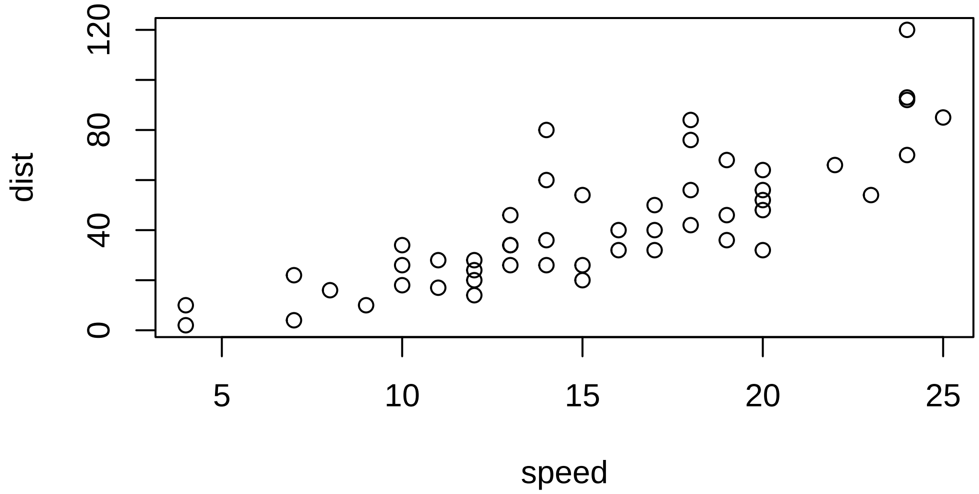
Class 05: Data Viz witth ggplot

Vanesa Fernandez

R has lot's of ways to make figures and graphs in particular. One that comes with R out of the box is called **"base" R** - the 'plot()' function

```
plot(cars)
```

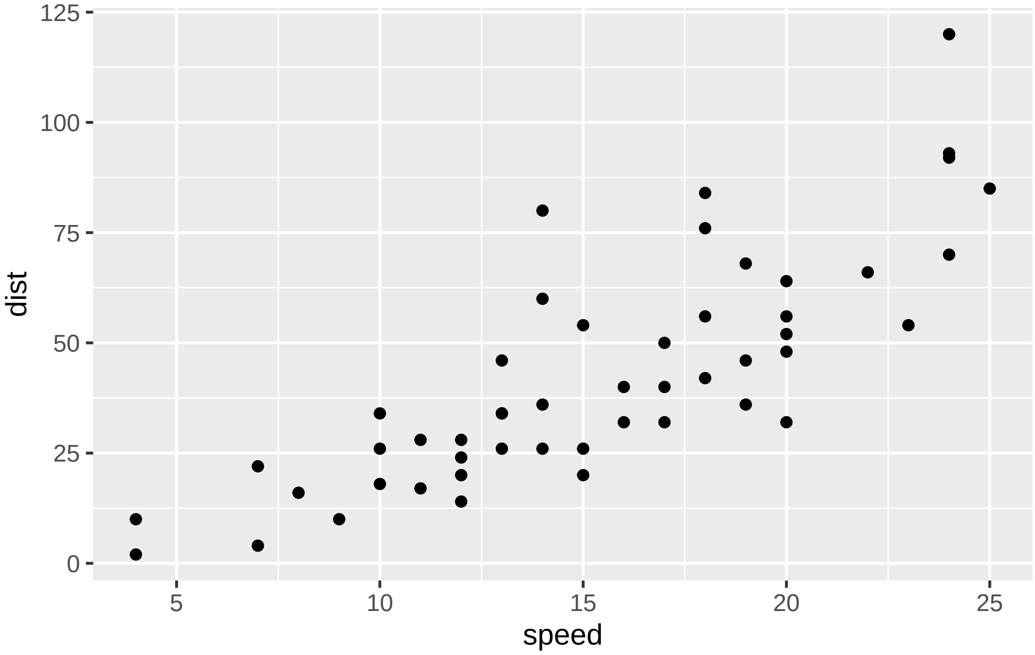


A very popular package in this area is called *ggplot2**

Before I can use any ad-on like this I must install it whit the `install.packages("ggplot2")` command/function

Then to use the package I need to load it with a `library(ggplot2)`) call

```
library(ggplot2)
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```

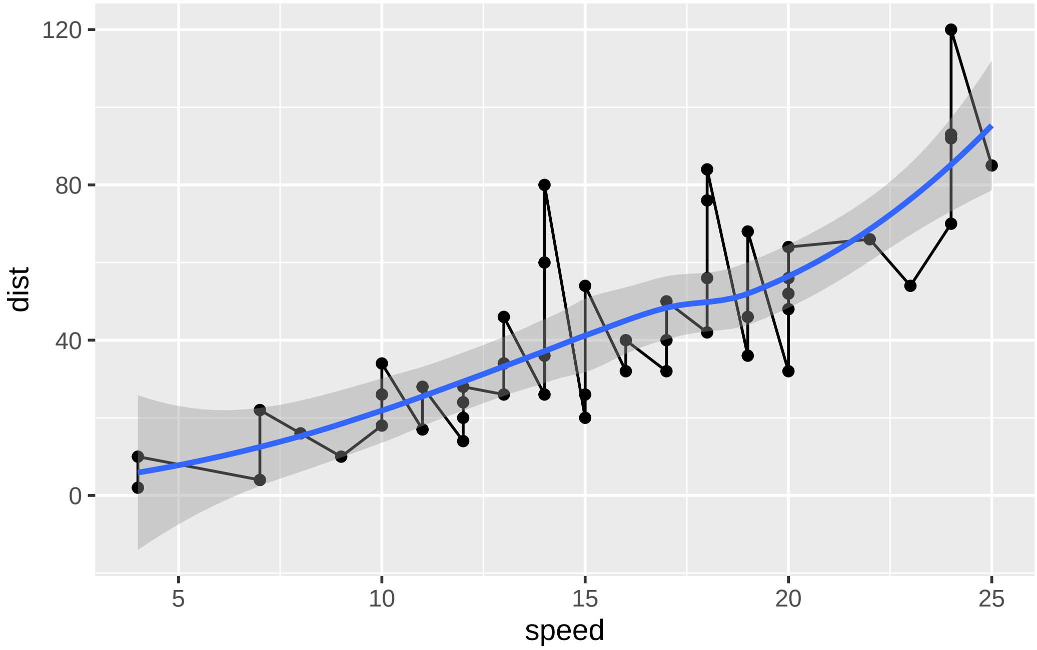


For “simple” plots like this one base R code will be much shorter than ggplot code.

Let’s fit a model and show it on my plot:

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

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



Every ggplot has at least 3 layers

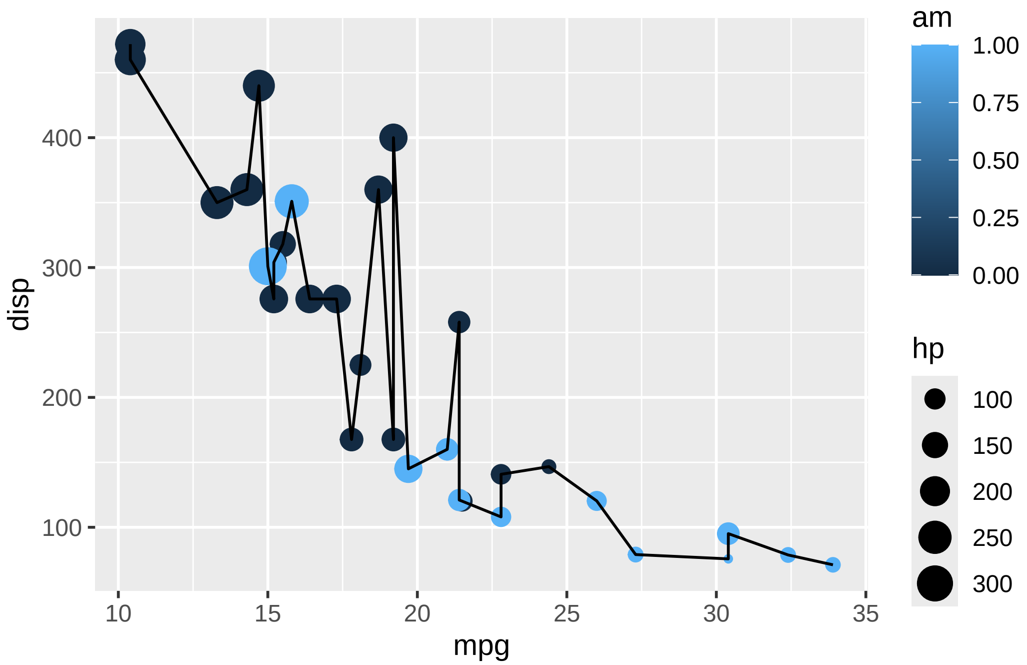
1st- **data** (data.frame with the numbers or stuff you want a plot) 2nd- **aes**thetics (mapping of your columns to your plot: position, size, line type/width, color, shape) 3rd- **geoms** (lots of these, these are `geompoint()`, `geom_line()`, `geom_col()`)

```
head(mtcars)
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

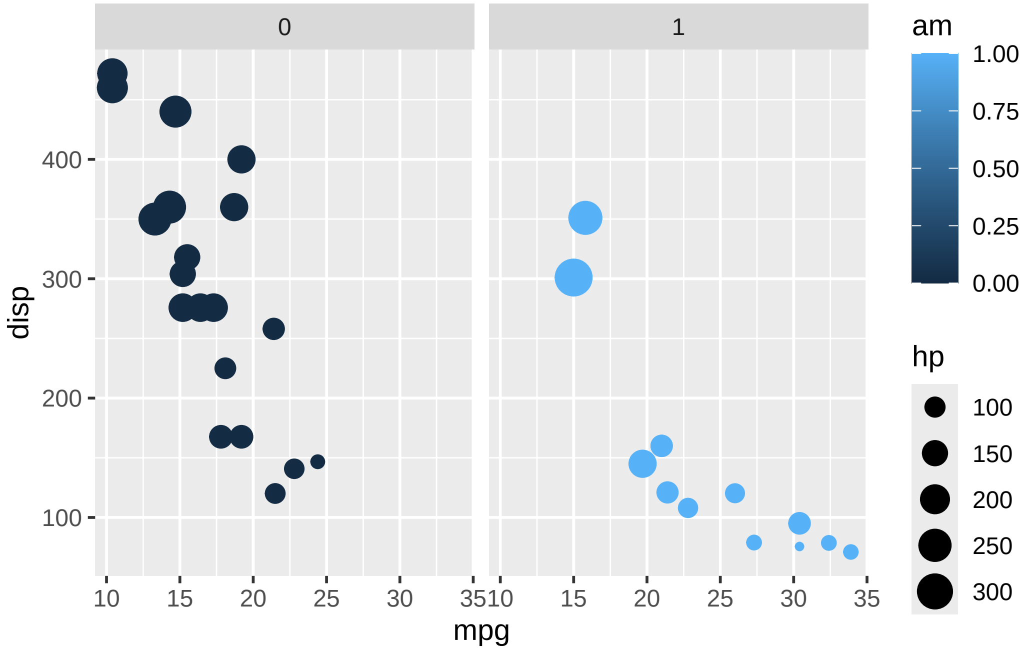
Make the ggplot of the `mtcars` data set using `mpg` vs `disp` and set the size of the points to the `hp`. and set the color to `am`

```
ggplot(mtcars) +
  aes(x=mpg, y=disp) +
  geom_point(aes(size=hp, col=am)) +
  geom_line()
```

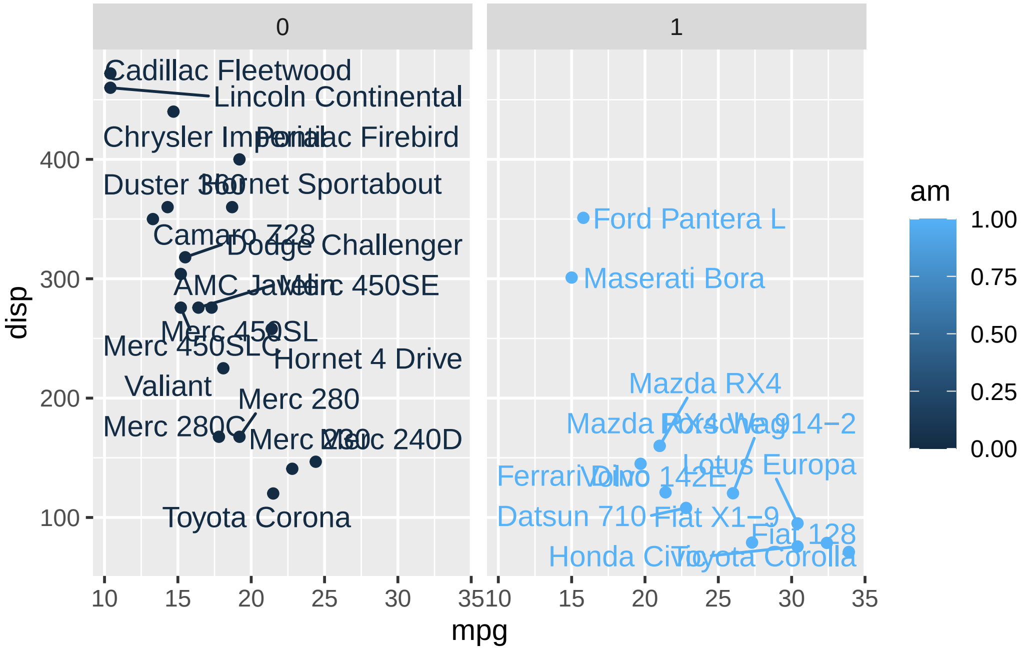


Now color all pts

```
ggplot(mtcars) +
  aes(x=mpg, y=disp, size=hp, col=am) +
  geom_point() +
  facet_wrap(~am)
```



```
library(ggrepel)

ggplot(mtcars) +
  aes(x=mpg, y=disp, col=am, label=rownames(mtcars)) +
  geom_point() +
  facet_wrap(~am) +
  geom_text_repel()
```



Going Further exercises

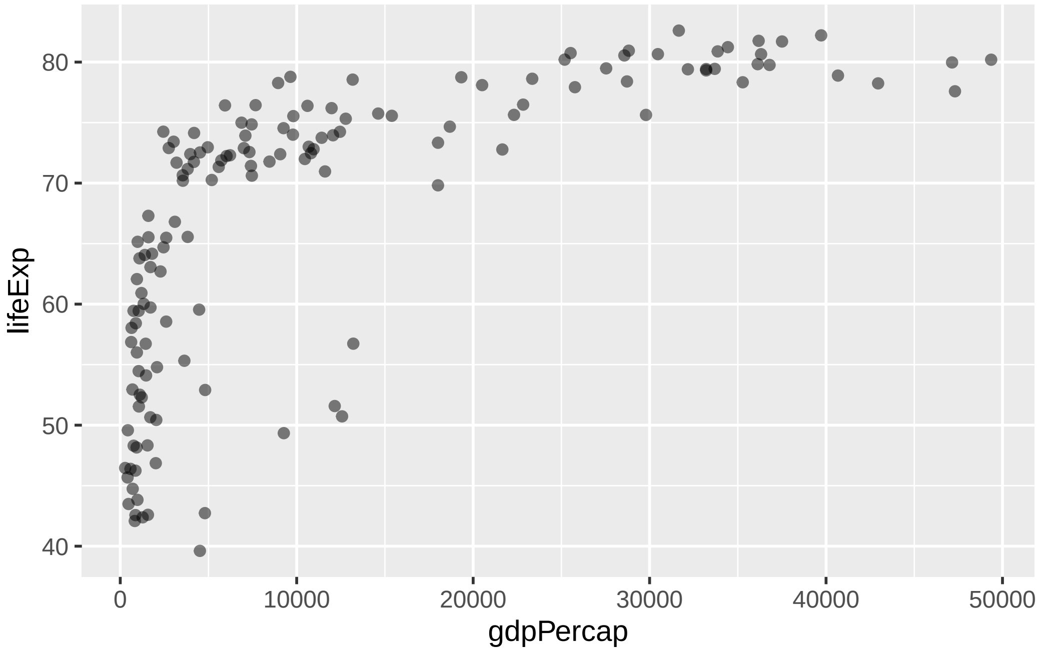
```
library(gapminder)
```

```
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
```

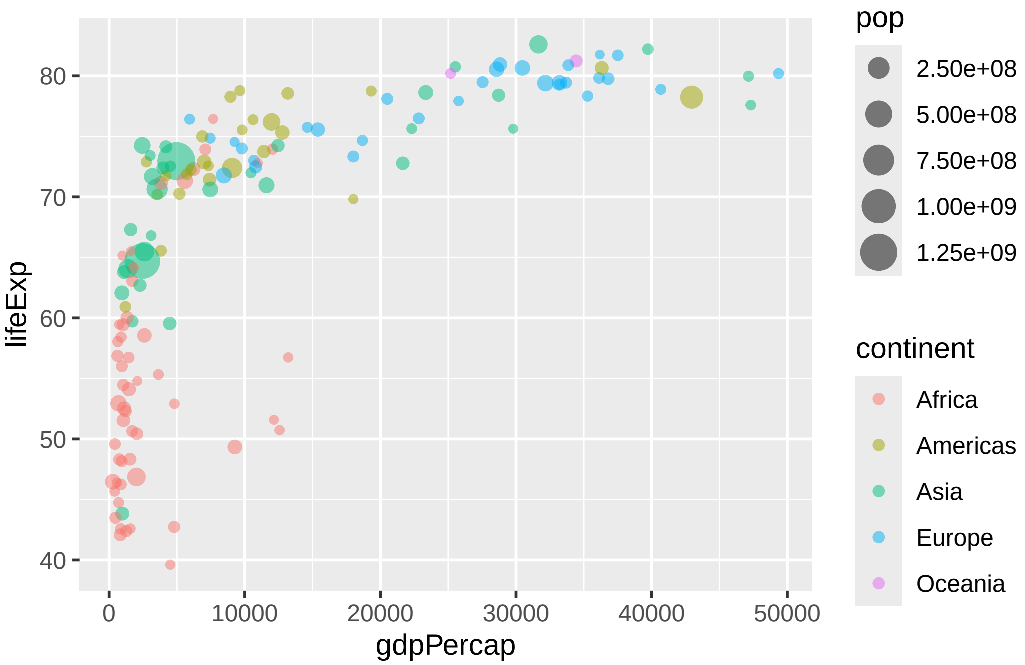
```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

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



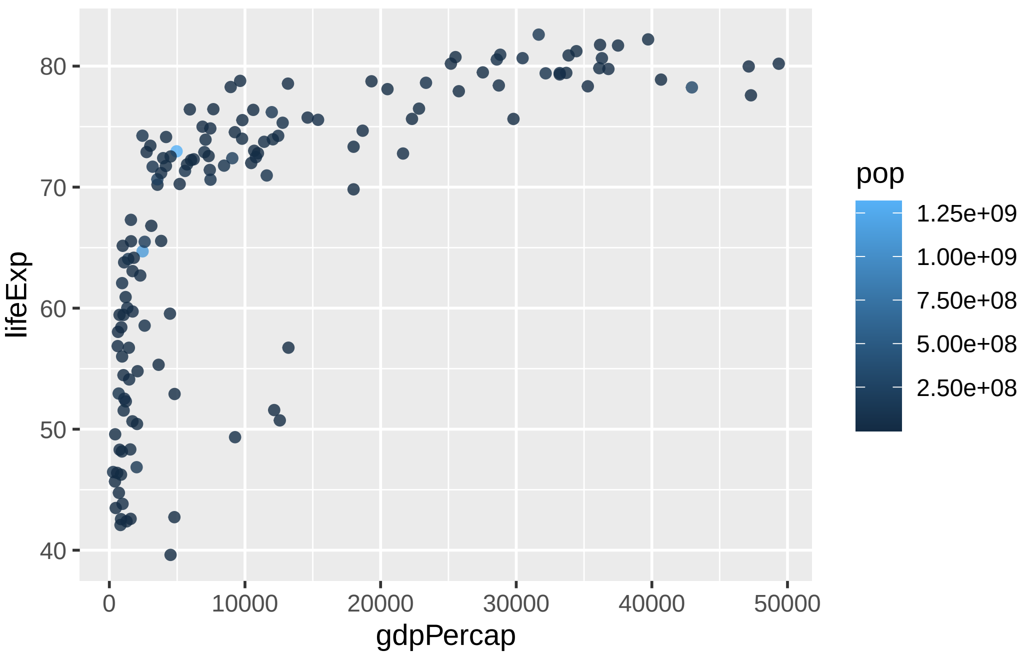
Adding more variables to `aes()`

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



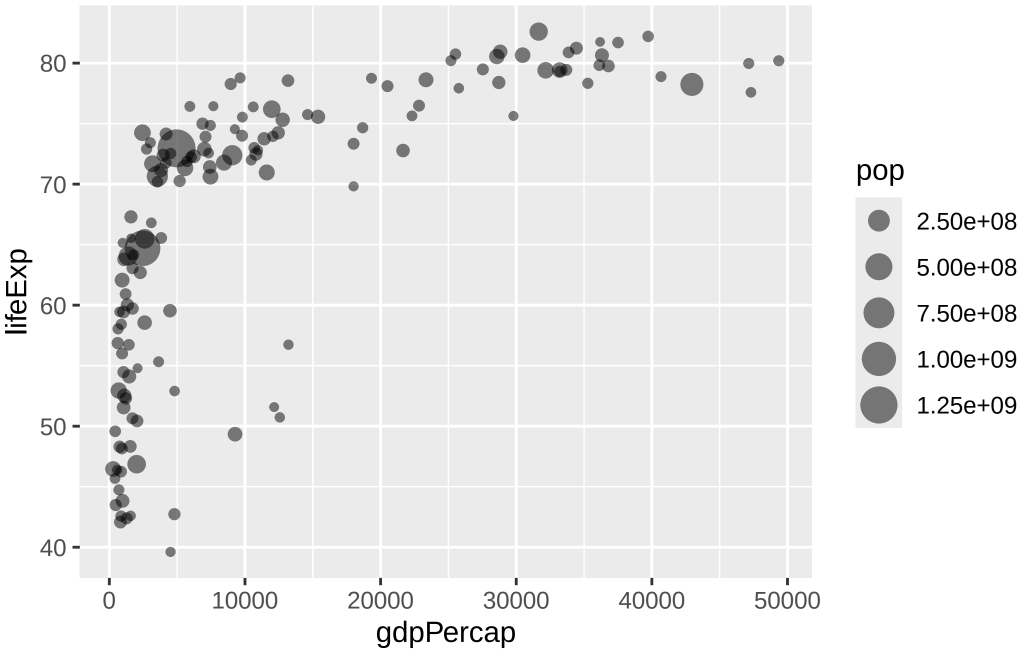
Color the points by the numeric variable population pop

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



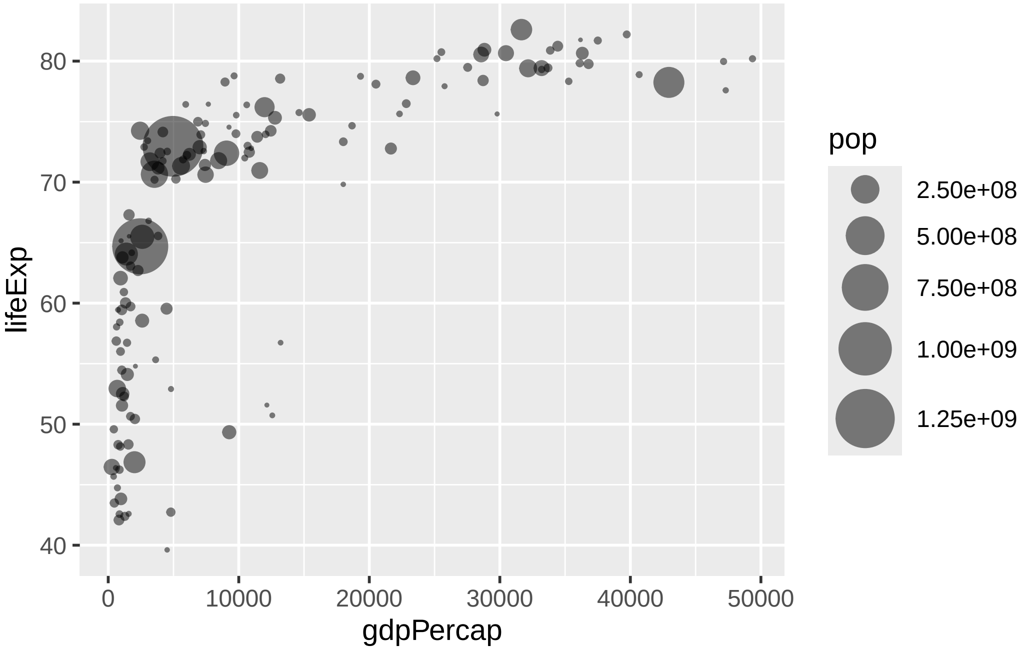
Adjusting Point size

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



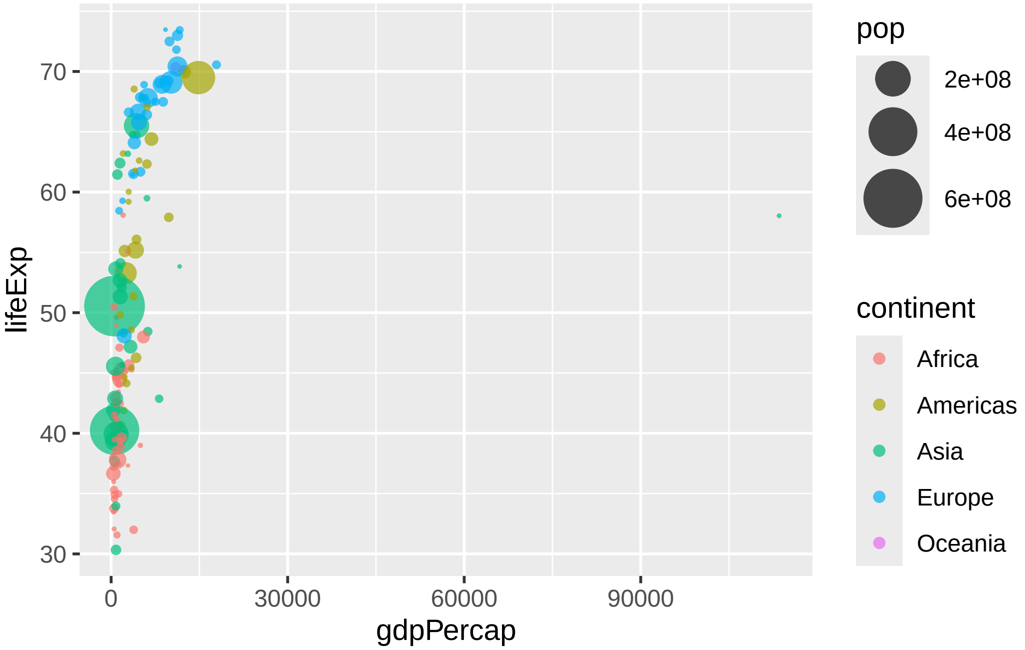
Scaling information

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



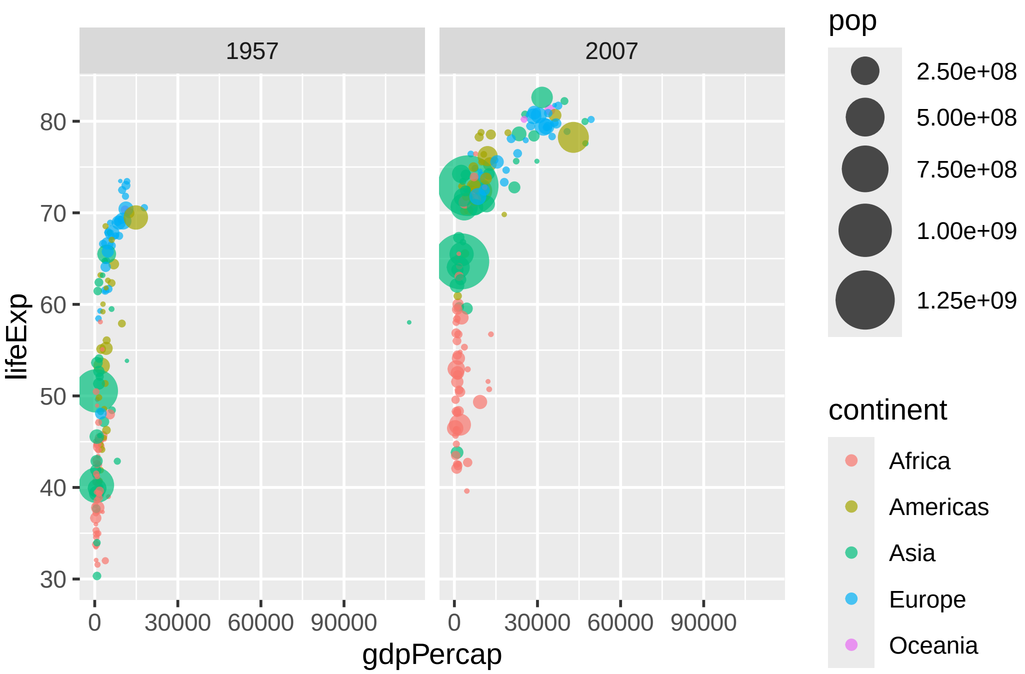
1957 plot

```
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)
```



1957 and 2007 `facet_wrap()` 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)
```



Gene expression

```
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
```

There are 5196 genes in this dataset.

```
unique(genes$State)
```

```
[1] "unchanging" "up"         "down"
```

The `table()` function is very useful to tell me how many entries of each type there are.

```
table(genes$State) / nrow(genes)
```

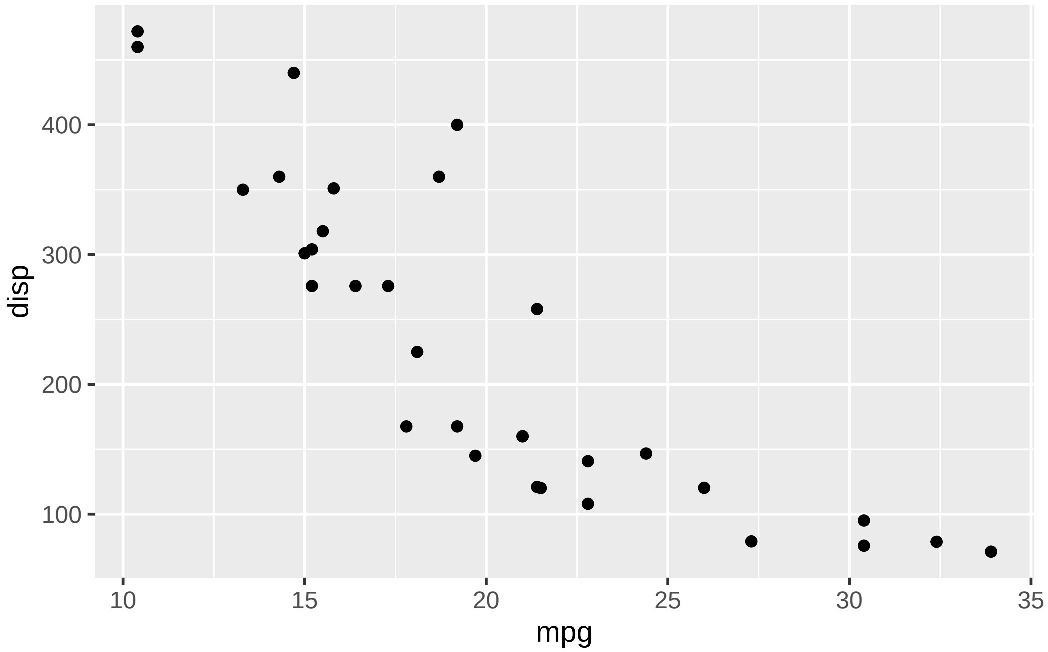
```

      down unchanging         up 
0.01385681 0.96170131 0.02444188 
```

The functions `nrow()`, `ncol()`, and `table()` are ones I want you to know.

> KEY POINTS Saving plots with **ggsave** Different plot "types" with different `geoms_**()` Faceting with `facet_wrap()` Multi-plot layout with the **patchwork** package

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

```
ggplot(mtcars) +
  aes(mpg, disp) +
  geom_point()
```



```
ggsave("myplot.pdf")
```

```
Saving 5.5 x 3.5 in image
```