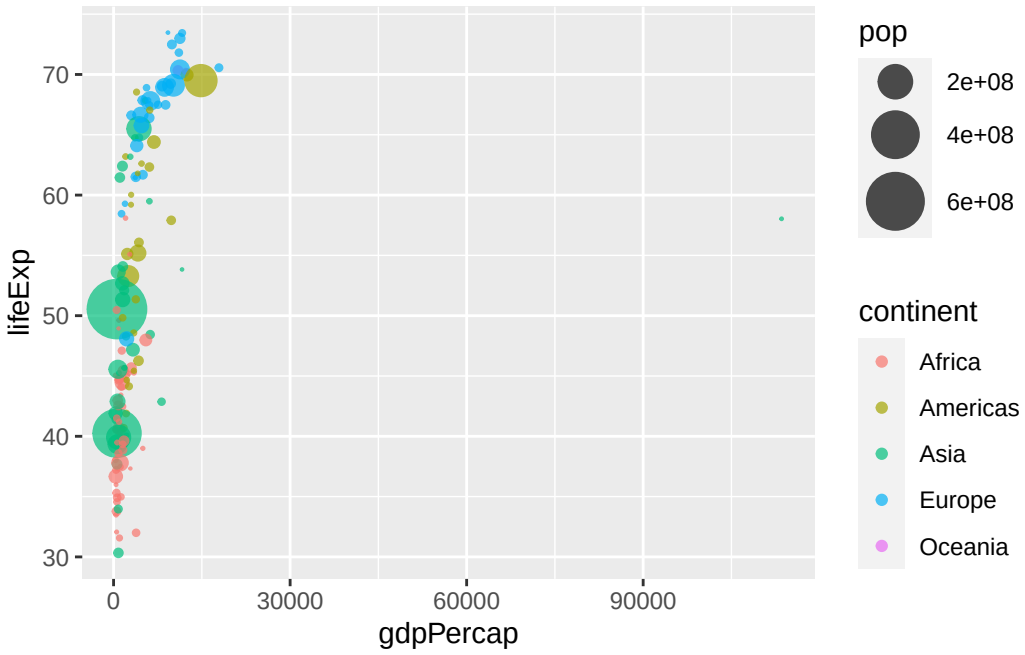
But it is not scaled, we want to scale it and reflect the actual population differences. Code using

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



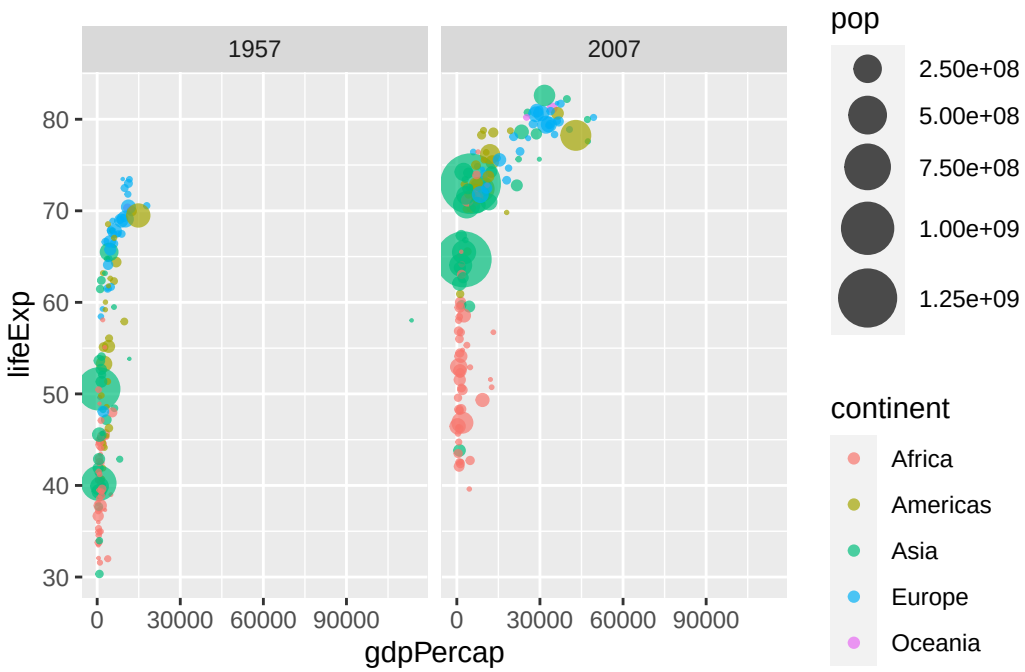
Now we want to compare 1957 vs 2007 Access 1957 data and plot

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

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



Time to compare 1957 vs 2007 using `facet_wrap(~year)`

```
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
80
70
60
50
40
30
lifeExp
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

Bar Charts