Class 5: Data visualization with ggplot2

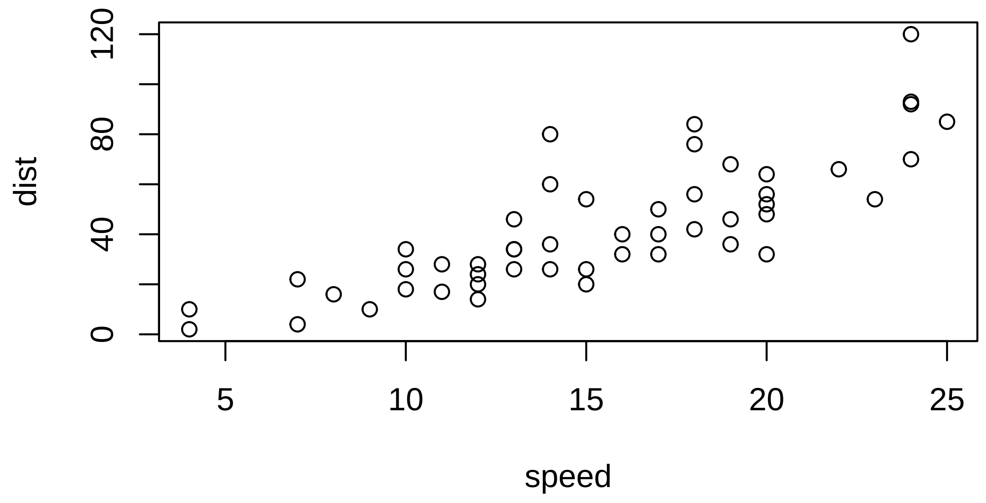
Kalisa Kang (PID: A16741690)

Table of contents

Today we will have our first play with the **ggplot2** package - one of the most popular graphics packages on the planet.

There are many plotting systems in R. These include so-called *"base"* plotting/graphics.

```
plot(cars)
```



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

If I want to use **ggplot2**, it takes some more work.

```
# ggplot(cars)
```

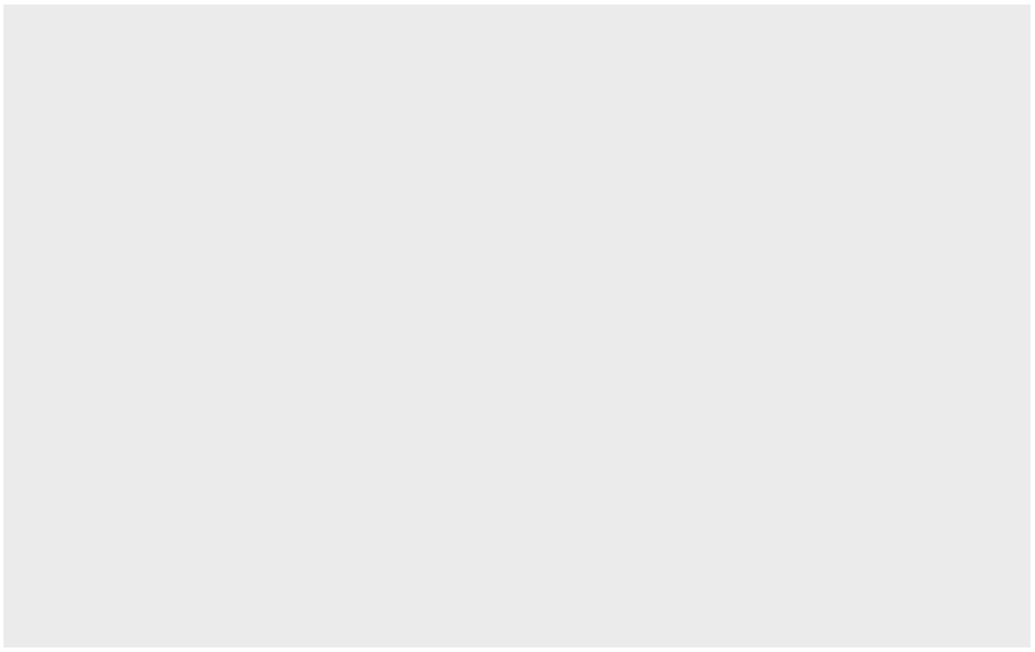
I need to install the package first. To do this, I can use the function `install.packages("ggplot2")`

Every time I want to use a package, I need to load it up with a `library()` call.

```
library(ggplot2)
```

Now finally, I can use ggplot2.

```
ggplot(cars)
```



Every ggplot has at least 3 things:

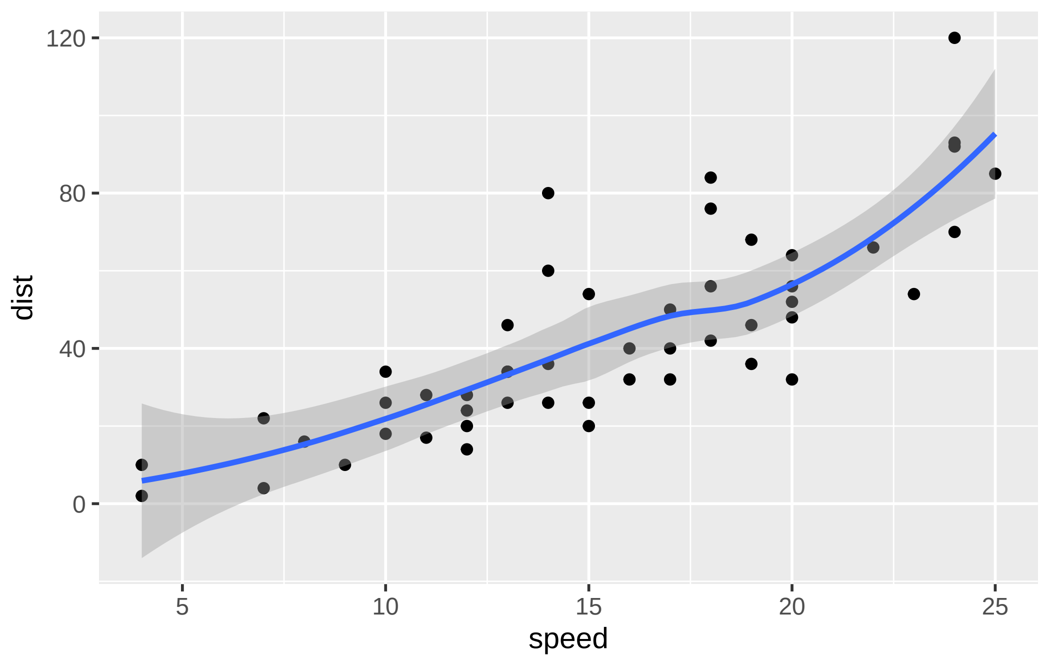
- **data** (the data.frame with the data you want to plot)
- **aes** (the aesthetic mapping of the data to the plot)
- **geom** (how you want the plot to look i.e., points, lines, columns, etc.)

```
head(cars)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

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

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

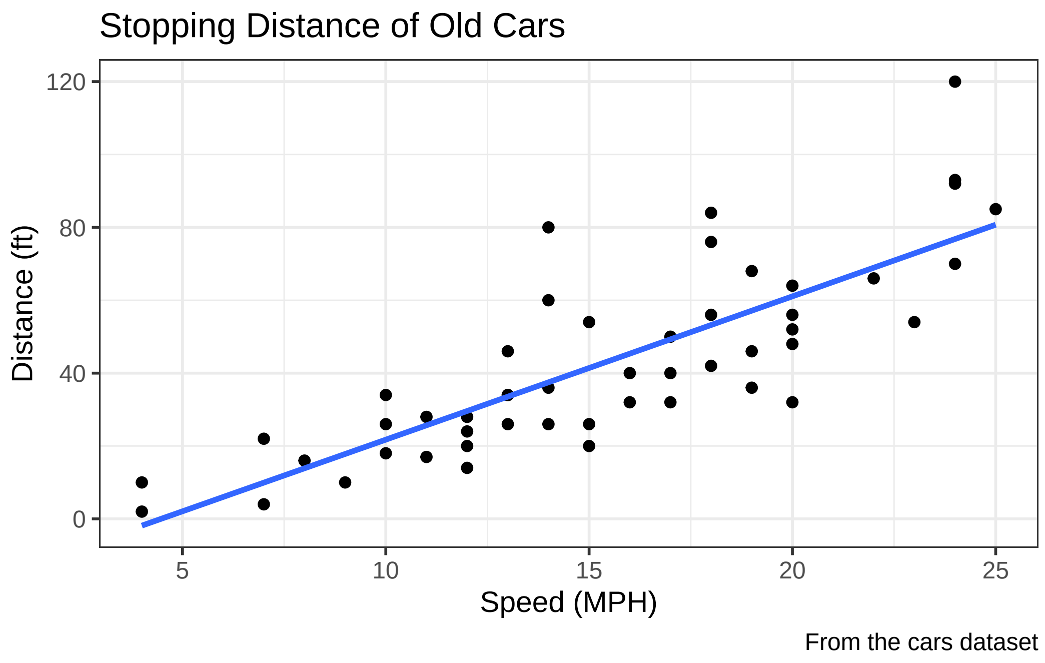


I want a linear model and no standard error bounds shown on my plot. I also want nicer axis labels, a title, etc.

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

```r
bp + geom_smooth(method = "lm", se = FALSE) +
  labs(title="Stopping Distance of Old Cars",
       x="Speed (MPH)",
       y="Distance (ft)",
       caption="From the cars dataset") +
  theme_bw()
```

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



A more complicated scatter plot

Here we make a plot of gene expression data:

```r
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
```

```r
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
```

> Q. Use the nrow() function to find out how many genes are in this dataset. What is your answer?

```r
nrow(genes)
```

```
[1] 5196
```

> Q. Use the colnames() function and the ncol() function on the genes data frame to find out what the column names are (we will need these later) and how many columns there are. How many columns did you find?

```r
colnames(genes)
```

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

```r
ncol(genes)
```

```
[1] 4
```

> Q. Use the table() function on the State column of this data.frame to find out how many 'up' regulated genes there are. What is your answer?

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

```

      down unchanging         up 
        72       4997        127 
```

> Q. Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset?

```r
round(sum(genes$State == "up")/nrow(genes) * 100, 2)
```

```
[1] 2.44
```

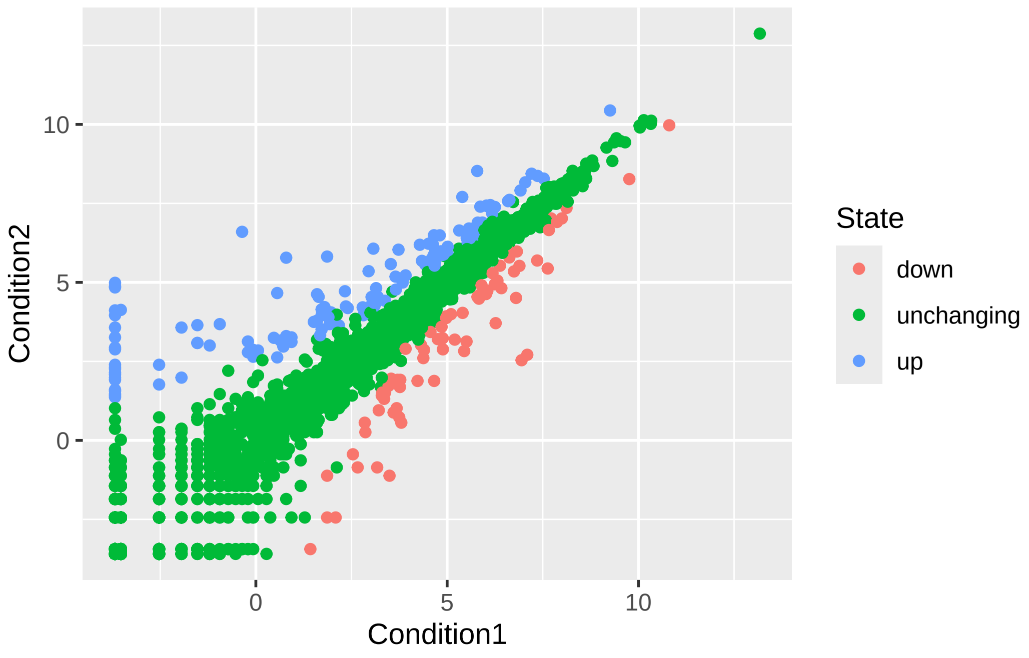
```r
n.gene <- nrow(genes)
n.up <- sum(genes$State == "up")

up.percent <- n.up/n.gene*100
round(up.percent, 2)
```

```
[1] 2.44
```

```r
head(genes, 2)
```

```
   Gene Condition1 Condition2      State
1 A4GNT  -3.680861  -3.440135 unchanging
2  AAAS   4.547958   4.386413 unchanging
```

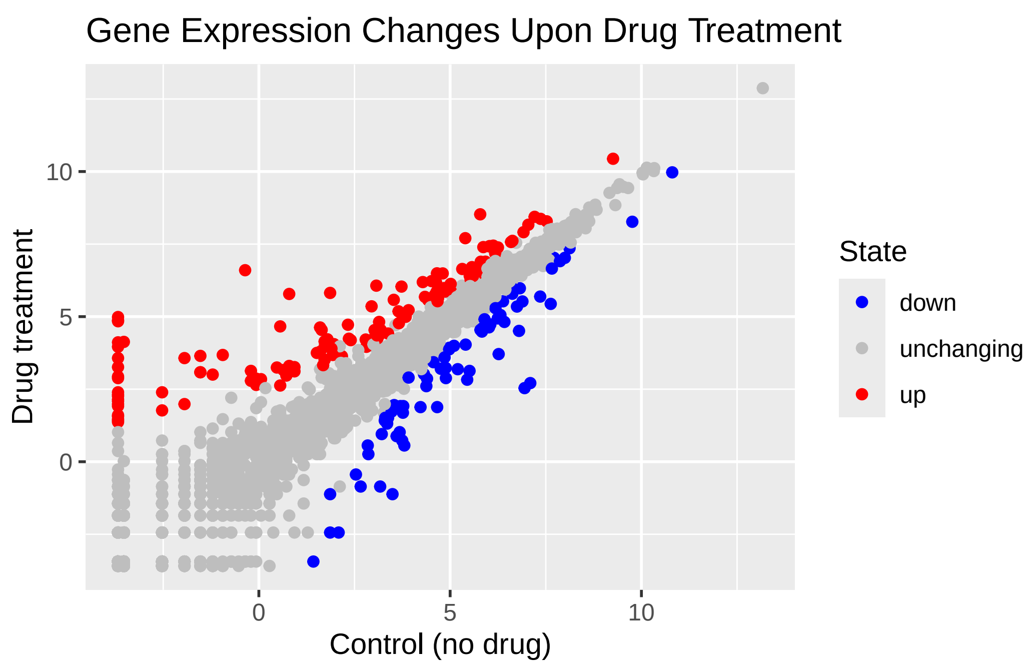
```r
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  geom_point()
```



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

Change the colors and add labels.

```
p + scale_color_manual(values=c("blue", "gray", "red")) + labs(title="Gene Expression Chan
```



Exploring the gapminder dataset

Here we will load up the gapminder dataset to get practice with different aes mappings.

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

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

> Q. How many entry rows are in this dataset?

```
nrow(gapminder)
```

```
[1] 1704
```

> Q. How many columns?

```
ncol(gapminder)
```

```
[1] 6
```

```r
dim(gapminder)
```

```
[1] 1704    6
```

```r
head(gapminder)
```

```
      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
4 Afghanistan      Asia 1967  34.020 11537966  836.1971
5 Afghanistan      Asia 1972  36.088 13079460  739.9811
6 Afghanistan      Asia 1977  38.438 14880372  786.1134
```

```r
table(gapminder$year)
```

```

1952 1957 1962 1967 1972 1977 1982 1987 1992 1997 2002 2007 
 142  142  142  142  142  142  142  142  142  142  142  142 
```

> Q. How many continents?

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

```

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

I can use the `unique()` function... The `length()` function tells us how many buckets there are!

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

```
[1] 5
```

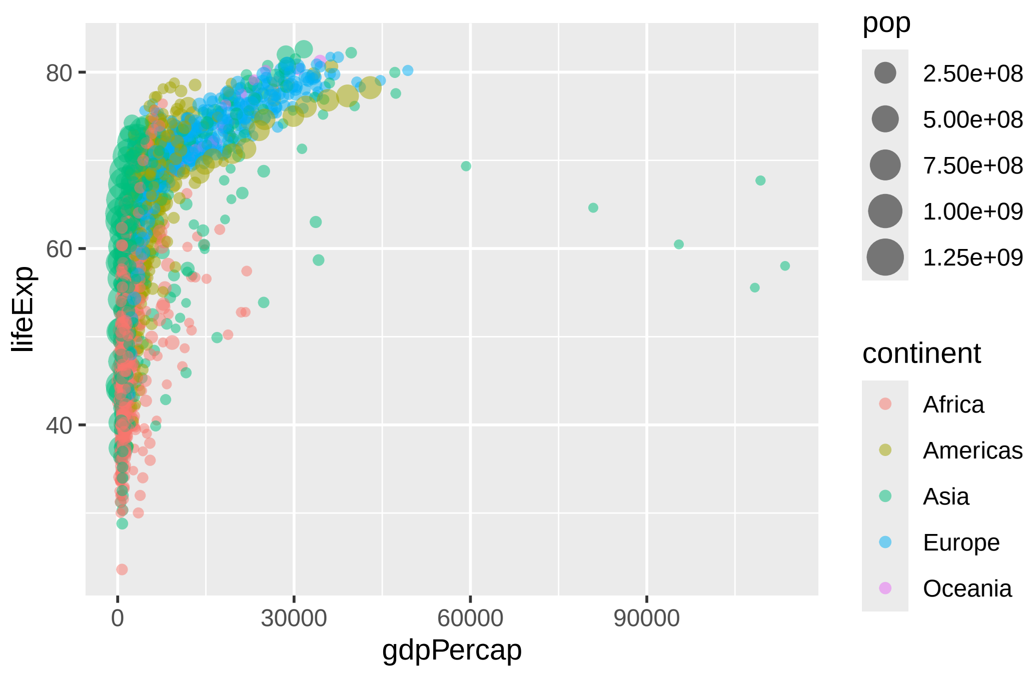
> Q. How many countries are there in this dataset?

```r
length(unique(gapminder$country))
```

```
[1] 142
```

Make a scatterplot. The `alpha()` function gives you different transparency levels, where 0 is completely transparent and 1 is not transparent. Putting `col="blue"` in the aesthetic function does not make the points blue. If you want to color by column, then put the col=column name in aes; but if you want to color everything, then put col=color in geom.

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent, size=pop) +
  geom_point(alpha=.5)
```



```
library(dplyr)
```

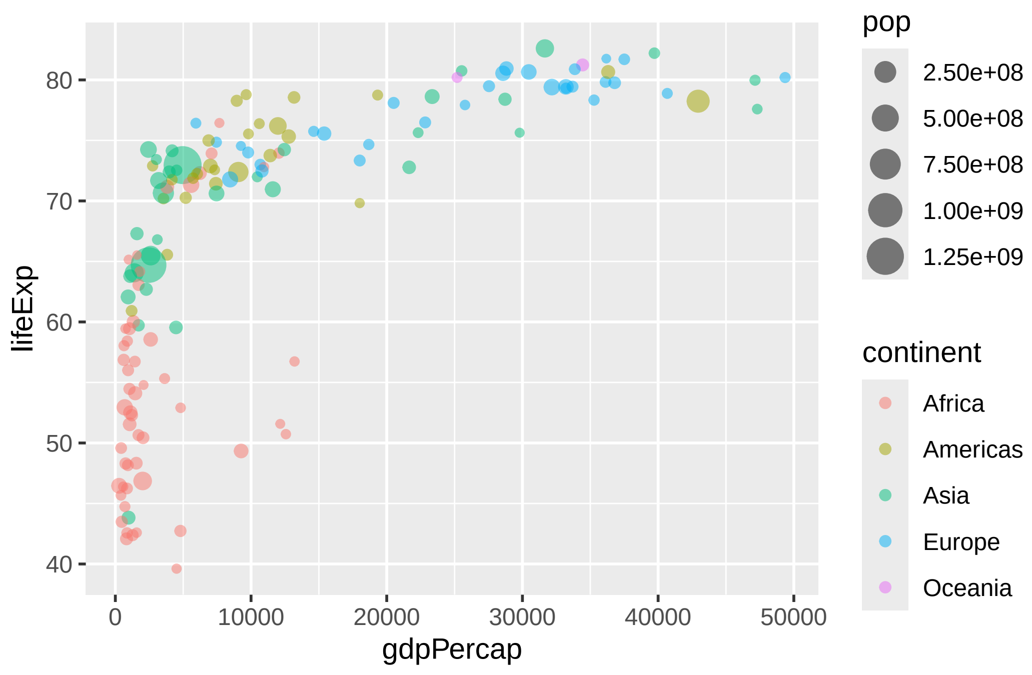
```
Attaching package: 'dplyr'

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

    filter, lag

The following objects are masked from 'package:base':
    intersect, setdiff, setequal, union
```

```
gapminder_2007 <- filter(gapminder, year==2007)

head(gapminder_2007)
```

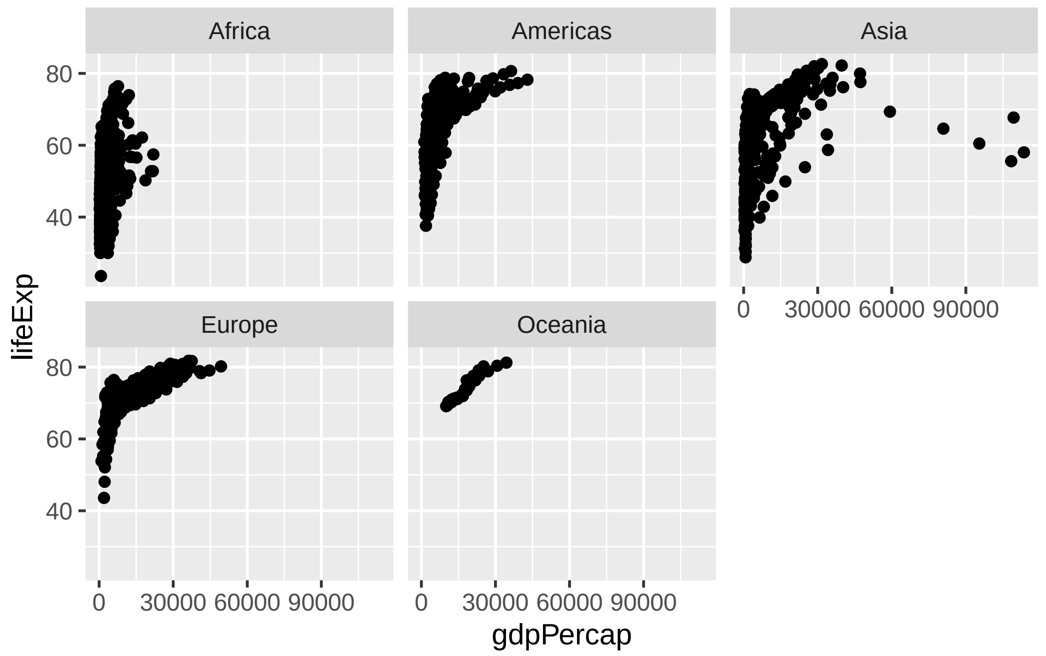
```
      country continent year lifeExp      pop  gdpPercap
1 Afghanistan      Asia 2007  43.828 31889923   974.5803
2     Albania    Europe 2007  76.423  3600523  5937.0295
3     Algeria    Africa 2007  72.301 33333216  6223.3675
4      Angola    Africa 2007  42.731 12420476  4797.2313
5   Argentina  Americas 2007  75.320 40301927 12779.3796
6   Australia   Oceania 2007  81.235 20434176 34435.3674
```

Plot of 2007 with population and continent data

```
ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, col=continent, size=pop) +
  geom_point(alpha=.5)
```



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


Africa
Americas
Asia
Europe
Oceania
lifeExp
gdpPercap