Class05

Yipeng Li(A16164737)

2023-04-18

Base R graphics vs ggplots 2

There are many graphics systems available in R, including so-called "base" R graphics and the very popular **ggplot2** package.

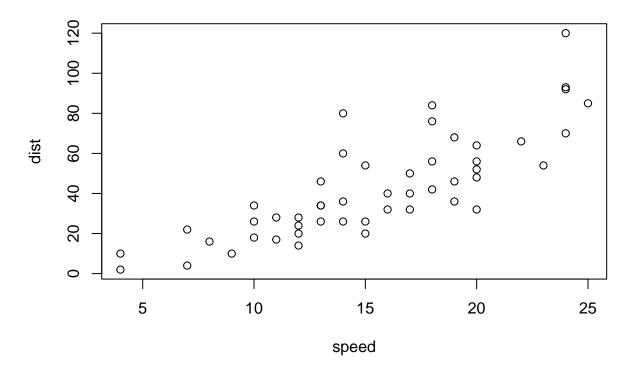
To compare these let's play with the inbuilt cars dataset.

head(cars)

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

To use "base" R I can simply call the plot() function:

```
plot(cars)
```



To use ggplot2 package I first need to install it with the function install.packages("ggplot2").

I will run this in my R console (i.e. the R brain) as I do not want to re-install it every time i ender my report...

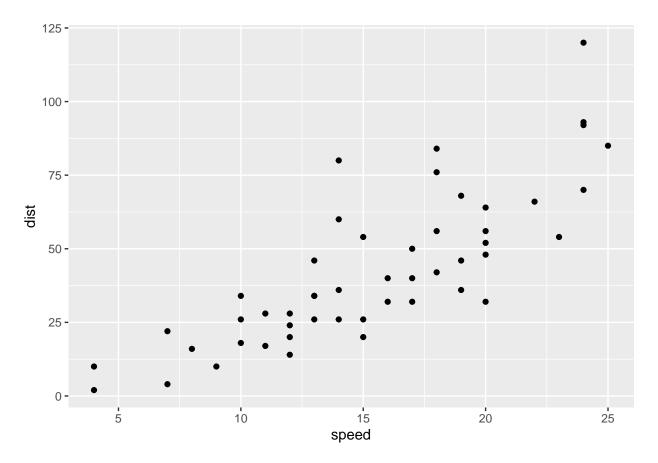
The main function in this package is called <code>ggplot()</code>. Can I just call it

library(ggplot2)
ggplot()

To make a figure with ggplot I need always at least 3 things:

- aes the aesthetic mapping of the data to the plot I want.
- the **geom** i.e. how I want to plot the data with different geometry

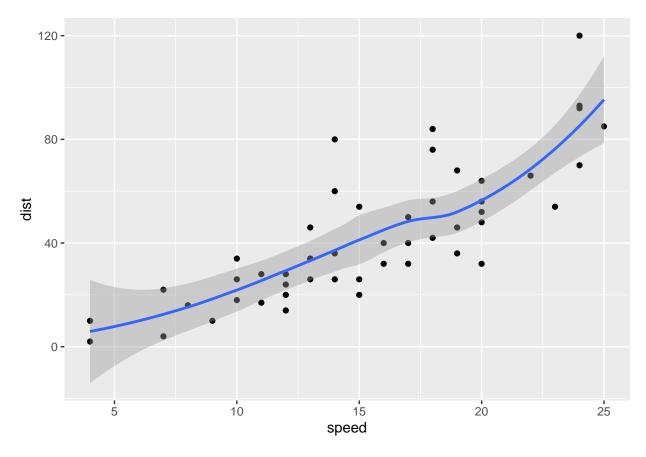
```
ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



If I want to add more things I can just keep addng layers, e.g.

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

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

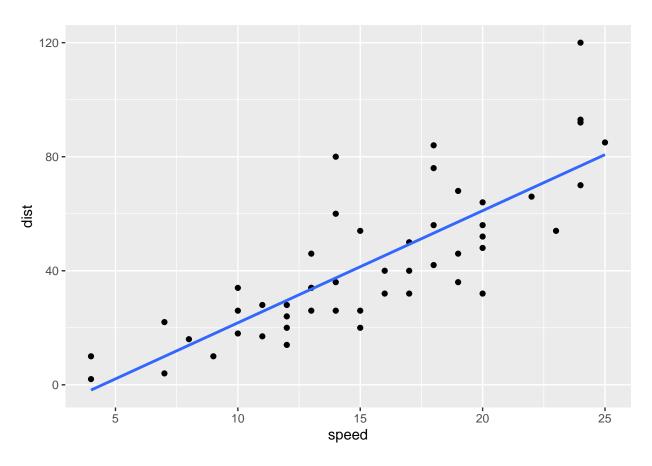


GGplot is much more verbose that base R plots for standard plots but it has a consistent layer system that I can use to make just about any plot.

Let's make a plot with a straight line fit -i.e. a linear model and no standard error shown.

```
ggplot(data=cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(se=FALSE, method="lm")
```

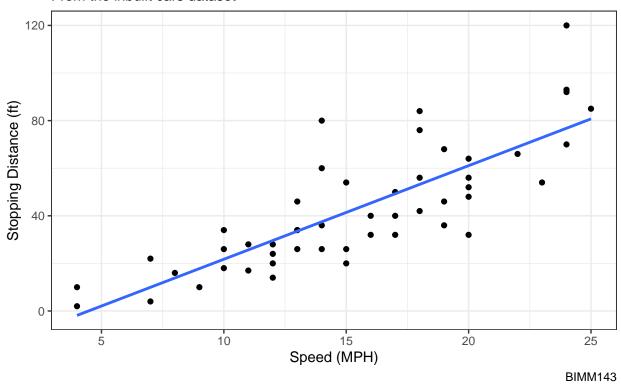
'geom_smooth()' using formula = 'y ~ x'



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

Speed and Stopping Distances of Cars

From the inbuilt cars dataset



A more complicated plot

Let's plot some gene expression data. The code bbelow reads the results on differential expression analysis where a new anti-viral drug is being tested.

```
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
          AATF
                5.0784720 5.0151916 unchanging
## 5
          AATK 0.4711421 0.5598642 unchanging
## 6 AB015752.4 -3.6808610 -3.5921390 unchanging
```

Q. How many genes are in this dataset?

```
nrow(genes)
```

```
## [1] 5196
```

Q. How can we summarize that last column - the "State" column?

down unchanging up ## 72 4997 127 Q. Fraction of total

##

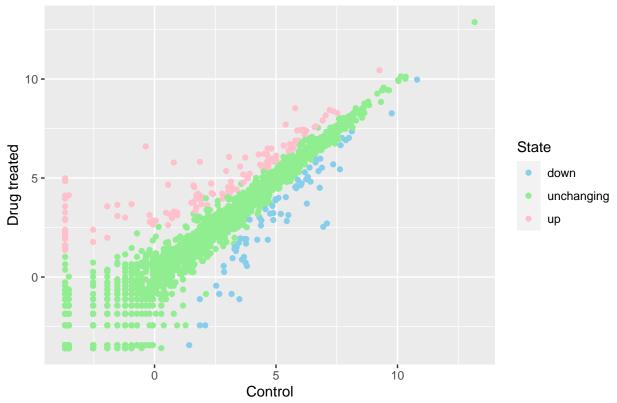
```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

```
## down unchanging up
## 1.39 96.17 2.44

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

I can know just call p when I want to plot or add to it

Gene Expression changes upon drug treatment

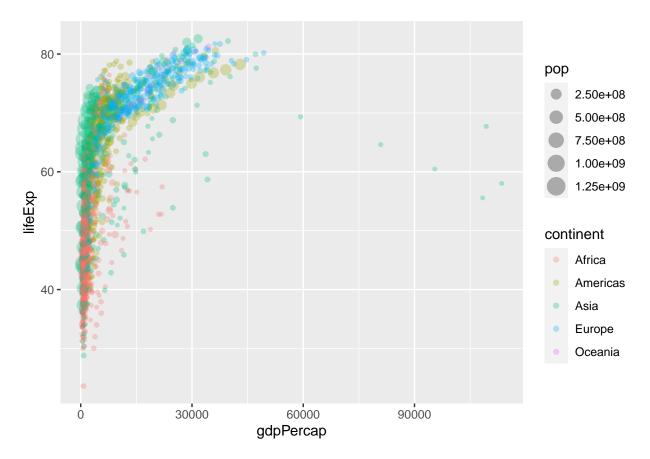


Going further

Here I read a slightly larger dataset

geom_point(alpha=0.3)

```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.tsv"</pre>
gapminder <- read.delim(url)</pre>
head(gapminder)
                                             pop gdpPercap
##
         country continent year lifeExp
## 1 Afghanistan
                      Asia 1952 28.801 8425333 779.4453
## 2 Afghanistan
                                 30.332 9240934 820.8530
                      Asia 1957
## 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
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop)+
```



A very useful layer to add sometimes is for "faceting"

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop)+
  geom_point(alpha=0.3) +
  facet_wrap(~continent)
```

