Class 5: Data visualization with ggplot

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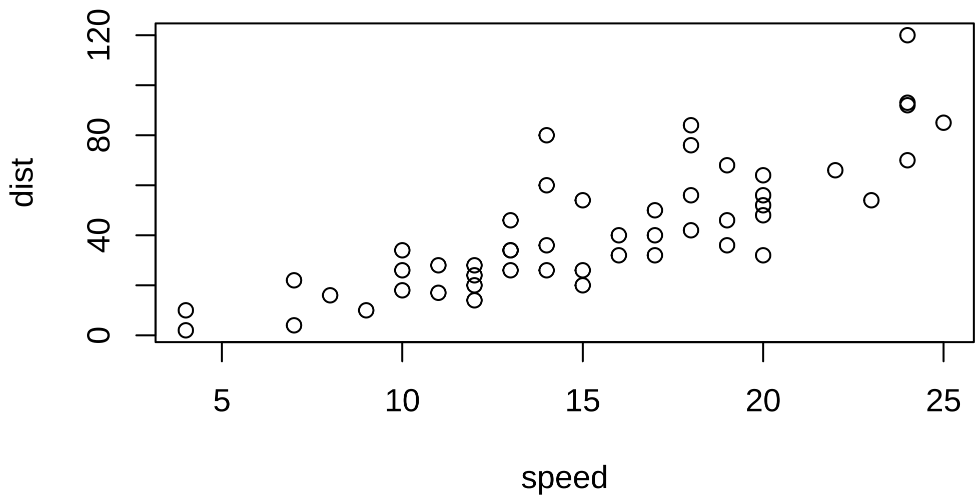
Table of contents

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 plots - 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 my computer. 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 I finally can use ggplot

```
ggplot(cars)
```

Every ggplot has at least 3 things:

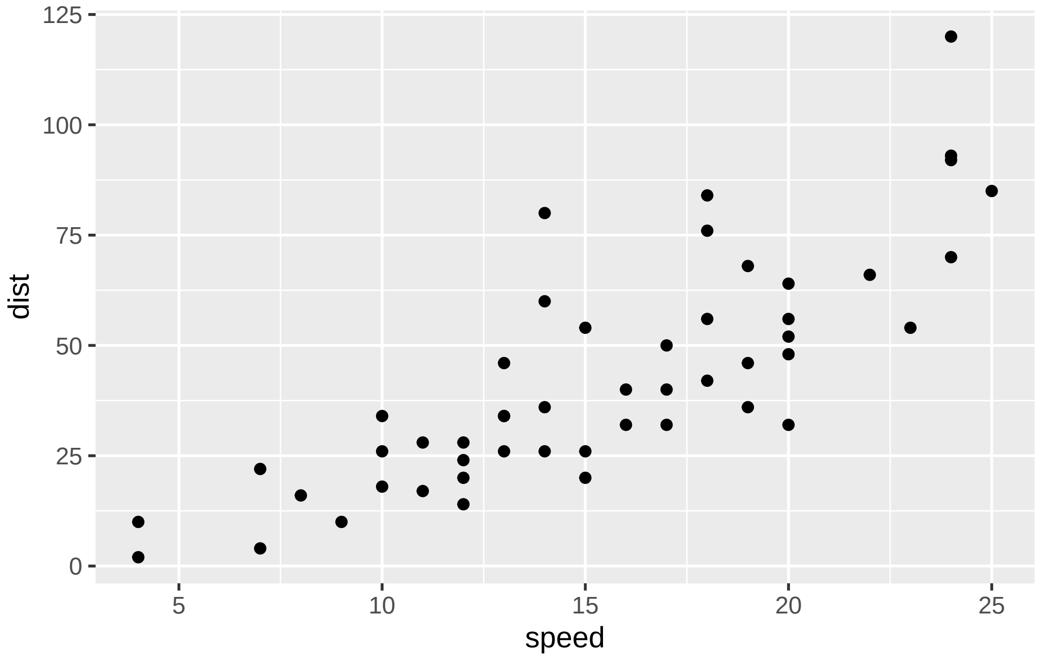
- **data** (the data.frame with the data you want to plot)
- **aes** (the aesthetic mapping of the data to the plot)
- **geom** (how do you want the plot to look, points, lines, etc.)

```
head(cars)
```

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

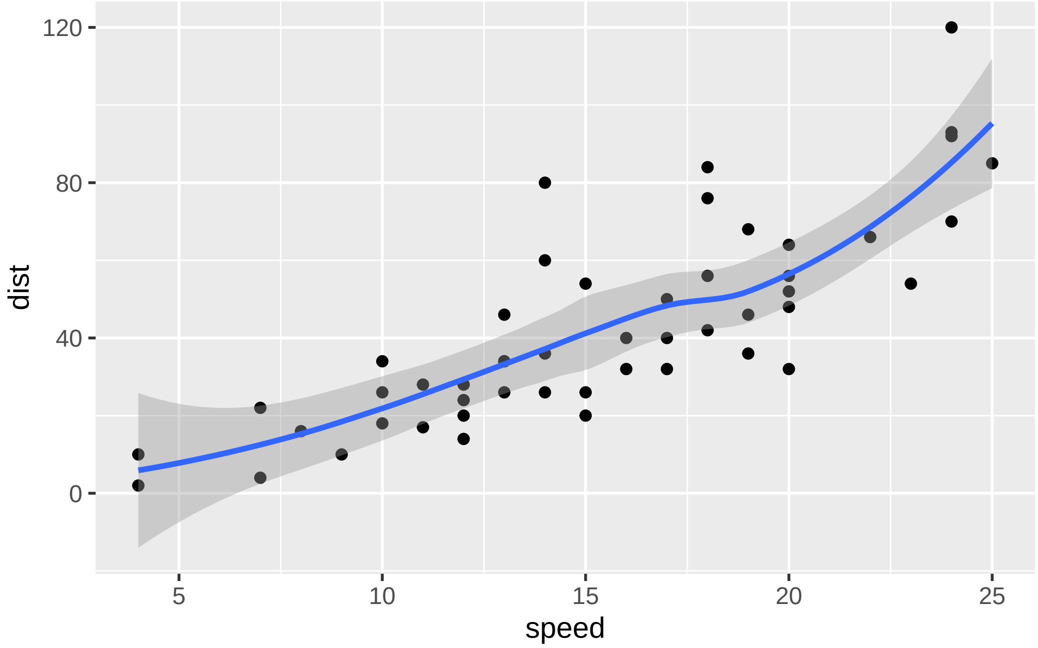
First point plot of cars

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



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

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

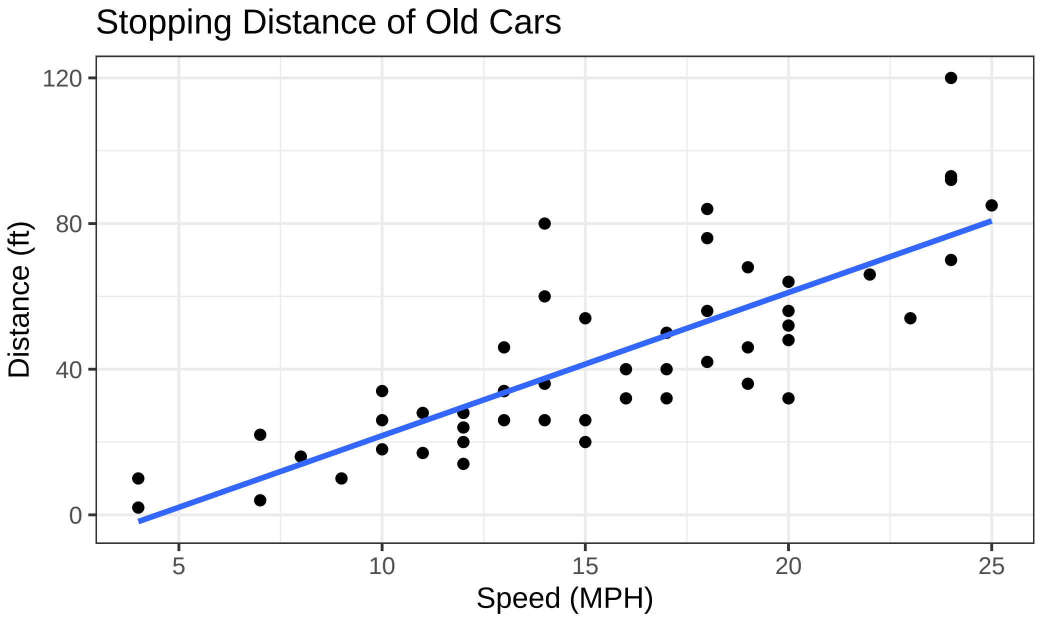


I want a linear model and no standard error bounds shown on my plot. I also want a nicer axis labels a title etc.

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

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



From the cars dataset

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)
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?

```
colnames(genes)
```

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

```
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?

```
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?

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

```
[1] 2.44
```

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

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

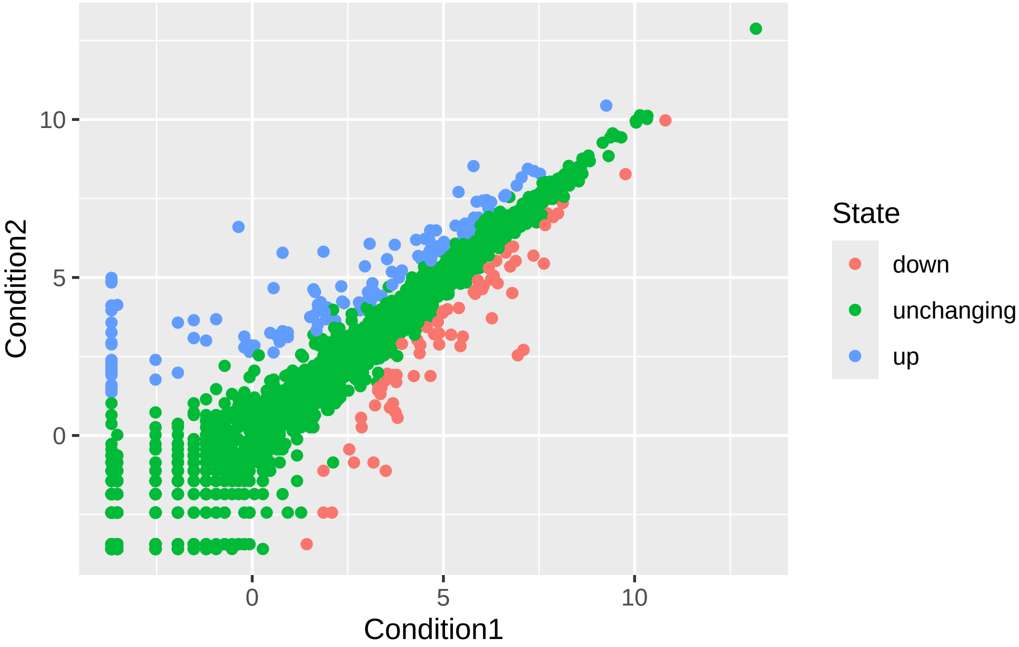
```
[1] 2.44
```

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

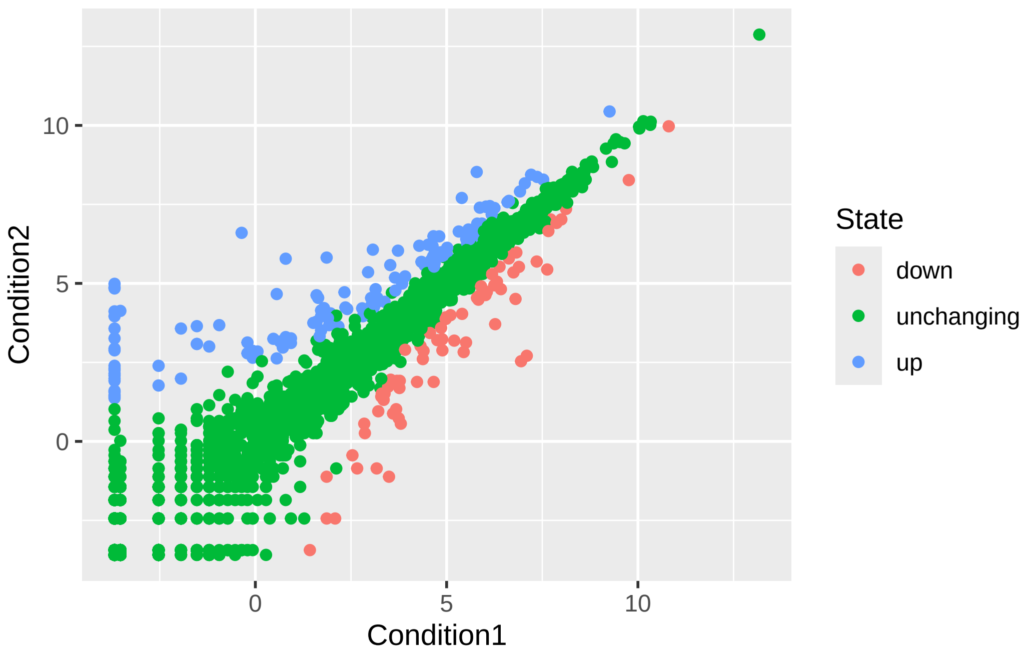
```
   Gene Condition1 Condition2      State
1 A4GNT  -3.680861  -3.440135 unchanging
2  AAAS   4.547958   4.386413 unchanging
```

```
library(ggplot2)
```

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

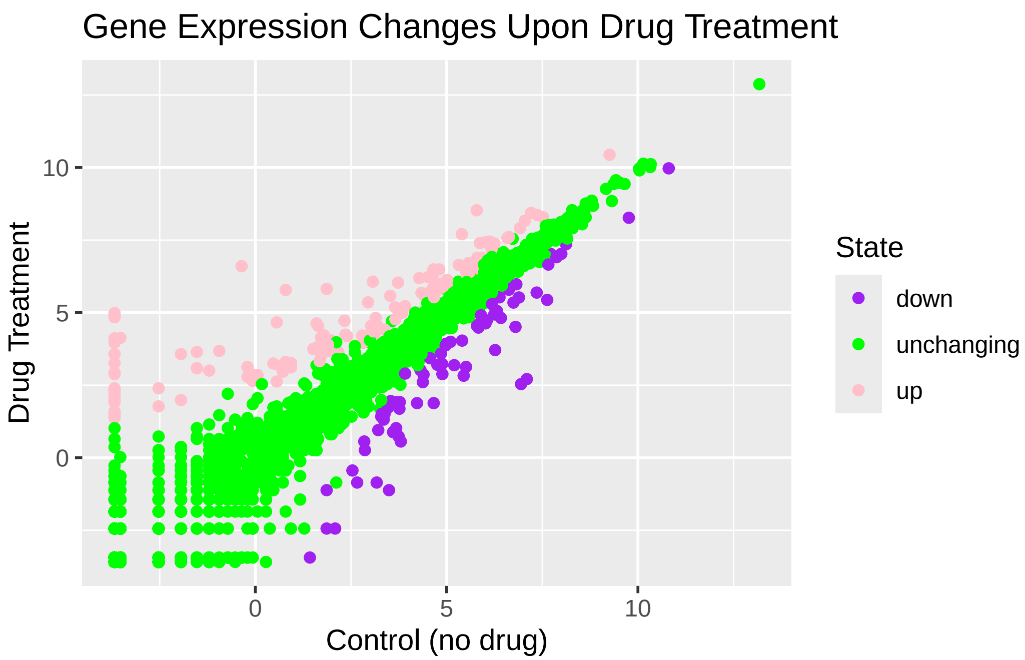


```
p <- ggplot(genes) +
     aes(x=Condition1, y=Condition2, col=State) +
     geom_point()
p
```



Change the colors

```
p + labs(title="Gene Expression Changes Upon Drug Treatment",
         x="Control (no drug)",
         y="Drug Treatment") +
  scale_color_manual(values=c("purple","green","pink"))
```



Exploring the gapminder dataset

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

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

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

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

```
nrow(gapminder)
```

```
[1] 1704
```

> Q. How many columns are in this dataset?

```
ncol(gapminder)
```

```
[1] 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 could use the `unique()` function…

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

```
[1] "Asia"     "Europe"   "Africa"   "Americas" "Oceania" 
```

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

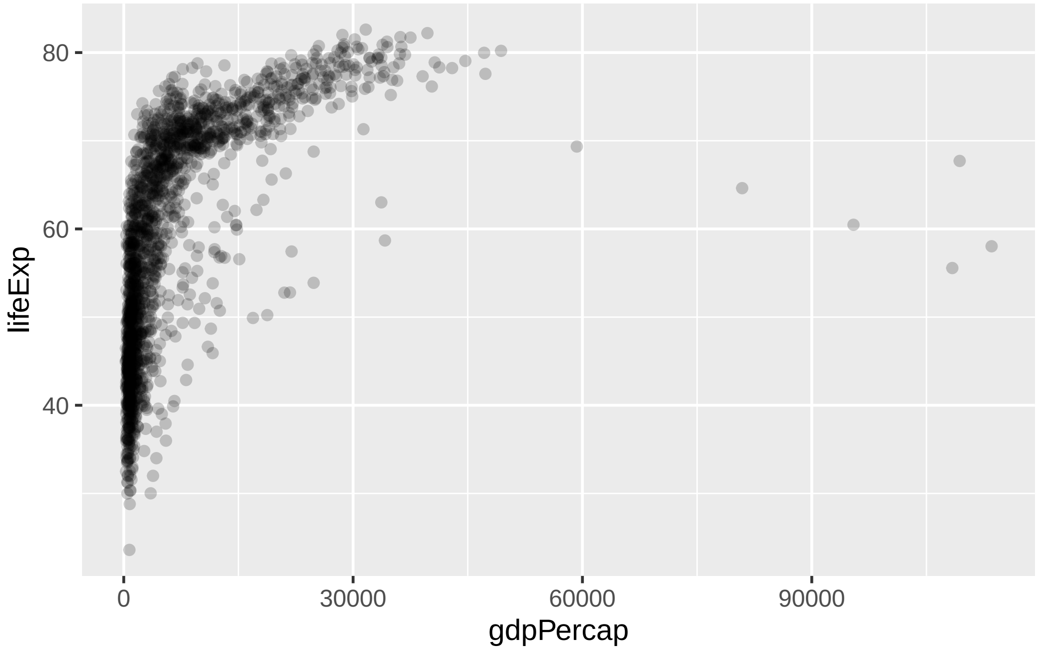
```
[1] 5
```

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

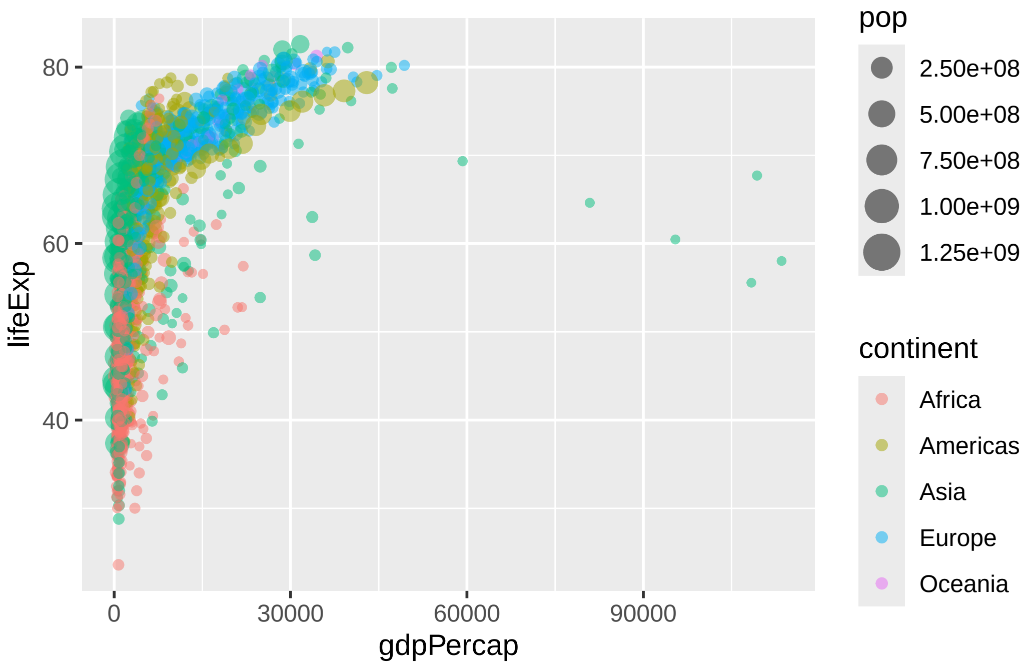
```r
length(unique(gapminder$country))
```

```
[1] 142
```

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp) +
  geom_point(alpha=0.2)
```



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



```r
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
```

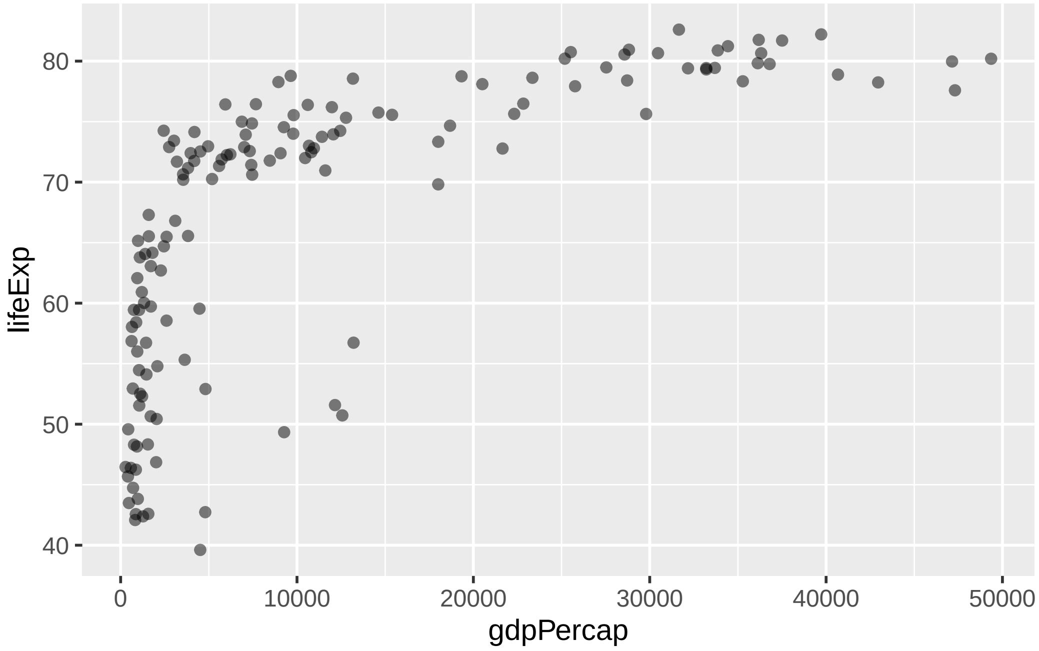
I need to install dplyr

```r
# install.packages("dplyr")  ## un-comment to install if needed
library(dplyr)

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

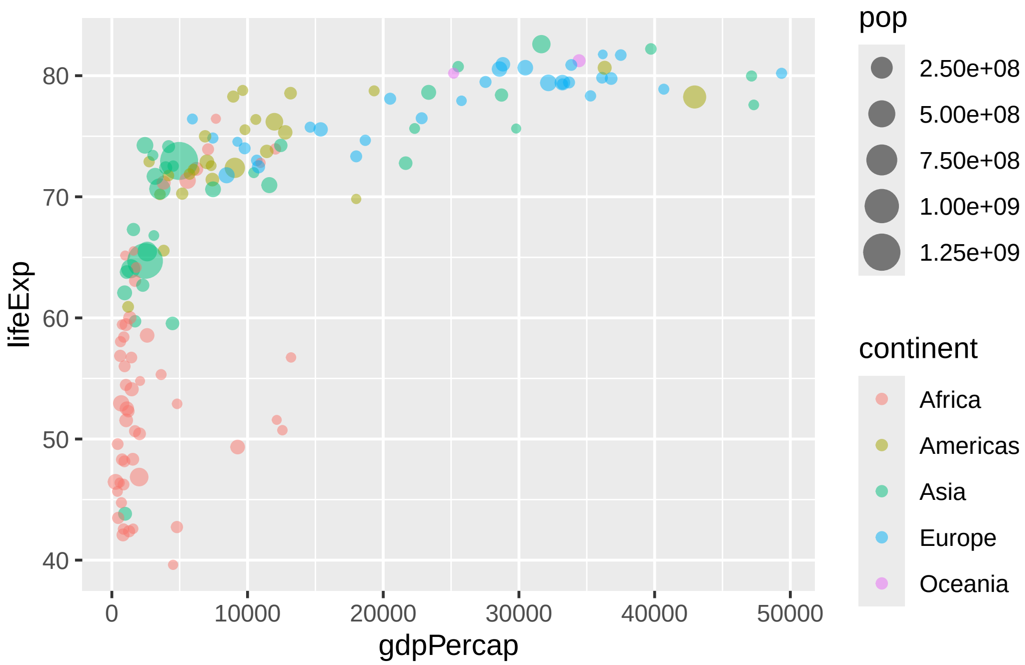
Plot of 2007 gapminder

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

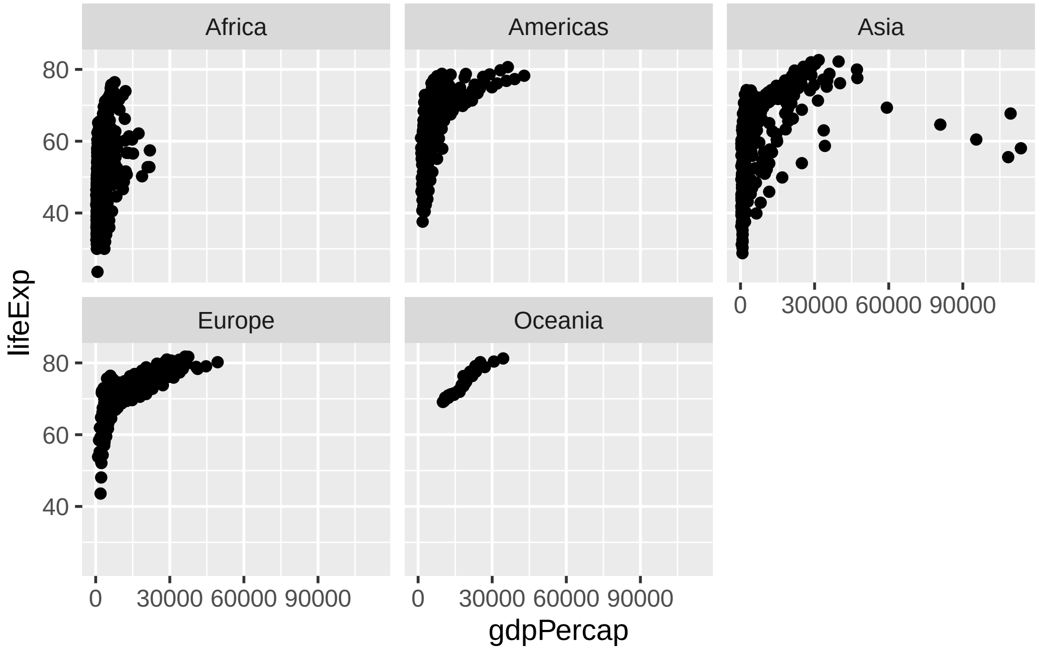


More aes

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



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


Africa
Americas
Asia
Europe
Oceania
lifeExp
80
60
40
0
30000
60000
90000
gdpPercap