Class 5: Data visualization with ggplot

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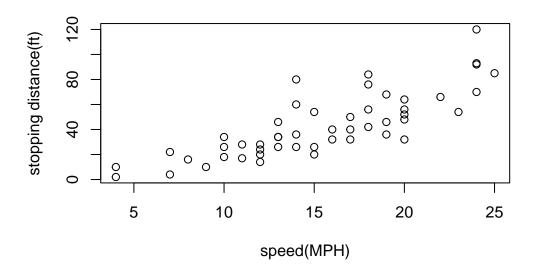
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Today we will have our first play with the **ggplot2** package - one of the most popular graphics packages on the planet. :D

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

```
plot(cars, xlab="speed(MPH)", ylab="stopping distance(ft)")
```



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 finally I can use ggplot!

```
ggplot(cars)
```

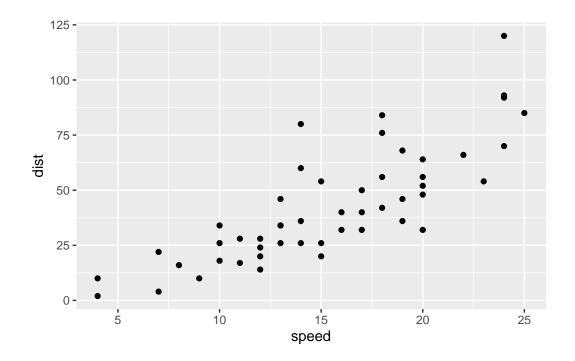
Every ggplot has at least 3 things:

- 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.)

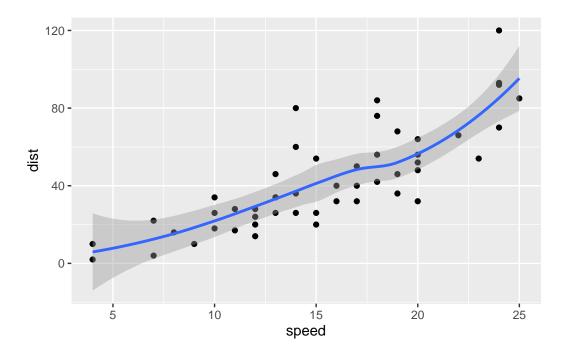
```
head(cars)
```

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

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

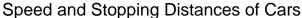


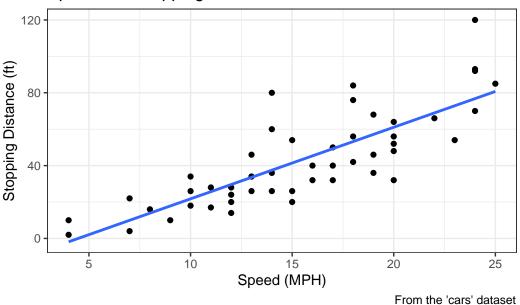
```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth()
```



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

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





A more complicated scatter plot

Here we make a plot of gene expression data

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

```
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
             5.0784720 5.0151916 unchanging
       AATF
       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?

```
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?

[1] 4

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
```

```
sum(genes$State =="up")
```

[1] 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.percent <- n.up/n.gene * 100</pre>
```

```
round (up.percent, 2)
[1] 2.44
  head(genes, 2)
  Gene Condition1 Condition2
1 A4GNT -3.680861 -3.440135 unchanging
```

geom_point()

p

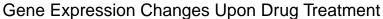
```
2 AAAS
          4.547958
                      4.386413 unchanging
  p <- ggplot(genes) +</pre>
    aes(x=Condition1, y=Condition2, col=State) +
```

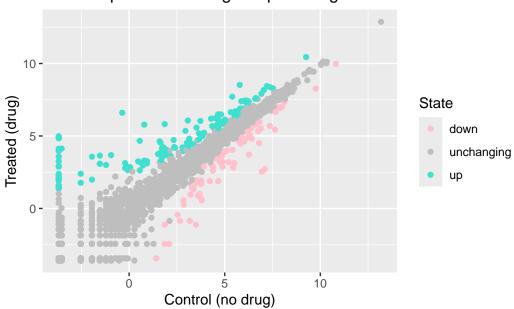
```
10-
                                                                              State
Condition2
                                                                                   down
                                                                                   unchanging
                                                                                   up
                       0
                                                          10
                                         5
                                  Condition1
```

State

```
p + labs(title="Gene Expression Changes Upon Drug Treatment",
 x="Control (no drug)",
 y="Treated (drug)") +
```

```
scale_color_manual( values=c("pink", "grey", "turquoise"))
```





Explore the gapminder dataset

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

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.
gapminder <- read.delim(url)
Q. how many rows and columns can be found in this dataframe?</pre>
```

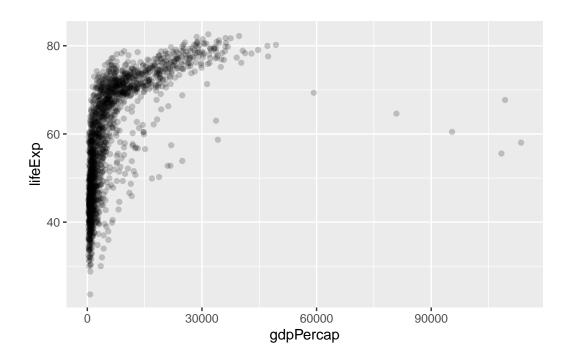
```
row <- nrow(gapminder)
column <- ncol(gapminder)
row</pre>
```

[1] 1704

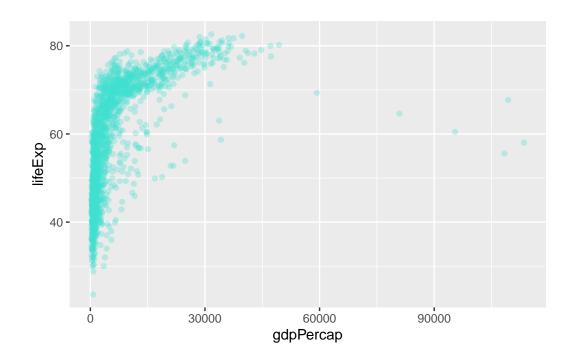
column

```
[1] 6
```

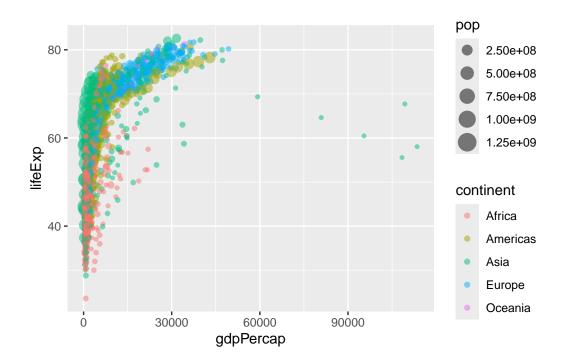
```
head(gapminder)
      country continent year lifeExp
                                            pop gdpPercap
1 Afghanistan
                    Asia 1952
                               28.801
                                       8425333 779.4453
2 Afghanistan
                    Asia 1957
                               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
                    Asia 1977 38.438 14880372 786.1134
6 Afghanistan
     Q. How many continents are there in the dataset?
  table(gapminder$continent)
  Africa Americas
                       Asia
                              Europe
                                      Oceania
     624
              300
                        396
                                 360
                                            24
I could use the unique() function...
  length(unique(gapminder$continent))
[1] 5
     Q. How many countries are there in this dataset?
  length(unique(gapminder$country))
[1] 142
  ggplot(gapminder) +
    aes(x=gdpPercap, y=lifeExp) +
    geom_point(alpha=0.2)
```



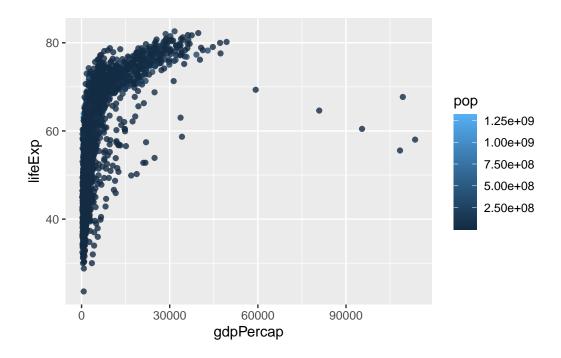
```
ggplot(gapminder) +
aes(x=gdpPercap, y=lifeExp) +
geom_point(col="turquoise", alpha=0.3)
```



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



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



```
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)</pre>
```

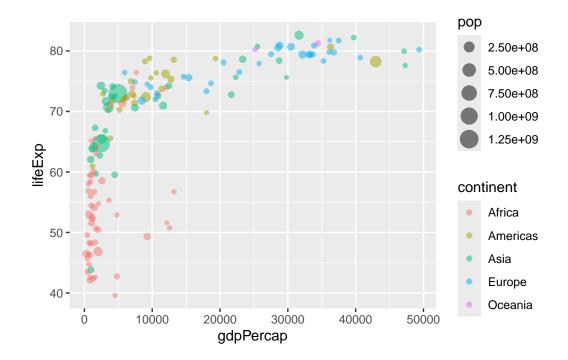
#install.packages("dplyr")

country continent year lifeExp pop gdpPercap 1 Afghanistan Asia 2007 43.828 31889923 974.5803

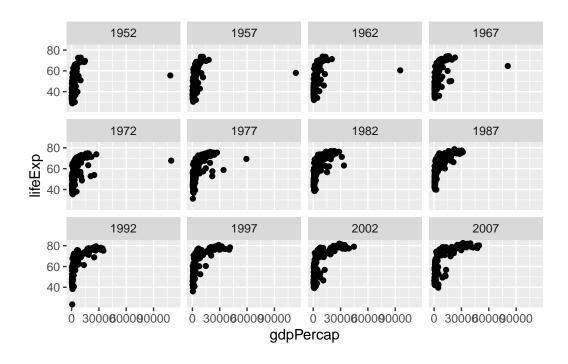
```
2
      Albania
                Europe 2007 76.423
                                      3600523 5937.0295
3
      Algeria
                Africa 2007
                              72.301 33333216
                                               6223.3675
4
      Angola
                 Africa 2007
                              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=0.5)
```



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



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

