

# Introduction to R

February 9, 2018

# R and RStudio

The image shows the RStudio interface with four key components highlighted by numbered callouts:

- 1) Script:** Points to the editor window containing R code. The code includes comments and functions for loading data, creating scatterplots, and adding regression lines.
- 2) Console:** Points to the terminal window showing the output of the R script, including variable types and values.
- 3) Workspace:** Points to the environment pane showing the objects loaded in memory, such as 'google' and 'reg1'.
- 4) Results/Plots:** Points to the plot window displaying a scatterplot titled 'Interest in Data Visualization Searches by Percent of Population with College Degrees'.

The scatterplot shows a positive correlation between the percentage of the population with college degrees (x-axis, 15 to 45) and the number of searches for 'Data Visualization' (y-axis, -1 to 3). A red regression line and a blue smoothed line are overlaid on the data points.

# What R can do

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Everything.<sup>1,2</sup>

1 Except think about your science

2 Occasionally in a non efficient way

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## What about RStudio?

- Makes your life easier
- Many handy tricks. So far we have seen:
  - ▶ Autocomplete suggestion (all alone or press tab)
  - ▶ Ctrl-Enter to send command to R
  - ▶ `str()` and `View()` objects in Environment

1 The mean

2 Data-frames

3 Visualisation

4 T-test

# Calculating a mean: Arithmetic and assignment

```
(2 + 3 + 5 + 1) / 4
```

```
[1] 2.75
```

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```
b <- 3
```

```
c <- 5
```

```
d <- 1
```

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```
b <- 3
```

```
c <- 5
```

```
d <- 1
```

```
(a + b + c + d) / 4
```

```
[1] 2.75
```

```
a <- 45
```

```
(a + b + c + d) / 4
```

```
[1] 13.5
```

# Calculating a mean: using vectors

```
c(2,3,5,1) # c is for concatenate
```

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[1] 2 3 5 1
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mydata <- c(2,3,5,1) # save the vector
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mydata <- c(2,3,5,1) # save the vector
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```
mydata <- (2,3,5,1) # c is missing => error!
```

```
Error: <text>:1:14: unexpected ','  
1: mydata <- (2,  
               ^
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```
Error: <text>:1:14: unexpected ',',  
1: mydata <- (2,  
  ^
```

Why bother with vectors?

```
mydata[2] <- 4  
mydata
```

```
[1] 2 4 5 1
```

# Calculating a mean: using functions

How to use a function?

```
?mean
```

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How to use a function?

```
?mean
```

```
mean(c(2,4,5,1))
```

```
[1] 3
```

```
mean(mydata)
```

```
[1] 3
```

```
mean(x = mydata)
```

```
[1] 3
```

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# Loading data

```
data("trees")
```

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```
data("trees")
```

```
str(trees)
```

```
'data.frame': 31 obs. of 3 variables:
```

```
$ Girth : num 8.3 8.6 8.8 10.5 10.7 10.8 11 11 11.1 11.2 ...
```

```
$ Height: num 70 65 63 72 81 83 66 75 80 75 ...
```

```
$ Volume: num 10.3 10.3 10.2 16.4 18.8 19.7 15.6 18.2 22.6 19.9 ...
```

Try also `summary`, `class`, `head`, `tail`

# Access

## Bracket-syntax

- Row: `dataframe[row, ]`
- Column: `dataframe[ , column]`
- Element: `dataframe[row, column]`

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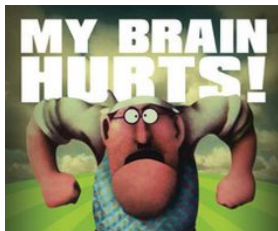
```
trees[,1]  
trees[1:8,]  
trees[c(2,1,2), 3]  
trees[, "Height"]
```

## Dollar-syntax

- Column `dataframe$column_name`
- Element `dataframe$column_name[row]`

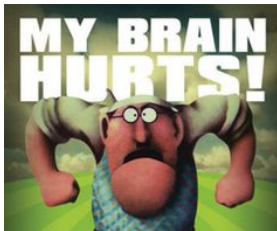
```
trees$Height
```

Finally time to think a tiny bit!



**Calculate the mean for all three variables in trees,  
excluding the last (31st) record.**

# Solution for one column



**Calculate the mean for all three variables in trees,  
excluding the last (31st) record.**

```
mean(trees$Girth[1:30])  
mean(trees[1:30, "Girth"])  
mean(trees$Girth[-31])  
mean(trees[-31, "Girth"])
```

# How to get the row means?

```
mean(trees[1,])  
mean(trees[2,])  
mean(trees[...])
```

# How to get the row means?

```
mean(trees[1,])  
mean(trees[2,])  
mean(trees[...])
```





# How to get the row means? For-loops

```
for (i in 1:N)
{
  something as a function of i
}
```

# How to get the row means? For-loops

```
for (i in 1:N)
{
  something as a function of i
}
```

```
ResultMean <- vector() # we will store the results there
for (i in 1:31)
{
  ResultMean[i] <- mean(as.numeric(trees[i,]))
}
```

# For-loops: your turn!

Load rock data.

```
data("rock")
```

**Use a for loop to obtain column averages**

# Solution

Load rock data.

```
data("rock")
```

**Use a for loop to obtain column averages**

```
storage <- vector(length = ncol(rock))  
for (i in 1:ncol(rock))  
{  
  storage[i] <- mean(rock[,i])  
}
```

# More concise alternative: apply functions

```
apply(X = dataframe, MARGIN = 1 (row) or 2 (col), FUN = function)
```

## More concise alternative: apply functions

```
apply(X = dataframe, MARGIN = 1 (row) or 2 (col), FUN = function)
```

```
apply(X = rock, MARGIN = 1, FUN = mean) #by row (not meaningful)  
apply(X = rock, MARGIN = 2, FUN = mean) #by column
```

## Even better (worse)...

```
colMeans(rock)  
rowMeans(rock)
```

# Even better (worse)...

```
colMeans(rock)
rowMeans(rock)
```

## Trade-off concision / flexibility

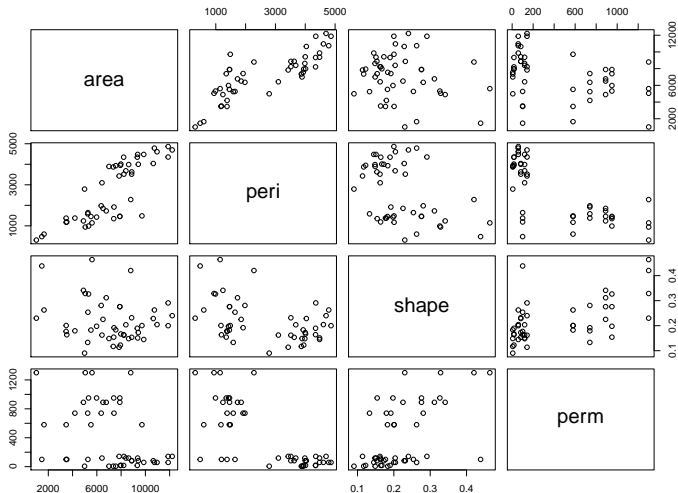
- colMeans shortest, but does only means
- apply very flexible, but does only array/matrix/data-frame
- for-loop looks complex, but infinitely flexible
- (NB: your computer does a for-loop whether you see it or not)



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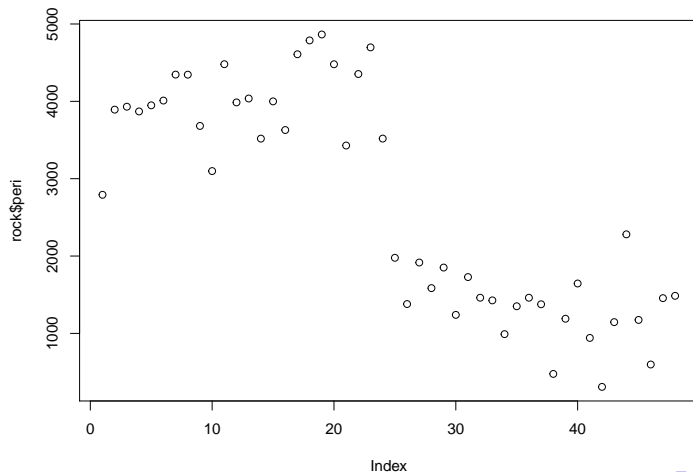
# plot function

```
plot(rock)
```



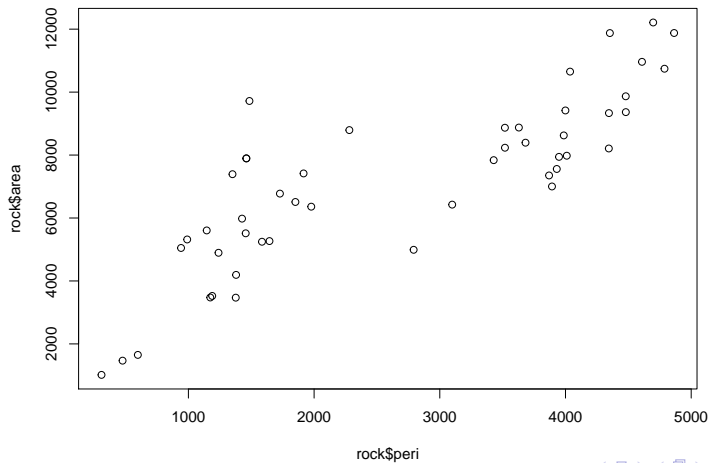
# plot function

```
plot(rock$peri)
```



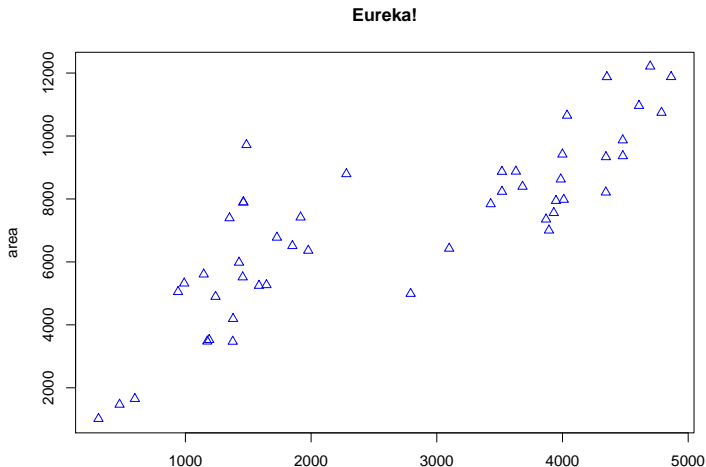
# plot function

```
plot(x = rock$peri, y = rock$area)
```



# plot function

```
plot(x = rock$peri, y = rock$area, main = "Eureka!",  
     xlab = "Perimeter", ylab = "area", col="blue", pch=2)
```

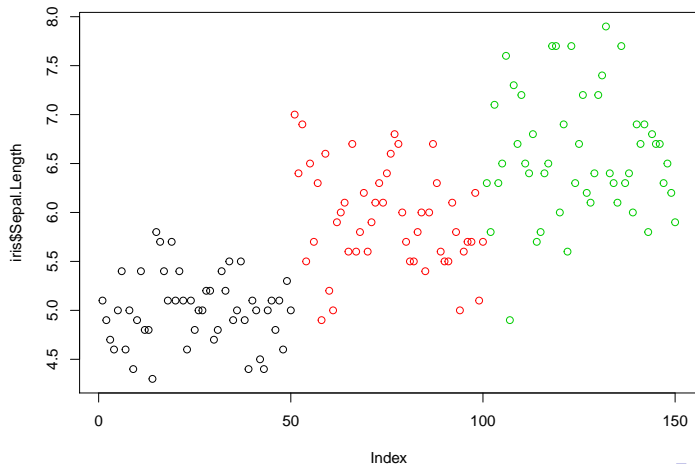


## plot function: back to the mean

```
data("iris")
```

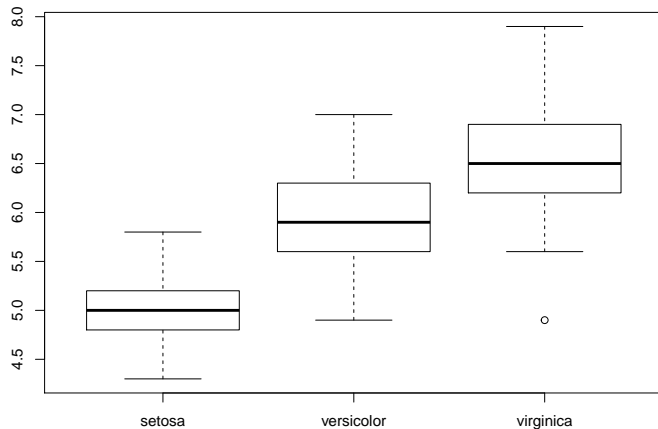
# plot function: back to the mean

```
plot(iris$Sepal.Length, col=iris$Species)
```



# boxplots

```
boxplot(iris$Sepal.Length ~ iris$Species)
```





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# Student's T.test introduction

```
?t.test
```

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```
t.test(1:10, y = c(7:20))
```

Welch Two Sample t-test

data: 1:10 and c(7:20)

t = -5.4349, df = 21.982, p-value = 1.855e-05

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-11.052802 -4.947198

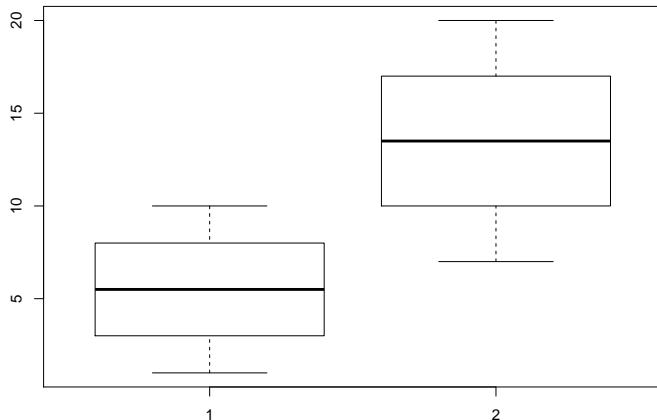
sample estimates:

mean of x mean of y

5.5 13.5

# T.test introduction

```
boxplot(c(1:10, 7:20) ~ c(rep(1,10), rep(2, 14)))
```



# Are irises different?

Use t-tests to compare species in the iris dataset



# Are irises different? Solution

## Use t-tests to compare species in the iris dataset

Sorry, I was mean and forgot to tell about subsetting, which you needed here.

Subset to the species *setosa*:

```
iris[iris$Species == "setosa", ]
```

One t-test for sepal length between *setosa* and *versicolor*:

```
t.test(x = iris$Sepal.Length[iris$Species == "setosa"],  
       y = iris$Sepal.Length[iris$Species == "versicolor"])
```