R

Programming

LEARN IN 1 DAY

KRISHNA RUNGTA

Learn R Programming in 1 Day

By Krishna Rungta

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Chapter 1: What is R Programming Language? Introduction & Basics

What is R?

R is a programming language developed by Ross Ihaka and Robert Gentleman in 1993. R possesses an extensive catalog of statistical and graphical methods. It includes machine learning algorithm, linear regression, time series, statistical inference to name a few. Most of the R libraries are written in R, but for heavy computational task, C, C++ and Fortran codes are preferred.

R is not only entrusted by academic, but many large companies also use R programming language, including Uber, Google, Airbnb, Facebook and so on.

Data analysis with R is done in a series of steps; programming, transforming, discovering, modeling and communicate the results

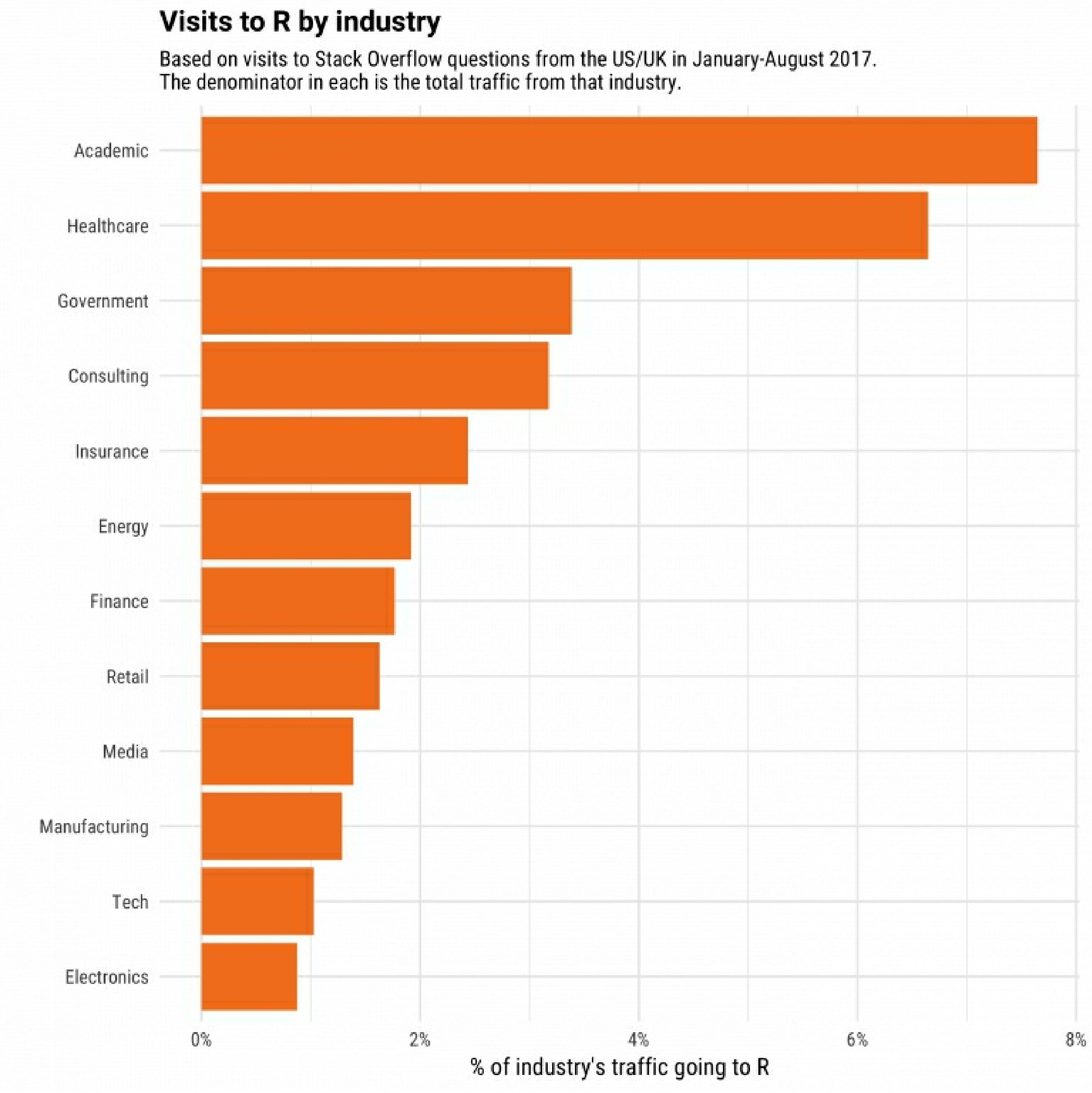
- **Program**: R is a clear and accessible programming tool
- **Transform**: R is made up of a collection of libraries designed specifically for data science
- **Discover**: Investigate the data, refine your hypothesis and analyze them
- **Model**: R provides a wide array of tools to capture the right model for your data
- **Communicate**: Integrate codes, graphs, and outputs to a report with R Markdown or build Shiny apps to share with the world

What is R used for?

- Statistical inference
- Data analysis
- Machine learning algorithm

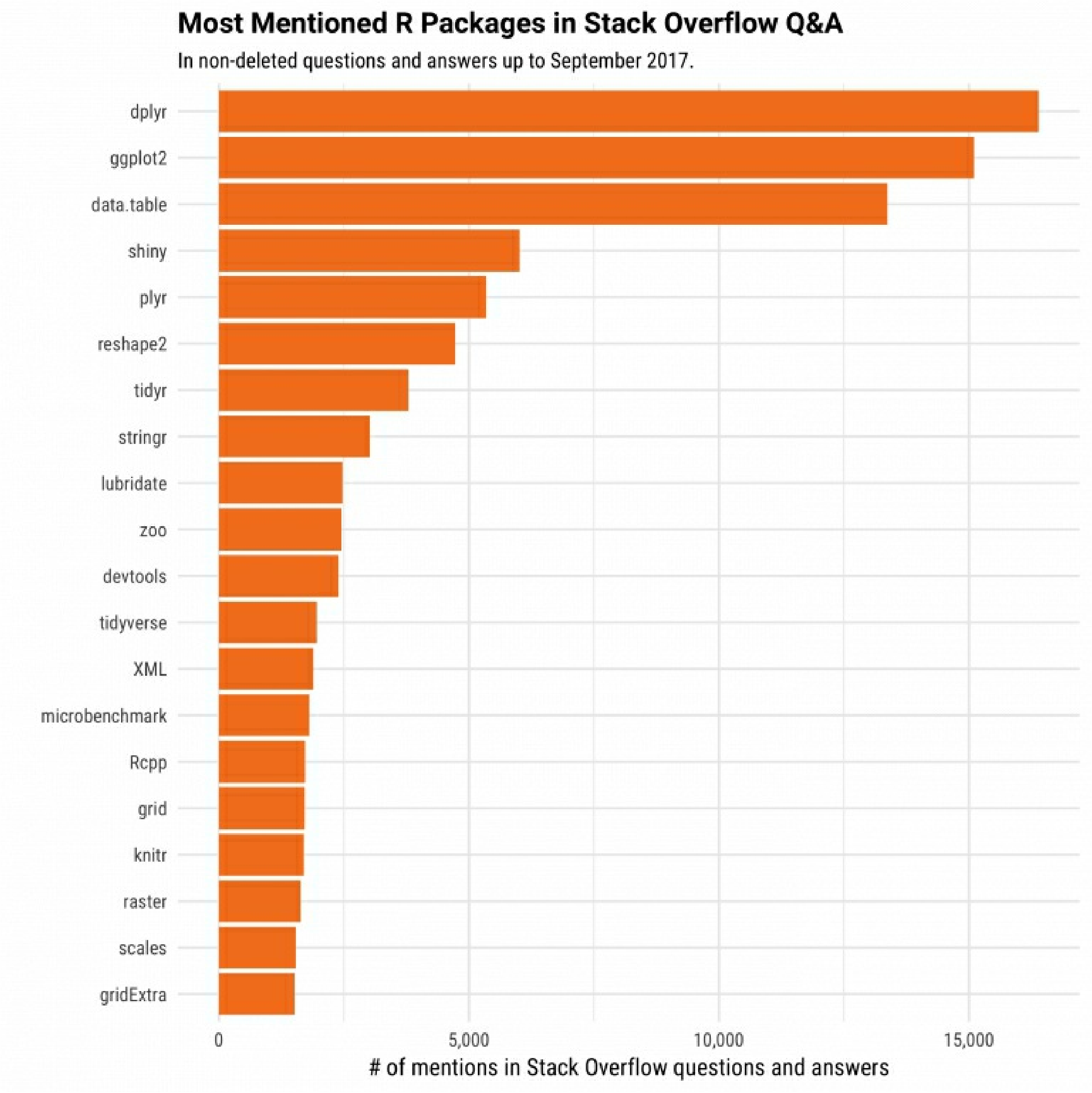
R by Industry

If we break down the use of R by industry, we see that academics come first. R is a language to do statistic. R is the first choice in the healthcare industry, followed by government and consulting.

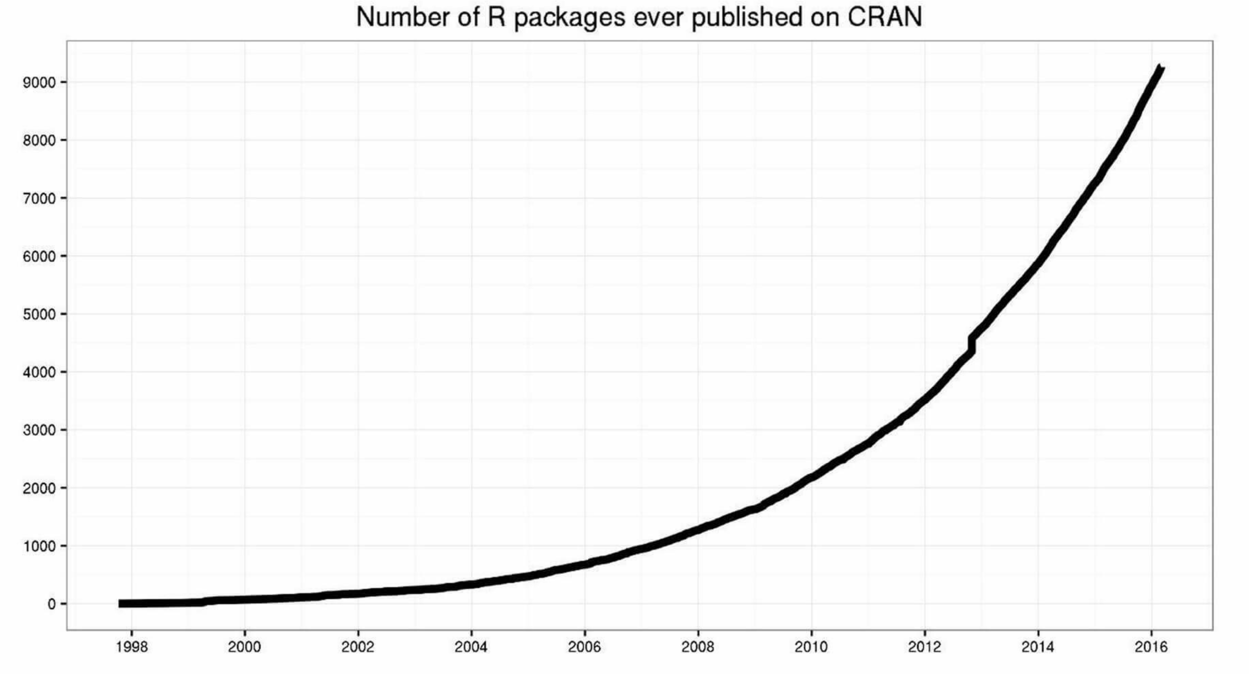


R package

The primary uses of R is and will always be, statistic, visualization, and machine learning. The picture below shows which R package got the most questions in Stack Overflow. In the top 10, most of them are related to the workflow of a data scientist: data preparation and communicate the results.



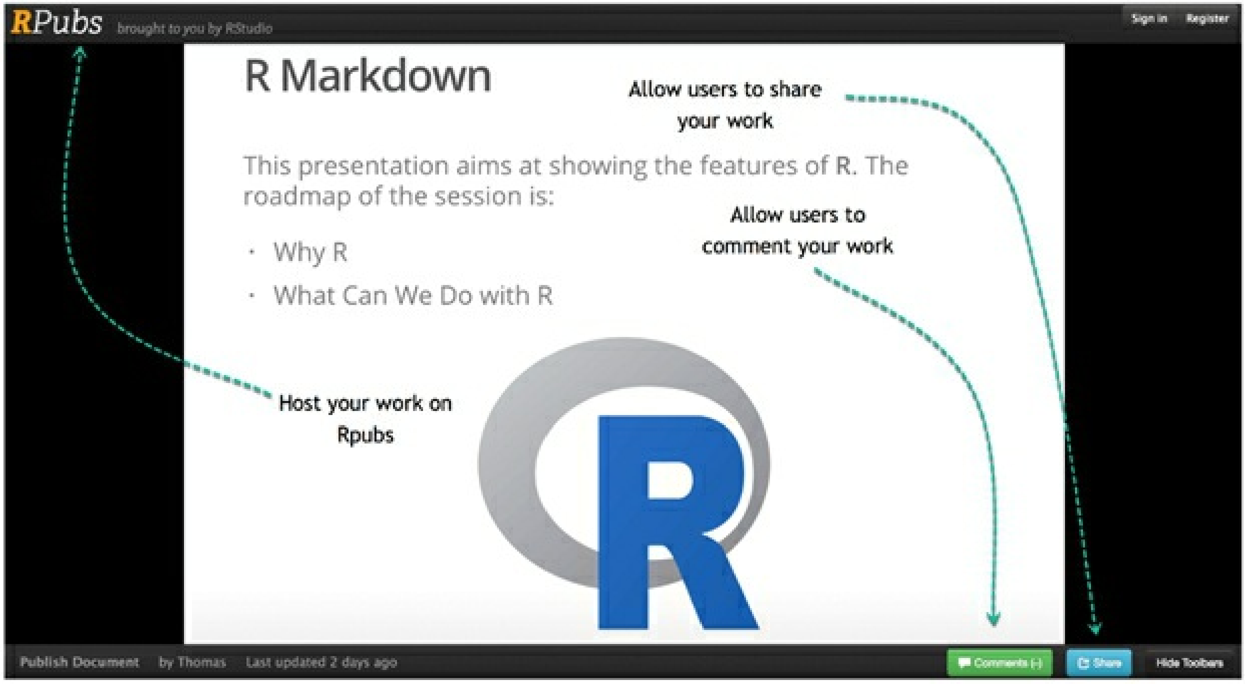
All the libraries of R, almost 12k, are stored in CRAN. CRAN is a free and open source. You can download and use the numerous libraries to perform Machine Learning or time series analysis.



Communicate with R

R has multiple ways to present and share work, either through a markdown document or a shiny app. Everything can be hosted in Rpub, GitHub or the business's website.

Below is an example of a presentation hosted on Rpub



R Markdown

This presentation aims at showing the features of R. The roadmap of the session is:

- Why R
- What Can We Do with R

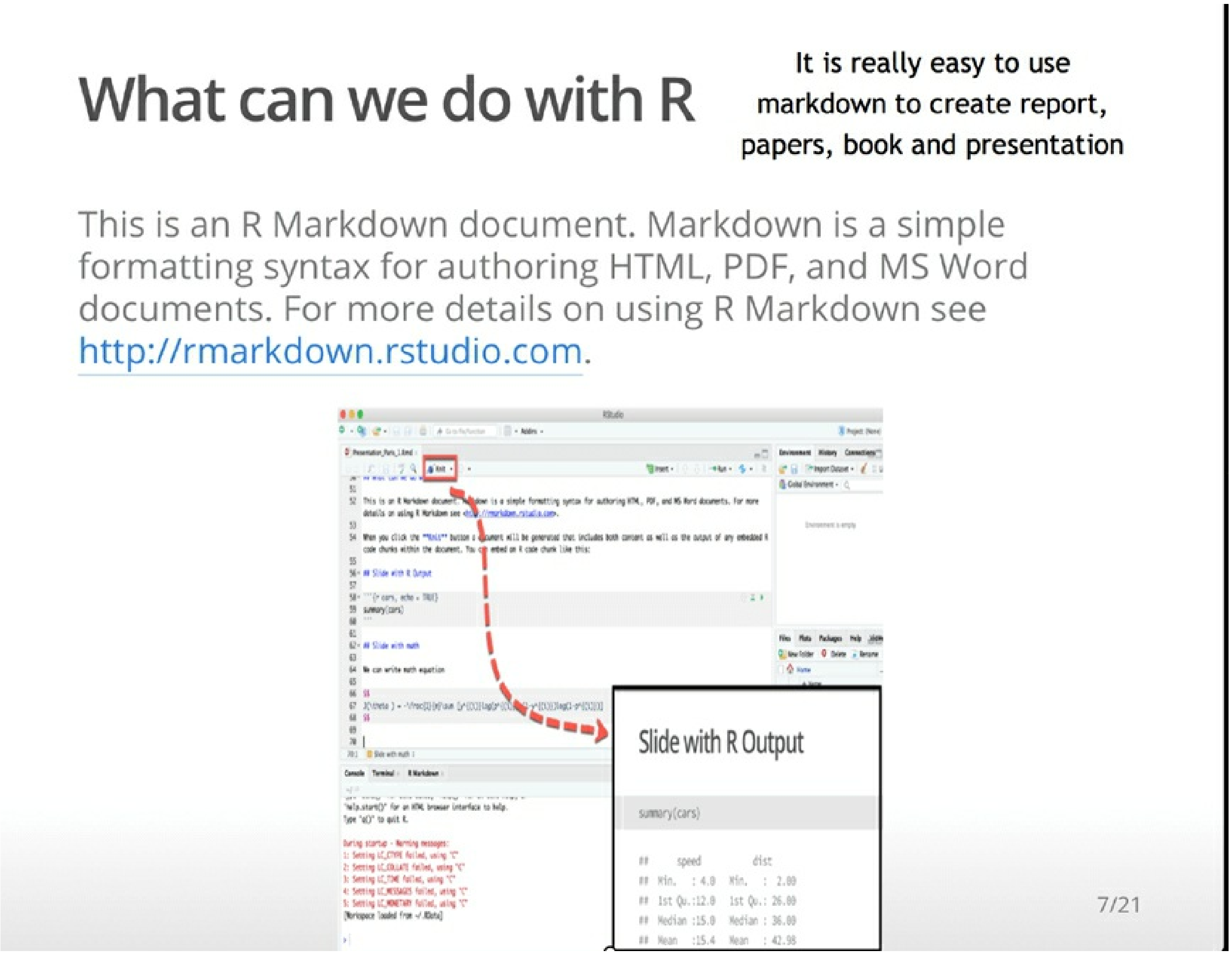
Allow users to share your work

Allow users to comment your work

Host your work on Rpubs

Rstudio accepts markdown to write a document. You can export the documents in different formats:

- Document :
    - HTML
    - PDF/Latex
    - Word
- Presentation
    - HTML
    - PDF beamer



What can we do with R

It is really easy to use markdown to create report, papers, book and presentation

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

~~~

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

Slide with R Output

```{r cars, echo = TRUE}
summary(cars)
~~~

## Slide with math

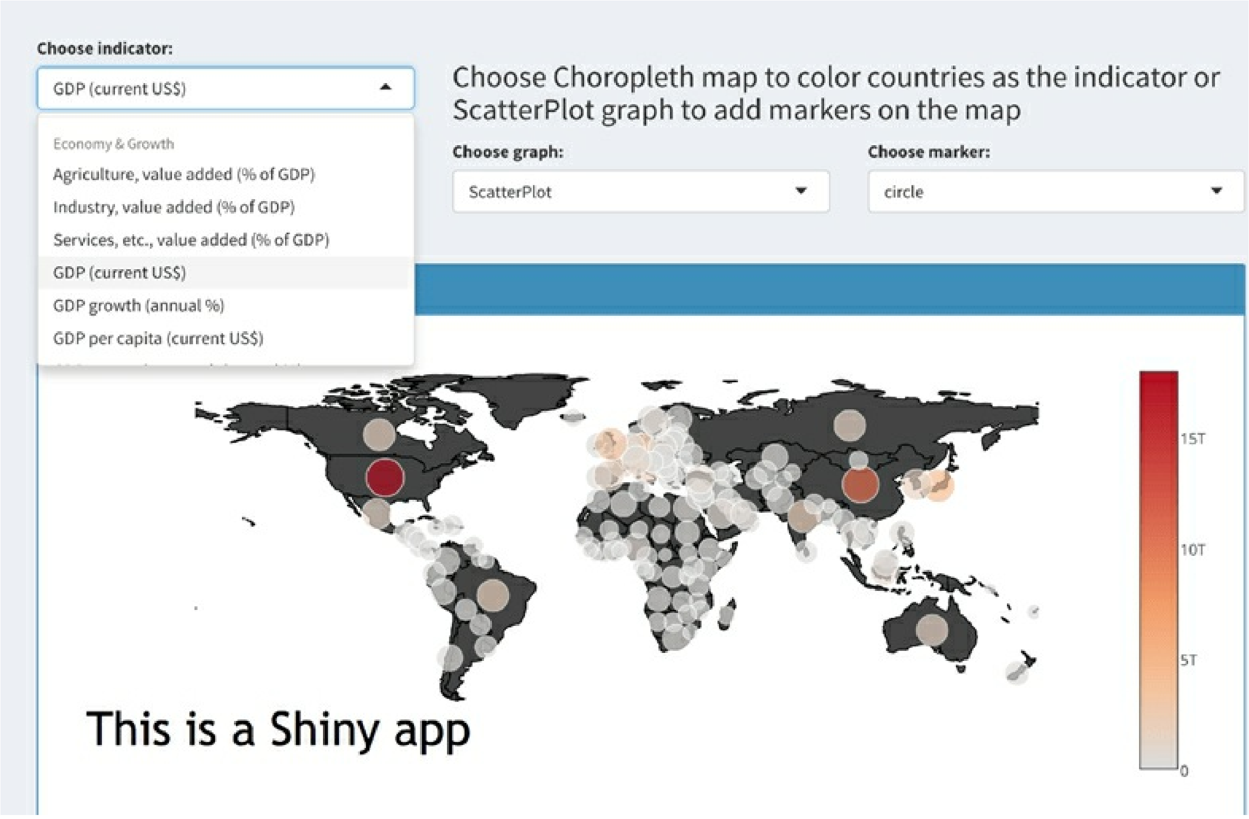
We can write math equation

$$
J(\theta ) = -\frac{1}{m}\sum [y^{(i)}\log(h^{(i)})+(1-y^{(i)})\log(1-h^{(i)})]
$$

```

```
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

During startup - Warning messages:
1: Setting LC_CTYPE failed, using "C"
2: Setting LC_COLLATE failed, using "C"
3: Setting LC_TIME failed, using "C"
4: Setting LC_MESSAGES failed, using "C"
5: Setting LC_MONETARY failed, using "C"
[Workspace loaded from ~/.RData]

>
```

Slide with R Output

```
summary(cars)
```

```
##      speed          dist
## Min.   : 4.0   Min.   :  2.00
## 1st Qu.:12.0   1st Qu.: 26.00
## Median :15.0   Median : 36.00
## Mean   :15.4   Mean   : 42.98
```

7/21

Rstudio has a great tool to create an App easily. Below is an example of app with the World Bank data.
```



Choose indicator: GDP (current US$)

Choose Choropleth map to color countries as the indicator or ScatterPlot graph to add markers on the map

Choose graph: ScatterPlot

Choose marker: circle

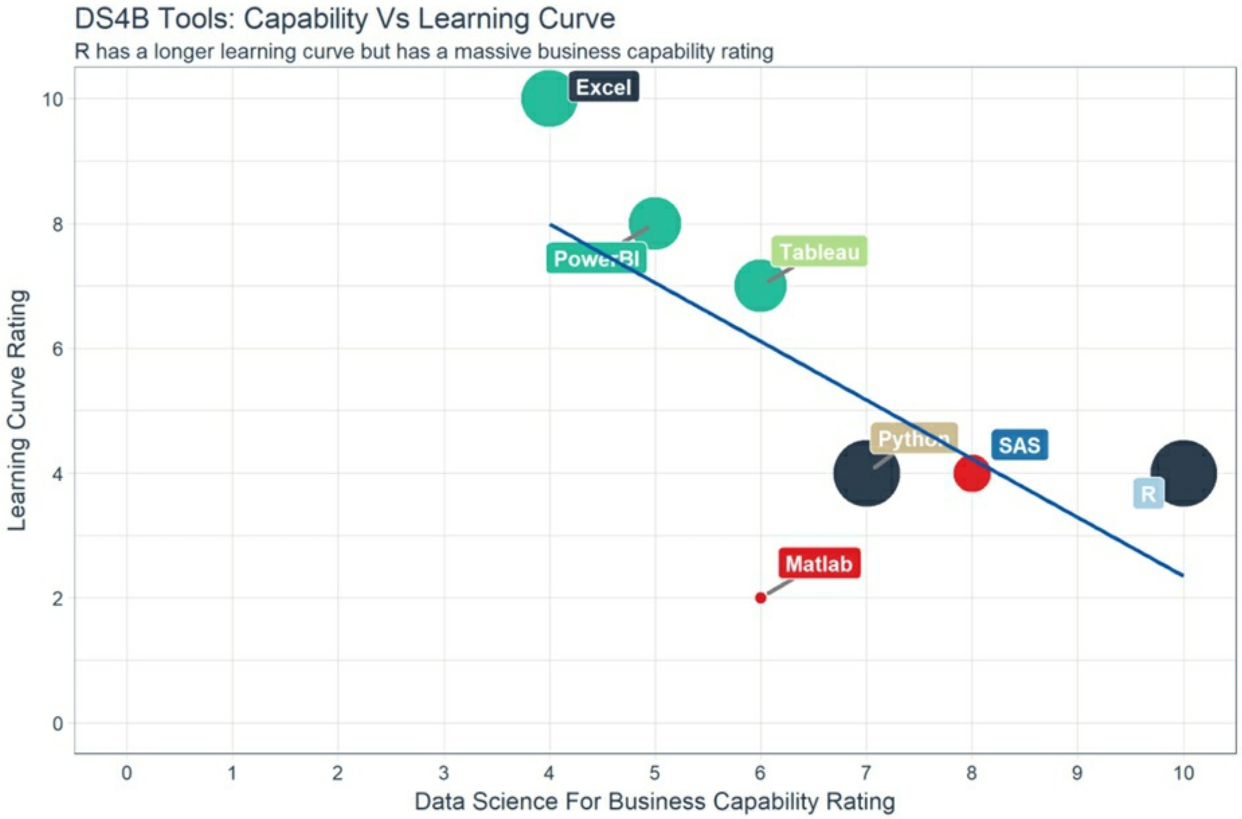
This is a Shiny app

Economy & Growth
Agriculture, value added (% of GDP)
Industry, value added (% of GDP)
Services, etc., value added (% of GDP)
GDP (current US$)
GDP growth (annual %)
GDP per capita (current US$)
15T
10T
5T
0

# Why use R?

Data science is shaping the way companies run their businesses. Without a doubt, staying away from Artificial Intelligence and Machine will lead the company to fail. The big question is which tool/language should you use?

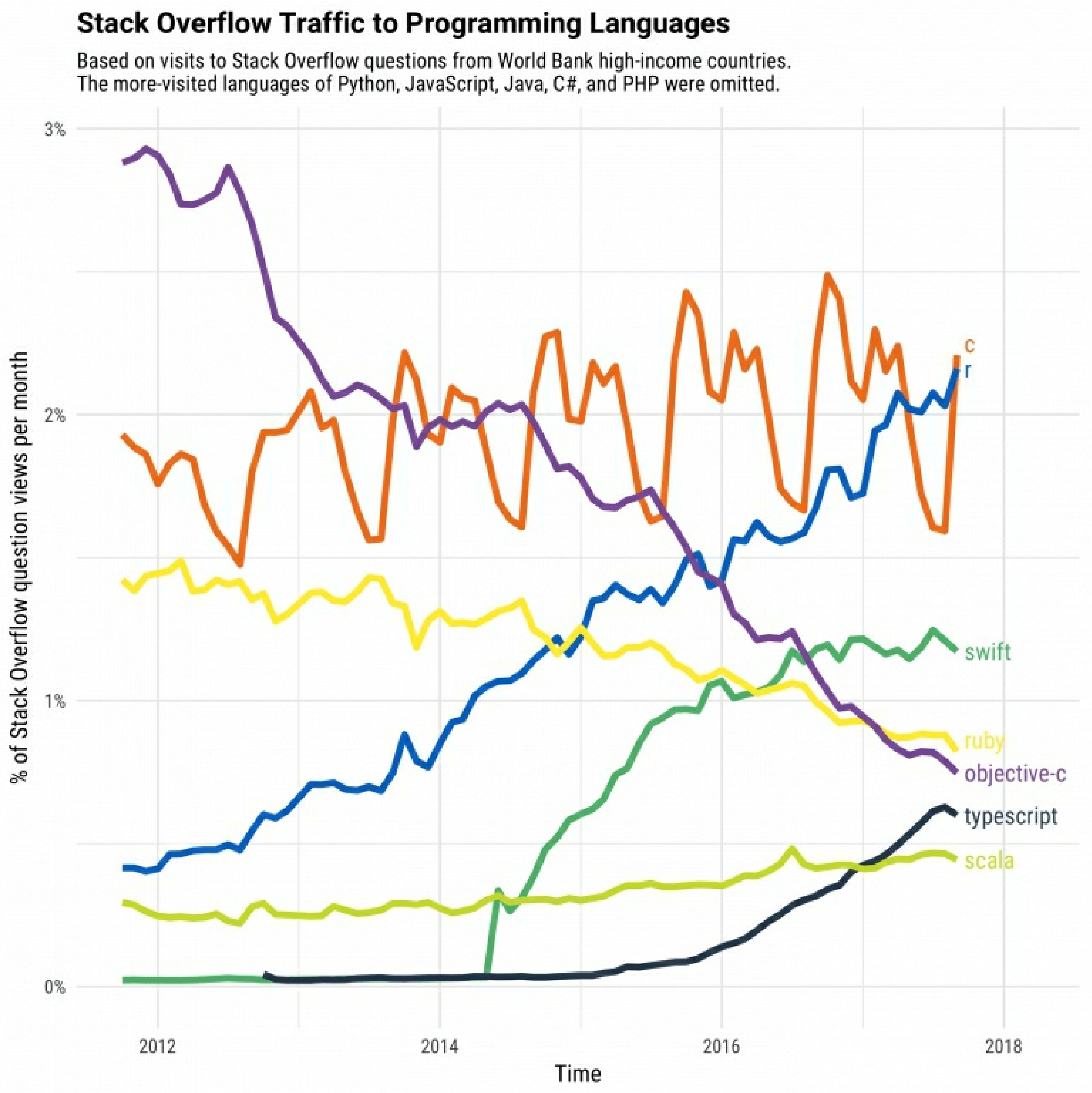
They are plenty of tools available in the market to perform data analysis. Learning a new language requires some time investment. The picture below depicts the learning curve compared to the business capability a language offers. The negative relationship implies that there is no free lunch. If you want to give the best insight from the data, then you need to spend some time learning the appropriate tool, which is R.



On the top left of the graph, you can see Excel and PowerBI. These two tools are simple to learn but don't offer outstanding business capability, especially in term of modeling. In the middle, you can see Python and SAS. SAS is a dedicated tool to run a statistical analysis for business, but it is not free. SAS is a click and run software. Python, however, is a language with a monotonous learning curve. Python is a fantastic tool to deploy Machine Learning and AI but lacks communication features. With an identical learning curve, R is a good trade-off between implementation and data analysis.

When it comes to data visualization (DataViz), you'd probably heard about Tableau. Tableau is, without a doubt, a great tool to discover patterns through graphs and charts. Besides, learning Tableau is not time-consuming. One big problem with data visualization is you might end up never finding a pattern or just create plenty of useless charts. Tableau is a good tool for quick visualization of the data or Business Intelligence. When it comes to statistics and decision-making tool, R is more appropriate.

Stack Overflow is a big community for programming languages. If you have a coding issue or need to understand a model, Stack Overflow is here to help. Over the year, the percentage of question-views has increased sharply for R compared to the other languages. This trend is of course highly correlated with the booming age of data science but, it reflects the demand of R language for data science.



In data science, there are two tools competing with each other. R and Python are probably the programming language that defines data science.

## Should you choose R?

Data scientist can use two excellent tools: R and Python. You may not have time to learn them both, especially if you get started to learn data science. **Learning statistical modeling and algorithm** is far more important than to learn a programming language. A programming language is a tool to compute and communicate your discovery. The most important task in data science is the way you deal with the data: import, clean, prep, feature engineering, feature selection. This should be your primary focus. If you are trying to learn R and Python at the same time without a solid background in statistics, its plain stupid. Data scientist are not programmers. Their job is to understand the data, manipulate it and expose the best approach. If you are thinking about which language to learn, let's see which language is the most appropriate for you.

The principal audience for data science is business professional. In the business, one big implication is communication. There are many ways to communicate: report, web app, dashboard. You need a tool that does all this together.

## Is R difficult?

Years ago, R was a difficult language to master. The language was confusing and not as structured as the other programming tools. To overcome this major issue, Hadley Wickham developed a collection of packages called tidyverse. The rule of the game changed for the best. Data manipulation become trivial and intuitive. Creating a graph was not so difficult anymore.

The best algorithms for machine learning can be implemented with R. Packages like Keras and TensorFlow allow to create high-end machine learning technique. R also has a package to perform Xgboost, one the best algorithm for Kaggle competition.

R can communicate with the other language. It is possible to call Python, Java, C++ in R. The world of big data is also accessible to R. You can connect R with different databases like Spark or Hadoop.

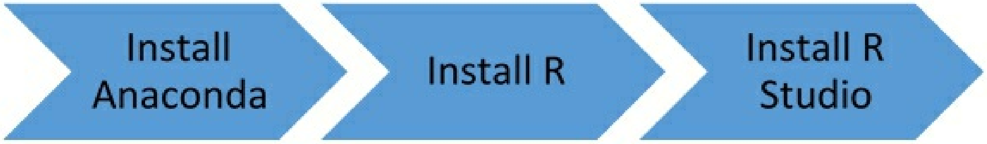
Finally, R has evolved and allowed parallelizing operation to speed up the computation. In fact, R was criticized for using only one CPU at a time. The parallel package lets you to perform tasks in different cores of the machine.

## Summary

In a nutshell, R is a great tool to explore and investigate the data. Elaborate analysis like clustering, correlation, and data reduction are done with R. This is the most crucial part, without a good feature engineering and model, the deployment of the machine learning will not give meaningful results.

# Chapter 2: How to Download & Install R, RStudio, Anaconda on Mac or Windows

R is a programming language. To use R, we need to install an **Integrated Development Environment** (IDE). **Rstudio** is the Best IDE available as it is user-friendly, open-source and is part of the Anaconda platform.



## Install Anaconda

### What is Anaconda?

Anaconda free open source is distributing both Python and R programming language. Anaconda is widely used in the scientific community and data scientist to carry out Machine Learning project or data analysis.

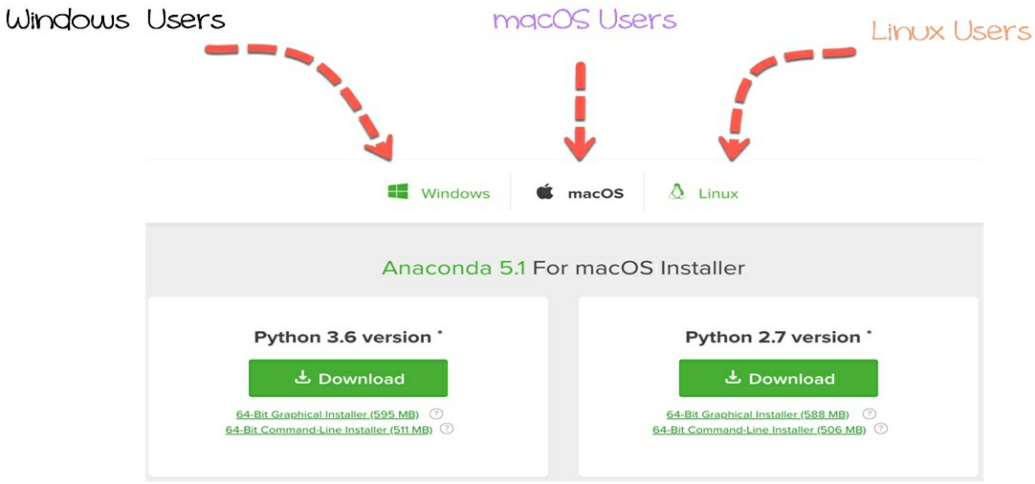
### Why use Anaconda?

Anaconda will help you to manage all the libraries required for Python, or R. Anaconda will install all the required libraries and IDE into one single folder to simplify package management. Otherwise, you would need to install them separately.

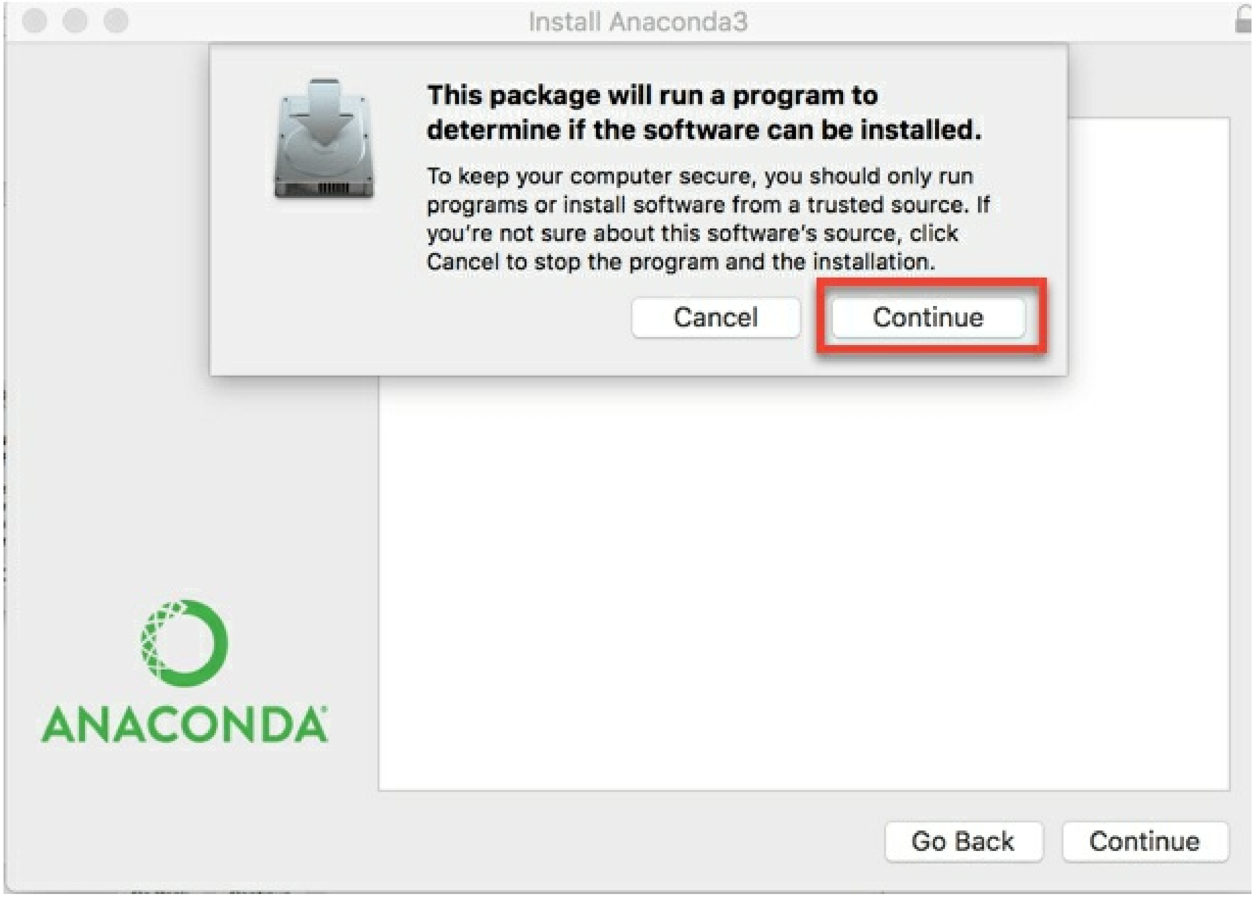
# Mac User

**Step 1) Go to https://www.anaconda.com/download/ and Download** Anaconda for Python 3.6 for your OS.

By default, Chrome selects the downloading page of your system. In this tutorial, installation is done for Mac. If you run on Windows or Linux, download Anaconda 5.1 for Windows installer or Anaconda 5.1 for Linux installer.


Windows Users
macOS Users
Linux Users
Windows
macOS
Linux
Anaconda 5.1 For macOS Installer
Python 3.6 version *
Download
64-Bit Graphical Installer (595 MB)
64-Bit Command-Line Installer (511 MB)
Python 2.7 version *
Download
64-Bit Graphical Installer (588 MB)
64-Bit Command-Line Installer (506 MB)

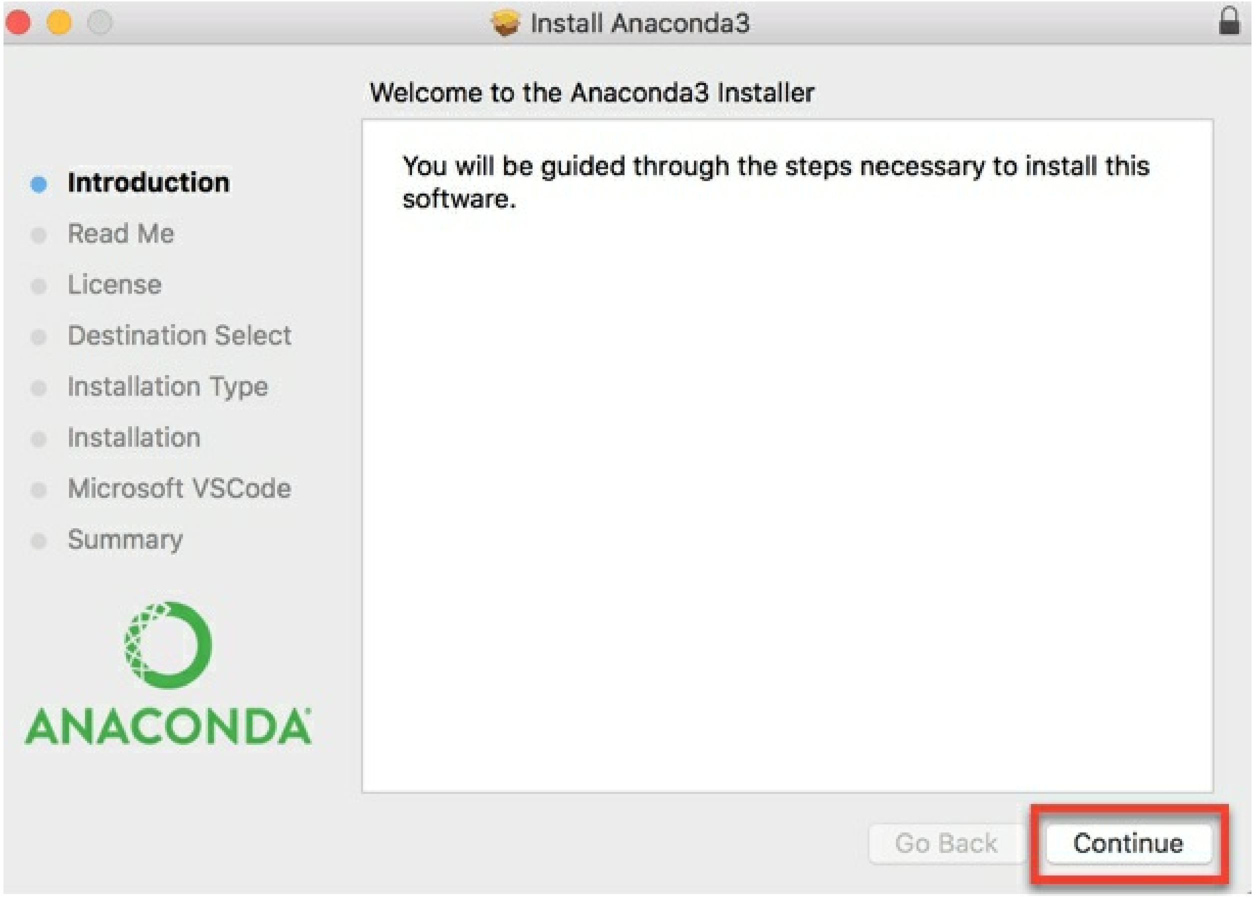
**Step 2)** You are now ready to install Anaconda. Double-click on the downloaded file to begin the installation. It is .dmg for mac and .exe for windows. You will be asked to confirm the installation. Click **Continue** button.



**This package will run a program to determine if the software can be installed.**

To keep your computer secure, you should only run programs or install software from a trusted source. If you're not sure about this software's source, click Cancel to stop the program and the installation.

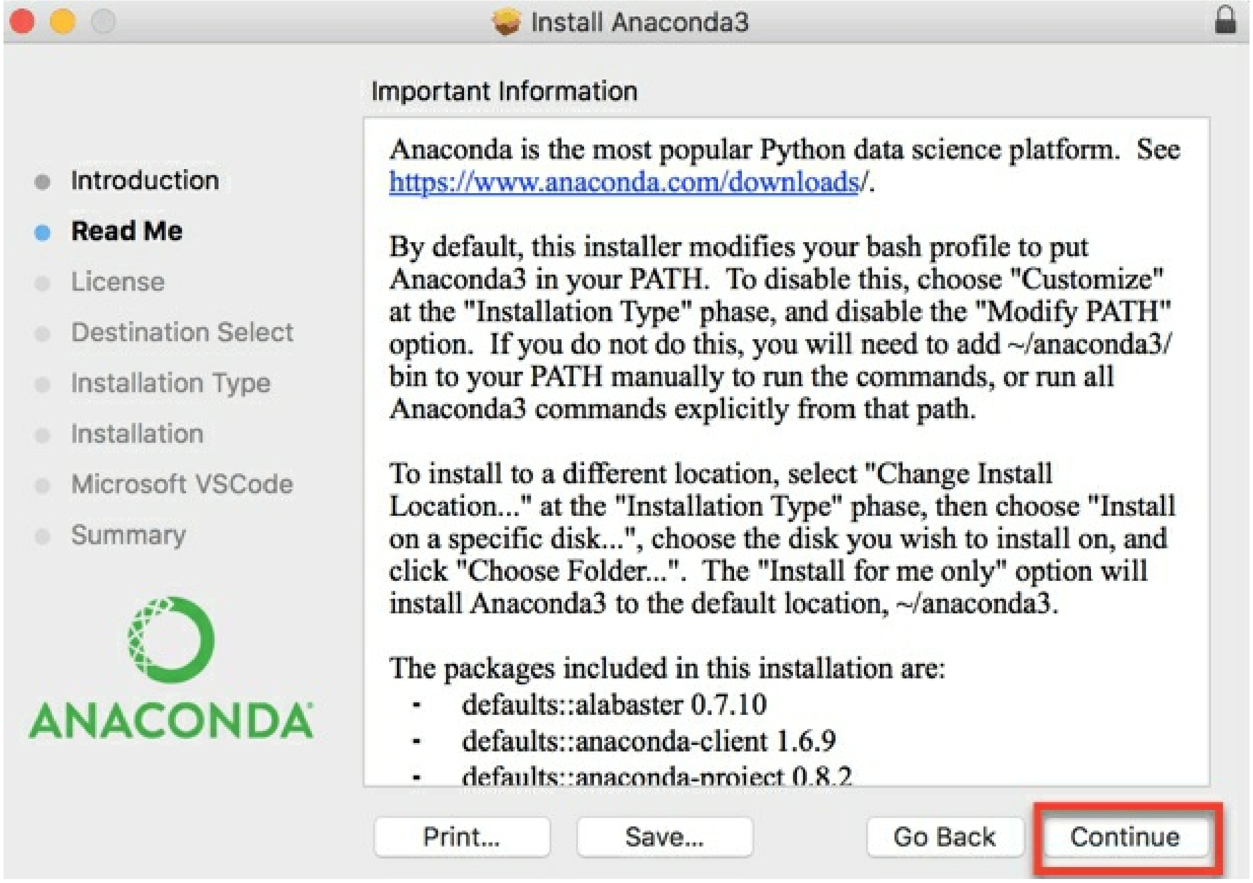
You are redirected to the **Anaconda3 Installer**.



Welcome to the Anaconda3 Installer

You will be guided through the steps necessary to install this software.

**Step 3)** Next window displays the **ReadMe**. After you are done reading the document, click **Continue**



Important Information

Anaconda is the most popular Python data science platform. See https://www.anaconda.com/downloads/.

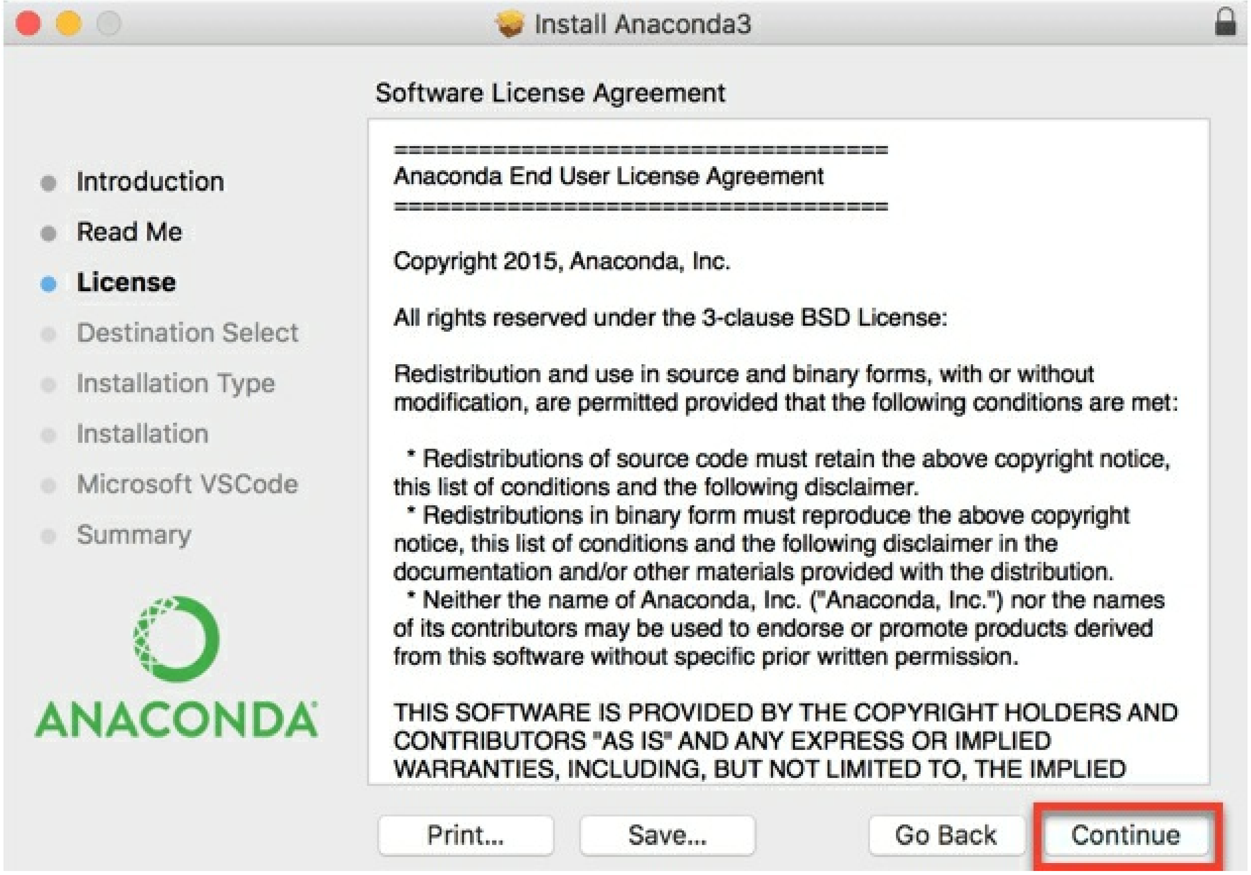
By default, this installer modifies your bash profile to put Anaconda3 in your PATH. To disable this, choose "Customize" at the "Installation Type" phase, and disable the "Modify PATH" option. If you do not do this, you will need to add ~/anaconda3/bin to your PATH manually to run the commands, or run all Anaconda3 commands explicitly from that path.

To install to a different location, select "Change Install Location..." at the "Installation Type" phase, then choose "Install on a specific disk...", choose the disk you wish to install on, and click "Choose Folder...". The "Install for me only" option will install Anaconda3 to the default location, ~/anaconda3.

The packages included in this installation are:

- defaults::alabaster 0.7.10
- defaults::anaconda-client 1.6.9
- defaults::anaconda-project 0.8.2

**Step 4)** This window shows the Anaconda End User License Agreement. Click Continue to agree.



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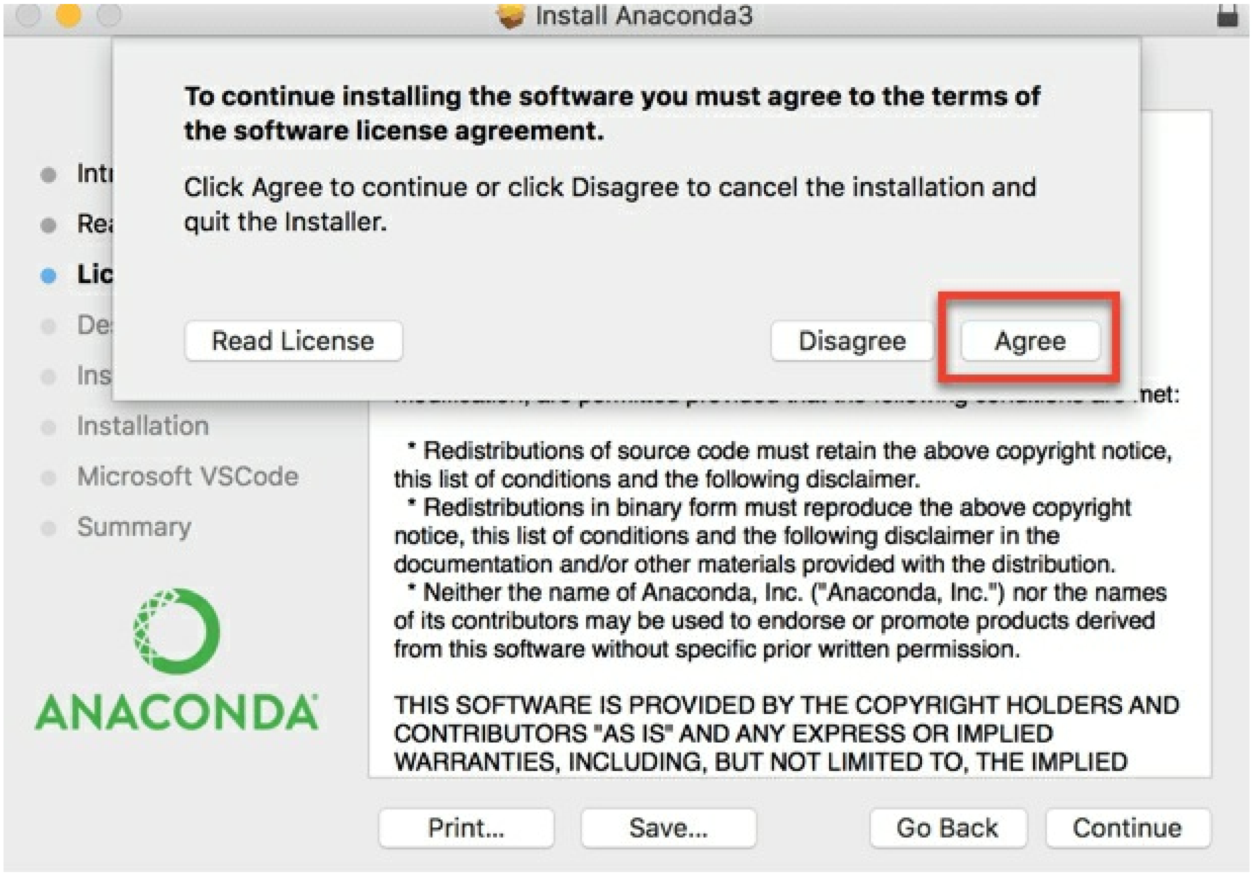
**Step 5)** You are prompted to agree, click **Agree** to go to the next step.



**To continue installing the software you must agree to the terms of the software license agreement.**

Click Agree to continue or click Disagree to cancel the installation and quit the Installer.

net:

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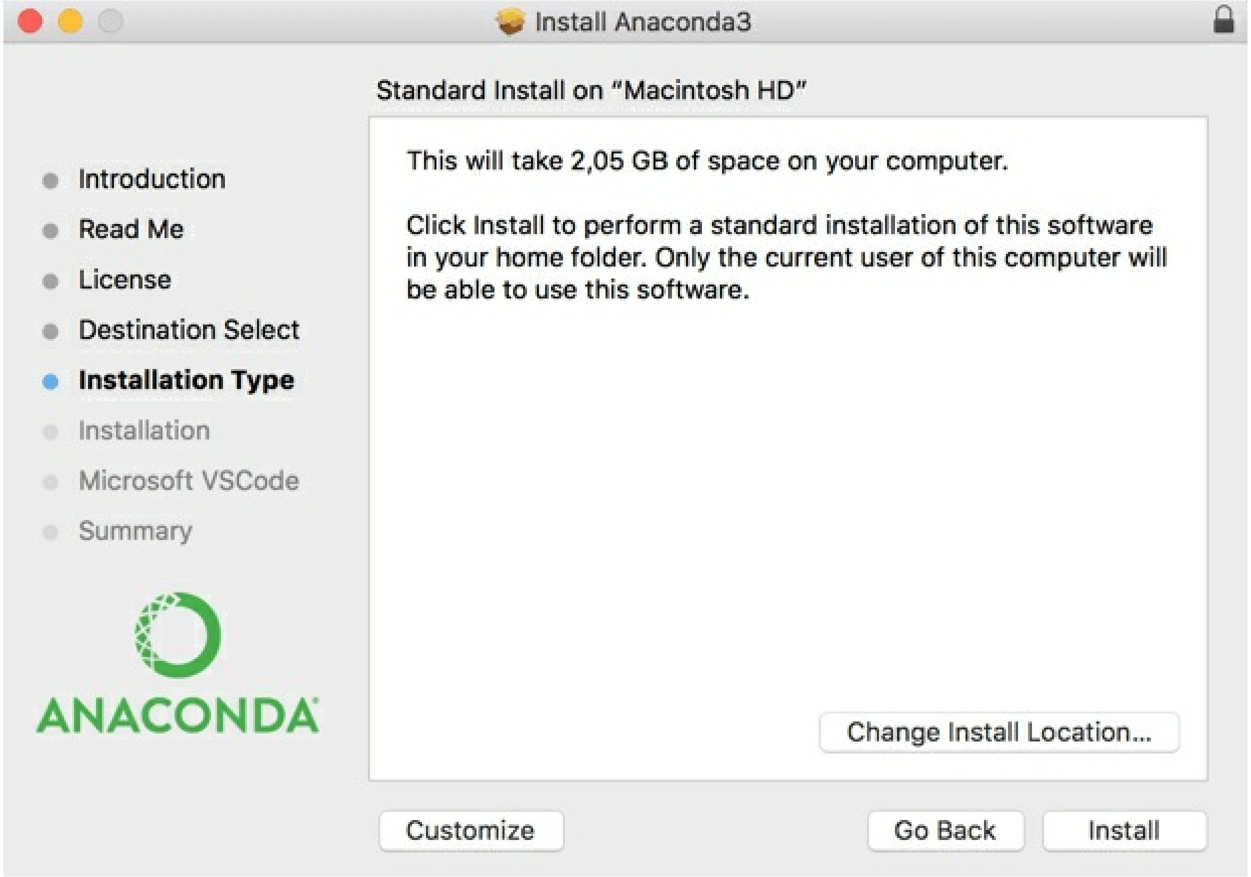
**Step 6)** Click **Change Install Location** to set the location of Anaconda. By default, Anaconda is installed in the user environment: **Users/YOURNAME/**.

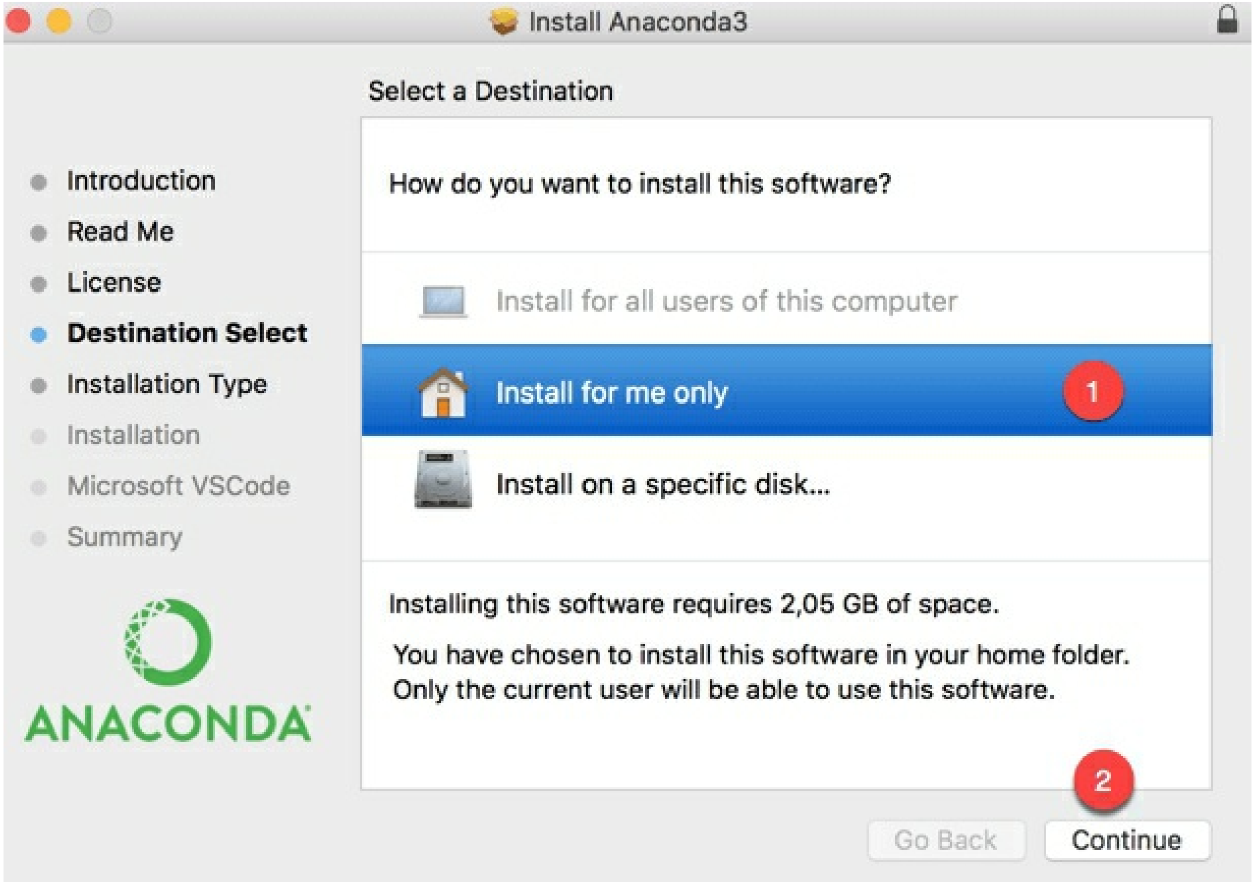


Standard Install on "Macintosh HD"

This will take 2,05 GB of space on your computer.

Click Install to perform a standard installation of this software in your home folder. Only the current user of this computer will be able to use this software.

Select the destination by clicking on **Install for me only**. It means Anaconda will be accessible only to this user.



Select a Destination

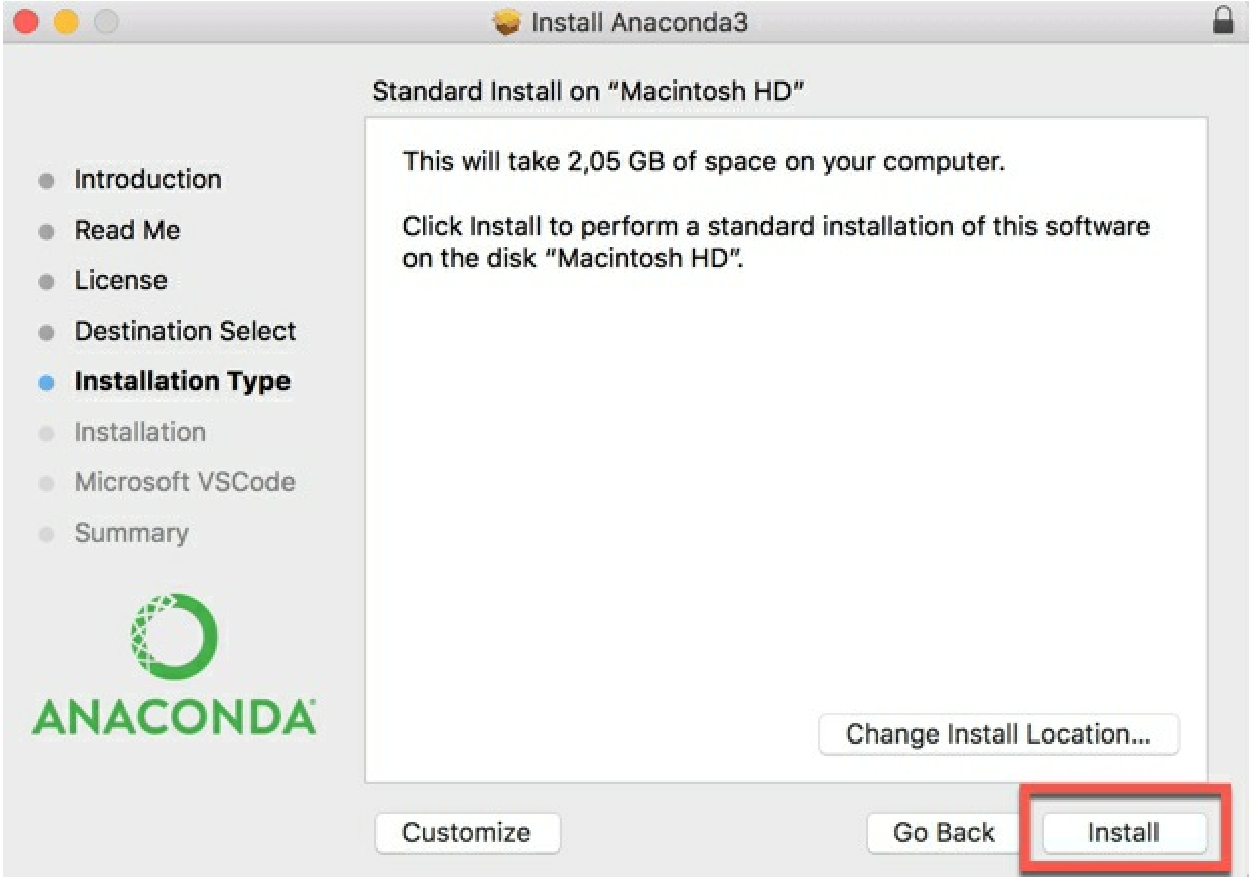
How do you want to install this software?

Install for all users of this computer
Install for me only
1
Install on a specific disk...

Installing this software requires 2,05 GB of space.

You have chosen to install this software in your home folder. Only the current user will be able to use this software.

**Step 7)** You can install Anaconda now. Click **Install** to proceed. Anaconda takes around 2.5 GB on your hard drive.



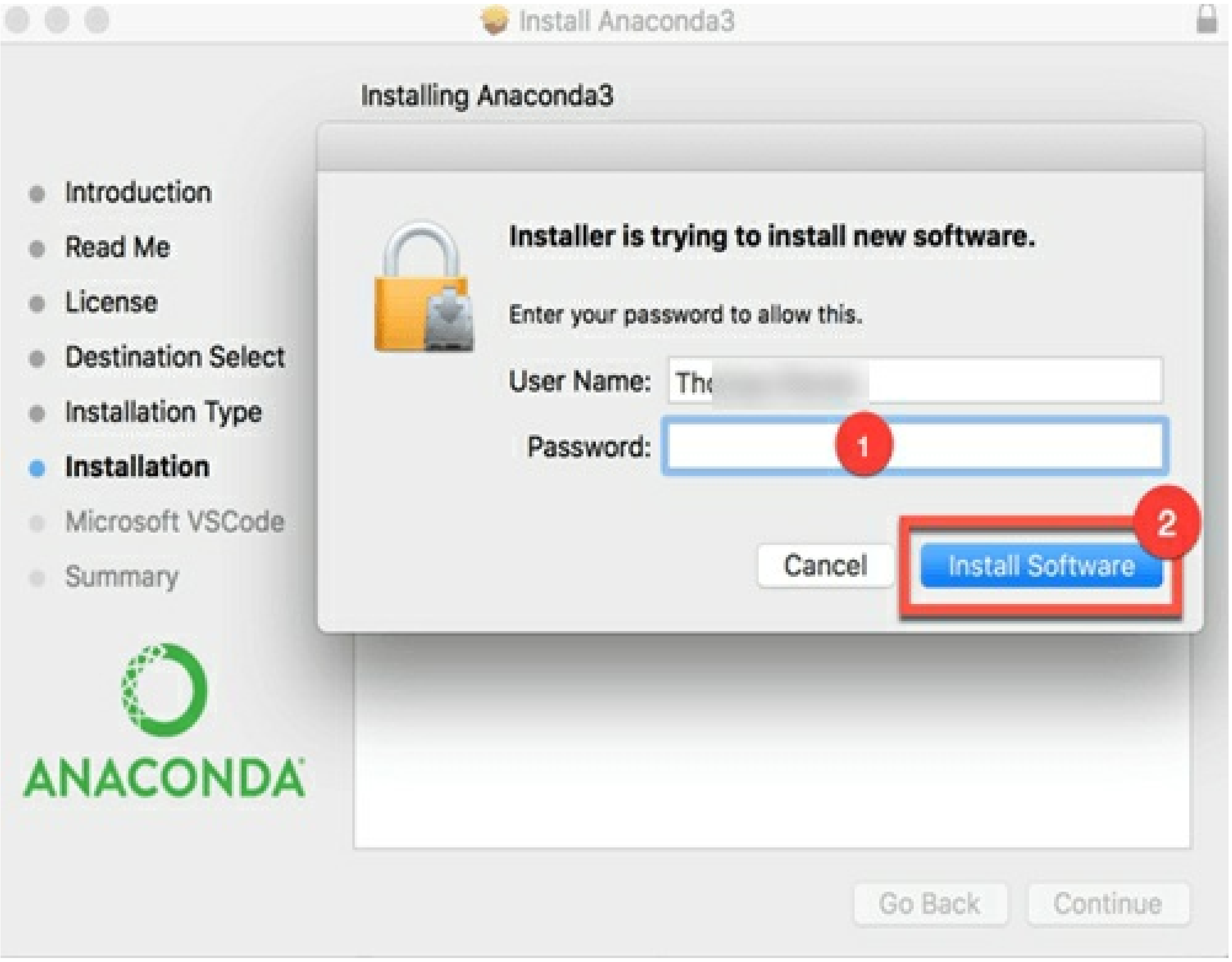
Install Anaconda3

Standard Install on "Macintosh HD"

This will take 2,05 GB of space on your computer.

Click Install to perform a standard installation of this software on the disk "Macintosh HD".

A message box is prompt. You need to confirm by typing your password. Hit **Install Software**



Installing Anaconda3

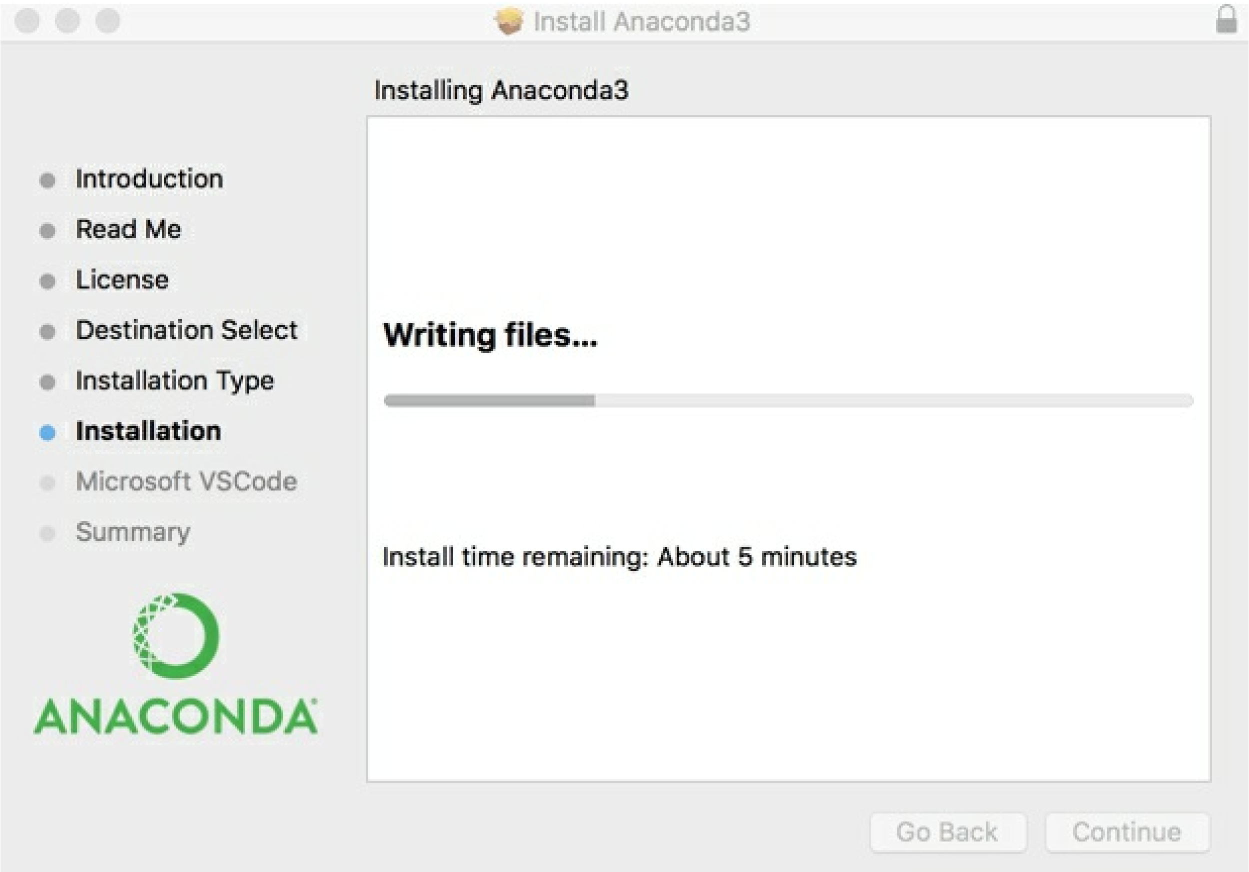
**Installer is trying to install new software.**

Enter your password to allow this.

User Name: Th[redacted]

Password:

The installation may take sometimes. It depends on your machine.

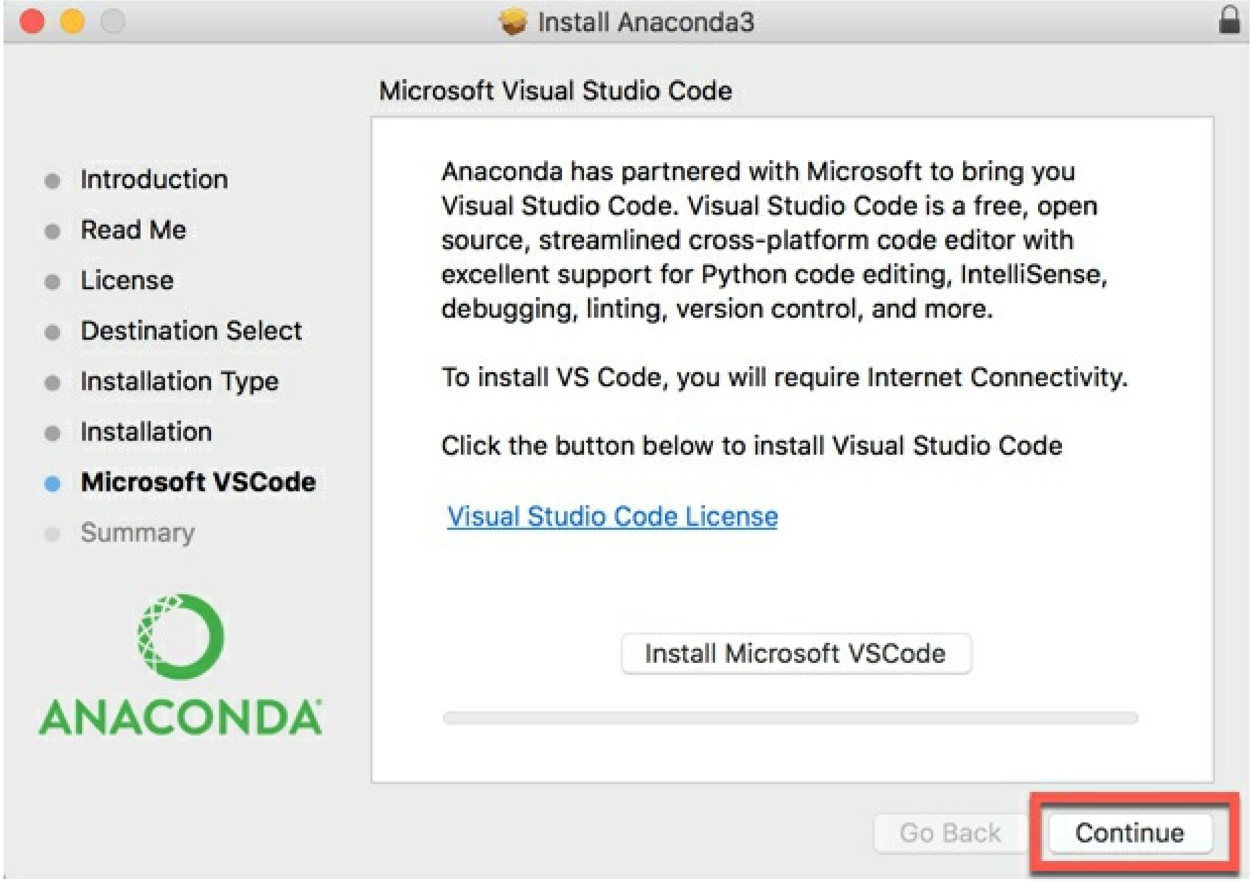


Installing Anaconda3

Writing files...

Install time remaining: About 5 minutes

**Step 8)** Anaconda asks you if you want to install Microsoft VSCode. You can ignore it and hit Continue



Microsoft Visual Studio Code

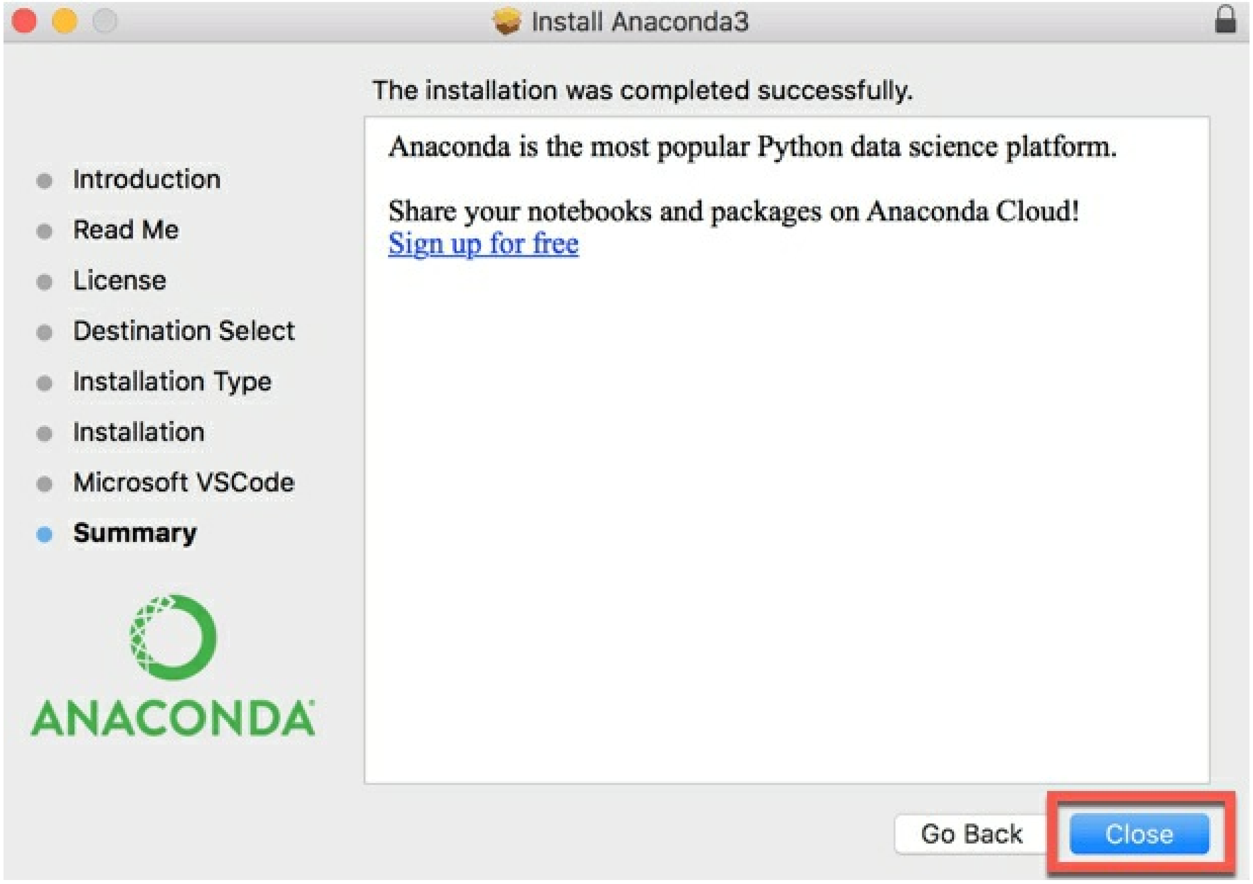
Anaconda has partnered with Microsoft to bring you Visual Studio Code. Visual Studio Code is a free, open source, streamlined cross-platform code editor with excellent support for Python code editing, IntelliSense, debugging, linting, version control, and more.

To install VS Code, you will require Internet Connectivity.

Click the button below to install Visual Studio Code

Visual Studio Code License

**Step 9)** The installation is completed. You can close the window.

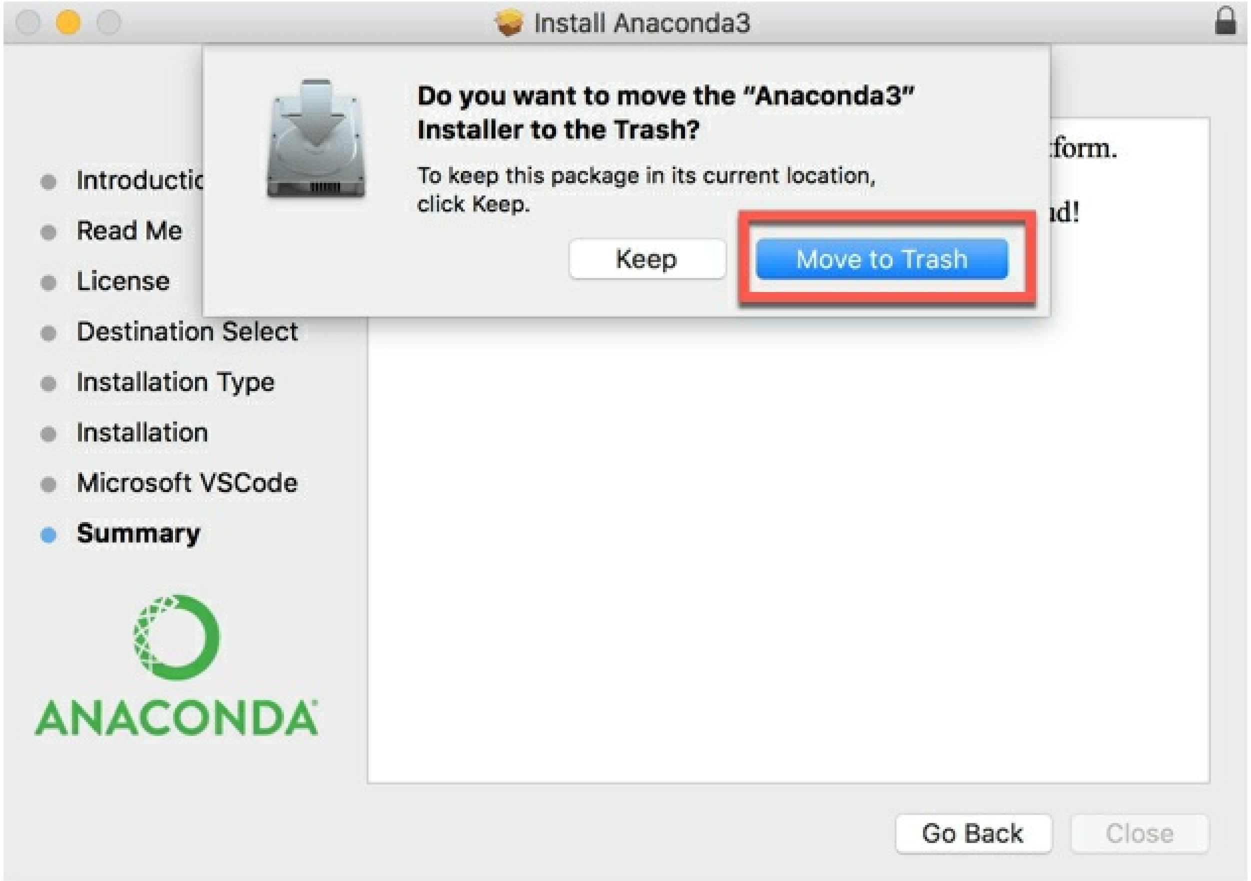


The installation was completed successfully.

Anaconda is the most popular Python data science platform.

Share your notebooks and packages on Anaconda Cloud!
Sign up for free

You are asked if you want to move "Anaconda3" installer to the Trash. Click **Move to Trash**



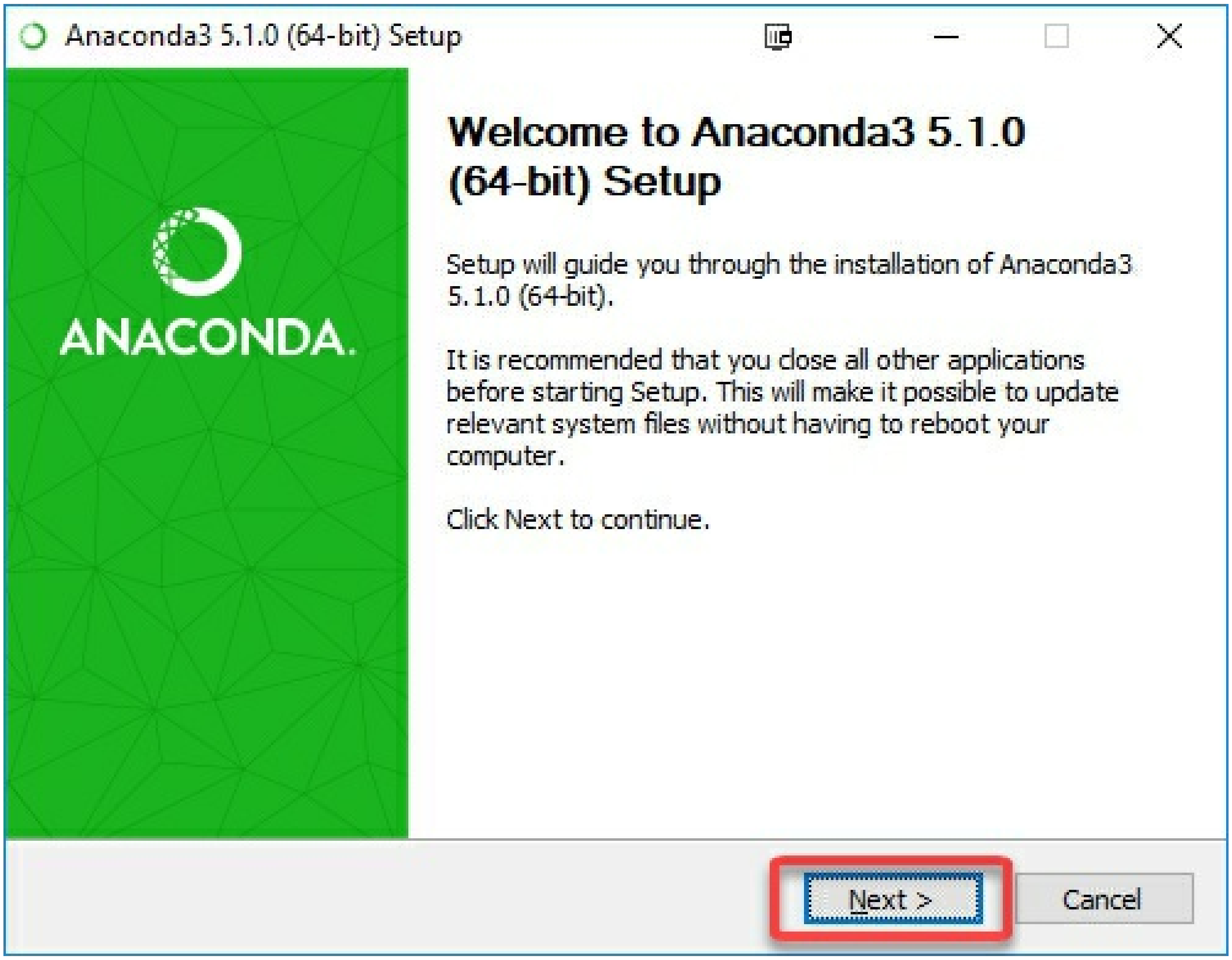
**Do you want to move the "Anaconda3" Installer to the Trash?**

To keep this package in its current location, click Keep.

**You are done with the installation of Anaconda on a macOS system**

## Windows User

**Step 1)** Open the downloaded exe and click Next



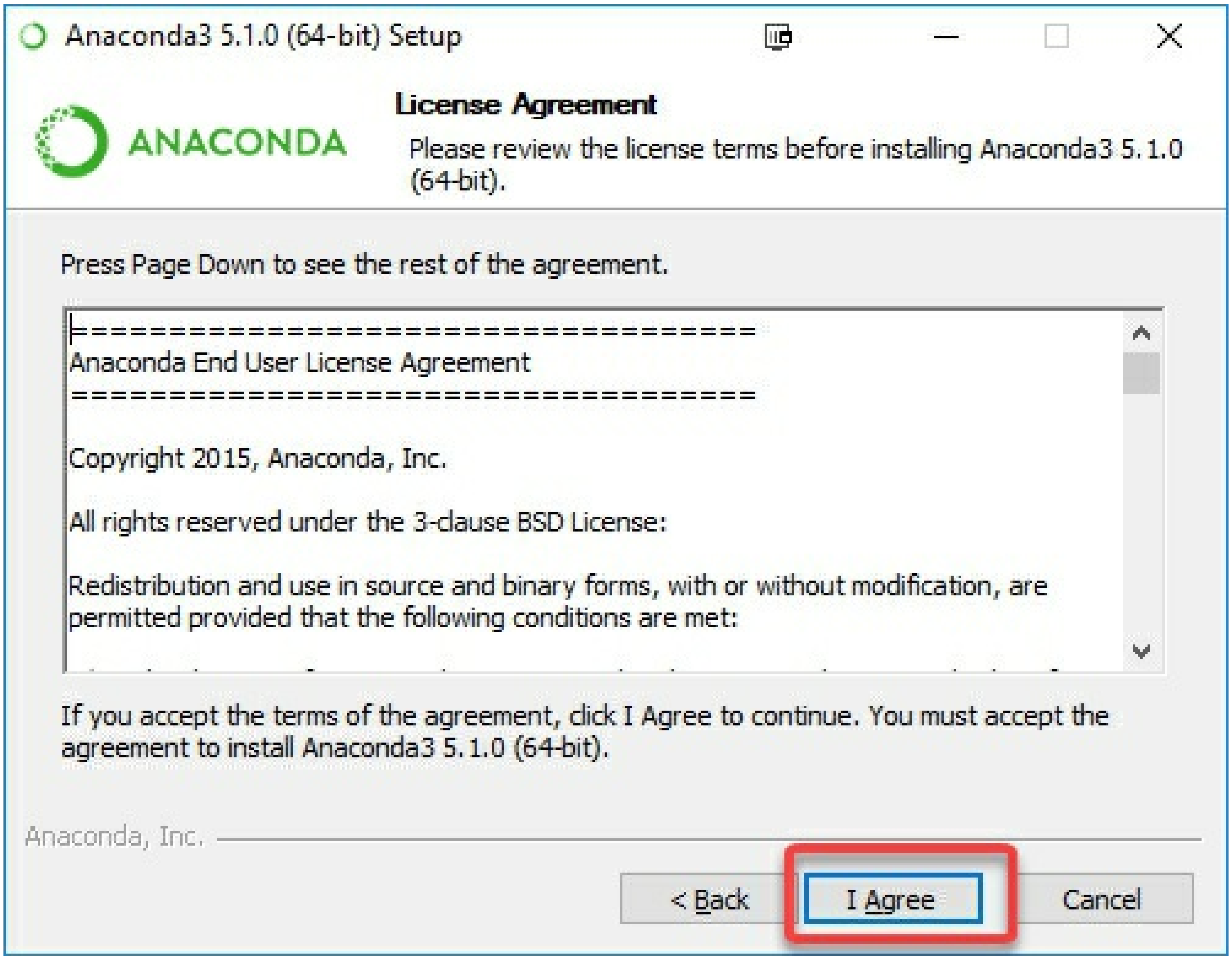
**Welcome to Anaconda3 5.1.0 (64-bit) Setup**

Setup will guide you through the installation of Anaconda3 5.1.0 (64-bit).

It is recommended that you close all other applications before starting Setup. This will make it possible to update relevant system files without having to reboot your computer.

Click Next to continue.

**Step 2)** Accept the License Agreement



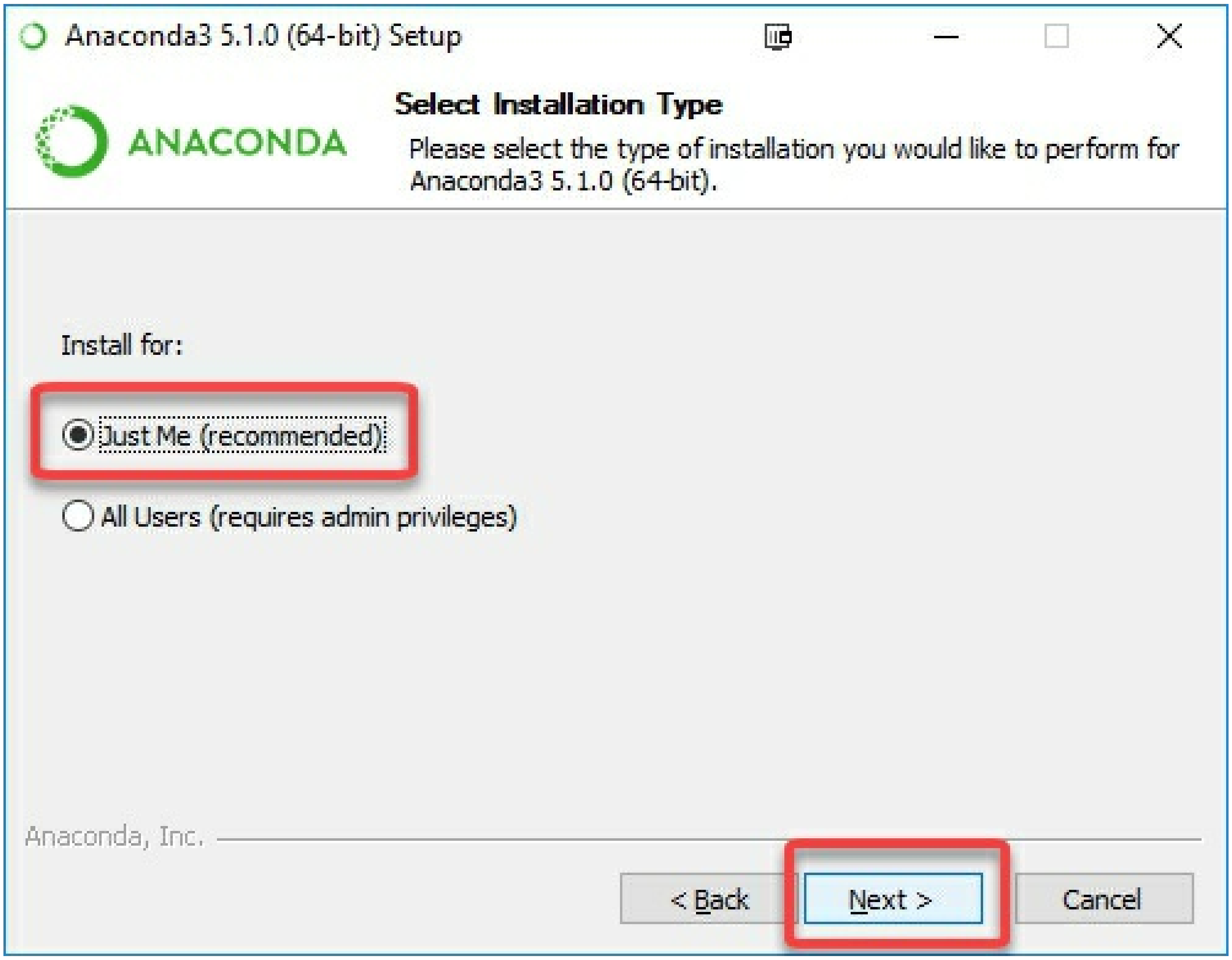
Press Page Down to see the rest of the agreement.

```
====================================
Anaconda End User License Agreement
====================================

Copyright 2015, Anaconda, Inc.

All rights reserved under the 3-clause BSD License:

Redistribution and use in source and binary forms, with or without modification, are
permitted provided that the following conditions are met:
```

If you accept the terms of the agreement, click I Agree to continue. You must accept the agreement to install Anaconda3 5.1.0 (64-bit).

Anaconda3 5.1.0 (64-bit) Setup
ANACONDA
License Agreement
Please review the license terms before installing Anaconda3 5.1.0 (64-bit).
Anaconda, Inc.
< Back
I Agree
Cancel

Step 3) Select Just Me and click Next



Anaconda3 5.1.0 (64-bit) Setup

Select Installation Type

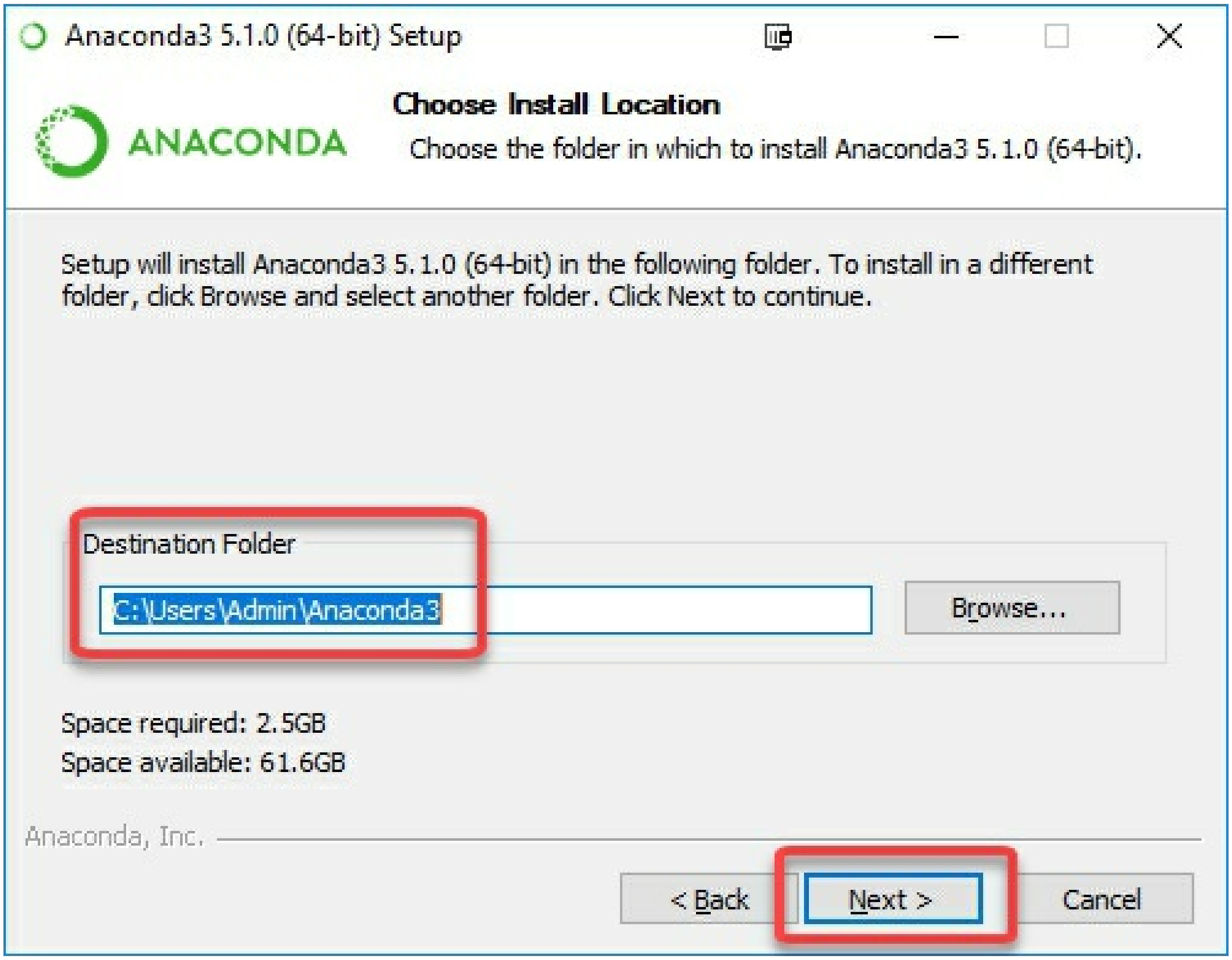
Please select the type of installation you would like to perform for Anaconda3 5.1.0 (64-bit).

Install for:

● Just Me (recommended)

○ All Users (requires admin privileges)

Step 4) Select Destination Folder and Click Next



Anaconda3 5.1.0 (64-bit) Setup

Choose Install Location

Choose the folder in which to install Anaconda3 5.1.0 (64-bit).

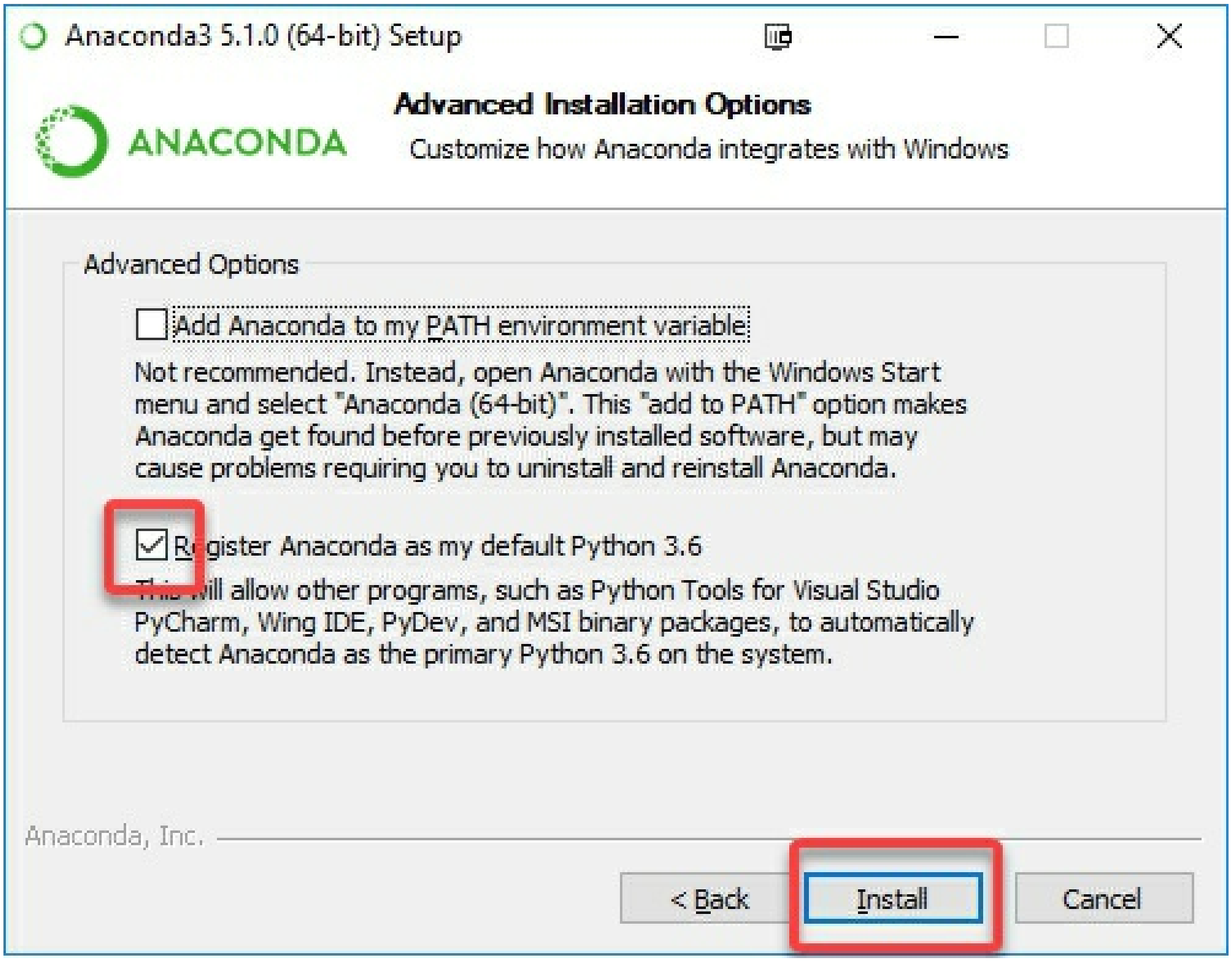
Setup will install Anaconda3 5.1.0 (64-bit) in the following folder. To install in a different folder, click Browse and select another folder. Click Next to continue.

Destination Folder

C:\Users\Admin\Anaconda3

Space required: 2.5GB
Space available: 61.6GB

Step 5) Click Install in next Screen



Anaconda3 5.1.0 (64-bit) Setup

Advanced Installation Options

Customize how Anaconda integrates with Windows

Advanced Options

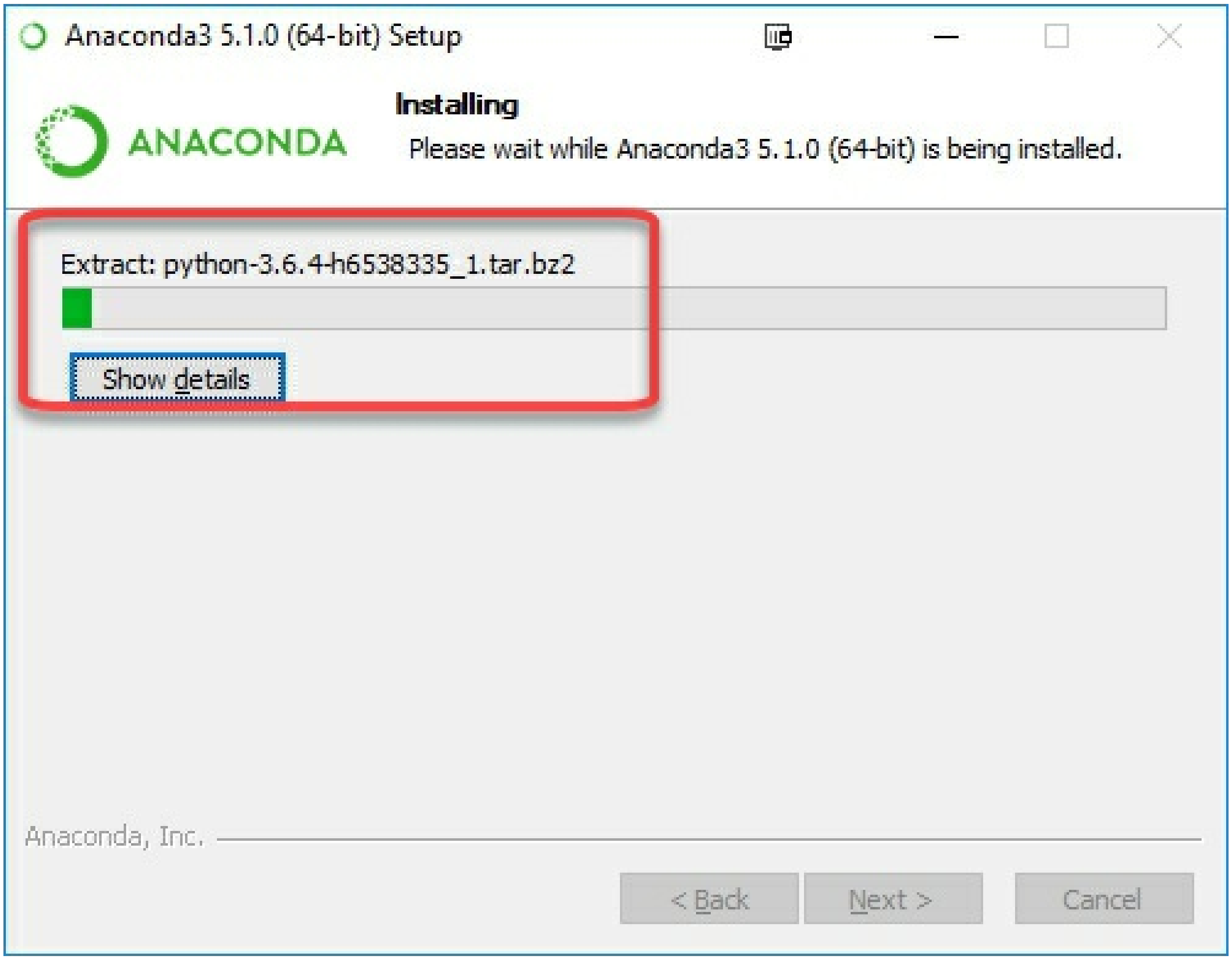
□ Add Anaconda to my PATH environment variable

Not recommended. Instead, open Anaconda with the Windows Start menu and select "Anaconda (64-bit)". This "add to PATH" option makes Anaconda get found before previously installed software, but may cause problems requiring you to uninstall and reinstall Anaconda.

☑ Register Anaconda as my default Python 3.6

This will allow other programs, such as Python Tools for Visual Studio PyCharm, Wing IDE, PyDev, and MSI binary packages, to automatically detect Anaconda as the primary Python 3.6 on the system.

Step 6) Installation will begin



Installing

Please wait while Anaconda3 5.1.0 (64-bit) is being installed.

Extract: python-3.6.4-h6538335_1.tar.bz2

Once done, Anaconda will be installed.

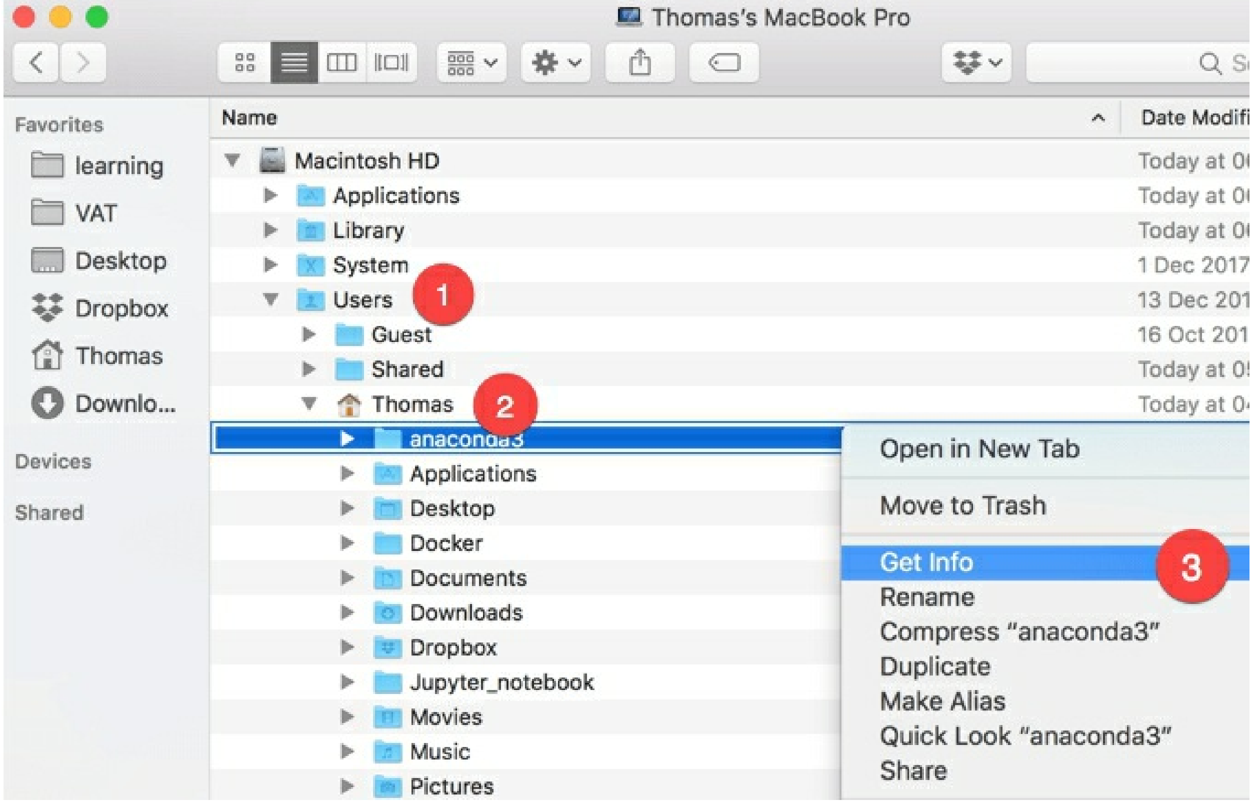
Install R

Mac users

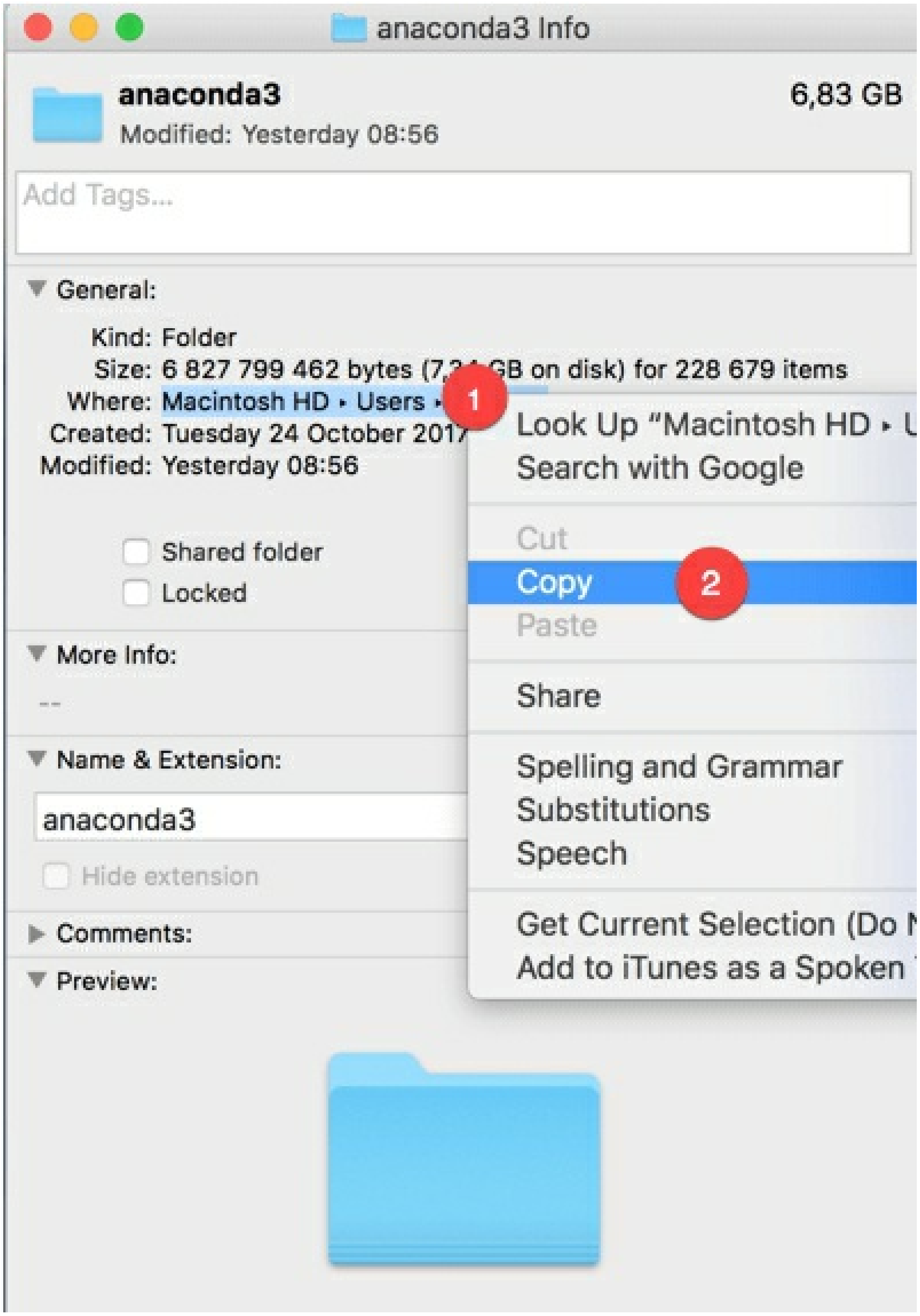
Step 1) Anaconda uses the **terminal** to install libraries. The terminal is a quick way to install libraries. We need to be sure to point the installation toward the right path. In our case, we set the location of Anaconda to the **Users/USERNAME/**. We can confirm this by checking **anaconda3** folder.

Open **Computer** and select **Users**, **USERNAME** and **anaconda3**.

It confirms that we installed Anaconda on the right path. Now, let's see how macOS write the path. Right-click, and then **Get Info**



Select the path **Where** and click **Copy**



anaconda3 Info

anaconda3 6,83 GB

Modified: Yesterday 08:56

Add Tags...

General:

Kind: Folder

Size: 6 827 799 462 bytes (7,24 GB on disk) for 228 679 items

Where: Macintosh HD ▸ Users ▸

Created: Tuesday 24 October 2017

Modified: Yesterday 08:56

□ Shared folder

□ Locked

More Info:

--

Name & Extension:

anaconda3

□ Hide extension

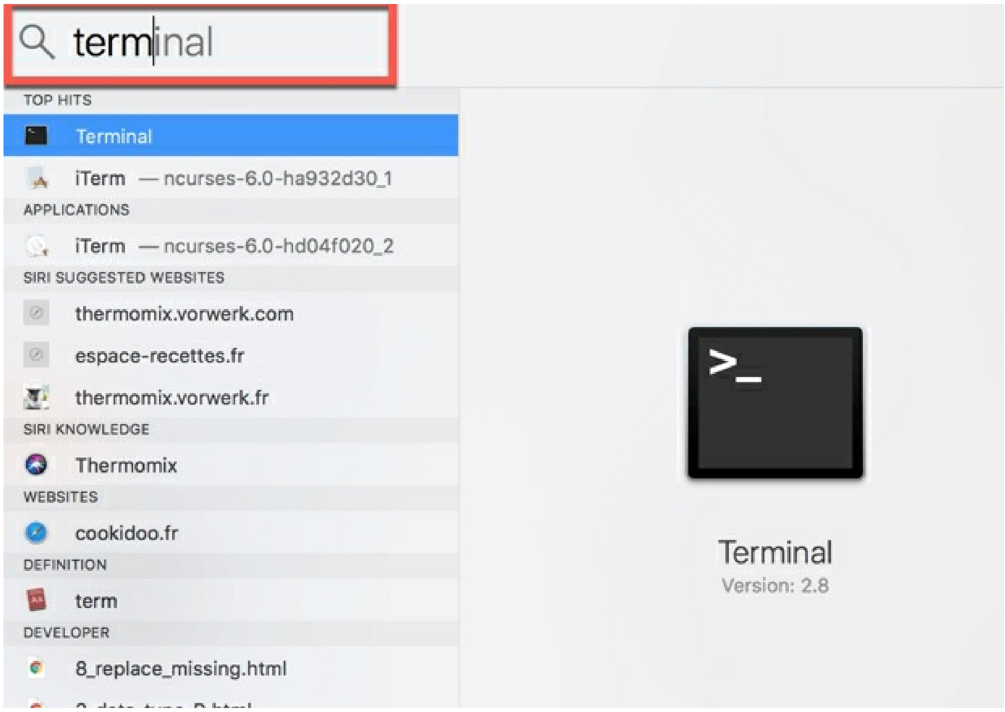
Comments:

Preview:

1
Look Up “Macintosh HD ▸ U
Search with Google
Cut
Copy
2
Paste
Share
Spelling and Grammar
Substitutions
Speech
Get Current Selection (Do N
Add to iTunes as a Spoken

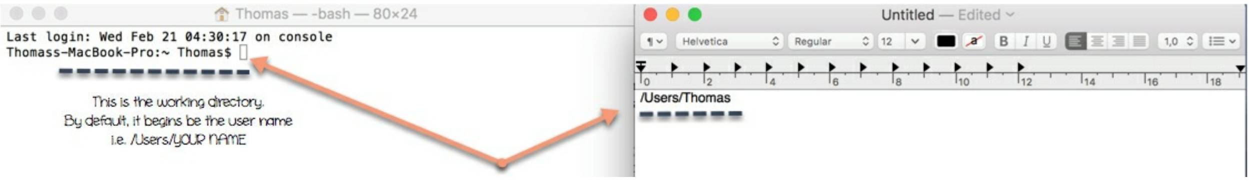
Step 2) For Mac user:

- The shortest way is to use the **Spotlight Search** and write **terminal**.



The terminal sets the default working directory to **Users/USERNAME**. As you can see in the figure below, the path of **anaconda3** and the working directory are identical. In macOS, the latest folder is shown before the **$**. For me, it is **Thomas**. The terminal will install all the libraries in this working directory.

If the path on the text editor does not match the working directory, you can change it by writing cd PATH in the terminal. **PATH** is the path you pasted in the text editor. Don't forget to wrap the PATH with **"PATH"**. This action will change the working directory to **PATH**.



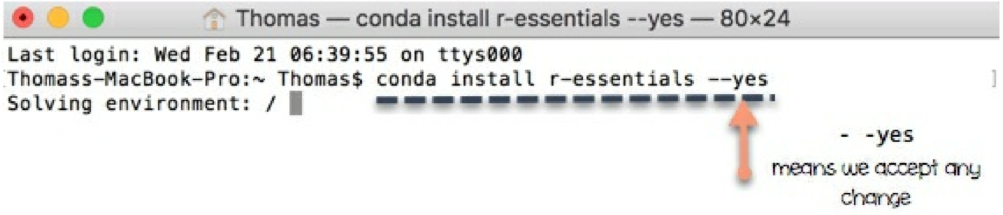
```
Last login: Wed Feb 21 04:30:17 on console
Thomass-MacBook-Pro:~ Thomas$
```

```
/Users/Thomas
```

Step 4) We are ready to install R. I recommend you to install all packages and dependencies with the conda command in the terminal.

```
## In the terminalconda install r-essentials --yes
```

r-essentials means conda will install **R** and all the necessary libraries used by data scientist.

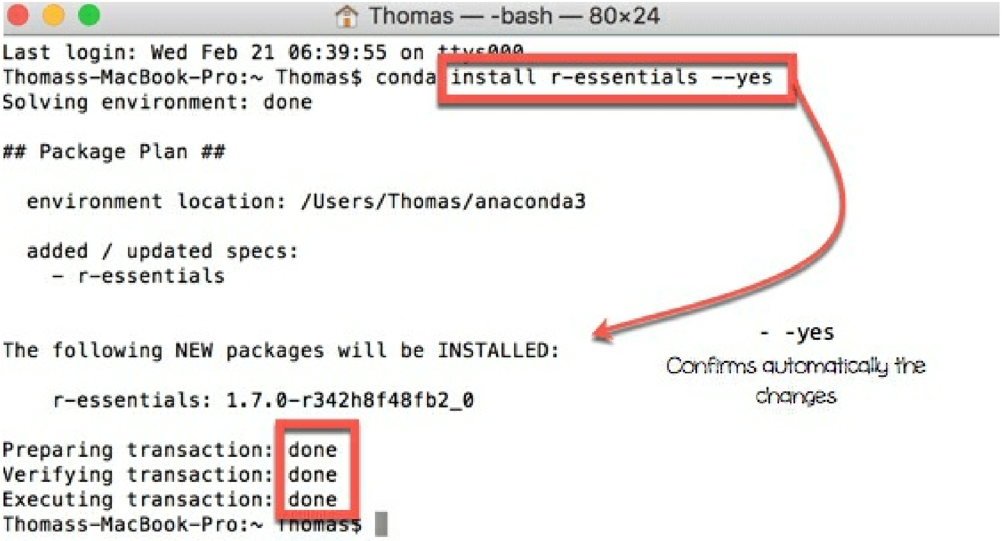


```
Last login: Wed Feb 21 06:39:55 on ttys000
Thomass-MacBook-Pro:~ Thomas$ conda install r-essentials --yes
Solving environment: /
```

- -yes
means we accept any change

Conda is downloading the libraries

It takes some time to upload all the libraries. Be patient...you are all set.

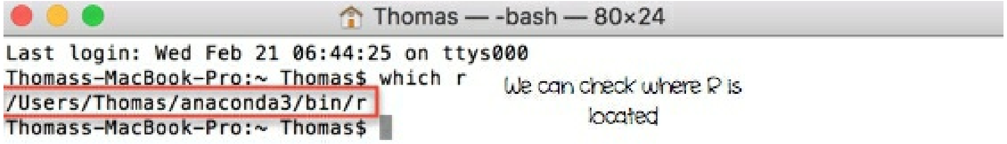


```
Last login: Wed Feb 21 06:39:55 on ttys000
Thomass-MacBook-Pro:~ Thomas$ conda install r-essentials --yes
Solving environment: done

## Package Plan ##

  environment location: /Users/Thomas/anaconda3

  added / updated specs:
    - r-essentials


The following NEW packages will be INSTALLED:

    r-essentials: 1.7.0-r342h8f48fb2_0

Preparing transaction: done
Verifying transaction: done
Executing transaction: done
Thomass-MacBook-Pro:~ Thomas$
```

- -yes
Confirms automatically the changes

In the terminal, you should see Executing transaction: done. If so, you have successfully installed **R**.

You can check where R is located.

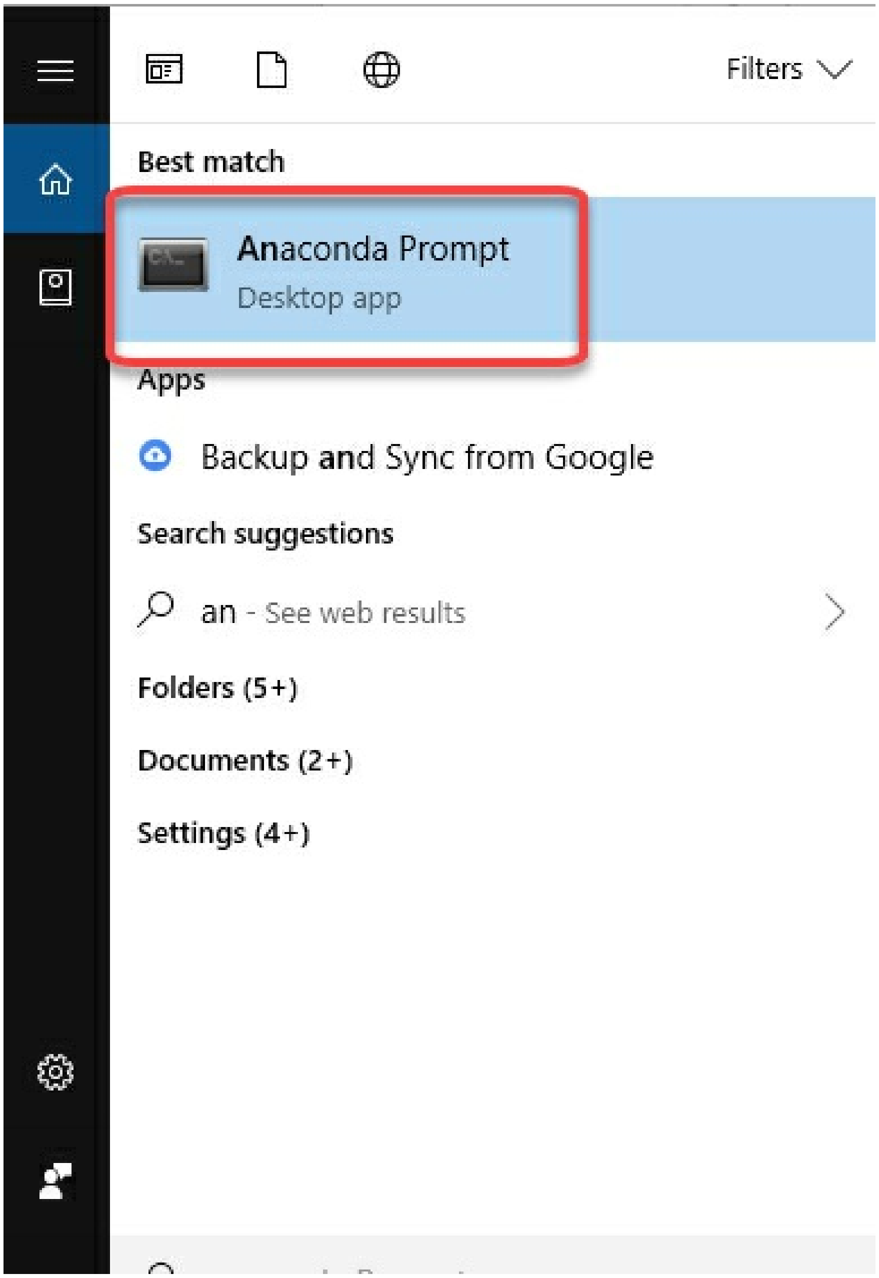


```
Last login: Wed Feb 21 06:44:25 on ttys000
Thomass-MacBook-Pro:~ Thomas$ which r
/Users/Thomas/anaconda3/bin/r
Thomass-MacBook-Pro:~ Thomas$
```

We can check where R is located

Windows User

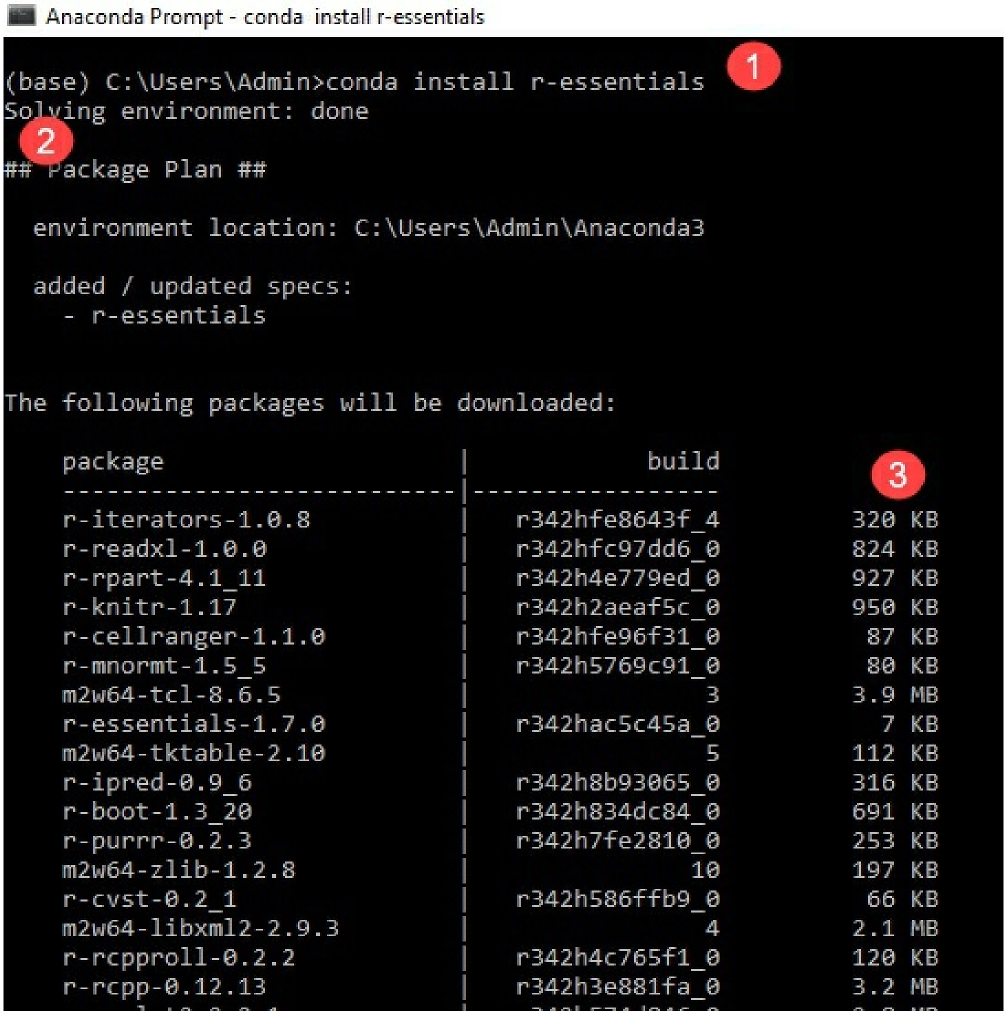
Step 1) Open the Anaconda command prompt



Step 2) In the command prompt

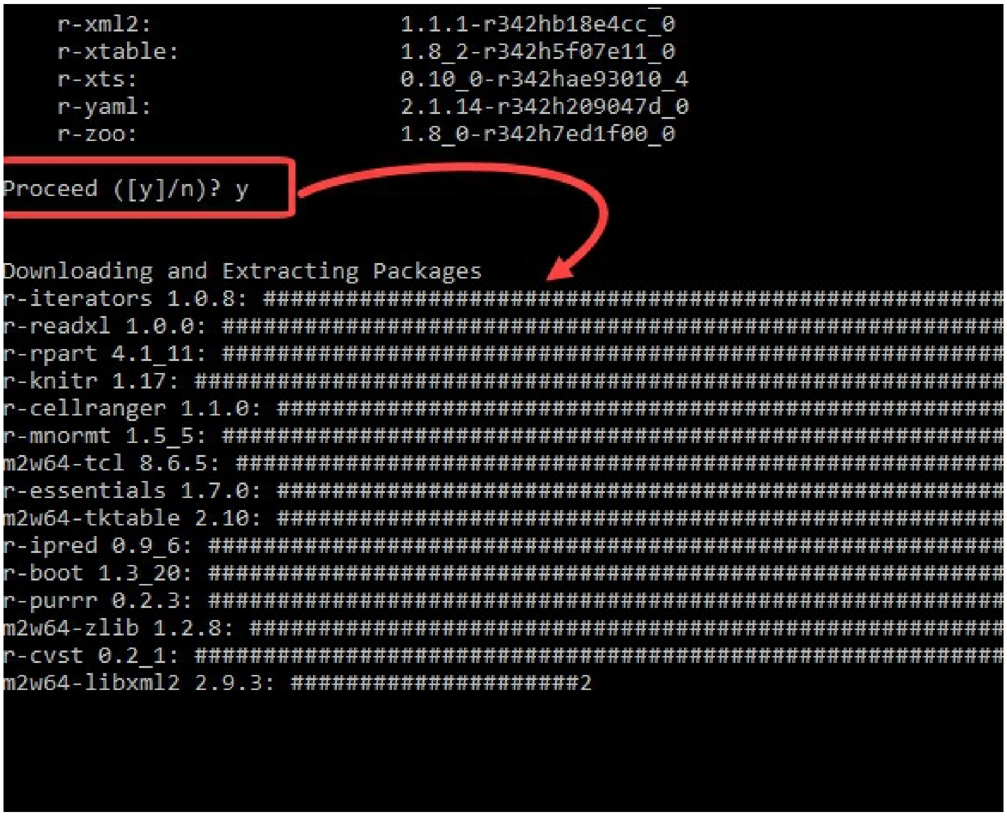
1. Enter the R install command
2. Environment will be determined

3. List of packages to be installed will be listed



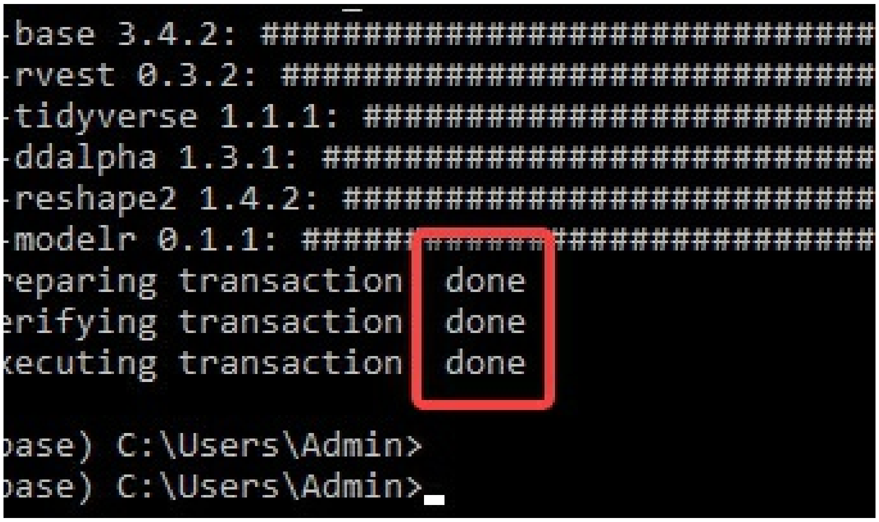
```
(base) C:\Users\Admin>conda install r-essentials
Solving environment: done

## Package Plan ##

  environment location: C:\Users\Admin\Anaconda3

  added / updated specs:
    - r-essentials


The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    r-iterators-1.0.8          |   r342hfe8643f_4         320 KB
    r-readxl-1.0.0             |   r342hfc97dd6_0         824 KB
    r-rpart-4.1_11             |   r342h4e779ed_0         927 KB
    r-knitr-1.17               |   r342h2aeaf5c_0         950 KB
    r-cellranger-1.1.0         |   r342hfe96f31_0          87 KB
    r-mnormt-1.5_5             |   r342h5769c91_0          80 KB
    m2w64-tcl-8.6.5            |                3         3.9 MB
    r-essentials-1.7.0         |   r342hac5c45a_0           7 KB
    m2w64-tktable-2.10         |                5         112 KB
    r-ipred-0.9_6              |   r342h8b93065_0         316 KB
    r-boot-1.3_20              |   r342h834dc84_0         691 KB
    r-purrr-0.2.3              |   r342h7fe2810_0         253 KB
    m2w64-zlib-1.2.8           |               10         197 KB
    r-cvst-0.2_1               |   r342h586ffb9_0          66 KB
    m2w64-libxml2-2.9.3        |                4         2.1 MB
    r-rcpproll-0.2.2           |   r342h4c765f1_0         120 KB
    r-rcpp-0.12.13             |   r342h3e881fa_0         3.2 MB
```

Step 3) Enter y and hit the return key to start installation



```
    r-xml2:                  1.1.1-r342hb18e4cc_0
    r-xtable:                1.8_2-r342h5f07e11_0
    r-xts:                   0.10_0-r342hae93010_4
    r-yaml:                  2.1.14-r342h209047d_0
    r-zoo:                   1.8_0-r342h7ed1f00_0

Proceed ([y]/n)? y

Downloading and Extracting Packages
r-iterators 1.0.8: ######################################################
r-readxl 1.0.0: #########################################################
r-rpart 4.1_11: #########################################################
r-knitr 1.17: ###########################################################
r-cellranger 1.1.0: #####################################################
r-mnormt 1.5_5: #########################################################
m2w64-tcl 8.6.5: ########################################################
r-essentials 1.7.0: #####################################################
m2w64-tktable 2.10: #####################################################
r-ipred 0.9_6: ##########################################################
r-boot 1.3_20: ##########################################################
r-purrr 0.2.3: ##########################################################
m2w64-zlib 1.2.8: #######################################################
r-cvst 0.2_1: ###########################################################
m2w64-libxml2 2.9.3: #####################2
```

Step 4) Installation will take time, and you will get done message.



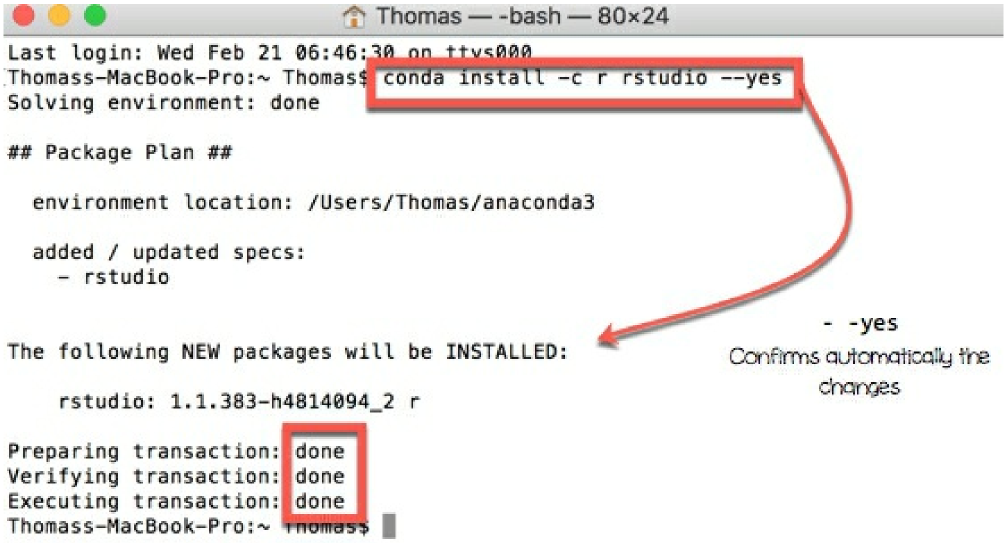
```
-base 3.4.2: #############################
-rvest 0.3.2: ############################
-tidyverse 1.1.1: ########################
-ddalpha 1.3.1: ##########################
-reshape2 1.4.2: #########################
-modelr 0.1.1: ###########################
reparing transaction  done
erifying transaction  done
xecuting transaction  done

ase) C:\Users\Admin>
ase) C:\Users\Admin>
```

Install Rstudio

Mac User

In the terminal, write the following code:

```
## In the terminalconda install -c r rstudio --yes
```



```
Last login: Wed Feb 21 06:46:30 on ttys000
Thomass-MacBook-Pro:~ Thomas$ conda install -c r rstudio --yes
Solving environment: done

## Package Plan ##

  environment location: /Users/Thomas/anaconda3

  added / updated specs:
    - rstudio


The following NEW packages will be INSTALLED:

    rstudio: 1.1.383-h4814094_2 r

Preparing transaction: done
Verifying transaction: done
Executing transaction: done
Thomass-MacBook-Pro:~ Thomas$
```

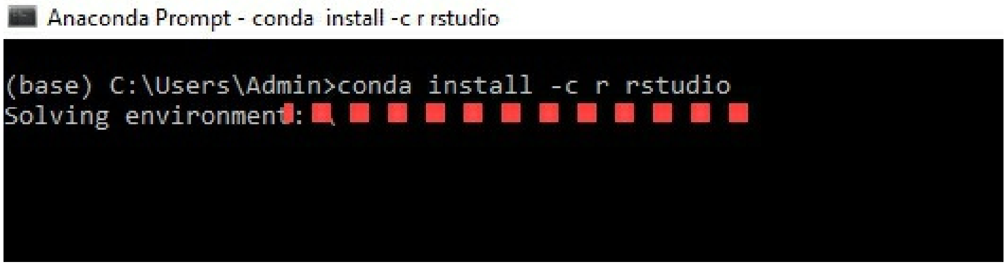
- -yes
Confirms automatically the changes

In the terminal, you should see Executing transaction: done. If so, you have successfully installed **Rstudio**.

You are all set now, congratulation!

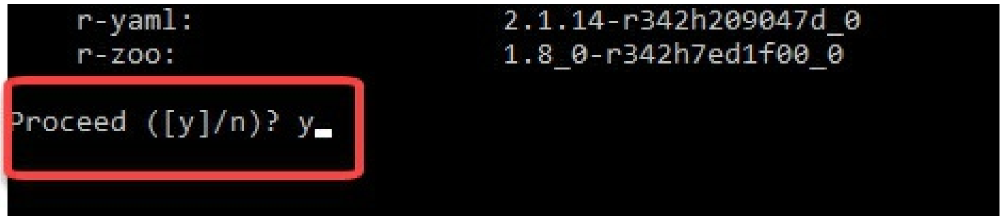
Windows User

Step 1) Enter command to install R Studio in the Anaconda prompt



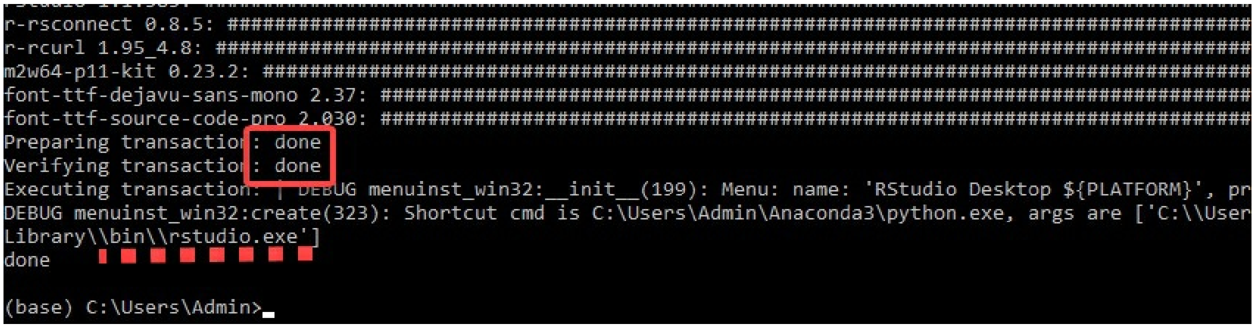
```
(base) C:\Users\Admin>conda install -c r rstudio
Solving environment: \
```

Step 2) You will be shown a list of packages that will be installed. Enter y



```
    r-yaml:                      2.1.14-r342h209047d_0
    r-zoo:                       1.8_0-r342h7ed1f00_0

Proceed ([y]/n)? y
```

Step 3) R Studio will be installed



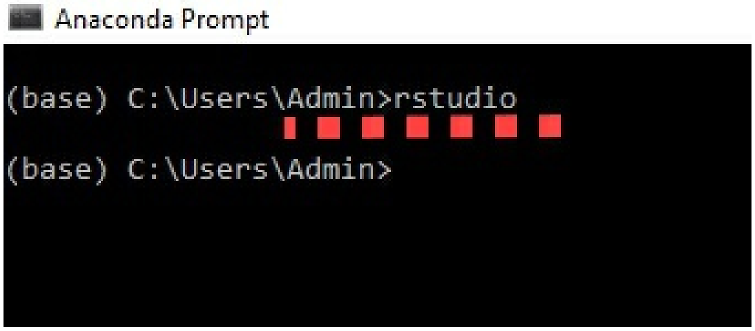
```
r-rsconnect 0.8.5: ###########################################################################
r-rcurl 1.95_4.8: ############################################################################
m2w64-p11-kit 0.23.2: ########################################################################
font-ttf-dejavu-sans-mono 2.37: ##############################################################
font-ttf-source-code-pro 2.030: ##############################################################
Preparing transaction: done
Verifying transaction: done
Executing transaction: | DEBUG menuinst_win32:__init__(199): Menu: name: 'RStudio Desktop ${PLATFORM}', pr
DEBUG menuinst_win32:create(323): Shortcut cmd is C:\Users\Admin\Anaconda3\python.exe, args are ['C:\\User
Library\\bin\\rstudio.exe']
done

(base) C:\Users\Admin>
```

Warning

Avoid as much as you can to install a library using pip for Python, and R. Conda libraries gather a lot of packages, you don't need to install libraries outside of conda environment.

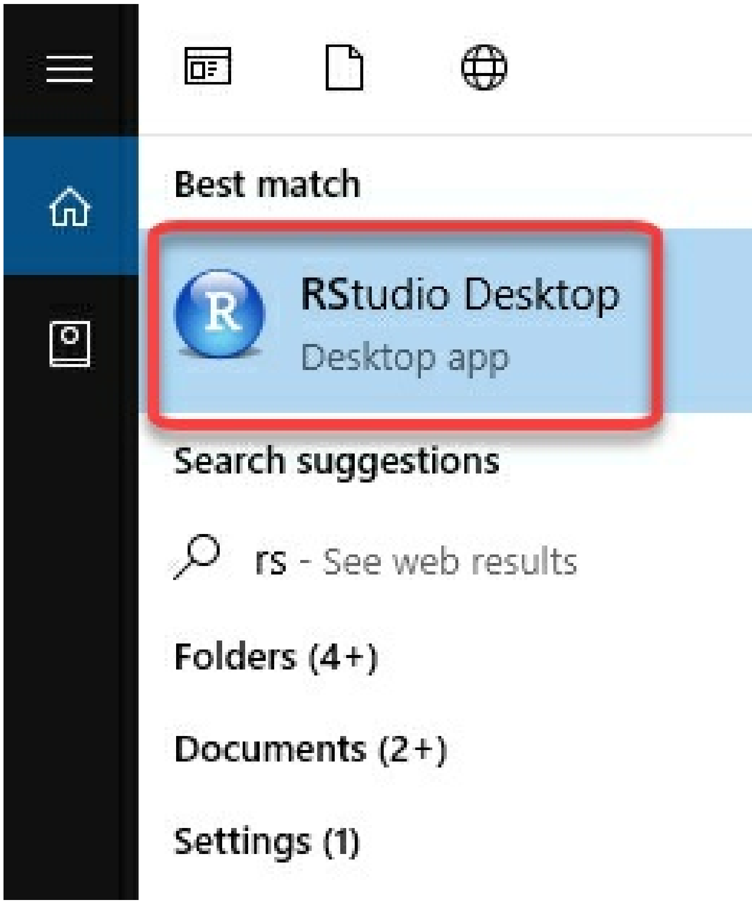
Run Rstudio

Directly run the command line from the terminal to open Rstudio. You open the terminal and write rstudio. You can also use Desktop Shortcut

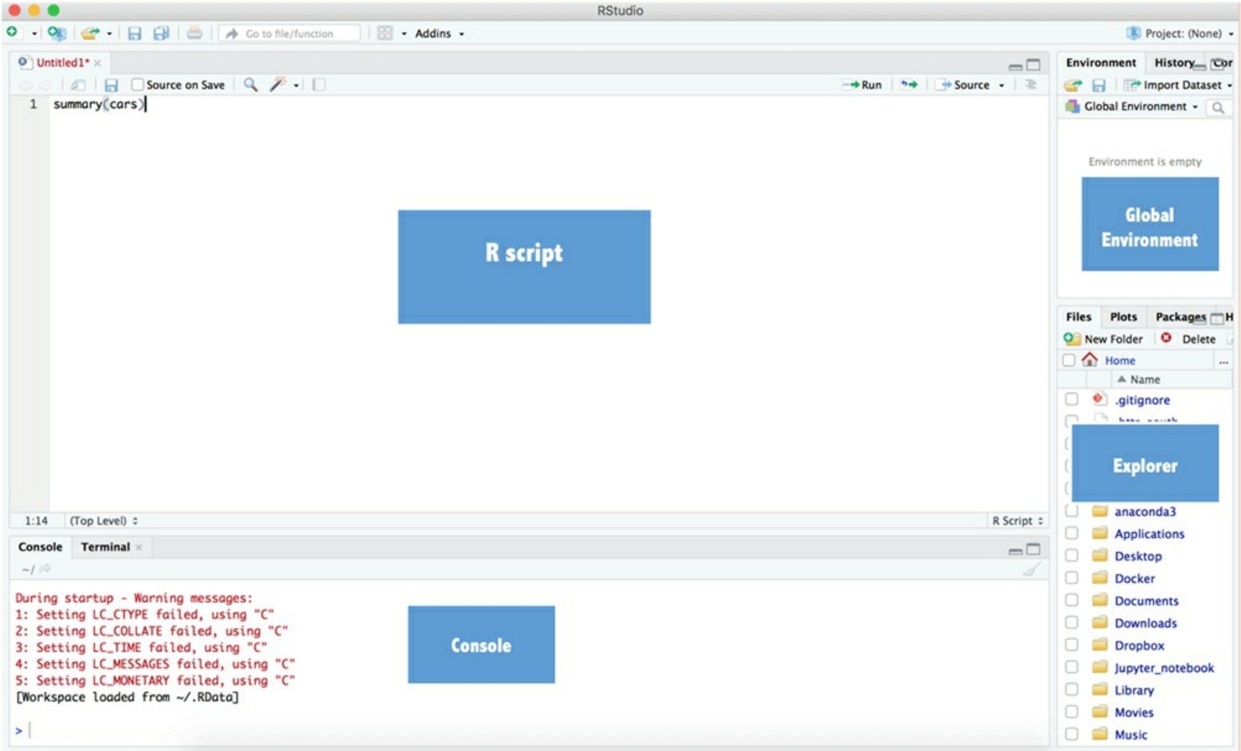


```
(base) C:\Users\Admin>rstudio

(base) C:\Users\Admin>
```

Or



A new window will be opened with **Rstudio**.



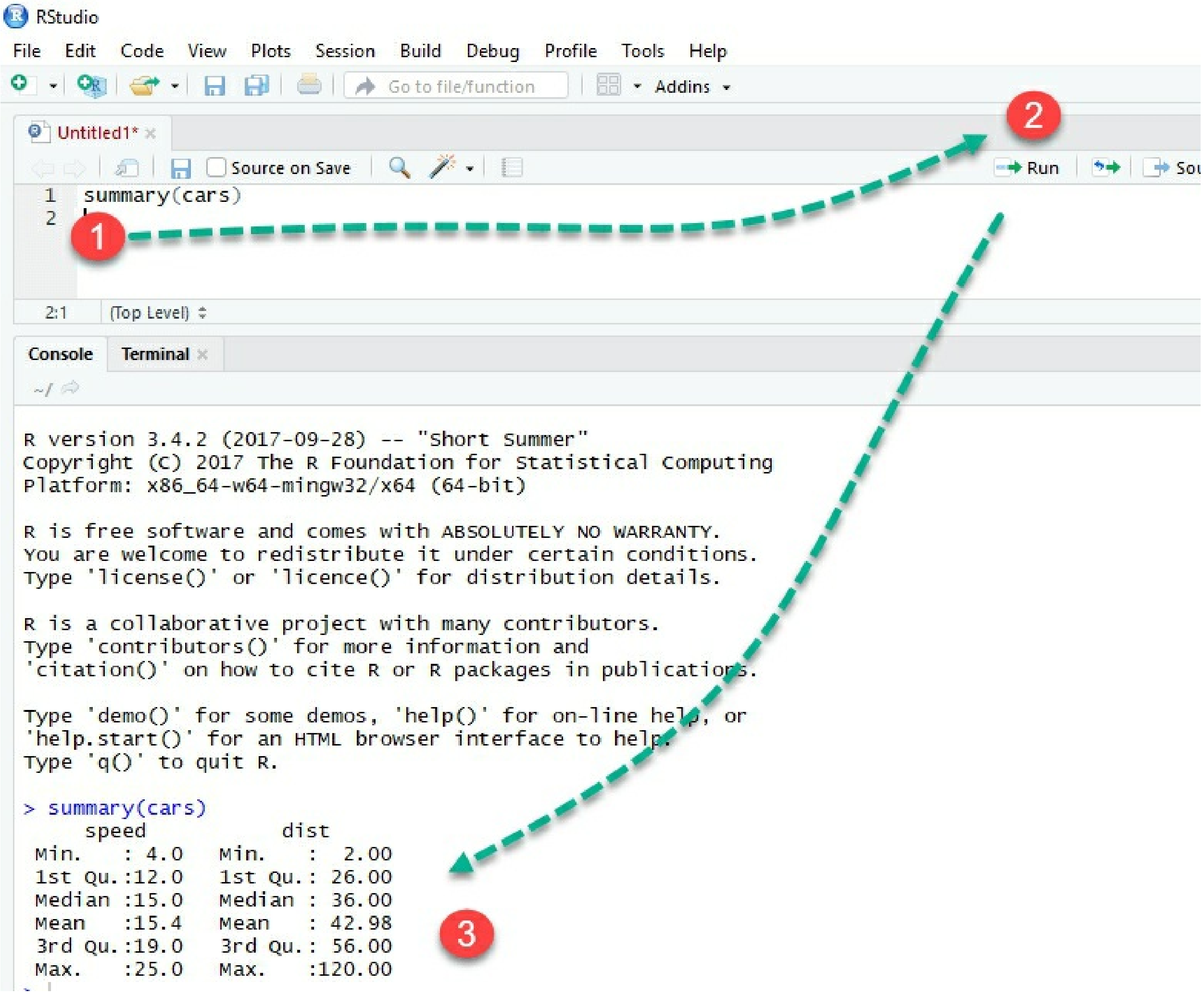
```
summary(cars)
```

```
During startup - Warning messages:
1: Setting LC_CTYPE failed, using "C"
2: Setting LC_COLLATE failed, using "C"
3: Setting LC_TIME failed, using "C"
4: Setting LC_MESSAGES failed, using "C"
5: Setting LC_MONETARY failed, using "C"
[Workspace loaded from ~/.RData]

>
```

Test

Open Rstudio from the terminal and open a script. Write the following command:

1. ## In Rstudio **summary**(cars)
2. Click Run
3. Check Output



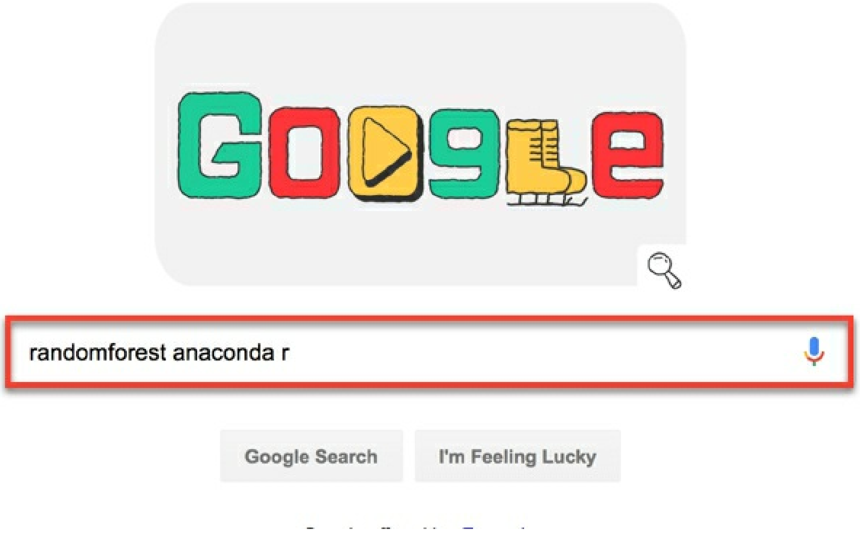
```
summary(cars)
```

```
R version 3.4.2 (2017-09-28) -- "Short Summer"
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> summary(cars)
     speed           dist       
 Min.   : 4.0   Min.   :  2.00  
 1st Qu.:12.0   1st Qu.: 26.00  
 Median :15.0   Median : 36.00  
 Mean   :15.4   Mean   : 42.98  
 3rd Qu.:19.0   3rd Qu.: 56.00  
 Max.   :25.0   Max.   :120.00  
```

If you can see the summary statistics, it works. You can close Rstudio without saving the files.

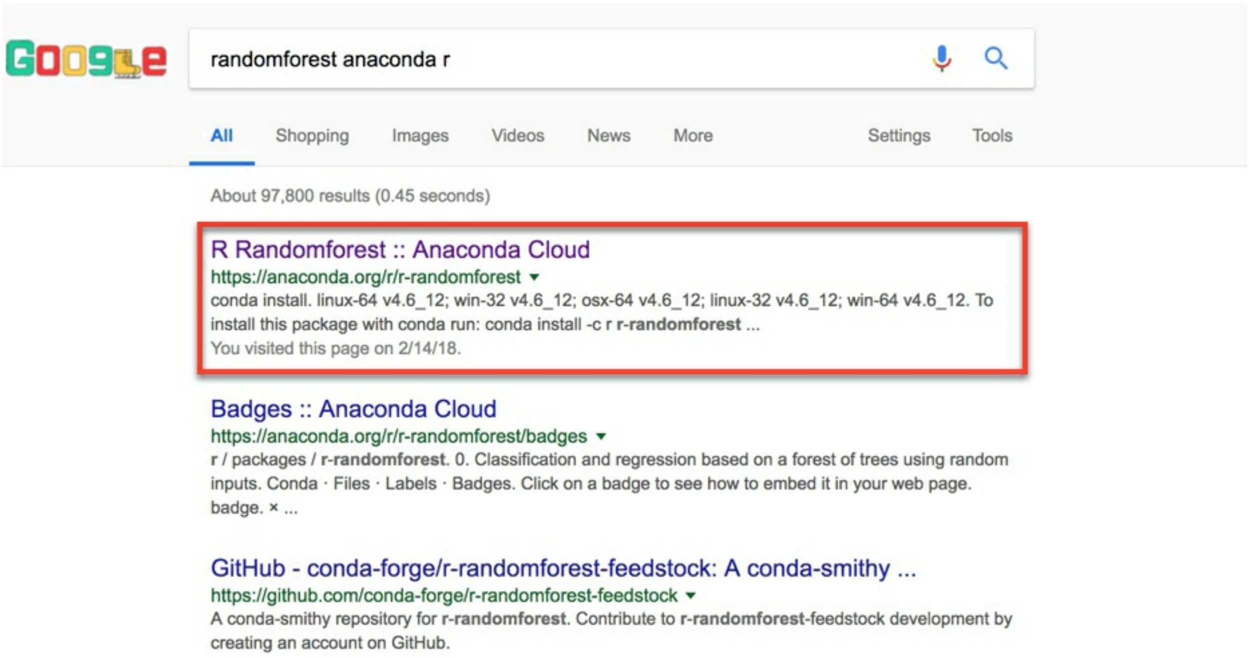
Install package

Install package with anaconda is trivial. You go to your favorite browser, type the name of the library followed by **anaconda r**.



randomforest anaconda r

You choose the link that points to anaconda. You copy and paste the library into the terminal.



randomforest anaconda r

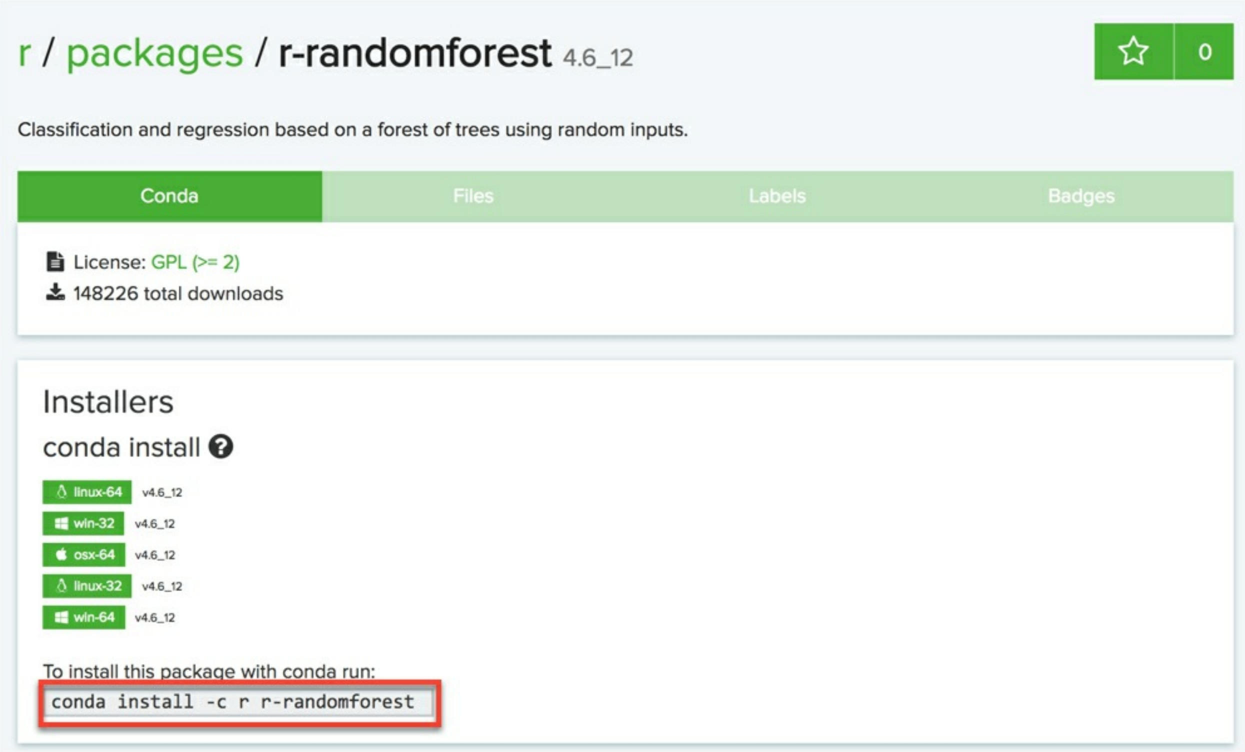
About 97,800 results (0.45 seconds)

R Randomforest :: Anaconda Cloud
https://anaconda.org/r/r-randomforest ▾
conda install. linux-64 v4.6_12; win-32 v4.6_12; osx-64 v4.6_12; linux-32 v4.6_12; win-64 v4.6_12. To install this package with conda run: conda install -c r **r-randomforest** ...
You visited this page on 2/14/18.

Badges :: Anaconda Cloud
https://anaconda.org/r/r-randomforest/badges ▾
r / packages / **r-randomforest**. 0. Classification and regression based on a forest of trees using random inputs. Conda · Files · Labels · Badges. Click on a badge to see how to embed it in your web page. badge. × ...

GitHub - conda-forge/r-randomforest-feedstock: A conda-smithy ...
https://github.com/conda-forge/r-randomforest-feedstock ▾
A conda-smithy repository for **r-randomforest**. Contribute to **r-randomforest**-feedstock development by creating an account on GitHub.

For instance, we need to install randomForest for the tutorial on random forest; we go **https://anaconda.org/r/r-randomforest.**



r / packages / r-randomforest 4.6_12

Classification and regression based on a forest of trees using random inputs.

License: GPL (>= 2)
148226 total downloads

Installers

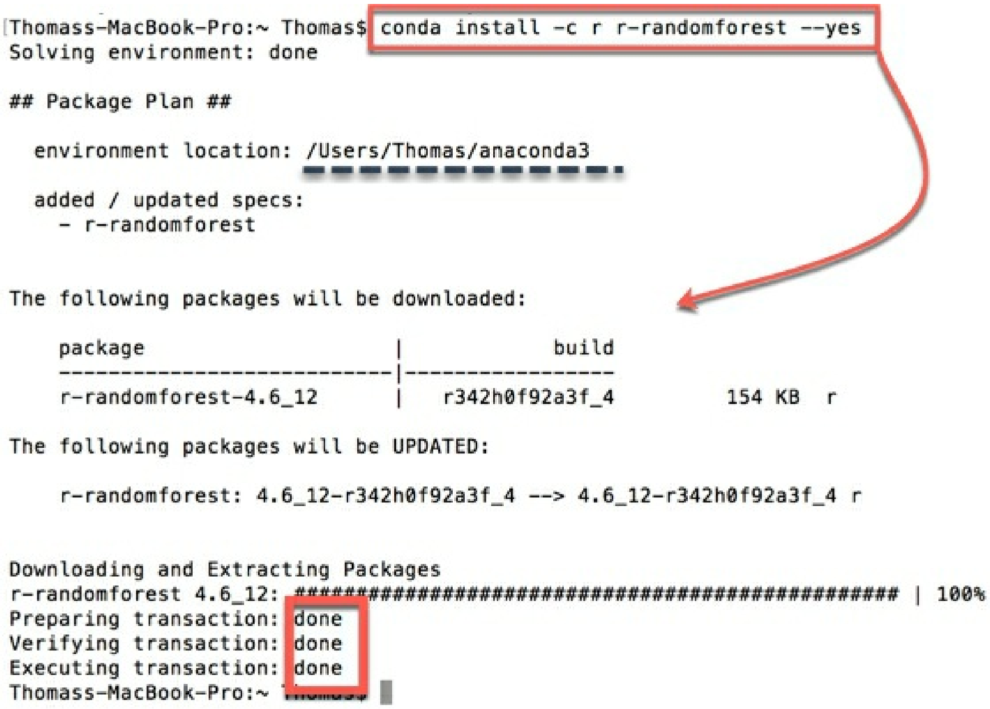
conda install

linux-64	v4.6_12
win-32	v4.6_12
osx-64	v4.6_12
linux-32	v4.6_12
win-64	v4.6_12

To install this package with conda run:

```
conda install -c r r-randomforest
```

Run conda install -c r r-randomforest --yes from the terminal.



```
Thomass-MacBook-Pro:~ Thomas$ conda install -c r r-randomforest --yes
Solving environment: done

## Package Plan ##

  environment location: /Users/Thomas/anaconda3

  added / updated specs:
    - r-randomforest


The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    r-randomforest-4.6_12      |   r342h0f92a3f_4         154 KB  r

The following packages will be UPDATED:

    r-randomforest: 4.6_12-r342h0f92a3f_4 --> 4.6_12-r342h0f92a3f_4 r


Downloading and Extracting Packages
r-randomforest 4.6_12: ################################################ | 100%
Preparing transaction: done
Verifying transaction: done
Executing transaction: done
Thomass-MacBook-Pro:~ Thomas$
```

The installation is completed.

Note that Thorough this tutorial, you won't need to install many libraries as the most used libraries came with the r-essential conda library. It includes ggplot for the graph and caret for the machine learning project.

Open a library

To run the R function randomForest(), we need to open the library containing the function. In the Rstudio script, we can write library(randomForest)

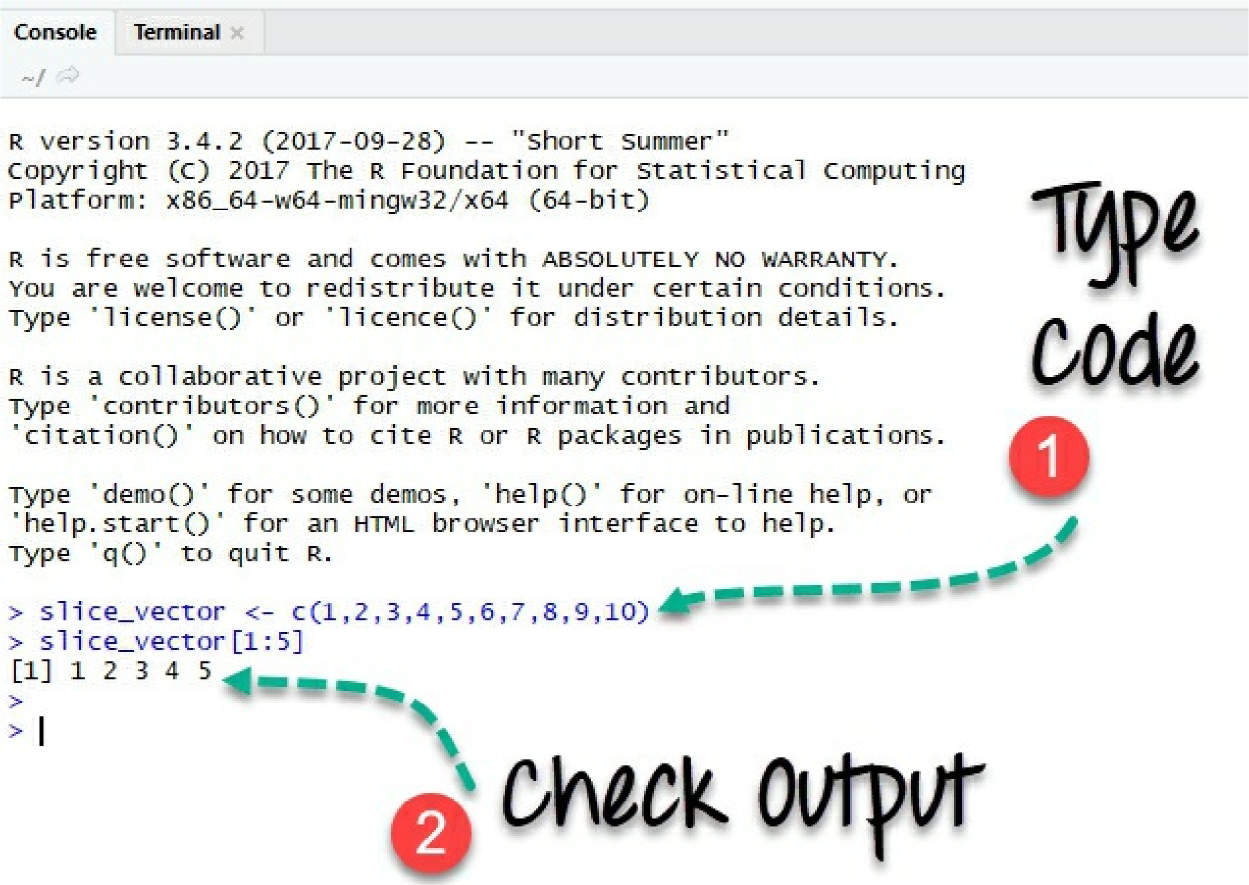
```
## In Rstudiolibrary(randomForest)
## randomForest 4.6-12
## Type rfNews() to see new features/changes/bug fixes.
```

Warning: Avoid as much as possible to open unnecessary packages. You might ended up creating conflicts between libraries.

Run R code

We have two ways to run codes in R

1. We can run the codes inside the Console. Our data will be stored in the Global Environment but no history is recorded. We won't be able to replicate the results once R is closed. We need to write the codes all over again. This method is not recommended if we want to replicate our save our codes



```
R version 3.4.2 (2017-09-28) -- "Short Summer"
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> slice_vector <- c(1,2,3,4,5,6,7,8,9,10)
> slice_vector[1:5]
[1] 1 2 3 4 5
>
> |
```
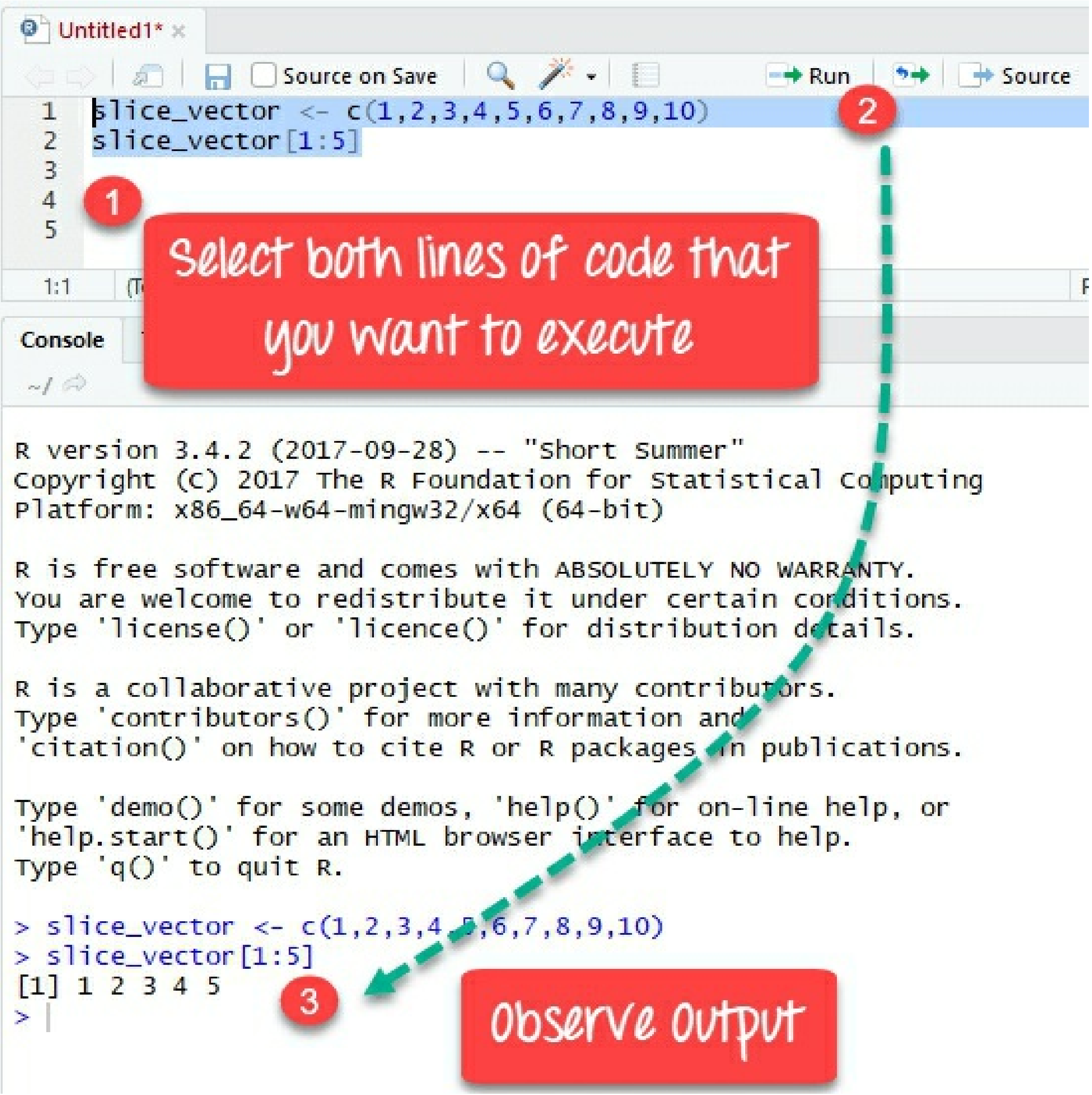

2. Write the code in the script. We can write as many lines of codes as we want. To run the code, we simple select the rows we want to return. Finally, click on run. We can see the output in the Console. We can save our script and open it later. Our results won't we lost.



```
1  slice_vector <- c(1,2,3,4,5,6,7,8,9,10)
2  slice_vector[1:5]
3
4
5
```

1 Select both lines of code that you want to execute

2

```
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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> slice_vector <- c(1,2,3,4,5,6,7,8,9,10)
> slice_vector[1:5]
[1] 1 2 3 4 5
> 
```
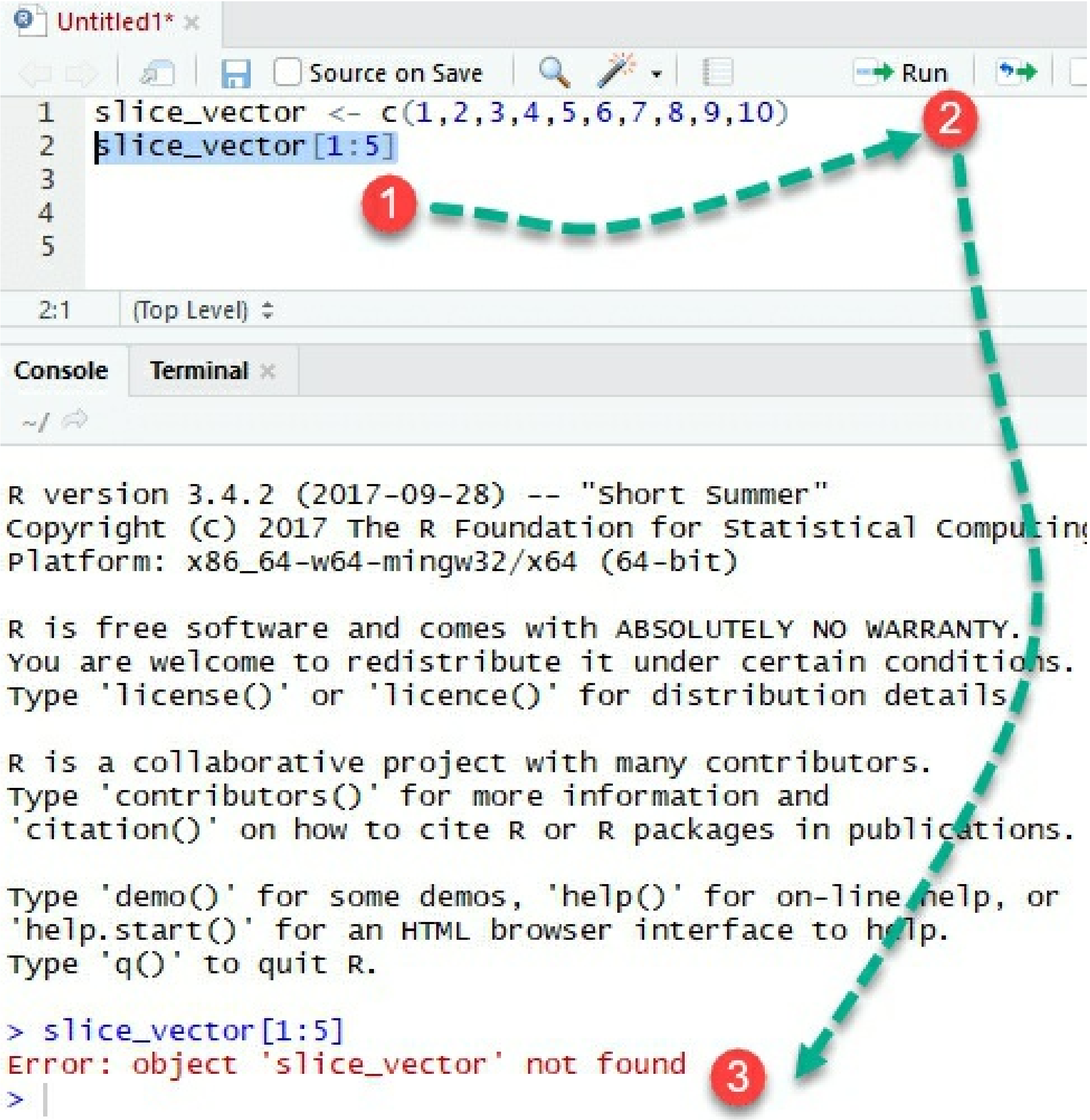

3 Observe output

Warning: In we point the cursor at the second row (i.e., slice_vector[1:5]), the Console displays an error. That's, we didn't run the line number 1.



```r
slice_vector <- c(1,2,3,4,5,6,7,8,9,10)
slice_vector[1:5]
```

```
R version 3.4.2 (2017-09-28) -- "Short Summer"
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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> slice_vector[1:5]
Error: object 'slice_vector' not found
>
```
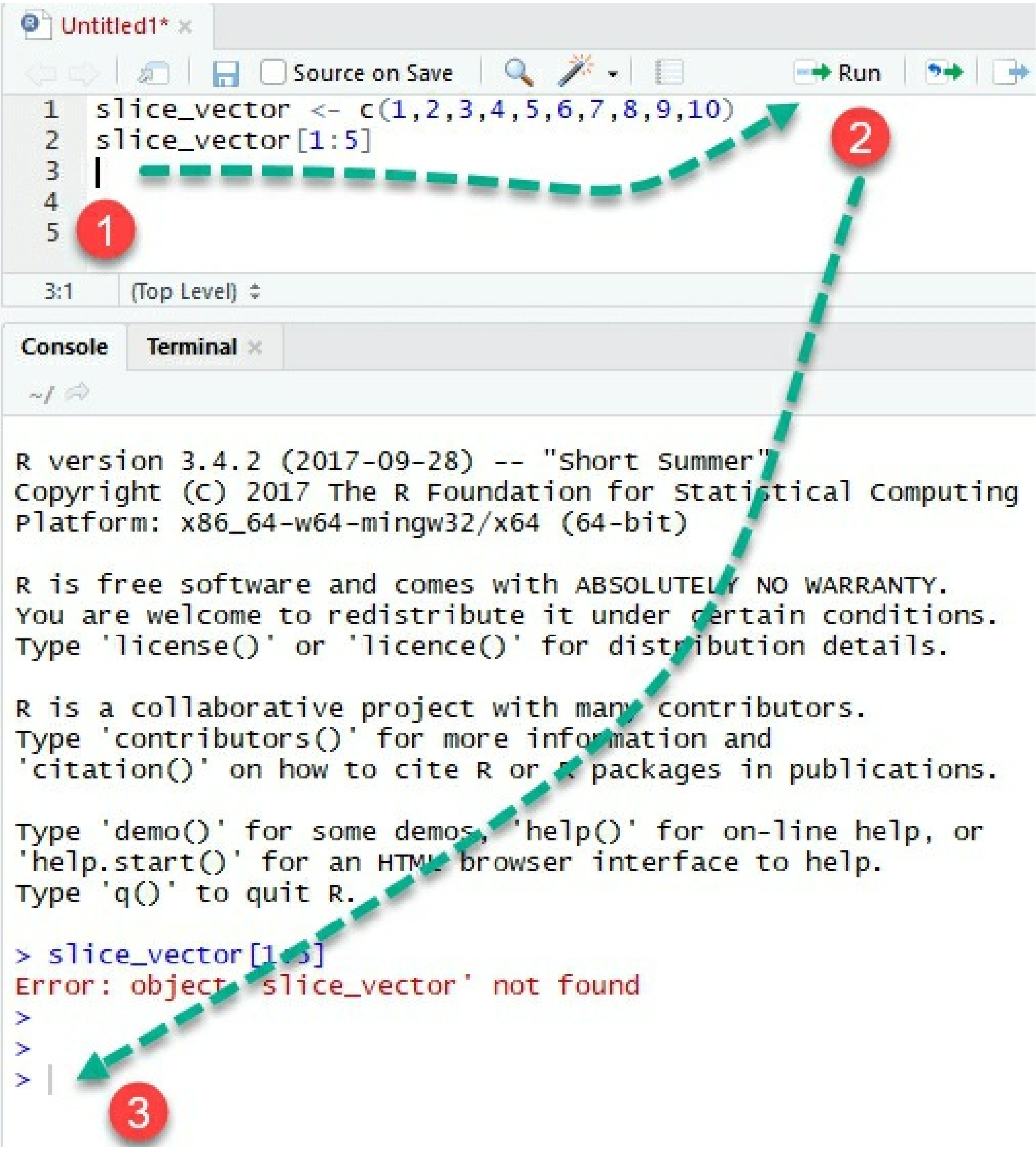

Similarly, if we point the cursor to an empty row and click on run, R return an empty output.



```
slice_vector <- c(1,2,3,4,5,6,7,8,9,10)
slice_vector[1:5]
```

```
R version 3.4.2 (2017-09-28) -- "Short Summer"
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'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> slice_vector[1:5]
Error: object 'slice_vector' not found
>
>
>
```

Chapter 3: R Data Types, Arithmetic & Logical Operators with Example

Basic data types

R Programming works with numerous data types, including

- Scalars
- Vectors (numerical, character, logical)
- Matrices
- Data frames
- Lists

Basics types

- 4.5 is a decimal value called **numerics**.
- 4 is a natural value called **integers**. Integers are also numerics.
- TRUE or FALSE is a Boolean value called **logical**.
- The value inside " " or ' ' are text (string). They are called **characters**.

We can check the type of a variable with the class function

Example 1:

```
# Declare variables of different types
# Numeric
x <- 28
class(x)
```

Output:

```
## [1] "numeric"
```

Example 2:

```
# String
y <- "R is Fantastic"
class(y)
```

Output:

```
## [1] "character"
```

Example 3:

```
# Boolean
z <- TRUE
class(z)
```

Output:

```
## [1] "logical"
```

Variables

Variables store values and are an important component in programming, especially for a data scientist. A variable can store a number, an object, a statistical result, vector, dataset, a model prediction basically anything R outputs. We can use that variable later simply by calling the name of the variable.

To declare a variable, we need to assign a variable name. The name should not have space. We can use _ to connect to words.

To add a value to the variable, use <- or =.

Here is the syntax:

```
# First way to declare a variable:  use the `<-`
name_of_variable <- value
# Second way to declare a variable:  use the `=`
```

```
name_of_variable = value
```

In the command line, we can write the following codes to see what happens:

Example 1:

```
# Print variable x
x <- 42
x
```

Output:

```
## [1] 42
```

Example 2:

```
y  <- 10
y
```

Output:

```
## [1] 10
```

Example 3:

```
# We call x and y and apply a subtraction
x-y
```

Output:

```
## [1] 32
```

Vectors

A vector is a one-dimensional array. We can create a vector with all the basic data type we learnt before. The simplest way to build a vector in R, is to use the c command.

Example 1:

```
# Numerical
vec_num <- c(1, 10, 49)
vec_num
```

Output:

```
## [1]  1 10 49
```

Example 2:

```
# Character
vec_chr <- c("a", "b", "c")
vec_chr
```

Output:

```
## [1] "a" "b" "c"
```

Example 3:

```
# Boolean
vec_bool <-  c(TRUE, FALSE, TRUE)
vec_bool
```

Output:

```
##[1] TRUE FALSE TRUE
```

We can do arithmetic calculations on vectors.

Example 4:

```
# Create the vectors
vect_1 <- c(1, 3, 5)
vect_2 <- c(2, 4, 6)
# Take the sum of A_vector and B_vector
sum_vect <- vect_1 + vect_2
# Print out total_vector
sum_vect
```

Output:

```
[1]  3  7 11
```

Example 5:

In R, it is possible to slice a vector. In some occasion, we are interested in only the first five rows of a vector. We can use the [1:5] command to extract the value 1 to 5.

```
# Slice the first five rows of the vector
slice_vector <- c(1,2,3,4,5,6,7,8,9,10)
slice_vector[1:5]
```

Output:

```
## [1] 1 2 3 4 5
```

Example 6:

The shortest way to create a range of value is to use the: between two numbers. For instance, from the above example, we can write c(1:10) to create a vector of value from one to ten.

```
# Faster way to create adjacent values
c(1:10)
```

Output:

```
## [1]  1  2  3  4  5  6  7  8  9 10
```

Arithmetic Operators

We will first see the basic arithmetic operations in R. The following operators stand for:

Operator	**Description**
+	Addition
-	Subtraction
*	Multiplication
/	Division

^ or **	Exponentiation

Example 1:

```
# An addition
3 + 4
```

Output:

```
## [1] 7
```

You can easily copy and paste the above R code into Rstudio Console. The **output** is displayed after the character #. For instance, we write the code print('Guru99') the output will be ##[1] Guru99.

The ## means we print an output and the number in the square bracket ([1]) is the number of the display

The sentences starting with # **annotation**. We can use # inside an R script to add any comment we want. R won't read it during the running time.

Example 2:

```
# A multiplication
3*5
```

Output:

```
## [1] 15
```

Example 3:

```
# A division
(5+5)/2
```

Output:

```
## [1] 5
```

Example 4:

```
# Exponentiation
2^5
```

Output:

Example 5:

```
## [1] 32
```

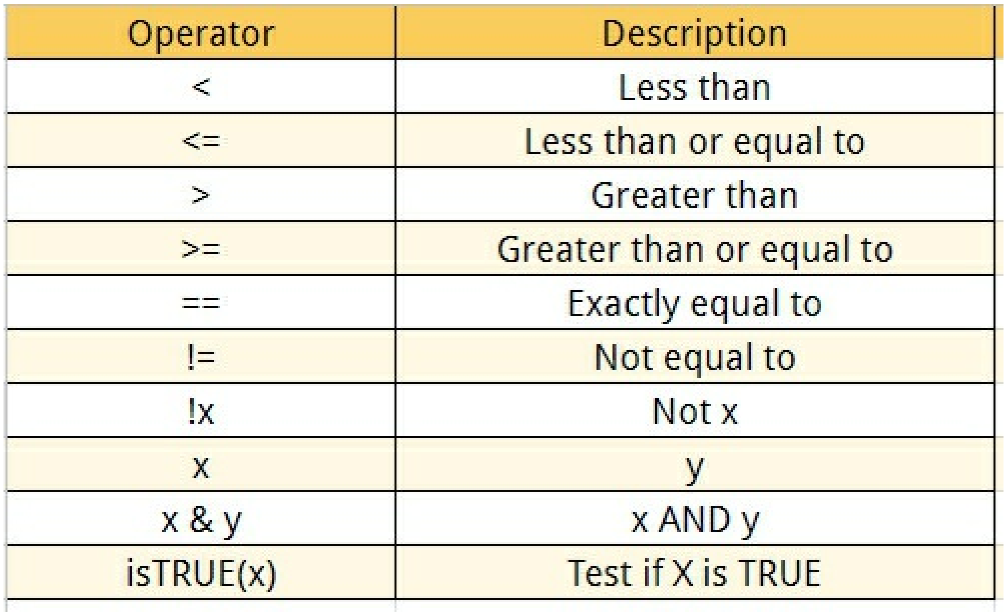
```
# Modulo
28%%6
```

Output:

```
## [1] 4
```

Logical Operators

With logical operators, we want to return values inside the vector based on logical conditions. Following is a detailed list of logical operators available in R



Operator	Description
<	Less than
<=	Less than or equal to
>	Greater than
>=	Greater than or equal to
==	Exactly equal to
!=	Not equal to
!x	Not x
x	y
x & y	x AND y
isTRUE(x)	Test if X is TRUE

The logical statements in R are wrapped inside the []. We can add many conditional statements as we like but we need to include them in a parenthesis. We can follow this structure to create a conditional statement:

```
variable_name[(conditional_statement)]
```

With variable_name referring to the variable, we want to use for the statement. We create the logical statement i.e. variable_name > 0. Finally, we use the square bracket to finalize the logical statement. Below, an example of a logical statement.

Example 1:

```
# Create a vector from 1 to 10
logical_vector <- c(1:10)
logical_vector>5
```

Output:

```
## [1]FALSE FALSE FALSE FALSE
FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
```

In the output above, R reads each value and compares it to the statement logical_vector>5. If the value is strictly superior to five, then the condition is TRUE, otherwise FALSE. R returns a vector of TRUE and FALSE.

Example 2:

In the example below, we want to extract the values that only meet the condition 'is strictly superior to five'. For that, we can wrap the condition inside a square bracket precede by the vector containing the values.

```
# Print value strictly above 5
logical_vector[(logical_vector>5)]
```

Output:

```
## [1]  6  7  8  9 10
```

Example 3:

```
# Print 5 and 6
logical_vector <- c(1:10)
logical_vector[(logical_vector>4) & (logical_vector<7)]
```

Output:

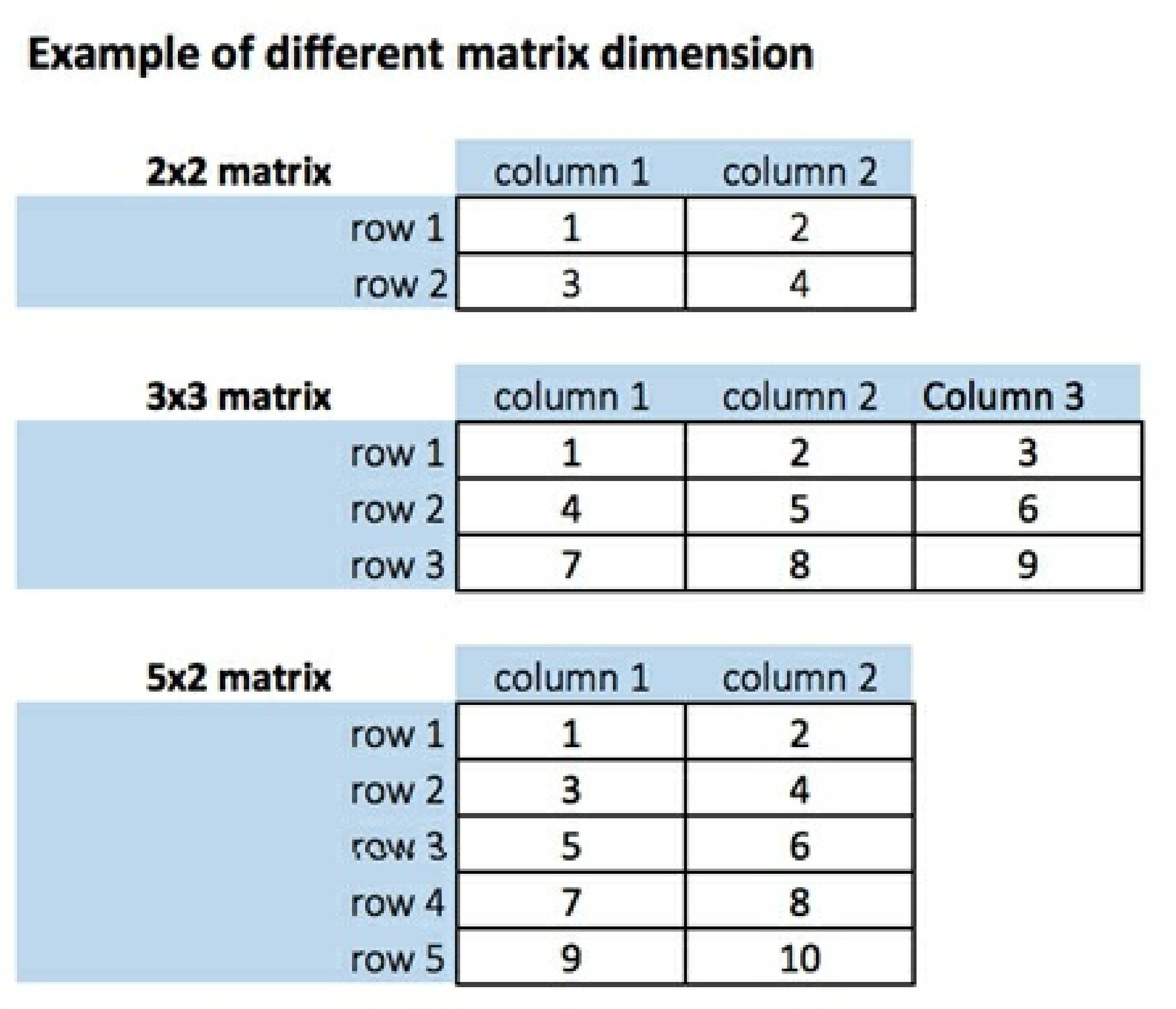
```
## [1] 5 6
```

Chapter 4: R Matrix Tutorial: Create, Print, add Column, Slice

What is a Matrix?

A matrix is a 2-dimensional array that has m number of rows and n number of columns. In other words, matrix is a combination of two or more vectors with the same data type.

Note: It is possible to create more than two dimensions arrays with R.



Example of different matrix dimension

2x2 matrix	column 1	column 2
row 1	1	2
row 2	3	4

3x3 matrix	column 1	column 2	Column 3
row 1	1	2	3
row 2	4	5	6
row 3	7	8	9

5x2 matrix	column 1	column 2
row 1	1	2
row 2	3	4
row 3	5	6
row 4	7	8
row 5	9	10

How to Create a Matrix in R

We can create a matrix with the function matrix(). This function takes three arguments:

```
matrix(data, nrow, ncol, byrow = FALSE)
```

Arguments:

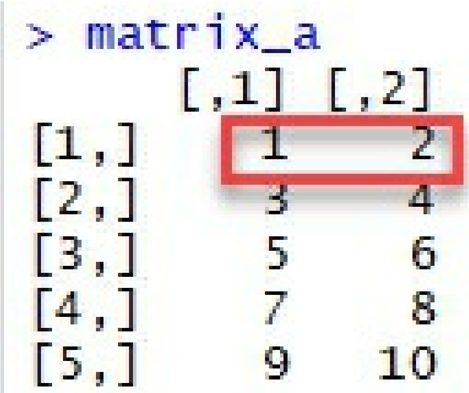
- **data**: The collection of elements that R will arrange into the rows and columns of the matrix \
- **nrow**: Number of rows

- **ncol**: Number of columns
- **byrow**: The rows are filled from the left to the right. We use `byrow = FALSE` (default values), if we want the matrix to be filled by the columns i.e. the values are filled top to bottom.

Let's construct two 5x2 matrix with a sequence of number from 1 to 10, one with byrow = TRUE and one with byrow = FALSE to see the difference.

```
# Construct a matrix with 5 rows that contain the numbers 1 up
to 10 and byrow =  TRUE
matrix_a <-matrix(1:10, byrow = TRUE, nrow = 5)
matrix_a
```

Output:



```
> matrix_a
     [,1] [,2]
[1,]    1    2
[2,]    3    4
[3,]    5    6
[4,]    7    8
[5,]    9   10
```

Print dimension of the matrix with dim()

```
# Print dimension of the matrix with dim()
dim(matrix_a)
```

Output:

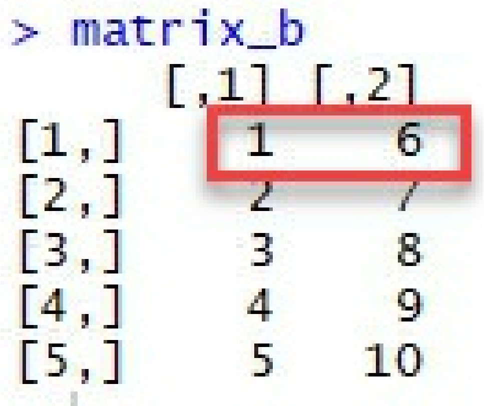
```
## [1] 5 2
```

Construct a matrix with 5 rows that contain the numbers 1 up to 10 and byrow = FALSE

```
# Construct a matrix with 5 rows that contain the numbers 1 up
```

```
to 10 and byrow =  FALSE
matrix_b <-matrix(1:10, byrow = FALSE, nrow = 5)
matrix_b
```

Output:



```
> matrix_b
     [,1] [,2]
[1,]    1    6
[2,]    2    7
[3,]    3    8
[4,]    4    9
[5,]    5   10
```

Print dimension of the matrix with dim()

```
# Print dimension of the matrix with dim()
dim(matrix_b)
```

Output:

```
## [1] 5 2
```

Note: Using command matrix_b <-matrix(1:10, byrow = FALSE, ncol = 2) will have same effect as above.

You can also create a 4x3 matrix using ncol. R will create 3 columns and fill the row from top to bottom. Check an example

```
matrix_c <-matrix(1:12, byrow = FALSE, ncol = 3)
matrix_c
```

Output:

```
##      [,1] [,2] [,3]
## [1,]    1    5    9
## [2,]    2    6   10
## [3,]    3    7   11
## [4,]    4    8   12
```

Example:

```
dim(matrix_c)
```

Output:

```
## [1] 4 3
```

Add a Column to a Matrix with the cbind()

You can add a column to a matrix with the cbind() command. cbind() means column binding. cbind()can concatenate as many matrix or columns as specified. For example, our previous example created a 5x2 matrix. We concatenate a third column and verify the dimension is 5x3

Example:

```
# concatenate c(1:5) to the matrix_a
matrix_a1 <- cbind(matrix_a, c(1:5))
# Check the dimension
dim(matrix_a1)
```

Output:

```
## [1] 5 3
```

Example:

```
matrix_a1
```

Output

```
##      [,1] [,2] [,3]
## [1,]    1    2    1
## [2,]    3    4    2
## [3,]    5    6    3
## [4,]    7    8    4
## [5,]    9   10    5
```

Example:

We can also add more than one column. Let's see the next sequence of number to the matrix_a2 matrix. The dimension of the new matrix will be 4x6 with number from 1 to 24.

```
matrix_a2 <-matrix(13:24, byrow = FALSE, ncol = 3)
```

Output:

```
##      [,1] [,2] [,3]
## [1,]   13   17   21
## [2,]   14   18   22
## [3,]   15   19   23
## [4,]   16   20   24
```

Example:

```
matrix_c <-matrix(1:12, byrow = FALSE, ncol = 3)
matrix_d <- cbind(matrix_a2, matrix_c)
dim(matrix_d)
```

Output:

```
## [1] 4 6
```

NOTE: The number of rows of matrices should be equal for cbind work

cbind()concatenate columns, rbind() appends rows. Let's add one row to our matrix_c matrix and verify the dimension is 6x3

```
matrix_c <-matrix(1:12, byrow = FALSE, ncol = 3)
# Create a vector of 3 columns
add_row <- c(1:3)
# Append to the matrix
matrix_c <- rbind(matrix_b, add_row)
# Check the dimension
```

```
dim(matrix_c)
```

Output:

```
## [1] 6 3
```

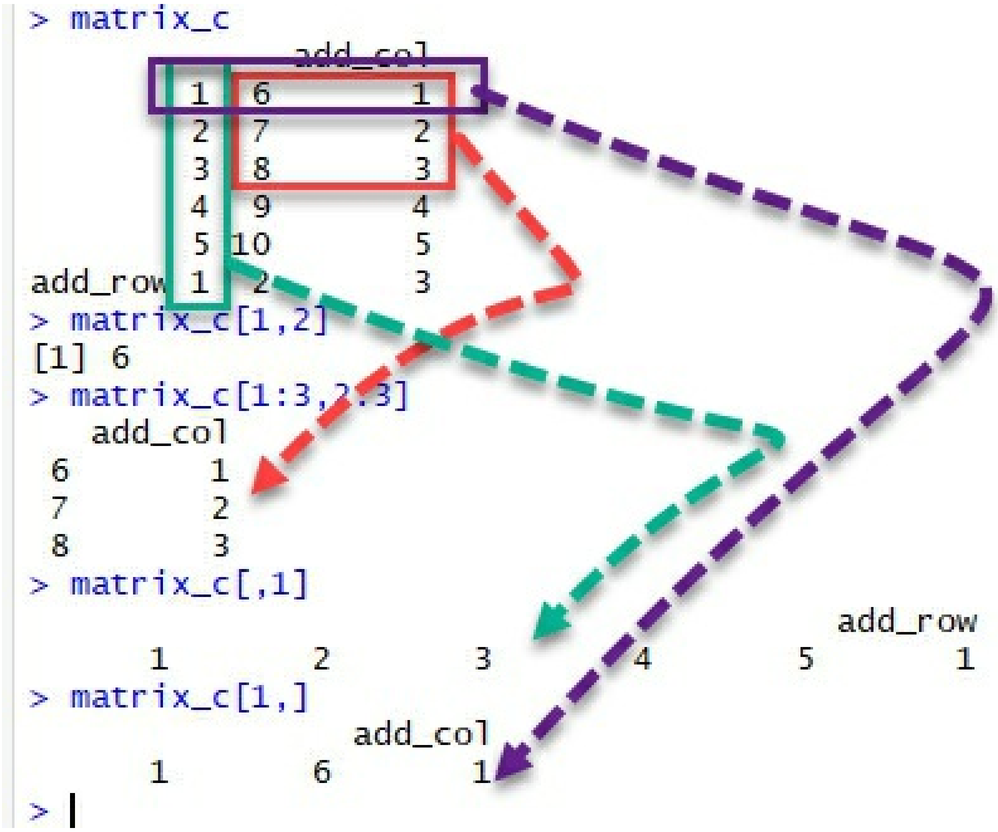
Slice a Matrix

We can select elements one or many elements from a matrix by using the square brackets [ ]. This is where slicing comes into the picture.

For example:

- matrix_c[1,2] selects the element at the first row and second column.
- matrix_c[1:3,2:3] results in a matrix with the data on the rows 1, 2, 3 and columns 2, 3,
- matrix_c[,1] selects all elements of the first column.
- matrix_c[1,] selects all elements of the first row.

Here is the output you get for the above codes



```
> matrix_c
              add_col
        1  6       1
        2  7       2
        3  8       3
        4  9       4
        5 10       5
add_row 1  2       3
> matrix_c[1,2]
[1] 6
> matrix_c[1:3,2:3]
   add_col
 6       1
 7       2
 8       3
> matrix_c[,1]
                                        add_row
      1       2       3       4       5       1
> matrix_c[1,]
                add_col
      1       6       1
> 
```

Chapter 5: Factor in R: Categorical & Continuous Variables

What is Factor in R?

Factors are variables in R which take on a limited number of different values; such variables are often referred to as categorical variables.

In a dataset, we can distinguish two types of variables: **categorical** and **continuous**.

- In a categorical variable, the value is limited and usually based on a particular finite group. For example, a categorical variable can be countries, year, gender, occupation.
- A continuous variable, however, can take any values, from integer to decimal. For example, we can have the revenue, price of a share, etc..

Categorical Variables

R stores categorical variables into a factor. Let's check the code below to convert a character variable into a factor variable. Characters are not supported in machine learning algorithm, and the only way is to convert a string to an integer.

Syntax

```
factor(x = character(), levels, labels = levels, ordered =
is.ordered(x))
```

Arguments:

- **x**: A vector of data. Need to be a string or integer, not decimal.
- **Levels**: A vector of possible values taken by x. This argument is optional. The default value is the unique list of items of the vector x.
- **Labels**: Add a label to the x data. For example, 1 can take the label `male` while 0, the label `female`.
- **ordered**: Determine if the levels should be ordered.

Example:

Let's create a factor data frame.

```
# Create gender vector
gender_vector <- c("Male", "Female", "Female", "Male", "Male")
class(gender_vector)
# Convert gender_vector to a factor
factor_gender_vector <-factor(gender_vector)
class(factor_gender_vector)
```

Output:

```
## [1] "character"
## [1] "factor"
```

It is important to transform a **string** into factor when we perform Machine Learning task.

A categorical variable can be divided into **nominal categorical variable** and **ordinal categorical variable**.

Nominal Categorical Variable

A categorical variable has several values but the order does not matter. For instance, male or female categorical variable do not have ordering.

```
# Create a color vector
color_vector <- c('blue', 'red', 'green', 'white', 'black',
'yellow')
# Convert the vector to factor
factor_color <- factor(color_vector)
factor_color
```

Output:

```
## [1] blue   red    green  white  black  yellow
## Levels: black blue green red white yellow
```

From the factor_color, we can't tell any order.

Ordinal Categorical Variable

Ordinal categorical variables do have a natural ordering. We can specify the order, from the lowest to the highest with order = TRUE and highest to lowest with order = FALSE.

Example:

We can use summary to count the values for each factor.

```
# Create Ordinal categorical vector
day_vector <- c('evening', 'morning', 'afternoon', 'midday',
'midnight', 'evening')
# Convert `day_vector` to a factor with ordered level
factor_day <- factor(day_vector, order = TRUE, levels
=c('morning', 'midday', 'afternoon', 'evening', 'midnight'))
# Print the new variable
factor_day
```

Output:

```
## [1] evening   morning   afternoon midday
midnight  evening
```

Example:

```
## Levels: morning < midday < afternoon < evening < midnight
# Append the line to above code
# Count the number of occurence of each level
```

```
summary(factor_day)
```

Output:

```
##   morning    midday afternoon   evening  midnight
##         1         1         1         2         1
```

R ordered the level from 'morning' to 'midnight' as specified in the levels parenthesis.

Continuous Variables

Continuous class variables are the default value in R. They are stored as numeric or integer. We can see it from the dataset below. mtcars is a built-in dataset. It gathers information on different types of car. We can import it by using mtcars and check the class of the variable mpg, mile per gallon. It returns a numeric value, indicating a continuous variable.

```
dataset <- mtcars
class(dataset$mpg)
```

Output

```
## [1] "numeric"
```

Chapter 6: R Data Frame: Create, Append, Select, Subset

What is a Data Frame?

A **data frame** is a list of vectors which are of equal length. A matrix contains only one type of data, while a data frame accepts different data types (numeric, character, factor, etc.).

In this tutorial, you will learn-

How to Create a Data Frame

We can create a data frame by passing the variable a,b,c,d into the data.frame() function. We can name the columns with name() and simply specify the name of the variables.

```
data.frame(df, stringsAsFactors = TRUE)
```

Arguments:

- **df**: It can be a matrix to convert as a data frame or a collection of variables to join
- **stringsAsFactors**: Convert string to factor by default

We can create our first data set by combining four variables of same length.

```
# Create a, b, c, d variables
a <- c(10,20,30,40)
```

```
b <- c('book', 'pen', 'textbook', 'pencil_case')
c <- c(TRUE,FALSE,TRUE,FALSE)
d <- c(2.5, 8, 10, 7)
# Join the variables to create a data frame
df <- data.frame(a,b,c,d)
df
```

Output:

```
##   a       b c d
## 1  1        book  TRUE   2.5
## 2  2         pen  TRUE   8.0
## 3  3    textbook  TRUE  10.0
## 4  4 pencil_case FALSE   7.0
```

We can see the column headers have the same name as the variables. We can change the column name with the function names(). Check the example below:

```
# Name the data frame
names(df) <- c('ID', 'items', 'store', 'price')
df
```

Output:

```
##   ID       items store price
## 1 10        book  TRUE   2.5
## 2 20         pen FALSE   8.0
## 3 30    textbook  TRUE  10.0
## 4 40 pencil_case FALSE   7.0
```

```
# Print the structure
str(df)
```

Output:

```
## 'data.frame':    4 obs. of  4 variables:
##  $ ID   : num  10 20 30 40
##  $ items: Factor w/ 4 levels "book","pen","pencil_case",..: 1
2 4 3
##  $ store: logi  TRUE FALSE TRUE FALSE
##  $ price: num  2.5 8 10 7
```

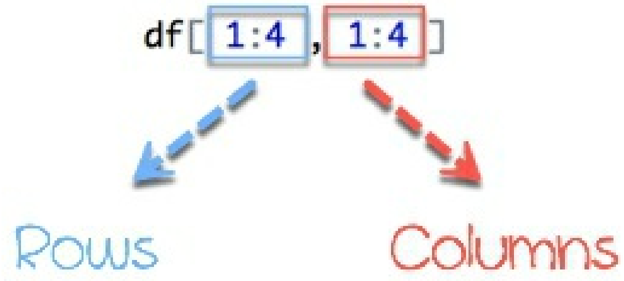
By default, data frame returns string variables as a factor.

Slice Data Frame

It is possible to SLICE values of a Data Frame. We select the rows and columns to return into bracket precede by the name of the data frame.

A data frame is composed of rows and columns, df[A, B]. A represents the rows and B the columns. We can slice either by specifying the rows and/or columns.

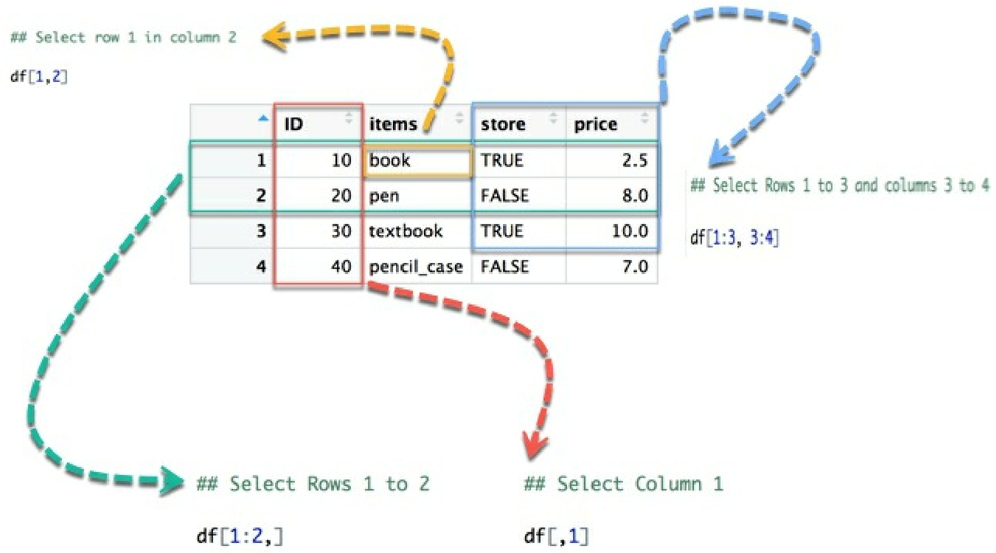
From picture 1, the left part represents the **rows,** and the right part is the **columns**. Note that the symbol : means **to**. For instance, 1:3 intends to select values from 1 **to** 3.



In below diagram we display how to access different selection of the data frame:

- The yellow arrow selects the **row** 1 in **column** 2
- The green arrow selects the **rows** 1 to 2
- The red arrow selects the **column** 1
- The blue arrow selects the **rows** 1 to 3 and **columns** 3 to 4

Note that, if we let the left part blank, R will select **all the rows**. By analogy, if we let the right part blank, R will select **all the columns**.



```
## Select row 1 in column 2

df[1,2]
```

	ID	items	store	price
1	10	book	TRUE	2.5
2	20	pen	FALSE	8.0
3	30	textbook	TRUE	10.0
4	40	pencil_case	FALSE	7.0

```
## Select Rows 1 to 3 and columns 3 to 4

df[1:3, 3:4]
```

```
## Select Rows 1 to 2

df[1:2,]
```

```
## Select Column 1

df[,1]
```

We can run the code in the console:

```
## Select row 1 in column 2
df[1,2]
```

Output:

```
## [1] book
## Levels: book pen pencil_case textbook
```

```
## Select Rows 1 to 2
df[1:2,]
```

Output:

```
##   ID items store price
## 1 10  book  TRUE   2.5
## 2 20   pen FALSE   8.0
```

```
## Select Columns 1
df[,1]
```

Output:

```
## [1] 10 20 30 40
```

```
## Select Rows 1 to 3 and columns 3 to 4
df[1:3, 3:4]
```

Output:

```
##   store price
## 1  TRUE   2.5
## 2 FALSE   8.0
## 3  TRUE  10.0
```

It is also possible to select the columns with their names. For instance, the code below extracts two columns: ID and store.

```
# Slice with columns name
df[, c('ID', 'store')]
```

Output:

```
##   ID store
## 1 10  TRUE
## 2 20 FALSE
## 3 30  TRUE
## 4 40 FALSE
```

Append a Column to Data Frame

You can also append a column to a Data Frame. You need to use the symbol $ to append a new variable.

```
# Create a new vector
quantity <- c(10, 35, 40, 5)

# Add `quantity` to the `df` data frame
df$quantity <- quantity
df
```

Output:

```
##   ID       items store price quantity
## 1 10        book  TRUE   2.5       10
## 2 20         pen FALSE   8.0       35
## 3 30    textbook  TRUE  10.0       40
## 4 40 pencil_case FALSE   7.0        5
```

Note: The number of elements in the vector has to be equal to the no of elements in data frame. Executing the following statement

```
quantity <- c(10, 35, 40)
# Add `quantity` to the `df` data frame
df$quantity <- quantity
```

Gives error:

```
Error in `$<-.data.frame`(`*tmp*`, quantity, value = c(10, 35,
40))
 replacement has 3 rows, data has
4
```

Select a Column of a Data Frame

Sometimes, we need to store a column of a data frame for future use or perform operation on a column. We can use the $ sign to select the column from a data frame.

```
# Select the column ID
df$ID
```

Output:

```
## [1] 1 2 3 4
```

Subset a Data Frame

In the previous section, we selected an entire column without condition. It is possible to **subset** based on whether or not a certain condition was true.

We use the subset() function.

```
subset(x, condition)
arguments:
- x: data frame used to perform the subset
- condition: define the conditional statement
```

We want to return only the items with price above 10, we can do:

```
# Select price above 5
subset(df, subset = price > 5)
```

Output:

```
ID       items store price
2 20         pen FALSE     8
3 30    textbook  TRUE    10
4 40 pencil_case FALSE     7
```

Chapter 7: List in R: Create, Select Elements with Example

What is a List?

A **list** is a great tool to store many kinds of object in the order expected. We can include matrices, vectors data frames or lists. We can imagine a list as a bag in which we want to put many different items. When we need to use an item, we open the bag and use it. A list is similar; we can store a collection of objects and use them when we need them.

How to Create a List

We can use list() function to create a list.

```
list(element_1, ...)
arguments:
-element_1: store any type of R object
-...: pass as many objects as specifying. each object needs to
be separated by a comma
```

In the example below, we create three different objects, a vector, a matrix and a data frame.

Step 1) Create a Vector

```
# Vector with numeric from 1 up to 5
vect  <- 1:5
```

Step 2) Create a Matrices

```
# A 2x 5 matrix
mat  <- matrix(1:9, ncol = 5)
```

```
dim(mat)
```

Output:

```
## [1] 2 5
```

Step 3) Create Data Frame

```
# select the 10th row of the built-in R data set EuStockMarkets
df <- EuStockMarkets[1:10,]
```

Step 4) Create a List

Now, we can put the three object into a list.

```
# Construct list with these vec, mat, and df:
my_list <- list(vect, mat, df)
my_list
```

Output:

```
## [[1]]
## [1] 1 2 3 4 5

## [[2]]
##       [,1] [,2] [,3] [,4] [,5]
## [1,]    1    3    5    7    9
## [2,]    2    4    6    8    1

## [[3]]
##          DAX    SMI    CAC   FTSE
##  [1,] 1628.75 1678.1 1772.8 2443.6
##  [2,] 1613.63 1688.5 1750.5 2460.2
##  [3,] 1606.51 1678.6 1718.0 2448.2
##  [4,] 1621.04 1684.1 1708.1 2470.4
##  [5,] 1618.16 1686.6 1723.1 2484.7
##  [6,] 1610.61 1671.6 1714.3 2466.8
##  [7,] 1630.75 1682.9 1734.5 2487.9
##  [8,] 1640.17 1703.6 1757.4 2508.4
##  [9,] 1635.47 1697.5 1754.0 2510.5
##  [10,] 1645.89 1716.3 1754.3 2497.4
```

Select Elements from List

After we built our list, we can access it quite easily. We need to use the [[index]] to select an element in a list. The value inside the double square bracket represents the position of the item in a list we want to extract. For instance, we pass 2 inside the parenthesis, R returns the second element listed.

Let's try to select the second items of the list named my_list, we use my_list[[2]]

```
# Print second element of the list
my_list[[2]]
```

Output:

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    3    5    7    9
## [2,]    2    4    6    8    1
```

Built-in Data Frame

Before to create our own data frame, we can have a look at the R data set available online. The prison dataset is a 714x5 dimension. We can get a quick look at the bottom of the data frame with tail() function. By analogy, head() displays the top of the data frame. You can specify the number of rows shown with head (df, 5). We will learn more about the function read.csv() in future tutorial.

```
PATH <-'https://raw.githubusercontent.com/guru99-edu/R-Programming/master/prison.csv'
df <- read.csv(PATH)[1:5]
head(df, 5)
```

Output:

```
##   X state year govelec black
## 1 1     1   80       0 0.2560
## 2 2     1   81       0 0.2557
## 3 3     1   82       1 0.2554
## 4 4     1   83       0 0.2551
## 5 5     1   84       0 0.2548
```

We can check the structure of the data frame with str:

```
# Structure of the data
str(df)
```

Output:

```
## 'data.frame':    714 obs. of  5 variables:
##  $ X      : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ state  : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ year   : int  80 81 82 83 84 85 86 87 88 89 ...
##  $ govelec: int  0 0 1 0 0 0 1 0 0 0 ...
##  $ black  : num  0.256 0.256 0.255 0.255 0.255 ...
```

All variables are stored in the **numerical** format.

Chapter 8: R Sort a Data Frame using Order()

In data analysis you can **sort** your data according to a certain variable in the dataset. In R, we can use the help of the function order(). In R, we can easily sort a vector of continuous variable or factor variable. Arranging the data can be of **ascending** or **descending** order.

Syntax:

```
sort(x, decreasing = FALSE, na.last = TRUE):
```

Argument:

- **x**: A vector containing continuous or factor variable
- **decreasing**: Control for the order of the sort method. By default, decreasing is set to `FALSE`.
- **last**: Indicates whether the `NA` 's value should be put last or not

Example 1

For instance, we can create a tibble data frame and sort one or multiple variables. A tibble data frame is a new approach to data frame. It improves the syntax of data frame and avoid frustrating data type formatting, especially for character to factor. It is also a convenient way to create a data frame by hand, which is our purpose here. To learn more about tibble, please refer to the vignette: https://cran.r-project.org/web/packages/tibble/vignettes/tibble.html

```
library(dplyr)
set.seed(1234)
data_frame <- tibble(
        c1 = rnorm(50, 5, 1.5),
        c2 = rnorm(50, 5, 1.5),
        c3 = rnorm(50, 5, 1.5),
        c4 = rnorm(50, 5, 1.5),
        c5 = rnorm(50, 5, 1.5)
)
# Sort by c1
df <-data_frame[order(data_frame$c1),]
head(df)
```

Output:

```
# A tibble: 6 x 5
##       c1       c2       c3       c4       c5
##     <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 1.481453 3.477557 4.246283 3.686611 6.0511003
## 2 1.729941 5.824996 4.525823 6.753663 0.1502718
## 3 2.556360 6.275348 2.524849 6.368483 5.4787404
## 4 2.827693 4.769902 5.120089 3.743626 4.0103449
## 5 2.988510 4.395902 2.077631 4.236894 4.6176880
## 6 3.122021 6.317305 5.413840 3.551145 5.6067027
```

Example 2

```
# Sort by c3 and c4
df <-data_frame[order(data_frame$c3, data_frame$c4),]
head(df)
```

Output:

```
# A tibble: 6 x 5
##        c1       c2       c3       c4       c5
##    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 2.988510 4.395902 2.077631 4.236894 4.617688
## 2 2.556360 6.275348 2.524849 6.368483 5.478740
## 3 3.464516 3.914627 2.730068 9.565649 6.016123
## 4 4.233486 3.292088 3.133568 7.517309 4.772395
## 5 3.935840 2.941547 3.242078 6.464048 3.599745
## 6 3.835619 4.947859 3.335349 4.378370 7.240240
```

Example 3

```
# Sort by c3(descending) and c4(acending)
df <-data_frame[order(-data_frame$c3, data_frame$c4),]
head(df)
```

Output:

```
# A tibble: 6 x 5
##         c1       c2       c3        c4       c5
##      <dbl>    <dbl>    <dbl>     <dbl>    <dbl>
## 1 4.339178 4.450214 8.087243 4.5010140 8.410225
## 2 3.959420 8.105406 7.736312 7.1168936 5.431565
## 3 3.339023 3.298088 7.494285 5.9303153 7.035912
## 4 3.397036 5.382794 7.092722 0.7163620 5.620098
## 5 6.653446 4.733315 6.520536 0.9016707 4.513410
## 6 4.558559 4.712609 6.380086 6.0562703 5.044277
```

Chapter 9: R Dplyr Tutorial: Data Manipulation(Join) & Cleaning(Spread)

Introduction to Data Analysis

Data analysis can be divided into three parts

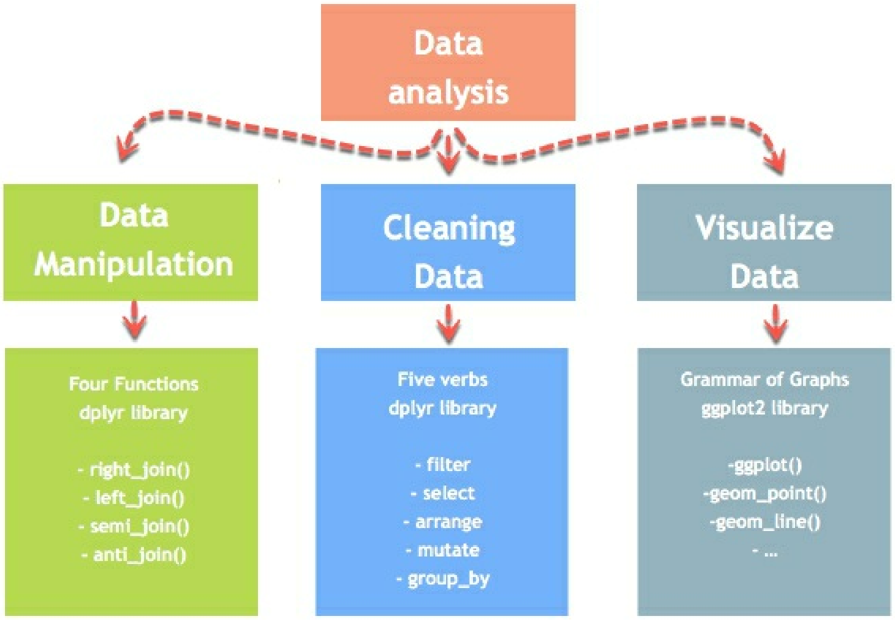
- Extraction: First, we need to collect the data from many sources and combine them.
- Transform: This step involves the data manipulation. Once we have consolidated all the sources of data, we can begin to clean the data.
- Visualize: The last move is to visualize our data to check irregularity.

One of the most significant challenges faced by data scientist is the data manipulation. Data is never available in the desired format. The data scientist needs to spend at least half of his time, cleaning and manipulating the data. That is one of the most critical assignments in the job. If the data manipulation process is not complete, precise and rigorous, the model will not perform correctly.

R has a library called dplyr to help in data transformation.

The dplyr library is fundamentally created around four functions to manipulate the data and five verbs to clean the data. After that, we can use the ggplot library to analyze and visualize the data.

In this tutorial, we will learn how to use the dplyr library to manipulate a data frame.



Merge with dplyr()

dplyr provides a nice and convenient way to combine datasets. We may have many sources of input data, and at some point, we need to combine them. A join with dplyr adds variables to the right of the original dataset. The beauty is dplyr is that it handles four types of joins similar to SQL

- Left_join()
- right_join()
- inner_join()
- full_join()

We will study all the joins types via an easy example.

First of all, we build two datasets. Table 1 contains two variables, ID, and y, whereas Table 2 gathers ID and z. In each situation, we need to have a **key-pair** variable. In our case, ID is our **key** variable. The function will look for identical values in both tables and bind the returning values to the right of table 1.

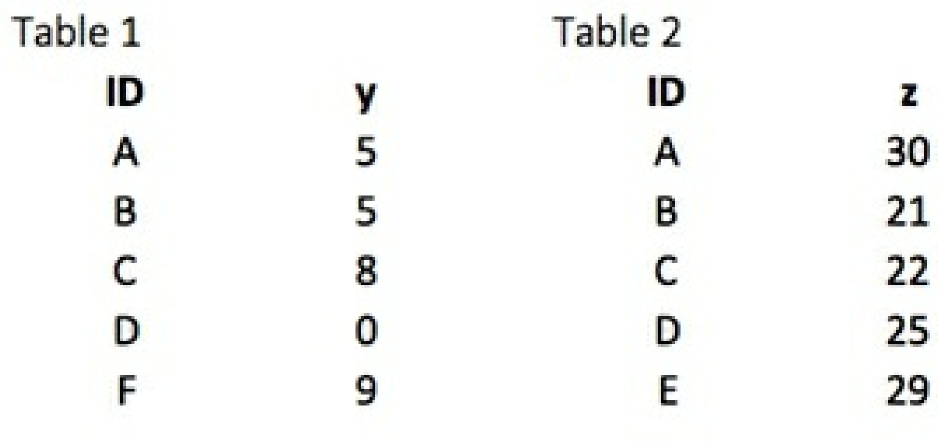


Table 1

ID	y
A	5
B	5
C	8
D	0
F	9

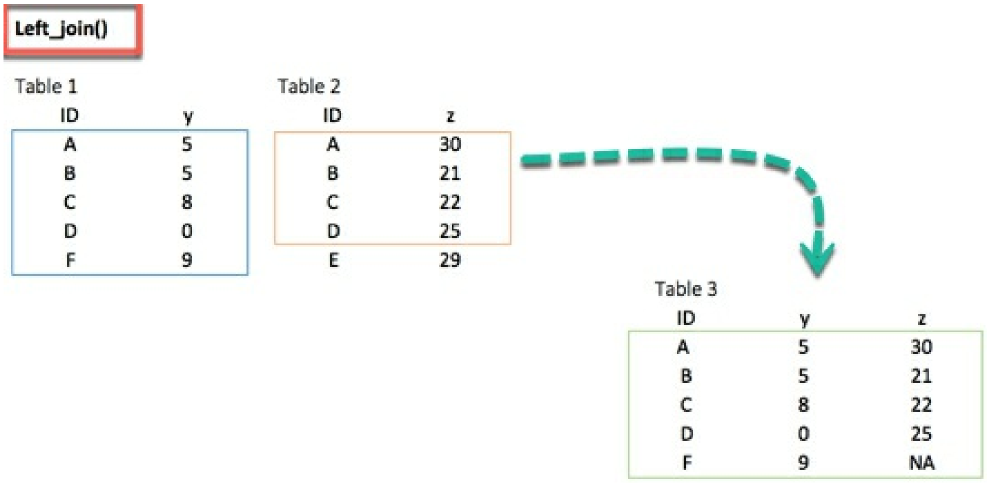
Table 2

ID	z
A	30
B	21
C	22
D	25
E	29

```
library(dplyr)
df_primary <- tribble(
  ~ID, ~y,
   "A", 5,
   "B", 5,
   "C", 8,
   "D", 0,
  "F", 9)
df_secondary <- tribble(
  ~ID, ~y,
   "A", 30,
   "B", 21,
   "C", 22,
   "D", 25,
   "E", 29)
```

left_join()

The most common way to merge two datasets is to use the left_join() function. We can see from the picture below that the key-pair matches perfectly the rows A, B, C and D from both datasets. However, E and F are left over. How do we treat these two observations? With the left_join(), we will keep all the variables in the original table and don't consider the variables that do not have a key-paired in the destination table. In our example, the variable E does not exist in table 1. Therefore, the row will be dropped. The variable F comes from the origin table; it will be kept after the left_join() and return NA in the column z. The figure below reproduces what will happen with a left_join().



Left_join()

Table 1

ID	y
A	5
B	5
C	8
D	0
F	9

Table 2

ID	z
A	30
B	21
C	22
D	25
E	29

Table 3

ID	y	z
A	5	30
B	5	21
C	8	22
D	0	25
F	9	NA

```
left_join(df_primary, df_secondary, by ='ID')
```

Output:

```
##
# A tibble: 5 x 3
##      ID   y.x   y.y
##   <chr> <dbl> <dbl>
## 1     A     5    30
## 2     B     5    21
## 3     C     8    22
## 4     D     0    25
## 5     F     9    NA
```

right_join()

The right_join() function works exactly like left_join(). The only difference is the row dropped. The value E, available in the destination data frame, exists in the new table and takes the value NA for the column y.

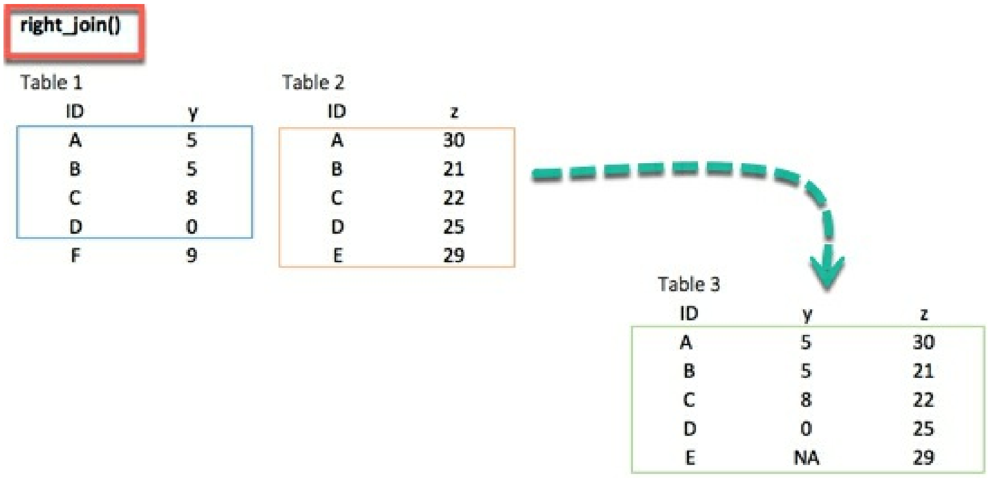


Table 1

ID	y
A	5
B	5
C	8
D	0
F	9

Table 2

ID	z
A	30
B	21
C	22
D	25
E	29

Table 3

ID	y	z
A	5	30
B	5	21
C	8	22
D	0	25
E	NA	29

```
right_join(df_primary, df_secondary, by = 'ID')
```

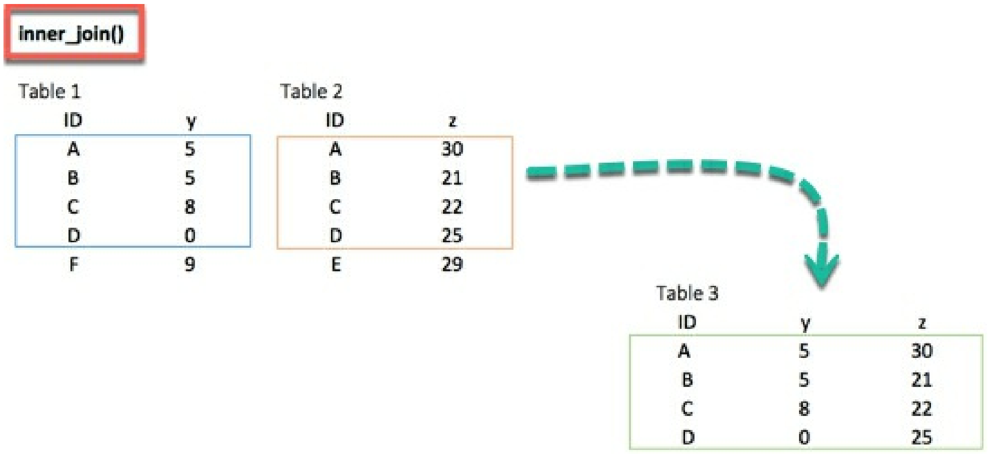
Output:

```
##
# A tibble: 5 x 3
##      ID   y.x   y.y
##   <chr> <dbl> <dbl>
## 1     A     5    30
## 2     B     5    21
## 3     C     8    22
## 4     D     0    25
## 5     E    NA    29
```

inner_join()

When we are 100% sure that the two datasets won't match, we can consider to return **only** rows existing in **both** dataset. This is possible when we need a clean dataset or when we don't want to impute missing values with the mean or median.

The inner_join()comes to help. This function excludes the unmatched rows.



inner_join()

Table 1

ID	y
A	5
B	5
C	8
D	0
F	9

Table 2

ID	z
A	30
B	21
C	22
D	25
E	29

Table 3

ID	y	z
A	5	30
B	5	21
C	8	22
D	0	25

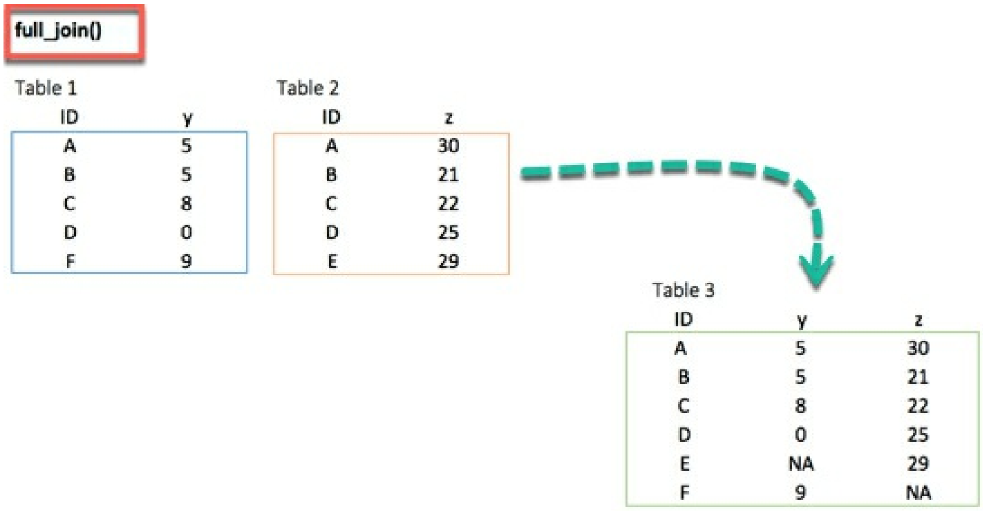
```
inner_join(df_primary, df_secondary, by ='ID')
```

output:

```
##
# A tibble: 4 x 3
##      ID   y.x   y.y
##   <chr> <dbl> <dbl>
## 1     A     5    30
## 2     B     5    21
## 3     C     8    22
## 4     D     0    25
```

full_join()

Finally, the full_join() function keeps all observations and replace missing values with NA.



full_join()

Table 1

ID	y
A	5
B	5
C	8
D	0
F	9

Table 2

ID	z
A	30
B	21
C	22
D	25
E	29

Table 3

ID	y	z
A	5	30
B	5	21
C	8	22
D	0	25
E	NA	29
F	9	NA

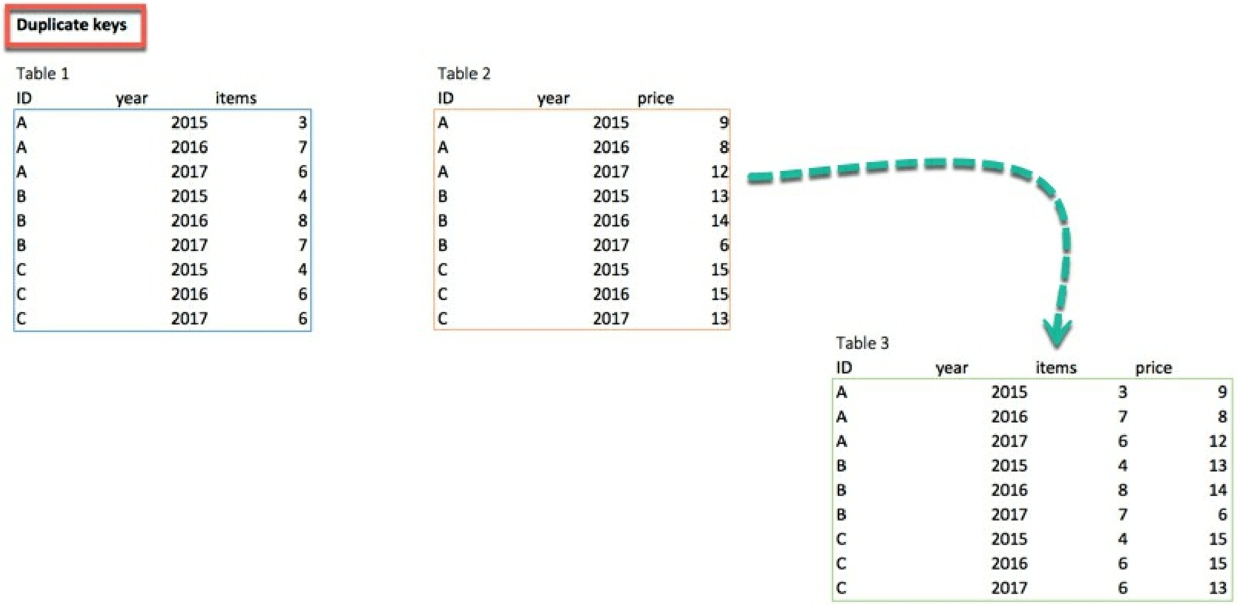
```
full_join(df_primary, df_secondary, by = 'ID')
```

Output:

```
## # A tibble: 6 x 3
##      ID   y.x   y.y
##   <chr> <dbl> <dbl>
## 1     A     5    30
## 2     B     5    21
## 3     C     8    22
## 4     D     0    25
## 5     F     9    NA
## 6     E    NA    29
```

Multiple keys pairs

Last but not least, we can have multiple keys in our dataset. Consider the following dataset where we have years or a list of products bought by the customer.



Duplicate keys

Table 1

ID	year	items
A	2015	3
A	2016	7
A	2017	6
B	2015	4
B	2016	8
B	2017	7
C	2015	4
C	2016	6
C	2017	6

Table 2

ID	year	price
A	2015	9
A	2016	8
A	2017	12
B	2015	13
B	2016	14
B	2017	6
C	2015	15
C	2016	15
C	2017	13

Table 3

ID	year	items	price
A	2015	3	9
A	2016	7	8
A	2017	6	12
B	2015	4	13
B	2016	8	14
B	2017	7	6
C	2015	4	15
C	2016	6	15
C	2017	6	13

If we try to merge both tables, R throws an error. To remedy the situation, we can pass two key-pairs variables. That is, ID and year which appear in both datasets. We can use the following code to merge table1 and table 2

```
df_primary <- tribble(
  ~ID, ~year, ~items,
  "A", 2015,3,
  "A", 2016,7,
  "A", 2017,6,
  "B", 2015,4,
  "B", 2016,8,
  "B", 2017,7,
  "C", 2015,4,
  "C", 2016,6,
  "C", 2017,6)
df_secondary <- tribble(
  ~ID, ~year, ~prices,
  "A", 2015,9,
  "A", 2016,8,
  "A", 2017,12,
  "B", 2015,13,
  "B", 2016,14,
  "B", 2017,6,
  "C", 2015,15,
  "C", 2016,15,
  "C", 2017,13)
```

```
left_join(df_primary, df_secondary, by = c('ID', 'year'))
```

Output:

```
## # A tibble: 9 x 4
##      ID  year items prices
##   <chr> <dbl> <dbl>  <dbl>
## 1     A  2015     3      9
## 2     A  2016     7      8
## 3     A  2017     6     12
## 4     B  2015     4     13
## 5     B  2016     8     14
## 6     B  2017     7      6
## 7     C  2015     4     15
## 8     C  2016     6     15
## 9     C  2017     6     13
```

Data Cleaning functions

Following are four important functions to tidy the data:

- gather(): Transform the data from wide to long
- spread(): Transform the data from long to wide
- separate(): Split one variable into two
- unit(): Unit two variables into one

We use the tidyr library. This library belongs to the collection of the library to manipulate, clean and visualize the data. If we install R with anaconda, the library is already installed. We can find the library here, https://anaconda.org/r/r-tidyr.

If not installed already, enter the following command

install tidyr : install.packages("tidyr")

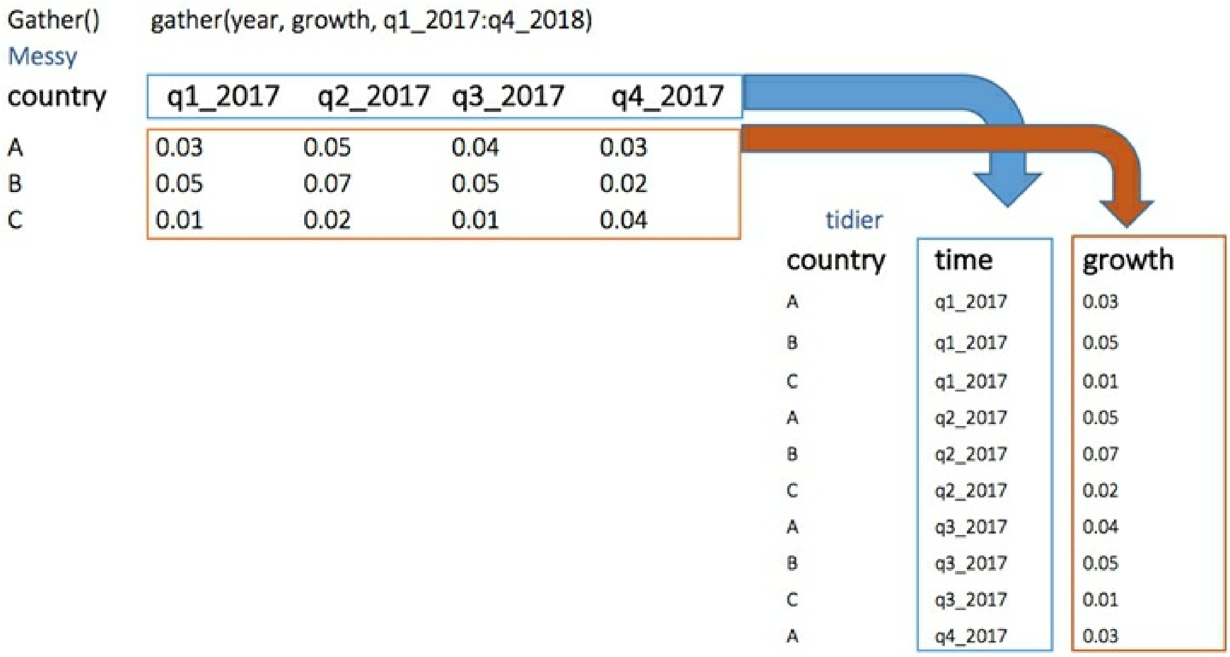
to install tidyr

gather()

The objectives of the gather() function is to transform the data from wide to long.

```
gather(data, key, value, na.rm = FALSE)
Arguments:
-data: The data frame used to reshape the dataset
-key: Name of the new column created
-value: Select the columns used to fill the key column
-na.rm: Remove missing values. FALSE by default
```

Below, we can visualize the concept of reshaping wide to long. We want to create a single column named growth, filled by the rows of the quarter variables.



country	q1_2017	q2_2017	q3_2017	q4_2017
A	0.03	0.05	0.04	0.03
B	0.05	0.07	0.05	0.02
C	0.01	0.02	0.01	0.04

country	time	growth
A	q1_2017	0.03
B	q1_2017	0.05
C	q1_2017	0.01
A	q2_2017	0.05
B	q2_2017	0.07
C	q2_2017	0.02
A	q3_2017	0.04
B	q3_2017	0.05
C	q3_2017	0.01
A	q4_2017	0.03

```
library(tidyr)
# Create a messy dataset
messy <- data.frame(
  country = c("A", "B", "C"),
  q1_2017 = c(0.03, 0.05, 0.01),
  q2_2017 = c(0.05, 0.07, 0.02),
  q3_2017 = c(0.04, 0.05, 0.01),
  q4_2017 = c(0.03, 0.02, 0.04))
messy
```

Output:

```
##   country q1_2017 q2_2017 q3_2017 q4_2017
## 1       A    0.03    0.05    0.04    0.03
## 2       B    0.05    0.07    0.05    0.02
## 3       C    0.01    0.02    0.01    0.04
```

```
# Reshape the data
tidier <-messy %>%
gather(quarter, growth, q1_2017:q4_2017)
tidier
```

Output:

```
##    country quarter growth
## 1        A q1_2017   0.03
## 2        B q1_2017   0.05
## 3        C q1_2017   0.01
## 4        A q2_2017   0.05
## 5        B q2_2017   0.07
## 6        C q2_2017   0.02
## 7        A q3_2017   0.04
## 8        B q3_2017   0.05
## 9        C q3_2017   0.01
## 10       A q4_2017   0.03
## 11       B q4_2017   0.02
## 12       C q4_2017   0.04
```

In the gather() function, we create two new variable quarter and growth because our original dataset has one group variable: i.e. country and the key-value pairs.

spread()

The spread() function does the opposite of gather.

```
spread(data, key, value)
arguments:
```

- data: The data frame used to reshape the dataset
- key: Column to reshape long to wide
- value: Rows used to fill the new column

We can reshape the tidier dataset back to messy with spread()

```
# Reshape the data
messy_1 <- tidier %>%
  spread(quarter, growth)
messy_1
```

Output:

```
##   country q1_2017 q2_2017 q3_2017 q4_2017
## 1       A    0.03    0.05    0.04    0.03
## 2       B    0.05    0.07    0.05    0.02
## 3       C    0.01    0.02    0.01    0.04
```

separate()

The separate() function splits a column into two according to a separator. This function is helpful in some situations where the variable is a date. Our analysis can require focussing on month and year and we want to separate the column into two new variables.

Syntax:

```
separate(data, col, into, sep= "", remove = TRUE)
arguments:
-data: The data frame used to reshape the dataset
-col: The column to split
-into: The name of the new variables
-sep: Indicates the symbol used that separates the variable,
i.e.:  "-", "_", "&"
-remove: Remove the old column. By default sets to TRUE.
```

We can split the quarter from the year in the tidier dataset by applying the separate() function.

```
separate_tidier <-tidier %>%
separate(quarter, c("Qrt", "year"), sep ="_")
head(separate_tidier)
```

Output:

```
##   country Qrt year growth
## 1       A  q1 2017   0.03
## 2       B  q1 2017   0.05
## 3       C  q1 2017   0.01
## 4       A  q2 2017   0.05
## 5       B  q2 2017   0.07
## 6       C  q2 2017   0.02
```

unite()

The unite() function concanates two columns into one.

Syntax:

```
unit(data, col, conc ,sep= "", remove = TRUE)
arguments:
-data: The data frame used to reshape the dataset
-col: Name of the new column
-conc: Name of the columns to concatenate
-sep: Indicates the symbol used that unites the variable,
i.e:  "-", "_", "&"
-remove: Remove the old columns. By default, sets to TRUE
```

In the above example, we separated quarter from year. What if we want to merge them. We use the following code:

```
unit_tidier <- separate_tidier %>%
  unite(Quarter, Qrt, year, sep ="_")
head(unit_tidier)
```

output:

```
##   country Quarter growth
## 1       A q1_2017   0.03
## 2       B q1_2017   0.05
## 3       C q1_2017   0.01
## 4       A q2_2017   0.05
## 5       B q2_2017   0.07
## 6       C q2_2017   0.02
```

Summary

Following are four important functions used in dplyr to merge two datasets.

Function	Objectives	Arguments	Multiple keys
left_join()	Merge two datasets. Keep all observations from the origin table	data, origin, destination, by = "ID"	origin, destination, by = c("ID", "ID2")
right_join()	Merge two datasets. Keep all observations from the destination table	data, origin, destination, by = "ID"	origin, destination, by = c("ID", "ID2")
inner_join()	Merge two datasets. Excludes all unmatched rows	data, origin, destination, by = "ID"	origin, destination, by = c("ID", "ID2")
full_join()	Merge two datasets. Keeps all observations	data, origin, destination, by = "ID"	origin, destination, by = c("ID", "ID2")

Using the tidyr Library you can transform a dataset with the gather(), spread(), separate() and unit() functions.

Function	Objectives	Arguments
gather()	Transform the data from wide to long	(data, key, value, na.rm = FALSE)
spread()	Transform the data from long to wide	(data, key, value)
separate()	Split one variables into two	(data, col, into, sep= "", remove = TRUE)
unit()	Unit two variables into one	(data, col, conc ,sep= "", remove = TRUE)

Chapter 10: Merge Data Frames in R: Full and Partial Match

Very often, we have data from multiple sources. To perform an analysis, we need to **merge** two dataframes together with one or more **common key variables**.

Full match

A full match returns values that have a counterpart in the destination table. The values that are not match won't be return in the new data frame. The partial match, however, return the missing values as NA.

We will see a simple **inner join**. The inner join keyword selects records that have matching values in both tables. To join two datasets, we can use merge() function. We will use three arguments :

```
merge(x, y, by.x = x, by.y = y)

Arguments:
-x: The origin data frame
-y: The data frame to merge
-by.x: The column used for merging in x data frame. Column x to
merge on
-by.y: The column used for merging in y data frame. Column y to
merge on
```

Example:

Create First Dataset with variables

- surname

- nationality

Create Second Dataset with variables

- surname
- movies

The common key variable is surname. We can merge both data and check if the dimensionality is 7x3.

We add stringsAsFactors=FALSE in the data frame because we don't want R to convert string as factor, we want the variable to be treated as character.

```
# Create origin dataframe(

producers <- data.frame(
    surname
=  c("Spielberg","Scorsese","Hitchcock","Tarantino","Polanski"),
    nationality = c("US","US","UK","US","Poland"),
    stringsAsFactors=FALSE)

# Create destination dataframe
movies <- data.frame(
    surname = c("Spielberg",
                "Scorsese",
                "Hitchcock",
                "Hitchcock",
                "Spielberg",
                "Tarantino",
                "Polanski"),
    title = c("Super 8",
                "Taxi Driver",
                "Psycho",
                "North by Northwest",
                "Catch Me If You Can",
                "Reservoir Dogs","Chinatown"),
                stringsAsFactors=FALSE)

# Merge two datasets
m1 <- merge(producers, movies, by.x = "surname")
m1
dim(m1)
```

Output:

```
surname          nationality             title
1 Hitchcock             UK              Psycho
2 Hitchcock             UK              North by Northwest
3 Polanski              Poland          Chinatown
4 Scorsese              US              Taxi Driver
5 Spielberg             US              Super 8
6 Spielberg             US              Catch Me If You Can
7 Tarantino             US              Reservoir Dogs
```

Let's merge data frames when the common key variables have different names.

We change surname to name in the movies data frame. We use the function identical(x1, x2) to check if both dataframes are identical.

```
# Change name of ` movies ` dataframe
colnames(movies)[colnames(movies) == 'surname'] <- 'name'
# Merge with different key value
m2 <- merge(producers, movies, by.x = "surname", by.y = "name")
# Print head of the data
head(m2)
```

Output:

```
##surname     nationality                title
## 1 Hitchcock          UK              Psycho
## 2 Hitchcock          UK              North by Northwest
## 3 Polanski          Poland           Chinatown
## 4 Scorsese           US              Taxi Driver
## 5 Spielberg          US              Super 8
## 6 Spielberg          US              Catch Me If You Can
```

```
# Check if data are identical
identical(m1, m2)
```

Output:

```
## [1] TRUE
```

This shows that merge operation is performed even if the column names are different.

Partial match

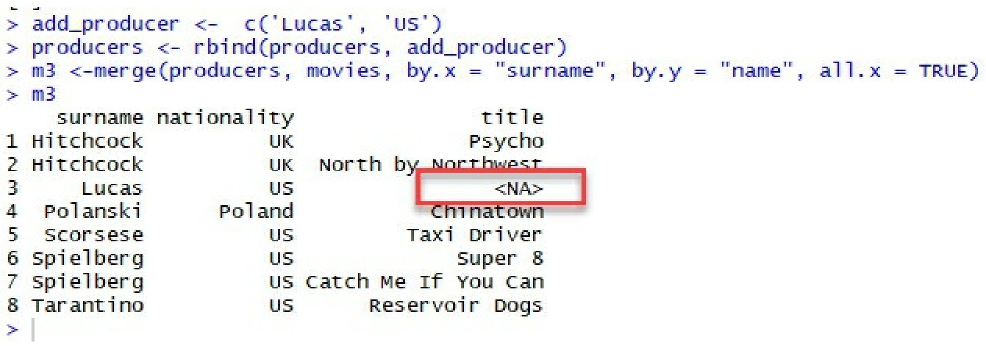
It is not surprising that two dataframes do not have the same common key variables. In the **full matching**, the dataframe returns **only** rows found in both x and y data frame. With **partial merging**, it is possible to keep the rows with no matching rows in the other data frame. These rows will have NA in those columns that are usually filled with values from y. We can do that by setting all.x= TRUE.

For instance, we can add a new producer, Lucas, in the producer data frame without the movie references in movies data frame. If we set all.x= FALSE, R will join only the matching values in both data set. In our case, the producer Lucas will not be join to the merge because it is missing from one dataset.

Let's see the dimension of each output when we specify all.x= TRUE and when we don't.

```
# Create a new producer
add_producer <-  c('Lucas', 'US')
#  Append it to the ` producer` dataframe
producers <- rbind(producers, add_producer)
# Use a partial merge
m3 <-merge(producers, movies, by.x = "surname", by.y = "name",
all.x = TRUE)
m3
```

Output:



```
> add_producer <-  c('Lucas', 'US')
> producers <- rbind(producers, add_producer)
> m3 <-merge(producers, movies, by.x = "surname", by.y = "name", all.x = TRUE)
> m3
    surname nationality                title
1 Hitchcock          UK               Psycho
2 Hitchcock          UK  North by Northwest
3     Lucas          US                 <NA>
4  Polanski      Poland            Chinatown
5  Scorsese          US          Taxi Driver
6 Spielberg          US              Super 8
7 Spielberg          US Catch Me If You Can
8 Tarantino          US       Reservoir Dogs
> 
```

```
# Compare the dimension of each data frame
dim(m1)
```

Output:

```
## [1] 7 3
```

```
dim(m2)
```

Output:

```
## [1] 7 3
```

```
dim(m3)
```

Output:

```
## [1] 8 3
```

As we can see, the dimension of the new data frame 8x3 compared with 7x3 for m1 and m2. R includes NA for the missing author in the books data frame.

Chapter 11: Functions in R Programming (with Example)

What is a Function in R?

A **function**, in a programming environment, is a set of instructions. A programmer builds a function to avoid **repeating the** same task, or reduce **complexity.**

A function should be

- written to carry out a specified a tasks
- may or may not include arguments
- contain a body
- may or may not return one or more values.

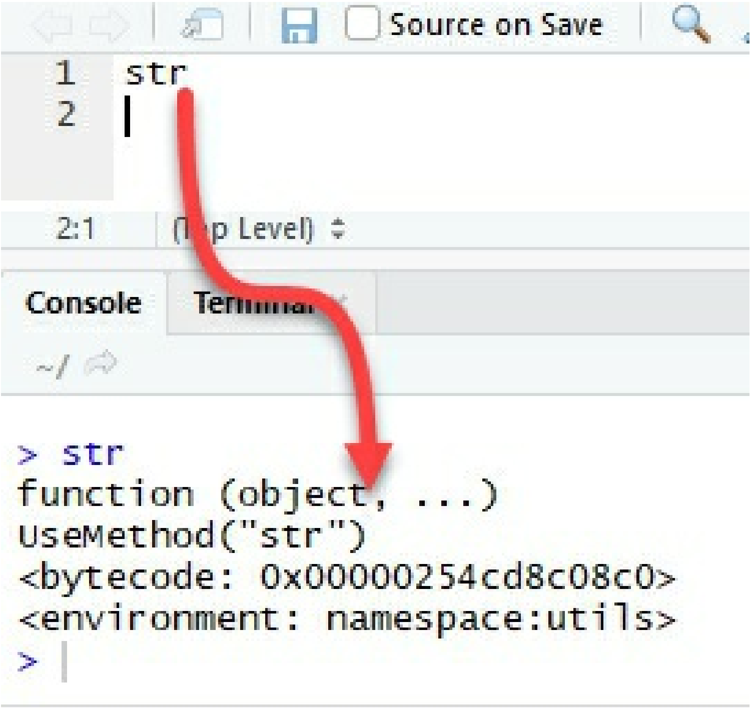
A general approach to a function is to use the argument part as **inputs**, feed the **body** part and finally return an **output**. The Syntax of a function is the following:

```
function (arglist)  {
  #Function body
}
```

R important built-in functions

There are a lot of built-in function in R. R matches your input parameters with its function arguments, either by value or by position, then executes the function body. Function arguments can have default values: if you do not specify these arguments, R will take the default value.

Note: It is possible to see the source code of a function by running the name of the function itself in the console.



```
str
```

```
> str
function (object, ...)
UseMethod("str")
<bytecode: 0x00000254cd8c08c0>
<environment: namespace:utils>
>
```

We will see three groups of function in action

- General function
- Maths function
- Statistical function

General functions

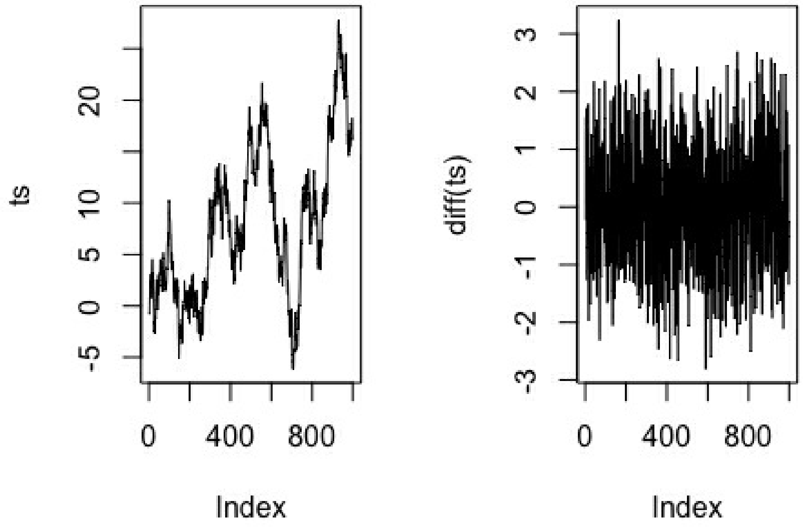
We are already familiar with general functions like cbind(), rbind(),range(),sort(),order() functions. Each of these functions has a specific task, takes arguments to return an output. Following are important functions one must know-

diff() function

If you work on **time series**, you need to stationary the series by taking their **lag values**. A **stationary process** allows constant mean, variance and autocorrelation over time. This mainly improves the prediction of a time series. It can be easily done with the function diff(). We can build a random time-series data with a trend and then use the function diff() to stationary the series. The diff() function accepts one argument, a vector, and return suitable lagged and iterated difference.

Note: We often need to create random data, but for learning and comparison we want the numbers to be identical across machines. To ensure we all generate the same data, we use the set.seed() function with arbitrary values of 123. The set.seed() function is generated through the process of pseudorandom number generator that make every modern computers to have the same sequence of numbers. If we don't use set.seed() function, we will all have different sequence of numbers.

```
set.seed(123)
## Create the data
x = rnorm(1000)
ts <- cumsum(x)
## Stationary the serie
diff_ts <- diff(ts)
par(mfrow=c(1,2))
## Plot the series
plot(ts, type='l')
plot(diff(ts), type='l')
```



length() function

In many cases, we want to know the **length** of a vector for computation or to be used in a for loop. The length() function counts the number of rows in vector x. The following codes import the cars dataset and return the number of rows.

Note: length() returns the number of elements in a vector. If the function is passed into a matrix or a data frame, the number of columns is returned.

```
dt <- cars
## number columns
length(dt)
```

Output:

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

```
## number rows
length(dt[,1])
```

Output:

```
## [1] 50
```

Math functions

R has an array of mathematical functions.

Operator	Description
abs(x)	Takes the absolute value of x
log(x,base=y)	Takes the logarithm of x with base y; if base is not specified, returns the natural logarithm
exp(x)	Returns the exponential of x
sqrt(x)	Returns the square root of x
factorial(x)	Returns the factorial of x (x!)

```
# sequence of number from 44 to 55 both including incremented by
1
x_vector <- seq(45,55, by = 1)
#logarithm
log(x_vector)
```

Output:

```
##  [1] 3.806662 3.828641 3.850148 3.871201 3.891820 3.912023
3.931826
##  [8] 3.951244 3.970292 3.988984 4.007333
```

```
#exponential
exp(x_vector)
```

```
#squared root
sqrt(x_vector)
```

Output:

```
##  [1] 6.708204 6.782330 6.855655 6.928203 7.000000 7.071068
7.141428
##  [8] 7.211103 7.280110 7.348469 7.416198
```

```
#factorial
```

```
factorial(x_vector)
```

Output:

```
##  [1] 1.196222e+56 5.502622e+57 2.586232e+59 1.241392e+61
6.082819e+62
##  [6] 3.041409e+64 1.551119e+66 8.065818e+67 4.274883e+69
2.308437e+71
## [11] 1.269640e+73
```

Statistical functions

R standard installation contains wide range of statistical functions. In this tutorial, we will briefly look at the most important function..

Basic statistic functions

Operator	**Description**
mean(x)	Mean of x
median(x)	Median of x
var(x)	Variance of x
sd(x)	Standard deviation of x
scale(x)	Standard scores (z-scores) of x
quantile(x)	The quartiles of x
summary(x)	Summary of x: mean, min, max etc..

```
speed <- dt$speed
speed
# Mean speed of cars dataset
mean(speed)
```

Output:

```
## [1] 15.4
```

```
# Median speed of cars dataset
median(speed)
```

Output:

```
## [1] 15
```

```
# Variance speed of cars dataset
var(speed)
```

Output:

```
## [1] 27.95918
```

```
# Standard deviation speed of cars dataset
sd(speed)
```

Output:

```
## [1] 5.287644
```

```
# Standardize vector speed of cars dataset
head(scale(speed), 5)
```

Output:

```
##           [,1]
## [1,] -2.155969
## [2,] -2.155969
## [3,] -1.588609
## [4,] -1.588609
## [5,] -1.399489
```

```
# Quantile speed of cars dataset
```

```
quantile(speed)
```

Output:

```
##   0%  25%  50%  75% 100%
##    4   12   15   19   25
```

```
# Summary speed of cars dataset
summary(speed)
```

Output:

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     4.0    12.0    15.0    15.4    19.0    25.0
```

Up to this point, we have learned a lot of R built-in functions.

Note: Be careful with the class of the argument, i.e. numeric, Boolean or string. For instance, if we need to pass a string value, we need to enclose the string in quotation mark: "ABC" .

Write function in R

In some occasion, we need to write our own function because we have to accomplish a particular task and no ready made function exists. A user-defined function involves a **name**, **arguments** and a **body**.

```
function.name <- function(arguments)
{
    computations on the arguments
    some other code
}
```

Note: A good practice is to name a user-defined function different from a built-in function. It avoids confusion.

One argument function

In the next snippet, we define a simple square function. The function accepts a value and returns the square of the value.

```
square_function<- function(n)
{
  # compute the square of integer `n`
  n^2
}
# calling the function and passing value 4
square_function(4)
```

Code Explanation:

- The function is named square_function; it can be called whatever we want.
- It receives an argument "n". We **didn't specify the type of variable so that the user can pass an integer, a vector or a matrix**
- The function takes the input "n" and returns the square of the input.

  When you are done using the function, we can remove it with the rm() function.

# after you create the function

```
rm(square_function)
square_function
```

On the console, we can see an error message :Error: object 'square_function' not found telling the function does not exist.

Environment Scoping

In R, the **environment** is a **collection** of objects like functions, variables, data frame, etc.

R opens an environment each time Rstudio is prompted.

The top-level environment available is the **global environment**, called R_GlobalEnv. And we have the **local environment.**

We can list the content of the current environment.

```
ls(environment())
```

Output

```
## [1]
"diff_ts"         "dt"              "speed"           "square_fun
## [5] "ts"              "x"               "x_vector"
```

You can see all the variables and function created in the R_GlobalEnv.

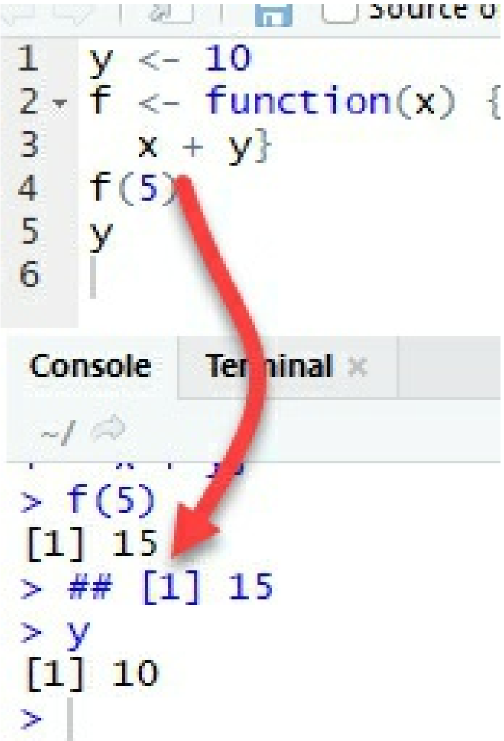
The above list will vary for you based on the historic code you execute in R Studio.

Note that n, the argument of the square_function function is **not in this global environment**.

A **new** environment is created for each function. In the above example, the function square_function() creates a new environment inside the global environment.

To clarify the difference between **global** and **local environment**, let's study the following example

These function takes a value x as an argument and add it to y define outside and inside the function



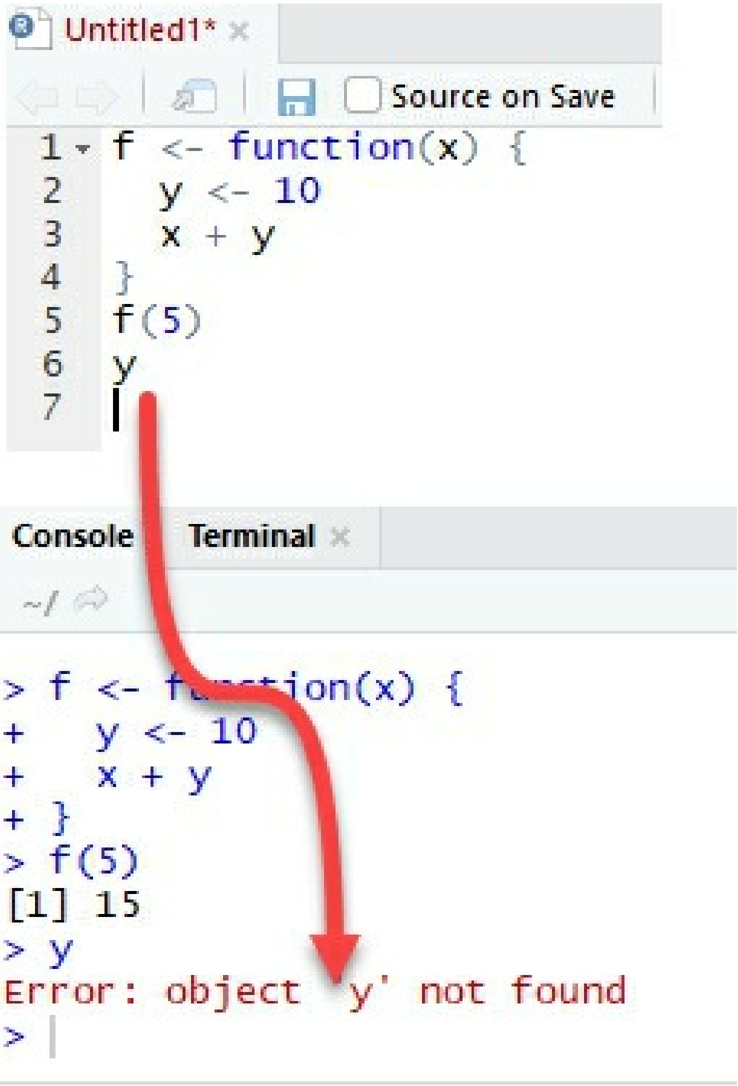
```r
y <- 10
f <- function(x) {
  x + y}
f(5)
y
```

```
> f(5)
[1] 15
> ## [1] 15
> y
[1] 10
>
```

The function f returns the output 15. This is because y is defined in the global environment. Any variable defined in the global environment can be used locally. The variable y has the value of 10 during all function calls and is accessible at any time.

Let's see what happens if the variable y is defined inside the function.

We need to dropp `y` prior to run this code using rm r

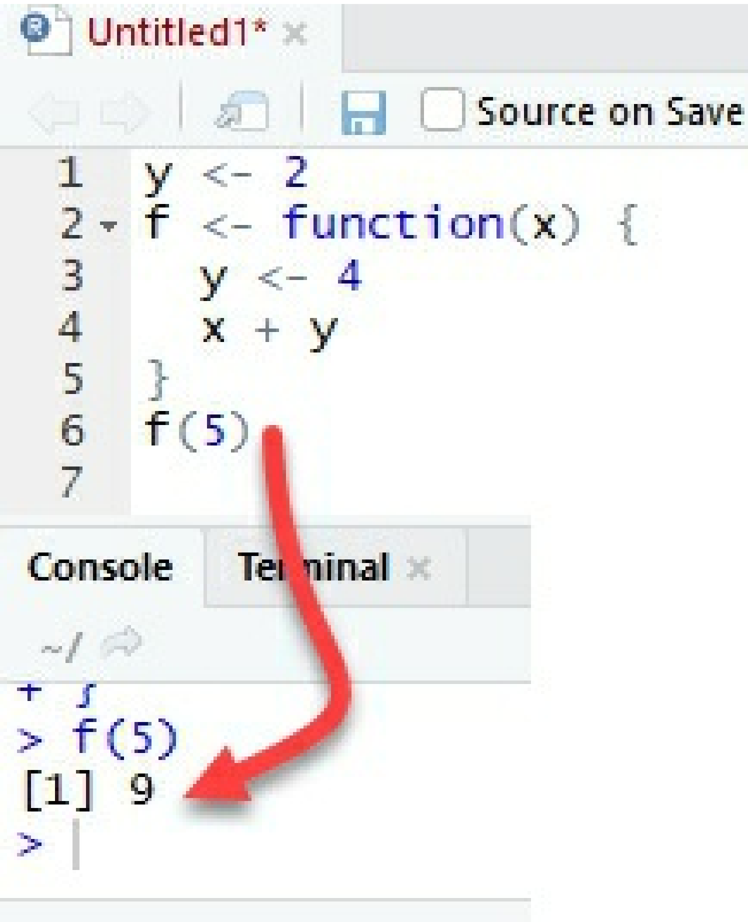


```
f <- function(x) {
  y <- 10
  x + y
}
f(5)
y
```

```
> f <- function(x) {
+   y <- 10
+   x + y
+ }
> f(5)
[1] 15
> y
Error: object 'y' not found
> 
```

The output is also 15 when we call f(5) but returns an error when we try to print the value y. The variable y is not in the global environment.

Finally, R uses the most recent variable definition to pass inside the body of a function. Let's consider the following example:



```
y <- 2
f <- function(x) {
  y <- 4
  x + y
}
f(5)
```

```
+ }
> f(5)
[1] 9
> 
```

R ignores the y values defined outside the function because we explicitly created a y variable inside the body of the function.

Multi arguments function

We can write a function with more than one argument. Consider the function called "times". It is a straightforward function multiplying two variables.

```
times <- function(x,y) {
  x*y
        }
times(2,4)
```

Output:

```
## [1] 8
```

When should we write function?

Data scientist need to do many repetitive tasks. Most of the time, we copy and paste chunks of code repetitively. For example, normalization of a variable is highly recommended before we run a machine learning algorithm. The formula to normalize a variable is:

$$normalize = \frac{x - x_{min}}{x_{max} - x_{min}}$$

We already know how to use the min() and max() function in R. We use the tibble library to create the data frame. Tibble is so far the most convenient function to create a data set from scratch.

```
library(tibble)
# Create a data frame
data_frame <- tibble(
  c1 = rnorm(50, 5, 1.5),
  c2 = rnorm(50, 5, 1.5),
  c3 = rnorm(50, 5, 1.5),
)
```

We will proceed in two steps to compute the function described above. In the first step, we will create a variable called c1_norm which is the rescaling of c1. In step two, we just copy and paste the code of c1_norm and change with c2 and c3.

Detail of the function with the column c1:

Nominator: : data_frame$c1 -min(data_frame$c1))

Denominator: max(data_frame$c1)-min(data_frame$c1))

Therefore, we can divide them to get the normalized value of column c1:

```
(data_frame$c1 -min(data_frame$c1))/(max(data_frame$c1)-
min(data_frame$c1))
```

We can create c1_norm, c2_norm and c3_norm:

```
Create c1_norm: rescaling of c1
data_frame$c1_norm <- (data_frame$c1 -
min(data_frame$c1))/(max(data_frame$c1)-min(data_frame$c1))
# show the first five values
head(data_frame$c1_norm, 5)
```

Output:

```
## [1] 0.3400113 0.4198788 0.8524394 0.4925860 0.5067991
```

It works. We can copy and paste

```
data_frame$c1_norm <- (data_frame$c1 -
min(data_frame$c1))/(max(data_frame$c1)-min(data_frame$c1))
```

then change c1_norm to c2_norm and c1 to c2. We do the same to create c3_norm

```
data_frame$c2_norm <- (data_frame$c2 -
min(data_frame$c2))/(max(data_frame$c2)-min(data_frame$c2))
data_frame$c3_norm <- (data_frame$c3 -
min(data_frame$c3))/(max(data_frame$c3)-min(data_frame$c3))
```

We perfectly rescaled the variables c1, c2 and c3.

However, this method is prone to mistake. We could copy and forget to change the column name after pasting. Therefore, a good practice is to write a function each time you need to paste same code more than twice. We can rearrange the code into a formula and call it whenever it is needed. To write our own function, we need to give:

- Name: normalize.
- the number of arguments: We only need one argument, which is the column we use in our computation.
- The body: this is simply the formula we want to return.

We will proceed step by step to create the function normalize.

Step 1) We create the **nominator**, which is . In R, we can store the nominator in a variable like this:

```
nominator <- x-min(x)
```

Step 2) We compute the **denominator:** . We can replicate the idea of step 1 and store the computation in a variable:

```
denominator <- max(x)-min(x)
```

Step 3) We perform the division between the nominator and denominator.

```
normalize <- nominator/denominator
```

Step 4) To return value to calling function we need to pass normalize inside return() to get the output of the function.

```
return(normalize)
```

Step 5) We are ready to use the function by wrapping everything inside the bracket.

```
normalize <- function(x){
  # step 1: create the nominator
  nominator <- x-min(x)
  # step 2: create the denominator
  denominator <- max(x)-min(x)
  # step 3: divide nominator by denominator
  normalize <- nominator/denominator
  # return the value
  return(normalize)
}
```

Let's test our function with the variable c1:

```
normalize(data_frame$c1)
```

It works perfectly. We created our first function.

Functions are more comprehensive way to perform a repetitive task.

We can use the normalize formula over different columns, like below:

```
data_frame$c1_norm_function <- normalize (data_frame$c1)
data_frame$c2_norm_function <- normalize     (data_frame$c2)
data_frame$c3_norm_function <- normalize     (data_frame$c3)
```

Even though the example is simple, we can infer the power of a formula. The above code is easier to read and especially avoid to mistakes when pasting codes.

Functions with condition

Sometimes, we need to include conditions into a function to allow the code to return different outputs.

In Machine Learning tasks, we need to split the dataset between a train set and a test set. The train set allows the algorithm to learn from the data. In order to test the performance of our model, we can use the test set to return the performance measure. R does not have a function to create two datasets. We can write our own function to do that. Our function takes two arguments and is called split_data(). The idea behind is simple, we multiply the length of dataset (i.e. number of observations) with 0.8. For instance, if we want to split the dataset 80/20, and our dataset contains 100 rows, then our function will multiply 0.8*100 = 80. 80 rows will be selected to become our training data.

We will use the airquality dataset to test our user-defined function. The airquality dataset has 153 rows. We can see it with the code below:

```
nrow(airquality)
```

Output:

```
## [1] 153
```

We will proceed as follow:

```
split_data <- function(df, train = TRUE)
Arguments:
-df: Define the dataset
-train: Specify if the function returns the train set or test
set. By default, set to TRUE
```

Our function has two arguments. The arguments train is a Boolean parameter. If it is set to TRUE, our function creates the train dataset, otherwise, it creates the test dataset.

We can proceed like we did we the normalise() function. We write the code as if it was only one-time code and then wrap everything with the condition into the body to create the function.

Step 1:

We need to compute the length of the dataset. This is done with the function nrow(). Nrow returns the total number of rows in the dataset. We call the variable length.

```
length<- nrow(airquality)
length
```

Output:

```
## [1] 153
```

Step 2:

We multiply the length by 0.8. It will return the number of rows to select. It should be 153*0.8 = 122.4

```
total_row <- length*0.8
total_row
```

Output:

```
## [1] 122.4
```

We want to select 122 rows among the 153 rows in the airquality dataset. We create a list containing values from 1 to total_row. We store the result in the variable called split

```
split <- 1:total_row
split[1:5]
```

Output:

```
## [1] 1 2 3 4 5
```

split chooses the first 122 rows from the dataset. For instance, we can see that our variable split gathers the value 1, 2, 3, 4, 5 and so on. These values will be the index when we will select the rows to return.

Step 3:

We need to select the rows in the airquality dataset based on the values stored in the split variable. This is done like this:

```
train_df <- airquality[split, ]
head(train_df)
```

Output:

```
##[1]    Ozone Solar.R Wind Temp Month Day
##[2]  51    13     137 10.3   76     6  20
##[3]  15    18      65 13.2   58     5  15
##[4]  64    32     236  9.2   81     7   3
##[5]  27    NA      NA  8.0   57     5  27
##[6]  58    NA      47 10.3   73     6  27
##[7]  44    23     148  8.0   82     6  13
```

Step 4:

We can create the test dataset by using the remaining rows, 123:153. This is done by using – in front of split.

```
test_df <- airquality[-split, ]
head(test_df)
```

Output:

```
##[1] Ozone Solar.R Wind Temp Month Day
```

```
##[2]  123    85     188  6.3   94     8  31
##[3]  124    96     167  6.9   91     9   1
##[4]  125    78     197  5.1   92     9   2
##[5]  126    73     183  2.8   93     9   3
##[6]  127    91     189  4.6   93     9   4
##[7]  128    47      95  7.4   87     9   5
```

Step 5:

We can create the condition inside the body of the function. Remember, we have an argument train that is a Boolean set to TRUE by default to return the train set. To create the condition, we use the if syntax:

```
  if (train ==TRUE){
    train_df <- airquality[split, ]
      return(train)
  } else {
    test_df <- airquality[-split, ]
      return(test)
  }
```

This is it, we can write the function. We only need to change airquality to df because we want to try our function to any data frame, not only airquality:

```
split_data <- function(df, train = TRUE){
  length<- nrow(df)
  total_row <- length *0.8
  split <- 1:total_row
  if (train ==TRUE){
    train_df <- df[split, ]
      return(train_df)
  } else {
    test_df <- df[-split, ]
      return(test_df)
  }
}
```

Let's try our function on the airquality dataset. we should have one train set with 122 rows and a test set with 31 rows.

```
train <- split_data(airquality, train = TRUE)
```

```
dim(train)
```

Output:

```
## [1] 122   6
```

```
test <- split_data(airquality, train = FALSE)
dim(test)
```

Output:

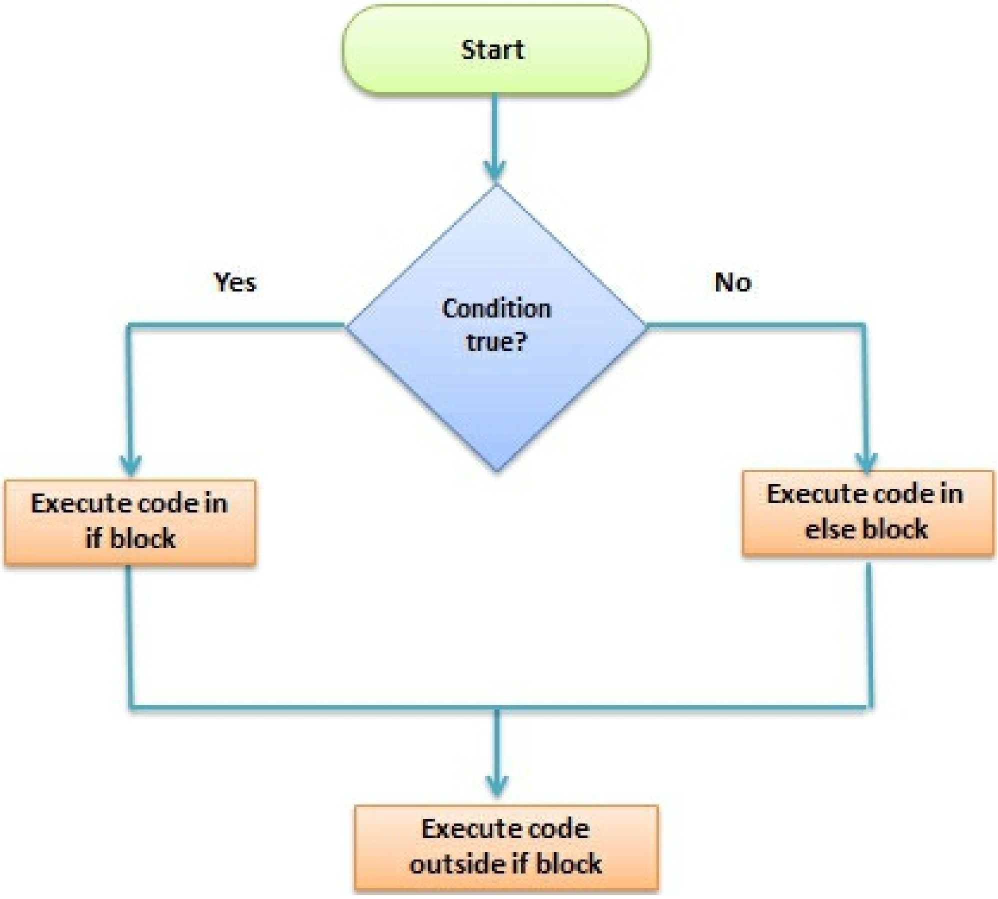
```
## [1] 31  6
```

Chapter 12: IF, ELSE, ELSE IF Statement in R

The if else statement

An if-else statement is a great tool for the developer trying to return an output based on a condition. In R, the syntax is:

```
if (condition) {
    Expr1
} else {
    Expr2
}
```



We want to examine whether a variable stored as "quantity" is above 20. If quantity is greater than 20, the code will print "You sold a lot!" otherwise Not enough for today.

```
# Create vector quantity
quantity <-  25
# Set the is-else statement
if (quantity > 20) {
    print('You sold a lot!')
} else {
    print('Not enough for today')
}
```

Output:

```
## [1] "You sold a lot!"
```

Note: Make sure you correctly write the indentations. Code with multiple conditions can become unreadable when the indentations are not in correct position.

The else if statement

We can further customize the control level with the else if statement. With elif, you can add as many conditions as we want. The syntax is:

```
if (condition1) {
    expr1
    } else if (condition2) {
    expr2
    } else if  (condition3) {
    expr3
    } else {
    expr4
}
```

We are interested to know if we sold quantities between 20 and 30. If we do, then the pint Average day. If quantity is > 30 we print What a great day!, otherwise Not enough for today.

You can try to change the amount of quantity.

```
# Create vector quantiy
quantity <-  10
# Create multiple condition statement
if (quantity <20) {
      print('Not enough for today')
} else if (quantity > 20  &quantity <= 30) {
     print('Average day')
} else {
      print('What a great day!')
}
```

Output:

```
## [1] "Not enough for today"
```

Example 2:

VAT has different rate according to the product purchased. Imagine we have three different kind of products with different VAT applied:

Categories	Products	VAT
A	Book, magazine, newspaper, etc..	8%
B	Vegetable, meat, beverage, etc..	10%
C	Tee-shirt, jean, pant, etc..	20%

We can write a chain to apply the correct VAT rate to the product a customer bought.

```
category <- 'A'
price <- 10
if (category =='A'){
  cat('A vat rate of 8% is applied.','The total price is',price
*1.08)
} else if (category =='B'){
    cat('A vat rate of 10% is applied.','The total price
is',price *1.10)
} else {
    cat('A vat rate of 20% is applied.','The total price
is',price *1.20)
}
```

Output:

```
# A vat rate of 8% is applied. The total price is 10.8
```

Chapter 13: For Loop in R with Examples for List and Matrix

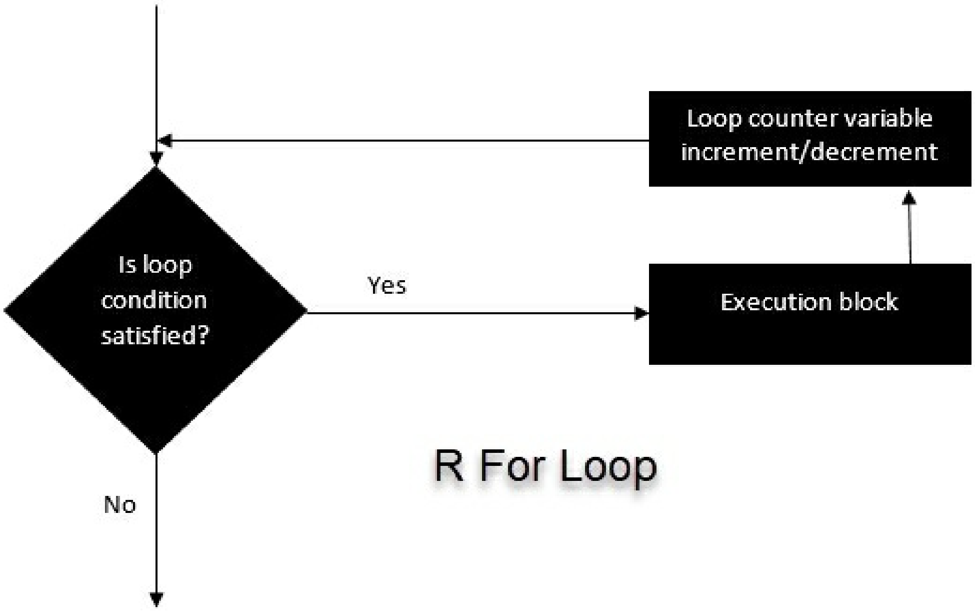
A for loop is very valuable when we need to iterate over a list of elements or a range of numbers. Loop can be used to iterate over a list, data frame, vector, matrix or any other object. The braces and square bracket are compulsory.

For Loop Syntax and Examples

```
For (i in vector) {
    Exp
}
```

Here,

R will loop over all the variables in vector and do the computation written inside the exp.


Loop counter variable increment/decrement
Is loop condition satisfied?
Yes
Execution block
R For Loop
No

Let's see a few examples.

Example 1: We iterate over all the elements of a vector and print the current value.

```
# Create fruit vector
fruit <- c('Apple', 'Orange', 'Passion fruit', 'Banana')
# Create the for statement
for ( i in fruit){
 print(i)
}
```

Output:

```
## [1] "Apple"
## [1] "Orange"
## [1] "Passion fruit"
## [1] "Banana"
```

Example 2: creates a non-linear function by using the polynomial of x between 1 and 4 and we store it in a list

```
# Create an empty list
list <- c()
# Create a for statement to populate the list
for (i in seq(1, 4, by=1)) {
  list[[i]] <- i*i
}
print(list)
```

Output:

```
## [1]   1  4 9 16
```

The for loop is very valuable for machine learning tasks. After we have trained a model, we need to regularize the model to avoid over-fitting. Regularization is a very tedious task because we need to find the value that minimizes the loss function. To help us detect those values, we can make use of a for loop to iterate over a range of values and define the best candidate.

For Loop over a list

Looping over a list is just as easy and convenient as looping over a vector. Let's see an example

```
# Create a list with three vectors
fruit <- list(Basket = c('Apple', 'Orange', 'Passion fruit',
'Banana'),
Money = c(10, 12, 15), purchase = FALSE)
for (p  in fruit)
{
        print(p)
}
```

Output:

```
## [1] "Apple" "Orange" "Passion fruit" "Banana"
## [1] 10 12 15
## [1] FALSE
```

For Loop over a matrix

A matrix has 2-dimension, rows and columns. To iterate over a matrix, we have to define two for loop, namely one for the rows and another for the column.

```
# Create a matrix
mat <- matrix(data = seq(10, 20, by=1), nrow = 6, ncol =2)
# Create the loop with r and c to iterate over the matrix
for (r in 1:nrow(mat))
    for (c in 1:ncol(mat))
         print(paste("Row", r, "and column",c, "have values of",
mat[r,c]))
```

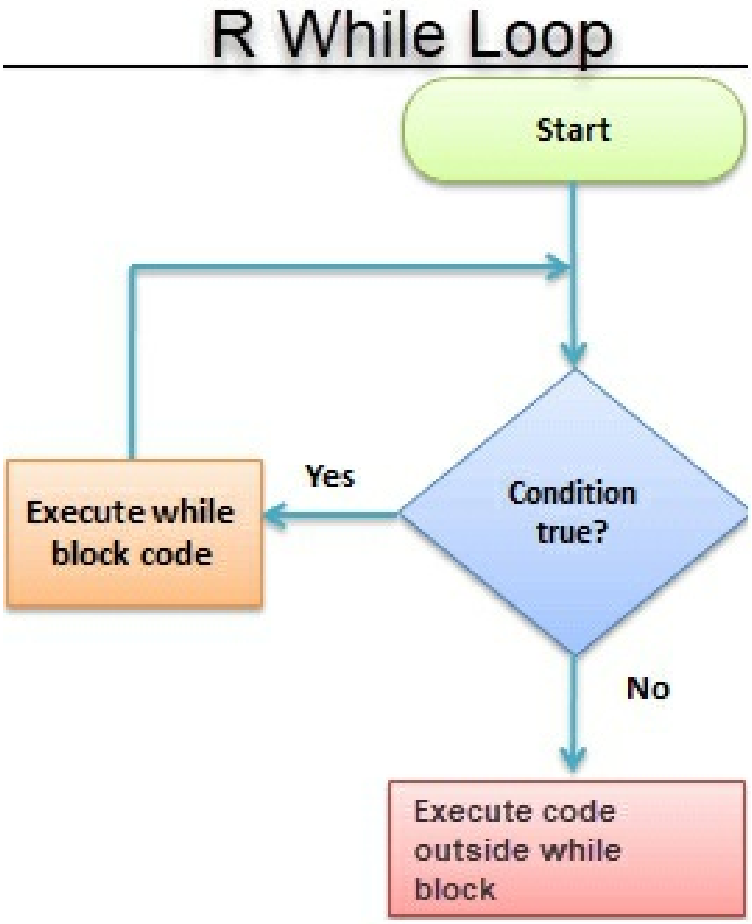
Output:

```
## [1] "Row 1 and column 1 have values of 10"
## [1] "Row 1 and column 2 have values of 16"
## [1] "Row 2 and column 1 have values of 11"
## [1] "Row 2 and column 2 have values of 17"
## [1] "Row 3 and column 1 have values of 12"
## [1] "Row 3 and column 2 have values of 18"
## [1] "Row 4 and column 1 have values of 13"
## [1] "Row 4 and column 2 have values of 19"
## [1] "Row 5 and column 1 have values of 14"
## [1] "Row 5 and column 2 have values of 20"
## [1] "Row 6 and column 1 have values of 15"
## [1] "Row 6 and column 2 have values of 10"
```

Chapter 14: While Loop in R with Example

A loop is a statement that keeps running until a condition is satisfied. The syntax for a while loop is the following:

```
while (condition) {
     Exp
}
```



While Loop Flow Chart

Note: Remember to write a closing condition at some point otherwise the loop will go on indefinitely.

Example 1:

Let's go through a very simple example to understand the concept of while loop. You will create a loop and after each run add 1 to the stored variable. You need to close the loop, therefore we explicitely tells R to stop looping when the variable reached 10.

Note: If you want to see current loop value, you need to wrap the variable inside the function print().

```
#Create a variable with value 1
begin <- 1

#Create the loop
while (begin <= 10){

#See which we are
cat('This is loop number',begin)

#add 1 to the variable begin after each loop
begin <- begin+1
print(begin)
}
```

Output:

```
## This is loop number 1[1] 2
## This is loop number 2[1] 3
## This is loop number 3[1] 4
## This is loop number 4[1] 5
## This is loop number 5[1] 6
## This is loop number 6[1] 7
## This is loop number 7[1] 8
## This is loop number 8[1] 9
## This is loop number 9[1] 10
## This is loop number 10[1] 11
```

Example 2:

You bought a stock at price of 50 dollars. If the price goes below 45, we want to short it. Otherwise, we keep it in our portfolio. The price can fluctuate between -10 to +10 around 50 after each loop. You can write the code as follow:

```
set.seed(123)
# Set variable stock and price
stock <- 50
price <- 50

# Loop variable counts the number of loops
loop <- 1

# Set the while statement
while (price > 45){

# Create a random price between 40 and 60
price <- stock + sample(-10:10, 1)

# Count the number of loop
loop = loop +1

# Print the number of loop
print(loop)
}
```

Output:

```
## [1] 2
## [1] 3
## [1] 4
## [1] 5
## [1] 6
## [1] 7
```

```
cat('it took',loop,'loop before we short the price. The lowest
price is',price)
```

Output:

```
## it took 7 loop before we short the price.The lowest price is
40
```

Chapter 15: apply(), lapply(), sapply(), tapply() Function in R with Examples

This tutorial aims at introducing the apply() function collection. The apply() function is the most basic of all collection. We will also learn sapply(), lapply() and tapply(). The apply collection can be viewed as a substitute to the loop

The apply() collection is bundled with **r essential** package if you install R with Anaconda. The apply() function can be feed with many functions to perform redundant application on a collection of object (data frame, list, vector, etc.). The purpose of apply() is primarily to avoid explicit uses of loop constructs. They can be used for an input list, matrix or array and apply a function. Any function can be passed into apply().

apply() function

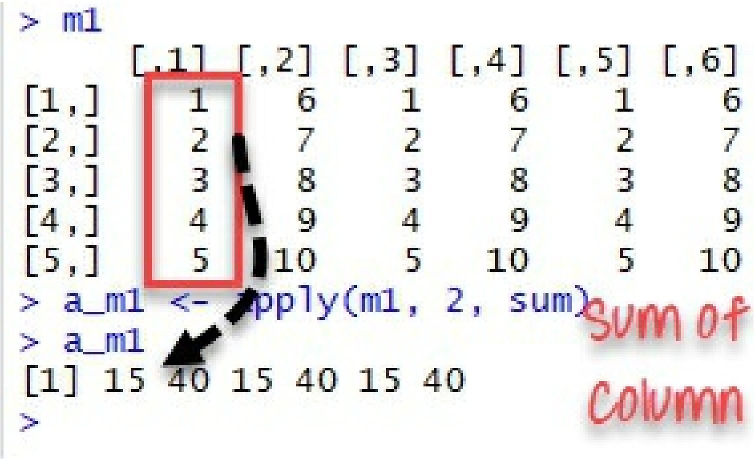
We use apply() over a matrice. This function takes 5 arguments:

```
apply(X, MARGIN, FUN)
Here:
-x: an array or matrix
-MARGIN:  take a value or range between 1 and 2 to define where
to apply the function:
-MARGIN=1`: the manipulation is performed on rows
-MARGIN=2`: the manipulation is performed on columns
-MARGIN=c(1,2)` the manipulation is performed on rows and
columns
-FUN: tells which function to apply. Built functions like mean,
median, sum, min, max and even user-defined functions can be
applied>
```

The simplest example is to sum a matrice over all the columns. The code apply(m1, 2, sum) will apply the sum function to the matrix 5x6 and return the sum of each column accessible in the dataset.

```
m1 <- matrix(C<-(1:10),nrow=5, ncol=6)
m1
a_m1 <- apply(m1, 2, sum)
a_m1
```

Output:



```
> m1
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    1    6    1    6    1    6
[2,]    2    7    2    7    2    7
[3,]    3    8    3    8    3    8
[4,]    4    9    4    9    4    9
[5,]    5   10    5   10    5   10
> a_m1 <- apply(m1, 2, sum)
> a_m1
[1] 15 40 15 40 15 40
>
```

Best practice: Store the values before printing it to the console.

lapply() function

```
lapply(X, FUN)
Arguments:
-X: A vector or an object
-FUN: Function applied to each element of x
```

l in lapply() stands for list. The difference between lapply() and apply() lies between the output return. The output of lapply() is a list. lapply() can be used for other objects like data frames and lists.

lapply() function does not need MARGIN.

A very easy example can be to change the string value of a matrix to lower case with tolower function. We construct a matrix with the name of the famous movies. The name is in upper case format.

```
movies <- c("SPYDERMAN","BATMAN","VERTIGO","CHINATOWN")
movies_lower <-lapply(movies, tolower)
str(movies_lower)
```

Output:

```
## List of 4
## $:chr"spyderman"
## $:chr"batman"
## $:chr"vertigo"
## $:chr"chinatown"
```

We can use unlist() to convert the list into a vector.

```
movies_lower <-unlist(lapply(movies,tolower))
str(movies_lower)
```

Output:

```
##  chr [1:4] "spyderman" "batman" "vertigo" "chinatown"
```

sapply() function

sapply() function does the same jobs as lapply() function but returns a vector.

```
sapply(X, FUN)
Arguments:
-X: A vector or an object
-FUN: Function applied to each element of x
```

We can measure the minimum speed and stopping distances of cars from the cars dataset.

```
dt <- cars
lmn_cars <- lapply(dt, min)
smn_cars <- sapply(dt, min)
lmn_cars
```

Output:

```
## $speed
## [1] 4
## $dist
## [1] 2
```

```
smn_cars
```

Output:

```
## speed  dist
##     4     2
```

```
lmxcars <- lapply(dt, max)
smxcars <- sapply(dt, max)
lmxcars
```

Output:

```
## $speed
## [1] 25
## $dist
## [1] 120
```

```
smxcars
```

Output:

```
## speed  dist
##    25   120
```

We can use a user built-in function into lapply() or sapply(). We create a function named avg to compute the average of the minimum and maximum of the vector.

```
avg <- function(x) {
  ( min(x) + max(x) ) / 2}
fcars <- sapply(dt, avg)
fcars
```

Output

```
## speed  dist
##  14.5  61.0
```

sapply() function is more efficient than lapply() in the output returned because sapply() store values direclty into a vector. In the next example, we will see this is not always the case.

We can summarize the difference between apply(), sapply() and `lapply() in the following table:

Function	**Arguments**	**Objective**	**Input**	**Output**
apply	apply(x, MARGIN, FUN)	Apply a function to the rows or columns or both	Data frame or matrix	vector, list, array
lapply	lapply(X, FUN)	Apply a function to all the elements of the input	List, vector or data frame	list
sapply	sappy(X FUN)	Apply a function to all the elements of the input	List, vector or data frame	vector or matrix

Slice vector

We can use lapply() or sapply() interchangeable to slice a data frame. We create a function, below_average(), that takes a vector of numerical values and returns a vector that only contains the values that are strictly above the average. We compare both results with the identical() function.

```
below_ave <- function(x) {
    ave <- mean(x)
    return(x[x > ave])
}
dt_s<- sapply(dt, below_ave)
dt_l<- lapply(dt, below_ave)
identical(dt_s, dt_l)
```

Output:

```
## [1] TRUE
```

tapply() function

The function tapply() computes a measure (mean, median, min, max, etc..) or a function for each factor variable in a vector.

```
tapply(X, INDEX, FUN = NULL)
Arguments:
-X: An object, usually a vector
-INDEX: A list containing factor
-FUN: Function applied to each element of x
```

Part of the job of a data scientist or researchers is to compute summaries of variables. For instance, measure the average or group data based on a characteristic. Most of the data are grouped by ID, city, countries, and so on. Summarizing over group reveals more interesting patterns.

To understand how it works, let's use the iris dataset. This dataset is very famous in the world of machine learning. The purpose of this dataset is to predict the class of each of the three flower species: Sepal, Versicolor, Virginica. The dataset collects information for each species about their length and width.

As a prior work, we can compute the median of the length for each species. tapply() is a quick way to perform this computation.

```
data(iris)
tapply(iris$Sepal.Width, iris$Species, median)
```

Output:

```
##     setosa versicolor  virginica
##        3.4        2.8        3.0
```

Chapter 16: Import Data into R: Read CSV, Excel, SPSS, Stata, SAS Files

Data could exist in various formats. For each format R has a specific function and argument. This tutorial explains how to import data to R.

Read CSV

One of the most widely data store is the .csv (comma-separated values) file formats. R loads an array of libraries during the start-up, including the utils package. This package is convenient to open csv files combined with the reading.csv() function. Here is the syntax for read.csv

```
read.csv(file, header = TRUE, sep = ",")
```

Argument:

- **file**: PATH where the file is stored
- **header**: confirm if the file has a header or not, by default, the header is set to TRUE
- **sep**: the symbol used to split the variable. By default, `,`.

We will read the data file name mtcats. The csv file is stored online. If your .csv file is stored locally, you can replace the PATH inside the code snippet. Don't forget to wrap it inside ' '. The PATH needs to be a string value.

For mac user, the path for the download folder is:

```
 "/Users/USERNAME/Downloads/FILENAME.csv"
```

For windows user:

```
"C:\Users\USERNAME\Downloads\FILENAME.csv"
```

Note that, we should always specify the extension of the file name.

- .csv
- .xlsx
- .txt
- ...

```
PATH <- 'https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/mtcars.csv'
df <- read.csv(PATH, header =  TRUE, sep = ',')
length(df)
```

Output:

```
## [1] 12
```

```
class(df$X)
```

Output:

```
## [1] "factor"
```

R, by default, returns character values as Factor. We can turn off this setting by adding stringsAsFactors = FALSE.

```
PATH <- 'https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/mtcars.csv'
df <-read.csv(PATH, header =TRUE, sep = ',', stringsAsFactors
=FALSE)
class(df$X)
```

Output:

```
## [1] "character"
```

The class for the variable X is now a character.

Read Excel files

Excel files are very popular among data analysts. Spreadsheets are easy to work with and flexible. R is equipped with a library readxl to import Excel spreadsheet.

Use this code

```
require(readxl)
```

to check if readxl is installed in your machine. If you install r with r-conda-essential, the library is already installed. You should see in the command window:

Output:

```
Loading required package: readxl.
```

If the package does not exit, you can install it with the conda library or in the terminal, use conda install -c mittner r-readxl.

Use the following command to load the library to import excel files.

```
library(readxl)
```

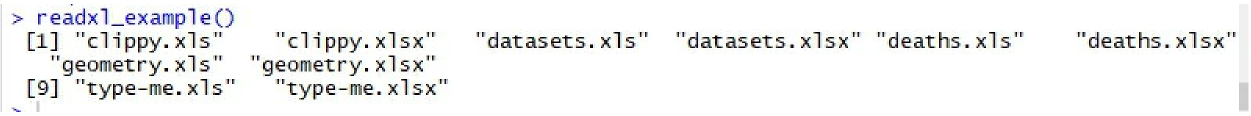
readxl_example()

We use the examples included in the package readxl during this tutorial.

Use code

```
readxl_example()
```

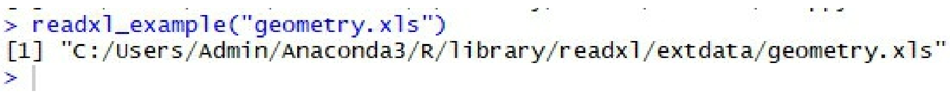
to see all the available spreadsheets in the library.



```
> readxl_example()
 [1] "clippy.xls"    "clippy.xlsx"   "datasets.xls"  "datasets.xlsx" "deaths.xls"    "deaths.xlsx"
   "geometry.xls"  "geometry.xlsx"
 [9] "type-me.xls"   "type-me.xlsx"
```

To check the location of the spreadsheet named clippy.xls, simple use

```
readxl_example("geometry.xls")
```



```
> readxl_example("geometry.xls")
[1] "C:/Users/Admin/Anaconda3/R/library/readxl/extdata/geometry.xls"
> 
```

If you install R with conda, the spreadsheets are located in Anaconda3/lib/R/library/readxl/extdata/filename.xls

read_excel()

The function read_excel() is of great use when it comes to opening xls and xlsx extention.

The syntax is:

```
read_excel(PATH, sheet = NULL, range= NULL, col_names = TRUE)
arguments:
-PATH: Path where the excel is located
-sheet: Select the sheet to import. By default, all
-range: Select the range to import. By default, all non-null
cells
-col_names: Select the columns to import. By default, all non-
null columns
```

We can import the spreadsheets from the readxl library and count the number of columns in the first sheet.

```
# Store the path of `datasets.xlsx`
example <- readxl_example("datasets.xlsx")
# Import the spreadsheet
df <- read_excel(example)
# Count the number of columns
length(df)
```

Output:

```
## [1] 5
```

excel_sheets()

The file datasets.xlsx is composed of 4 sheets. We can find out which sheets are available in the workbook by using excel_sheets() function

```
example <- readxl_example("datasets.xlsx")

excel_sheets(example)
```

Output:

```
[1] "iris"     "mtcars"   "chickwts" "quakes"
```

If a worksheet includes many sheets, it is easy to select a particular sheet by using the sheet arguments. We can specify the name of the sheet or the sheet index. We can verify if both function returns the same output with identical().

```
example <- readxl_example("datasets.xlsx")
quake <- read_excel(example, sheet = "quakes")
quake_1 <-read_excel(example, sheet = 4)
identical(quake, quake_1)
```

Output:

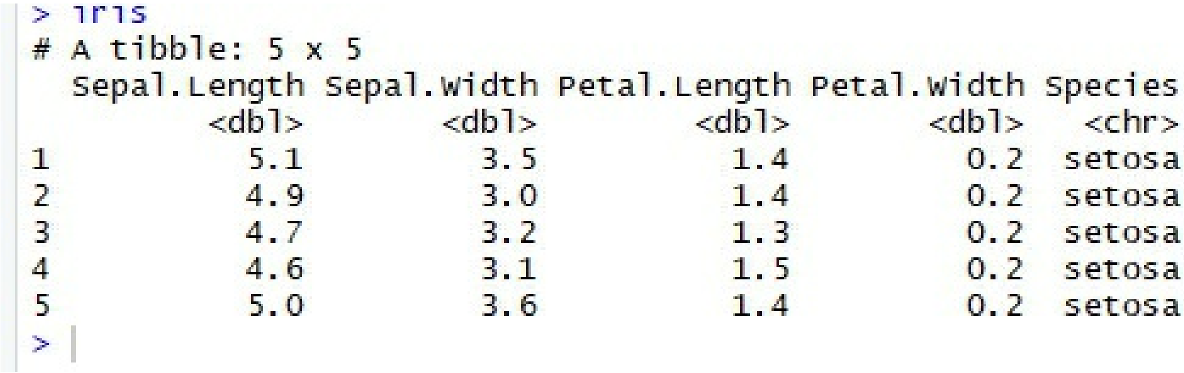
```
## [1] TRUE
```

We can control what cells to read in 2 ways

1. Use n_max argument to return n rows
2. Use range argument combined with cell_rows or cell_cols

For example, we set n_max equals to 5 to import the first five rows.

```
# Read the first five row: with header
iris <-read_excel(example, n_max =5, col_names =TRUE)
```



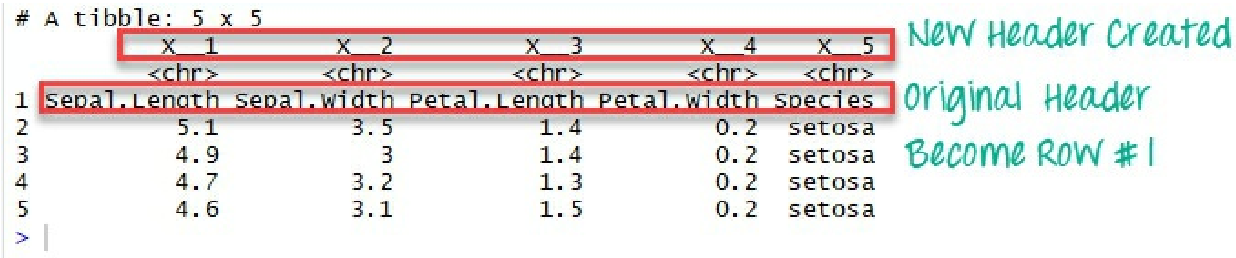
```
> iris
# A tibble: 5 x 5
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
         <dbl>       <dbl>        <dbl>       <dbl>   <chr>
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
> 
```

If we change col_names to FALSE, R creates the headers automatically.

```
# Read the first five row: without header
iris_no_header <-read_excel(example, n_max =5, col_names =FALSE)
```

iris_no_header

In the data frame iris_no_header, R created five new variables named X__1, X__2, X__3, X__4 and X__5



```
# A tibble: 5 x 5
          X__1        X__2         X__3        X__4    X__5
         <chr>       <chr>        <chr>       <chr>   <chr>
1 Sepal.Length Sepal.Width Petal.Length Petal.Width Species
2          5.1         3.5          1.4         0.2  setosa
3          4.9           3          1.4         0.2  setosa
4          4.7         3.2          1.3         0.2  setosa
5          4.6         3.1          1.5         0.2  setosa
> 
```

New Header Created

Original Header Become Row #1

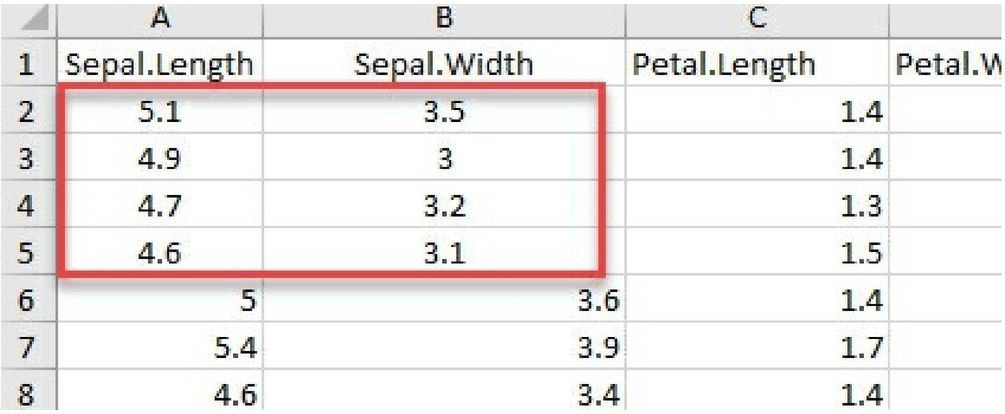
We can also use the argument range to select rows and columns in the spreadsheet. In the code below, we use the excel style to select the range A1 to B5.

```
# Read rows A1 to B5
example_1 <-read_excel(example, range = "A1:B5", col_names
=TRUE)
dim(example_1)
```

Output:

```
## [1] 4 2
```

We can see that the example_1 returns 4 rows with 2 columns. The dataset has header, that the reason the dimension is 4x2.



	A	B	C	
1	Sepal.Length	Sepal.Width	Petal.Length	Petal.W
2	5.1	3.5	1.4	
3	4.9	3	1.4	
4	4.7	3.2	1.3	
5	4.6	3.1	1.5	
6	5	3.6	1.4	
7	5.4	3.9	1.7	
8	4.6	3.4	1.4	

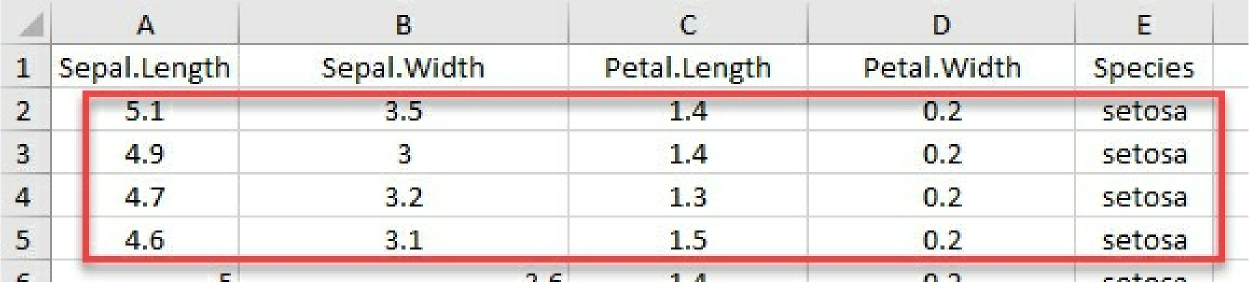
In the second example, we use the function cell_rows() which controls the range of rows to return. If we want to import the rows 1 to 5, we can set cell_rows(1:5). Note that, cell_rows(1:5) returns the same output as cell_rows(5:1).

```
# Read rows 1 to 5
example_2 <-read_excel(example, range =cell_rows(1:5),col_names
=TRUE)
dim(example_2)
```

Output:

```
## [1] 4 5
```

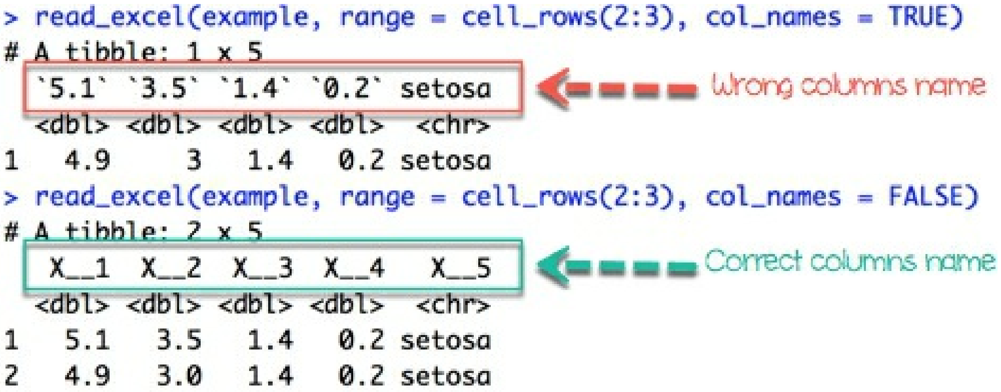
The example_2 however is a 4x5 matrix. The iris dataset has 5 columns with header. We return the first four rows with header of all columns



	A	B	C	D	E
1	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
2	5.1	3.5	1.4	0.2	setosa
3	4.9	3	1.4	0.2	setosa
4	4.7	3.2	1.3	0.2	setosa
5	4.6	3.1	1.5	0.2	setosa
6	5	3.6	1.4	0.2	setosa

In case we want to import rows which do not begin at the first row, we have to include col_names = FALSE. If we use range = cell_rows(2:5), it becomes obvious our data frame does not have header anymore.

```
iris_row_with_header <-read_excel(example, range
=cell_rows(2:3), col_names=TRUE)
iris_row_no_header <-read_excel(example, range
=cell_rows(2:3),col_names =FALSE)
```



```
> read_excel(example, range = cell_rows(2:3), col_names = TRUE)
# A tibble: 1 x 5
  `5.1` `3.5` `1.4` `0.2` setosa
  <dbl> <dbl> <dbl> <dbl>   <chr>
1   4.9     3   1.4   0.2 setosa
> read_excel(example, range = cell_rows(2:3), col_names = FALSE)
# A tibble: 2 x 5
   X__1  X__2  X__3  X__4   X__5
  <dbl> <dbl> <dbl> <dbl>   <chr>
1   5.1   3.5   1.4   0.2 setosa
2   4.9   3.0   1.4   0.2 setosa
```

```
We can select the columns with the letter, like in Excel.
# Select columns A and B
col <-read_excel(example, range =cell_cols("A:B"))
dim(col)
```

Output:

```
## [1] 150   2
```

Note : range = cell_cols("A:B"), returns output all cells with non-null value. The dataset contains 150 rows, therefore, read_excel() returns rows up to 150. This is verified with the dim() function.

read_excel() returns NA when a symbol without numerical value appears in the cell. We can count the number of missing values with the combination of two functions

1. sum
2. is.na

Here is the code

```
iris_na <-read_excel(example, na ="setosa")
```

```
sum(is.na(iris_na))
```

Output:

```
## [1] 50
```

We have 50 values missing, which are the rows belonging to the setosa species.

Import data from other Statistical software

We will import different files format with the heaven package. This package support SAS, STATA and SPSS softwares. We can use the following function to open different types of dataset, according to the extension of the file:

- SAS: read_sas()
- STATA: read_dta() (or read_stata(), which are identical)
- SPSS: read_sav() or read_por(). We need to check the extension

Only one argument is required within these function. We need to know the PATH where the file is stored. That's it, we are ready to open all the files from SAS, STATA and SPSS. These three function accepts an URL as well.

```
library(haven)
```

haven comes with conda r-essential otherwise go to the link or in the terminal conda install -c conda-forge r-haven

Read sas

For our example, we are going to use the admission dataset from IDRE.

```
PATH_sas <- 'https://github.com/guru99-edu/R-
Programming/blob/master/binary.sas7bdat?raw=true'
df <- read_sas(PATH_sas)
head(df)
```

Output:

```
## # A tibble: 6 x 4
##   ADMIT   GRE   GPA  RANK
##   <dbl> <dbl> <dbl> <dbl>
## 1     0   380  3.61     3
## 2     1   660  3.67     3
## 3     1   800  4.00     1
## 4     1   640  3.19     4
## 5     0   520  2.93     4
## 6     1   760  3.00     2
```

Read STATA

For STATA data files you can use read_dta(). We use exactly the same dataset but store in .dta file.

```
PATH_stata <- 'https://github.com/guru99-edu/R-
Programming/blob/master/binary.dta?raw=true'
df <- read_dta(PATH_stata)
head(df)
```

Output:

```
## # A tibble: 6 x 4
##   admit   gre   gpa  rank
##   <dbl> <dbl> <dbl> <dbl>
## 1     0   380  3.61     3
## 2     1   660  3.67     3
## 3     1   800  4.00     1
## 4     1   640  3.19     4
## 5     0   520  2.93     4
## 6     1   760  3.00     2
```

Read SPSS

We use the read_sav()function to open a SPSS file. The file extension ".sav"

```
PATH_spss <- 'https://github.com/guru99-edu/R-
Programming/blob/master/binary.sav?raw=true'
df <- read_sav(PATH_spss)
head(df)
```

Output:

```
## # A tibble: 6 x 4
##   admit   gre   gpa  rank
##   <dbl> <dbl> <dbl> <dbl>
## 1     0   380  3.61     3
## 2     1   660  3.67     3
## 3     1   800  4.00     1
## 4     1   640  3.19     4
## 5     0   520  2.93     4
## 6     1   760  3.00     2
```

Best practices for Data Import

When we want to import data into R, it is useful to implement following checklist. It will make it easy to import data correctly into R:

- The typical format for a spreadsheet is to use the first rows as the header (usually variables name).
- Avoid to name a dataset with blank spaces; it can lead to interpreting as a separate variable. Alternatively, prefer to use '_' or '-.'
- Short names are preferred
- Do not include symbol in the name: i.e: exchange_rate_$_€ is not correct. Prefer to name it: exchange_rate_dollar_euro
- Use NA for missing values otherwise; we need to clean the format later.

Summary

Following table summarizes the function to use in order to import different types of file in R. The column one states the library related to the function. The last column refers to the default argument.

Library	**Objective**	**Function**	**Default Arguments**
utils	Read CSV file	read.csv()	file, header =,TRUE, sep = ","
readxl	Read EXCEL file	read_excel()	path, range = NULL, col_names = TRUE
haven	Read SAS file	read_sas()	path
haven	Read STATA file	read_stata()	path
haven	Read SPSS fille	read_sav()	path

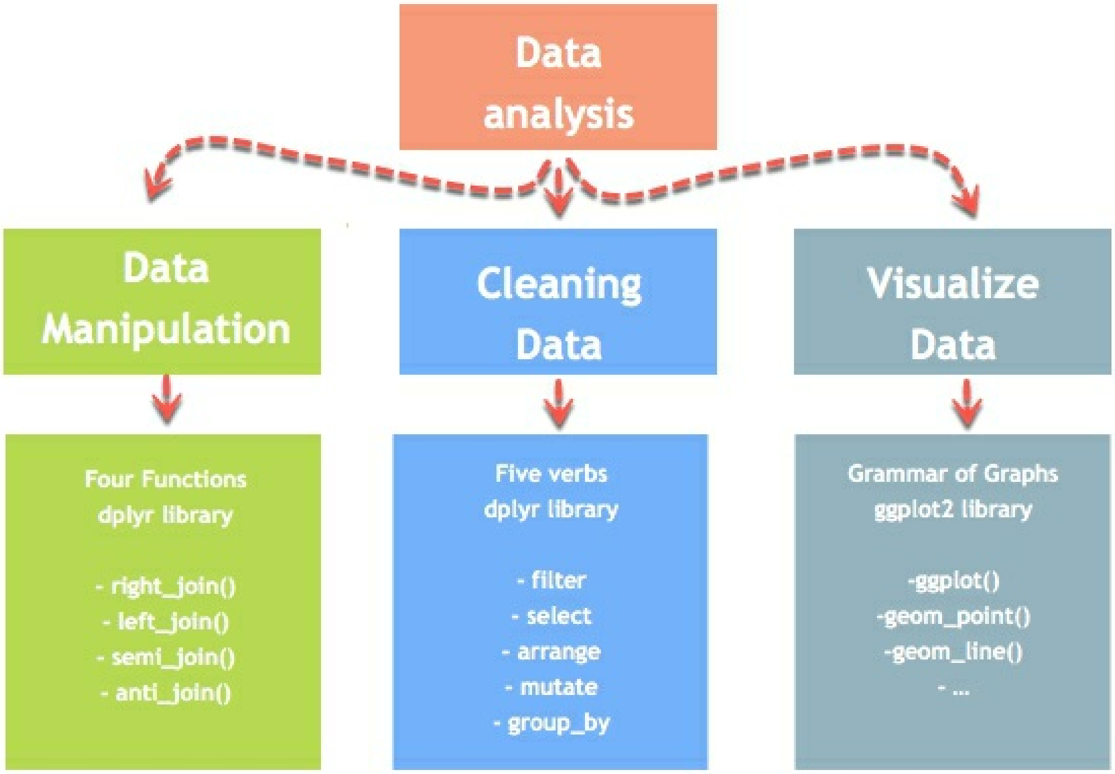
Following table shows the different ways to import a selection with read_excel() function.

Function	**Objectives**	**Arguments**
read_excel()	Read n number of rows	n_max = 10
	Select rows and columns like in excel	range = "A1:D10"
	Select rows with indexes	range= cell_rows(1:3)
	Select columns with letters	range = cell_cols("A:C")

Chapter 17: How to Replace Missing Values(NA) in R: na.omit & na.rm

Missing values in data science arise when an observation is missing in a column of a data frame or contains a character value instead of numeric value. Missing values must be dropped or replaced in order to draw correct conclusion from the data.

In this tutorial, we will learn how to deal with missing values with the dplyr library. dplyr library is part of an ecosystem to realize a data analysis.



mutate()

The fourth verb in the dplyr library is helpful to create new variable or change the values of an existing variable.

We will proceed in two parts. We will learn how to:

- exclude missing values from a data frame
- impute missing values with the mean and median

The verb mutate() is very easy to use. We can create a new variable following this syntax:

```
mutate(df, name_variable_1 = condition, ...)
arguments:
-df: Data frame used to create a new variable
-name_variable_1: Name and the formula to create the new
variable
-...: No limit constraint. Possibility to create more than one
variable inside mutate()
```

Exclude Missing Values (NA)

The na.omit() method from the dplyr library is a simple way to exclude missing observation. Dropping all the NA from the data is easy but it does not mean it is the most elegant solution. During analysis, it is wise to use variety of methods to deal with missing values

To tackle the problem of missing observations, we will use the titanic dataset. In this dataset, we have access to the information of the passengers on board during the tragedy. This dataset has many NA that need to be taken care of.

We will upload the csv file from the internet and then check which columns have NA. To return the columns with missing data, we can use the following code:

Let's upload the data and verify the missing data.

```
PATH <- "https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/test.csv"
df_titanic <- read.csv(PATH, sep = ",")
# Return the column names containing missing observations
list_na <- colnames(df_titanic)[ apply(df_titanic, 2, anyNA) ]
list_na
```

Output:

```
## [1] "age"  "fare"
```

Here,

```
colnames(df_titanic)[apply(df_titanic, 2, anyNA)]
```

Gives the name of columns that do not have data.

The columns age and fare have missing values.

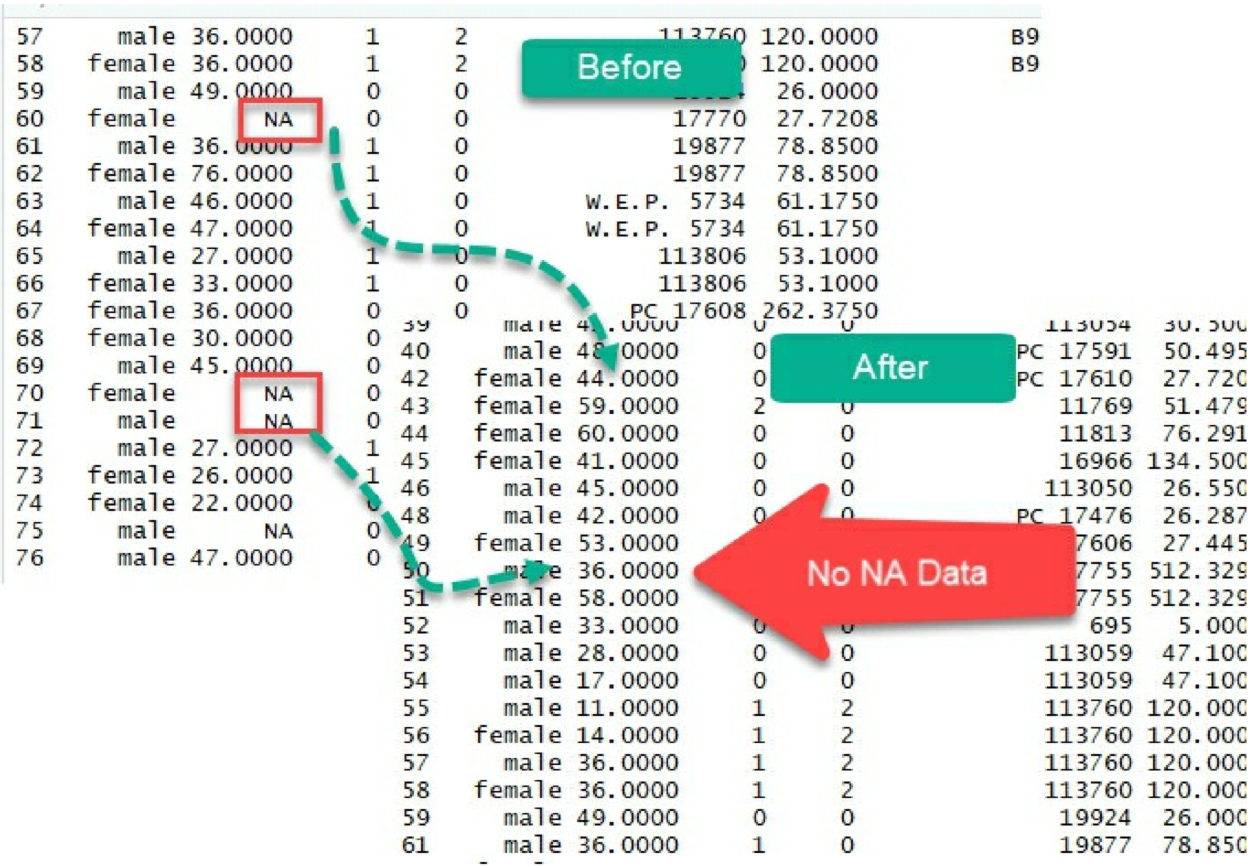
We can drop them with the na.omit().

```
library(dplyr)
# Exclude the missing observations
df_titanic_drop <-df_titanic %>%
na.omit()
dim(df_titanic_drop)
```

Output:

```
## [1] 1045   13
```

The new dataset contains 1045 rows compared to 1309 with the original dataset.



```
57     male 36.0000      1      2            113760 120.0000              B9
58   female 36.0000      1      2                   120.0000              B9
59     male 49.0000      0      0                    26.0000
60   female      NA      0      0             17770  27.7208
61     male 36.0000      1      0             19877  78.8500
62   female 76.0000      1      0             19877  78.8500
63     male 46.0000      1      0       W.E.P. 5734  61.1750
64   female 47.0000      1      0       W.E.P. 5734  61.1750
65     male 27.0000      1      0            113806  53.1000
66   female 33.0000      1      0            113806  53.1000
67   female 36.0000      0      0          PC 17608 262.3750
68   female 30.0000      0
69     male 45.0000      0
70   female      NA      0
71     male      NA      0
72     male 27.0000      1
73   female 26.0000      1
74   female 22.0000      0
75     male      NA      0
76     male 47.0000      0
```

```
40     male 48.0000      0              PC 17591  50.495
42   female 44.0000      0              PC 17610  27.720
43   female 59.0000      2                 11769  51.479
44   female 60.0000      0      0          11813  76.291
45   female 41.0000      0      0          16966 134.500
46     male 45.0000      0      0         113050  26.550
48     male 42.0000      0      0       PC 17476  26.287
49   female 53.0000                         7606  27.445
50     male 36.0000                         7755 512.329
51   female 58.0000                         7755 512.329
52     male 33.0000      0      0            695   5.000
53     male 28.0000      0      0         113059  47.100
54     male 17.0000      0      0         113059  47.100
55     male 11.0000      1      2         113760 120.000
56   female 14.0000      1      2         113760 120.000
57     male 36.0000      1      2         113760 120.000
58   female 36.0000      1      2         113760 120.000
59     male 49.0000      0      0          19924  26.000
61     male 36.0000      1      0          19877  78.850
```

Impute Missing data with the Mean and Median

We could also impute(populate) missing values with the median or the mean. A good practice is to create two separate variables for the mean and the median. Once created, we can replace the missing values with the newly formed variables.

We will use the apply method to compute the mean of the column with NA. Let's see an example

Step 1) Earlier in the tutorial, we stored the columns name with the missing values in the list called list_na. We will use this list

Step 2) Now we need to compute of the mean with the argument na.rm = TRUE. This argument is compulsory because the columns have missing data, and this tells R to ignore them.

```
# Create mean
average_missing <- apply(df_titanic[,colnames(df_titanic) %in%
list_na],
      2,
      mean,
      na.rm =  TRUE)
average_missing
```

Code Explanation:

We pass 4 arguments in the apply method.

- df: df_titanic[,colnames(df_titanic) %in% list_na]. This code will return the columns name from the list_na object (i.e. "age" and "fare")
- 2: Compute the function on the columns
- mean: Compute the mean
- na.rm = TRUE: Ignore the missing values

Output:

```
##      age     fare
## 29.88113 33.29548
```

We successfully created the mean of the columns containing missing observations. These two values will be used to replace the missing observations.

Step 3) Replace the NA Values

The verb mutate from the dplyr library is useful in creating a new variable. We don't necessarily want to change the original column so we can create a new variable without the NA. mutate is easy to use, we just choose a variable name and define how to create this variable. Here is the complete code

```
# Create a new variable with the mean and median
df_titanic_replace <- df_titanic %>%
   mutate(replace_mean_age  = ifelse(is.na(age),
average_missing[1], age),
   replace_mean_fare = ifelse(is.na(fare), average_missing[2],
fare))
```

Code Explanation:

We create two variables, replace_mean_age and replace_mean_fare as follow:

- replace_mean_age = ifelse(is.na(age), average_missing[1], age)
- replace_mean_fare = ifelse(is.na(fare), average_missing[2],fare)

If the column age has missing values, then replace with the first element of average_missing (mean of age), else keep the original values. Same logic for fare

```
sum(is.na(df_titanic_replace$age))
```

Output:

```
## [1] 263
```

Perform the replacement

```
sum(is.na(df_titanic_replace$replace_mean_age))
```

Output:

```
## [1] 0
```

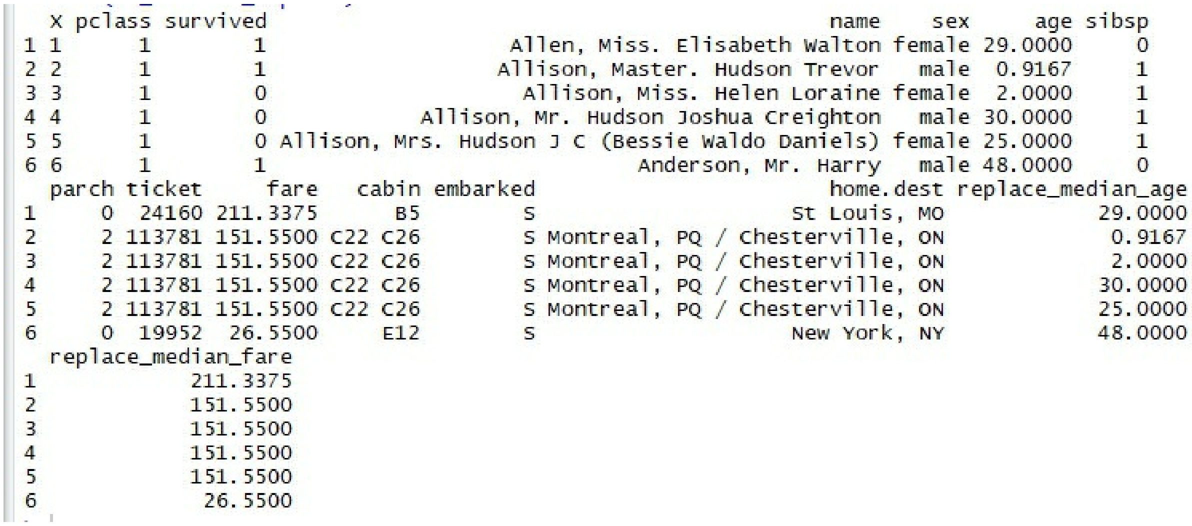
The original column age has 263 missing values while the newly created variable have replaced them with the mean of the variable age.

Step 4) We can replace the missing observations with the median as well.

```
median_missing <- apply(df_titanic[,colnames(df_titanic) %in%
list_na],
      2,
      median,
      na.rm =  TRUE)
```

```
df_titanic_replace <- df_titanic %>%
            mutate(replace_median_age  = ifelse(is.na(age),
median_missing[1], age),
            replace_median_fare = ifelse(is.na(fare),
median_missing[2], fare))
head(df_titanic_replace)
```

Output:



```
  X pclass survived                                            name    sex     age sibsp
1 1      1        1                   Allen, Miss. Elisabeth Walton female 29.0000     0
2 2      1        1                  Allison, Master. Hudson Trevor   male  0.9167     1
3 3      1        0                    Allison, Miss. Helen Loraine female  2.0000     1
4 4      1        0            Allison, Mr. Hudson Joshua Creighton   male 30.0000     1
5 5      1        0 Allison, Mrs. Hudson J C (Bessie Waldo Daniels) female 25.0000     1
6 6      1        1                             Anderson, Mr. Harry   male 48.0000     0
  parch ticket     fare   cabin embarked                       home.dest replace_median_age
1     0  24160 211.3375      B5        S                    St Louis, MO            29.0000
2     2 113781 151.5500 C22 C26        S Montreal, PQ / Chesterville, ON             0.9167
3     2 113781 151.5500 C22 C26        S Montreal, PQ / Chesterville, ON             2.0000
4     2 113781 151.5500 C22 C26        S Montreal, PQ / Chesterville, ON            30.0000
5     2 113781 151.5500 C22 C26        S Montreal, PQ / Chesterville, ON            25.0000
6     0  19952  26.5500     E12        S                    New York, NY            48.0000
  replace_median_fare
1            211.3375
2            151.5500
3            151.5500
4            151.5500
5            151.5500
6             26.5500
```

Step 5) A big data set could have lots of missing values and the above method could be cumbersome. We can execute all the above steps above in one line of code using sapply() method. Though we would not know the vales of mean and median.

sapply does not create a data frame, so we can wrap the sapply() function within data.frame() to create a data frame object.

```
# Quick code to replace missing values with the mean
df_titanic_impute_mean < -data.frame(
    sapply(
        df_titanic,
        function(x) ifelse(is.na(x),
            mean(x, na.rm = TRUE),
            x)))
```

Summary

We have three methods to deal with missing values:

- Exclude all of the missing observations
- Impute with the mean
- Impute with the median

The following table summarizes how to remove all the missing observations

Library	Objective	Code
base	List missing observations	`colnames(df)[apply(df, 2, anyNA)]`
dplyr	Remove all missing values	`na.omit(df)`

Imputation with mean or median can be done in two ways

- Using apply
- Using sapply

Method	Details	Advantages	Disadvantages
Step by step with apply	Check columns with missing, compute mean/median, store the value, replace with mutate()	You know the value of means/median	More execution time. Can be slow with big dataset
Quick way with sapply	Use sapply() and data.frame() to automatically search and replace missing values with mean/median	Short code and fast	Don't know the imputation values

Chapter 18: R Exporting Data to Excel, CSV, SAS, STATA, Text File

How to Export Data from R

In this tutorial, we will learn how to export data from R environment to different formats.

To export data to the hard drive, you need the file path and an extension. First of all, the path is the location where the data will be stored. In this tutorial, you will see how to store data on:

- The hard drive
- Google Drive
- Dropbox

Secondly, R allows the users to export the data into different types of files. We cover the essential file's extension:

- csv
- xlsx
- RDS
- SAS
- SPSS
- STATA

Overall, it is not difficult to export data from R.

Export to Hard drive

To begin with, you can save the data directly into the working directory. The following code prints the path of your working directory:

```
directory <-getwd()
directory
```

Output:

```
## [1] "/Users/15_Export_to_do"
```

By default, the file will be saved in the below path.

For Mac OS:

```
/Users/USERNAME/Downloads/
```

For Windows:

```
C:\Users\USERNAME\Documents\
```

You can, of course, set a different path. For instance, you can change the path to the download folder.

Create data frame

First of all, let's import the mtcars dataset and get the mean of mpg and disp grouped by gear.

```
library(dplyr)
df <-mtcars % > %
    select(mpg, disp, gear) % > %
    group_by(gear) % > %
    summarize(mean_mpg = mean(mpg), mean_disp = mean(disp))
df
```

Output::

```
## # A tibble: 3 x 3
##      gear mean_mpg mean_disp
##      <dbl>     <dbl>     lt;dbl>
## 1    3 16.10667  326.3000
## 2    4 24.53333  123.0167
## 3    5 21.38000  202.4800
```

The table contains three rows and three columns. You can create a CSV file with the function write.csv().

Export CSV

The basic syntax is:

```
write.csv(df, path)
arguments
-df: Dataset to save. Need to be the same name of the data frame
in the environment.
-path: A string. Set the destination path. Path + filename +
extension i.e. "/Users/USERNAME/Downloads/mydata.csv" or the
filename + extension if the folder is the same as the working
directory
```

Example:

```
write.csv(df, "table_car.csv")
```

Code Explanation

- write.csv(df, "table_car.csv"): Create a CSV file in the hard drive:
  - df: name of the data frame in the environment
  - "table_car.csv": Name the file table_car and store it as csv

Note: You can use the function write.csv2() to separate the rows with a semicolon.

```
write.csv2(df, "table_car.csv")
```

Note: For pedagogical purpose only, we created a function called open_folder() to open the directory folder for you. You just need to run the code below and see where the csv file is stored. You should see a file names table_car.csv.

```
# Run this code to create the function
open_folder <-function(dir){
        if (.Platform['OS.type'] == "windows"){
        shell.exec(dir)
        } else {
        system(paste(Sys.getenv("R_BROWSER"), dir))
  }
}
# Call the function to open the folder
open_folder(directory)
```

Export to Excel file

Export data to Excel is trivial for Windows users and trickier for Mac OS user. Both users will use the library xlsx to create an Excel file. The slight difference comes from the installation of the library. Indeed, the library xlsx uses Java to create the file. Java needs to be installed if not present in your machine.

Windows users

If you are a Windows user, you can install the library directly with conda:

```
conda install -c r r-xlsx
```

Once the library installed, you can use the function write.xlsx(). A new Excel workbook is created in the working directory

```
library(xlsx)
write.xlsx(df, "table_car.xlsx")
```

If you are a Mac OS user, you need to follow these steps:

- Step 1: Install the latest version of Java
- Step 2: Install library rJava
- Step 3: Install library xlsx

Step 1) You could download Java from official Oracle site and install it.

You can go back to Rstudio and check which version of Java is installed.

```
system("java -version")
```

At the time of the tutorial, the latest version of Java is 9.0.4.

Step 2) You need to install rjava in R. We recommended you to install R and Rstudio with Anaconda. Anaconda manages the dependencies between libraries. In this sense, Anaconda will handle the intricacies of rJava installation.

First of all, you need to update conda and then install the library. You can copy and paste the next two lines of code in the terminal.

```
conda - conda update
conda install -c r r-rjava
```

Next, open rjava in Rstudio

```
library(rJava)
```

Step 3) Finally, it is time to install xlsx. Once again, you can use conda to do it:

```
conda install -c r r-xlsx
```

Just as the windows users, you can save data with the function write.xlsx()

```
library(xlsx)
```

Output:

```
## Loading required package: xlsxjars
```

```
write.xlsx(df, "table_car.xlsx")
```

Export to different software

Exporting data to different software is as simple as importing them. The library "haven" provides a convenient way to export data to

- spss
- sas
- stata

First of all, import the library. If you don't have "haven", you can go here to install it.

```
library(haven)
```

SPSS file

Below is the code to export the data to SPSS software:

```
write_sav(df, "table_car.sav")
```

Export SAS file

Just as simple as spss, you can export to sas

```
write_sas(df, "table_car.sas7bdat")
```

Export STATA file

Finally, haven library allows writing .dta file.

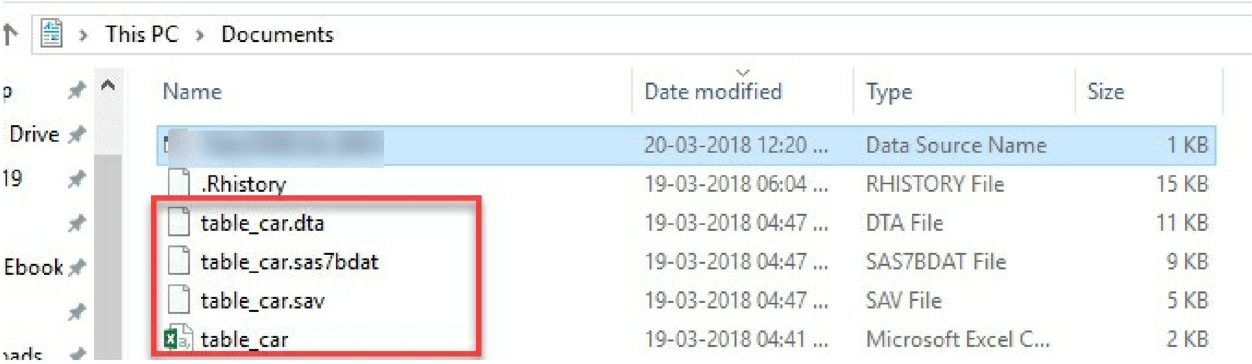
```
write_dta(df, "table_car.dta")
```

R

If you want to save a data frame or any other R object, you can use the save() function.

```
save(df, file ='table_car.RData')
```

You can check the files created above in the present working directory



Name	Date modified	Type	Size
[redacted]	20-03-2018 12:20 ...	Data Source Name	1 KB
.Rhistory	19-03-2018 06:04 ...	RHISTORY File	15 KB
table_car.dta	19-03-2018 04:47 ...	DTA File	11 KB
table_car.sas7bdat	19-03-2018 04:47 ...	SAS7BDAT File	9 KB
table_car.sav	19-03-2018 04:47 ...	SAV File	5 KB
table_car	19-03-2018 04:41 ...	Microsoft Excel C...	2 KB

Interact with the Cloud Services

Last but not least, R is equipped with fantastic libraries to interact with the cloud computing services. The last part of this tutorial deals with export/import files from:

- Google Drive
- Dropbox

Note: This part of the tutorial assumes you have an account with Google and Dropbox. If not, you can quickly create one for – Google Drive: https://accounts.google.com/SignUp?hl=en - Dropbox: https://www.dropbox.com/h

Google Drive

You need to install the library googledrive to access the function allowing to interact with Google Drive.

The library is not yet available at Anaconda. You can install it with the code below in the console.

```
install.packages("googledrive")
```

and you open the library.

```
library(googledrive)
```

For non-conda user, installing a library is easy, you can use the function install.packages('NAME OF PACKAGE) with the name of the package inside the parenthesis. Don't forget the ' '. Note that, R is supposed to install the package in the `libPaths() automatically. It is worth to see it in action.

Upload to Google Drive

To upload a file to Google drive, you need to use the function drive_upload().

Each time you restart Rstudio, you will be prompted to allow access tidyverse to Google Drive.

The basic syntax of drive_upload() is

```
drive_upload(file, path = NULL, name = NULL)
arguments:
- file: Full name of the file to upload (i.e., including the
extension)
- path: Location of the file- name: You can rename it as you
wish. By default, it is the local name.
```

After you launch the code, you need to confirm several questions

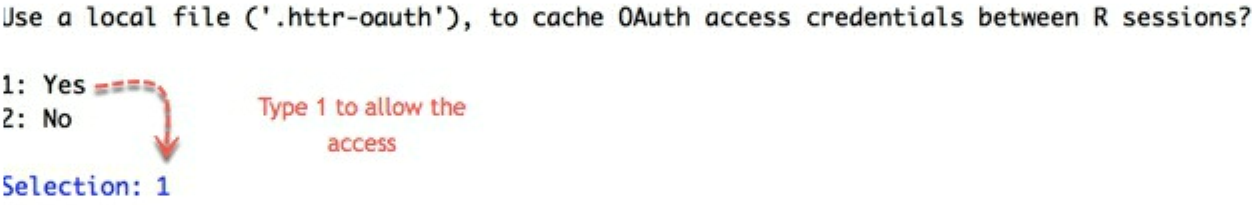
```
drive_upload%<("table_car.csv", name ="table_car")
```

Output:

```
## Local file:
## * table_car.csv
## uploaded into Drive file:
```

```
## * table_car: 1hwb57eT-9qSgDHt9CrVt5Ht7RHogQaMk
## with MIME type:
## * text/csv
```

You type 1 in the console to confirm the access



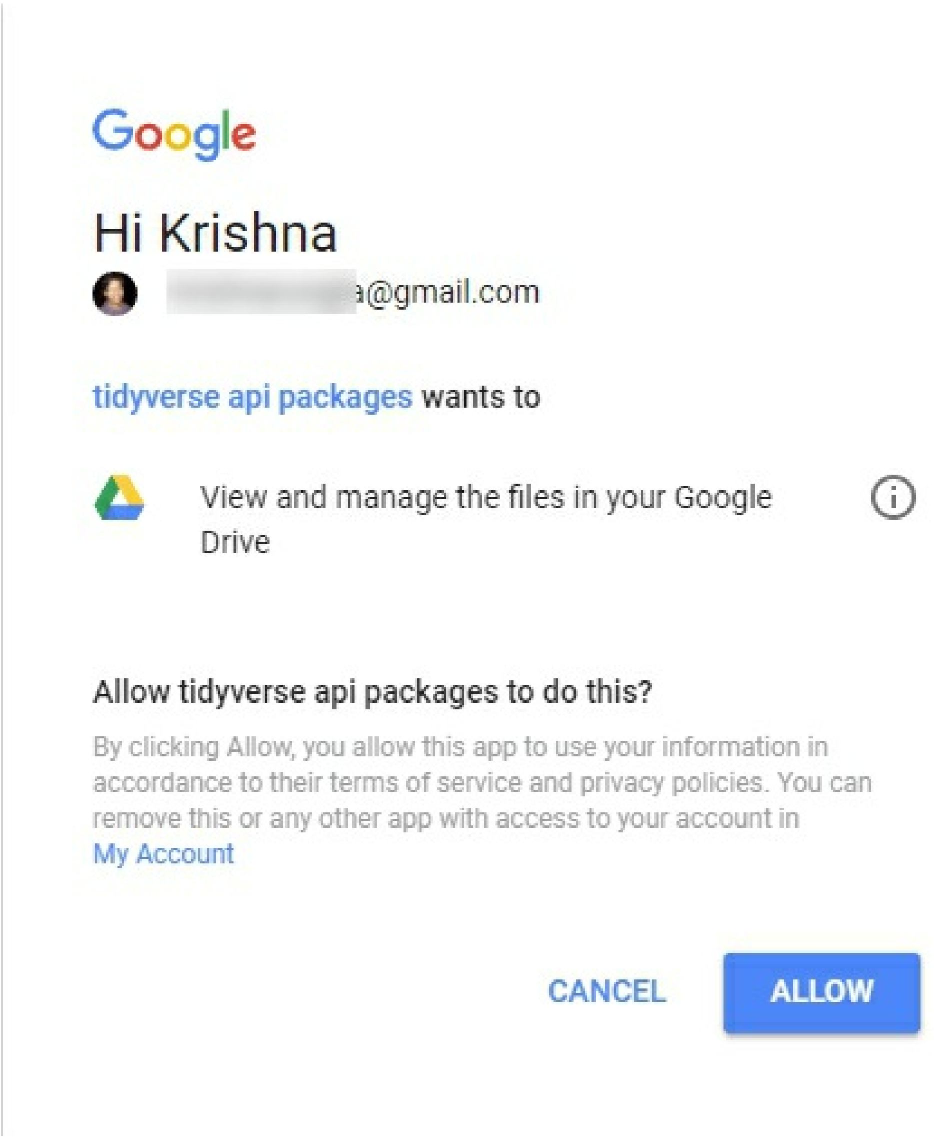
```
Use a local file ('.httr-oauth'), to cache OAuth access credentials between R sessions?

1: Yes
2: No

Selection: 1
```

Type 1 to allow the access

Then, you are redirected to Google API to allow the access. Click Allow.



Google

Hi Krishna

[redacted]a@gmail.com

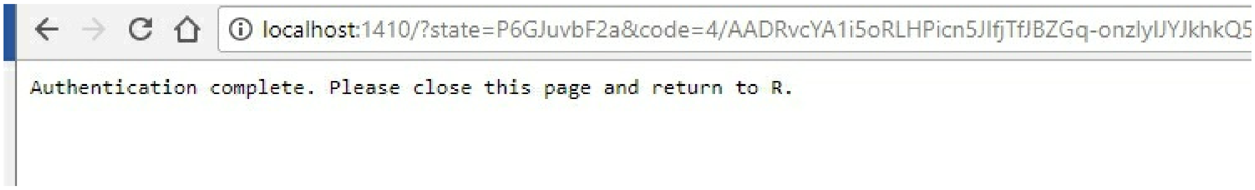
tidyverse api packages wants to

View and manage the files in your Google Drive

Allow tidyverse api packages to do this?

By clicking Allow, you allow this app to use your information in accordance to their terms of service and privacy policies. You can remove this or any other app with access to your account in My Account

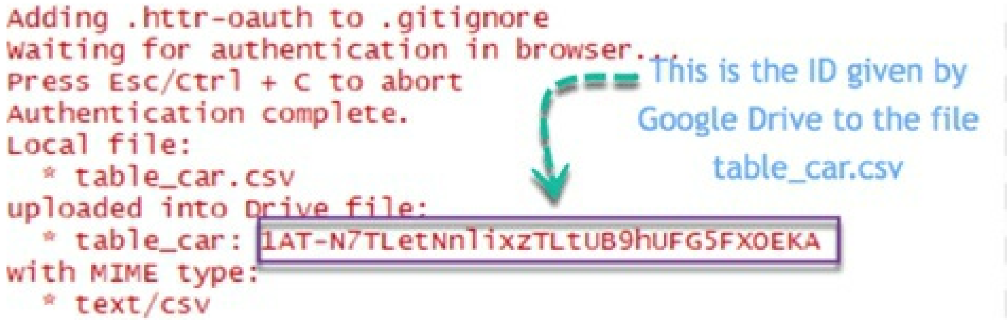
Once the authentication is complete, you can quit your browser.



localhost:1410/?state=P6GJuvbF2a&code=4/AADRvcYA1i5oRLHPicn5JlfjTfJBZGq-onzlylJYJkhkQ5

```
Authentication complete. Please close this page and return to R.
```

In the Rstudio's console, you can see the summary of the step done. Google successfully uploaded the file located locally on the Drive. Google assigned an ID to each file in the drive.



```
Adding .httr-oauth to .gitignore
Waiting for authentication in browser...
Press Esc/Ctrl + C to abort
Authentication complete.
Local file:
  * table_car.csv
uploaded into Drive file:
  * table_car: 1AT-N7TLetNnlixzTLtUB9hUFG5FXOEKA
with MIME type:
  * text/csv
```

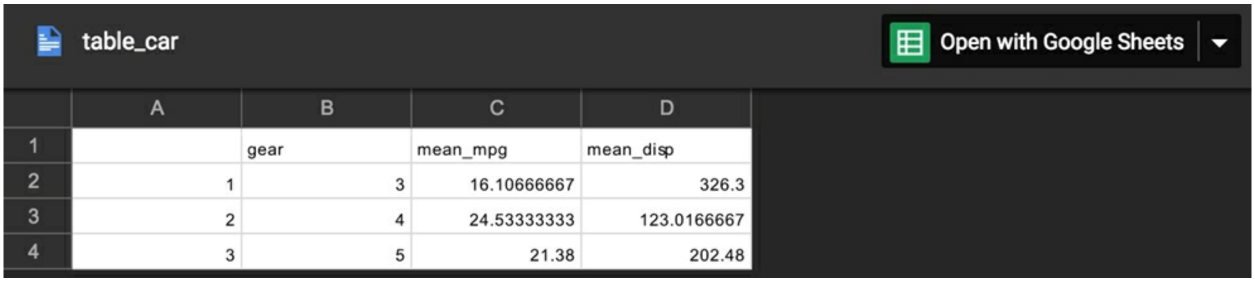
This is the ID given by Google Drive to the file table_car.csv

You can see this file in Google Spreadsheet.

```
drive_browse("table_car")
```

Output:

You will be redirected to Google Spreadsheet



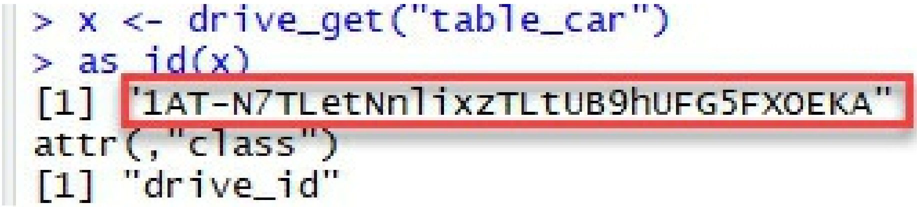
	A	B	C	D
1		gear	mean_mpg	mean_disp
2	1	3	16.10666667	326.3
3	2	4	24.53333333	123.0166667
4	3	5	21.38	202.48

Import from Google Drive

Upload a file from Google Drive with the ID is convenient. If you know the file name, you can get its ID as follow:

Note: Depending on your internet connection and the size of your Drive, it takes times.

```
x <-drive_get("table_car")
as_id(x)
```



```
> x <- drive_get("table_car")
> as_id(x)
[1] "1AT-N7TLetNnlixzTLtUB9hUFG5FXOEKA"
attr(,"class")
[1] "drive_id"
```

You stored the ID in the variable x. The function drive_download() allows downloading a file from Google Drive.

The basic syntax is:

```
drive_download(file, path = NULL, overwrite = FALSE)
arguments:
- file:  Name or id of the file to download
-path: Location to download the file. By default, it is
downloaded to the working directory and the name as in Google
Drive
-overwrite = FALSE: If the file already exists, don't overwrite
it. If set to TRUE, the old file is erased and replaced by the
new one.
```

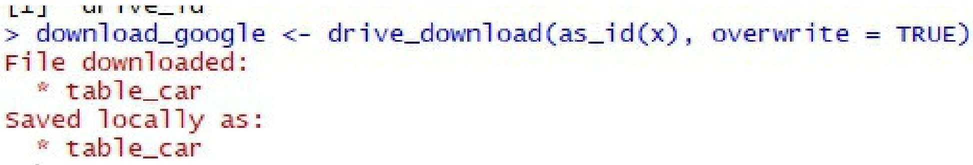
You can finally download the file:

```
download_google & lt; - drive_download(as_id(x), overwrite =
TRUE)
```

Code Explanation

- drive_download(): Function to download a file from Google Drive
- as_id(x): Use the ID to browse the file in Google Drive
- overwrite = TRUE: If file exists, overwrite it, else execution halted
  To see the name of the file locally, you can use:

Output:



```
> download_google <- drive_download(as_id(x), overwrite = TRUE)
File downloaded:
  * table_car
Saved locally as:
  * table_car
```

The file is stored in your working directory. Remember, you need to add the extenstion of the file to open it in R. You can create the full name with the function paste() (i.e. table_car.csv)

```
google_file <-download_google$local_path
google_file
path <-paste(google_file, ".csv", sep = "")
google_table_car <-read.csv(path)
google_table_car
```

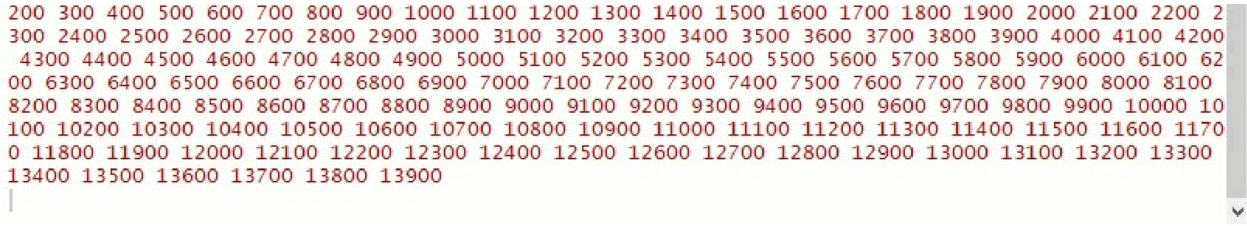
Output:

```
##   X gear mean_mpg mean_disp
## 1 1    3 16.10667  326.3000
## 2 2    4 24.53333  123.0167
## 3 3    5 21.38000  202.4800
```

Finally, you can remove the file from your Google drive.

```
## remove file
drive_find("table_car") %>%drive_rm()
```

Output:



```
200 300 400 500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2
300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 3500 3600 3700 3800 3900 4000 4100 4200
 4300 4400 4500 4600 4700 4800 4900 5000 5100 5200 5300 5400 5500 5600 5700 5800 5900 6000 6100 62
00 6300 6400 6500 6600 6700 6800 6900 7000 7100 7200 7300 7400 7500 7600 7700 7800 7900 8000 8100
8200 8300 8400 8500 8600 8700 8800 8900 9000 9100 9200 9300 9400 9500 9600 9700 9800 9900 10000 10
100 10200 10300 10400 10500 10600 10700 10800 10900 11000 11100 11200 11300 11400 11500 11600 1170
0 11800 11900 12000 12100 12200 12300 12400 12500 12600 12700 12800 12900 13000 13100 13200 13300
13400 13500 13600 13700 13800 13900
```

It's a slow process. Takes time to delete

Export to Dropbox

R interacts with Dropbox via the rdrop2 library. The library is not available at Anaconda as well. You can install it via the console

```
install.packages('rdrop2')
```

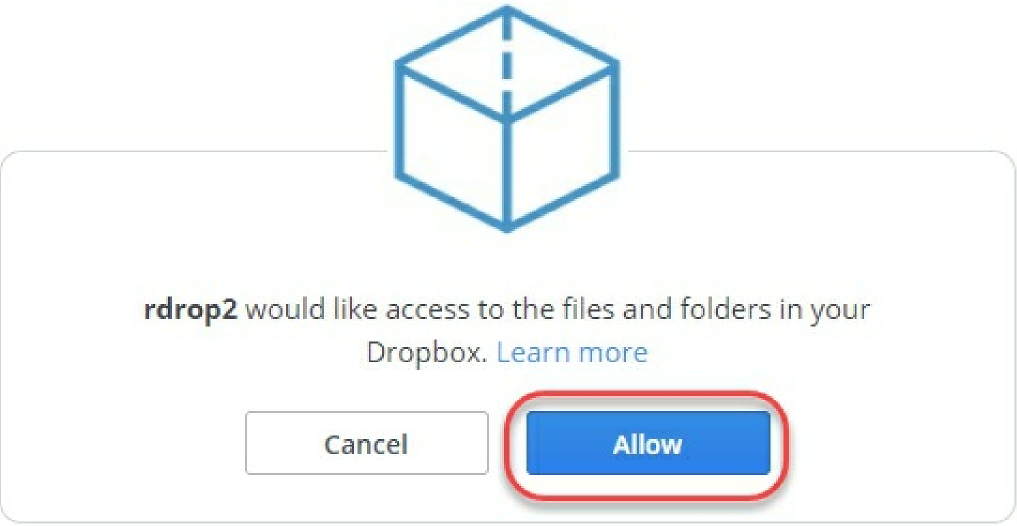
```
library(rdrop2)
```

You need to provide temporary access to Dropbox with your credential. After the identification is done, R can create, remove upload and download to your Dropbox.

First of all, you need to give access to your account. The credentials are cached during all session.

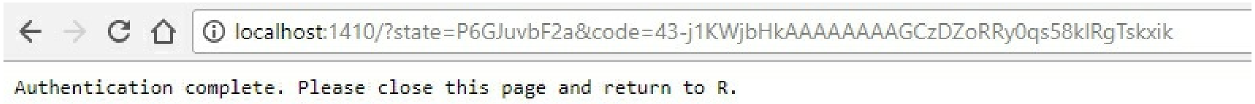
```
drop_auth()
```

You will be redirected to Dropbox to confirm the authentication.



rdrop2 would like access to the files and folders in your Dropbox. Learn more

You will get a confirmation page. You can close it and return to R



localhost:1410/?state=P6GJuvbF2a&code=43-j1KWjbHkAAAAAAAAGCzDZoRRy0qs58klRgTskxik

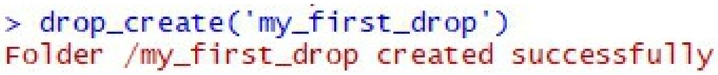
```
Authentication complete. Please close this page and return to R.
```

You can create a folder with the function drop_create().

- drop_create('my_first_drop'): Create a folder in the first branch of Dropbox
- drop_create('First_branch/my_first_drop'): Create a folder inside the existing First_branch folder.

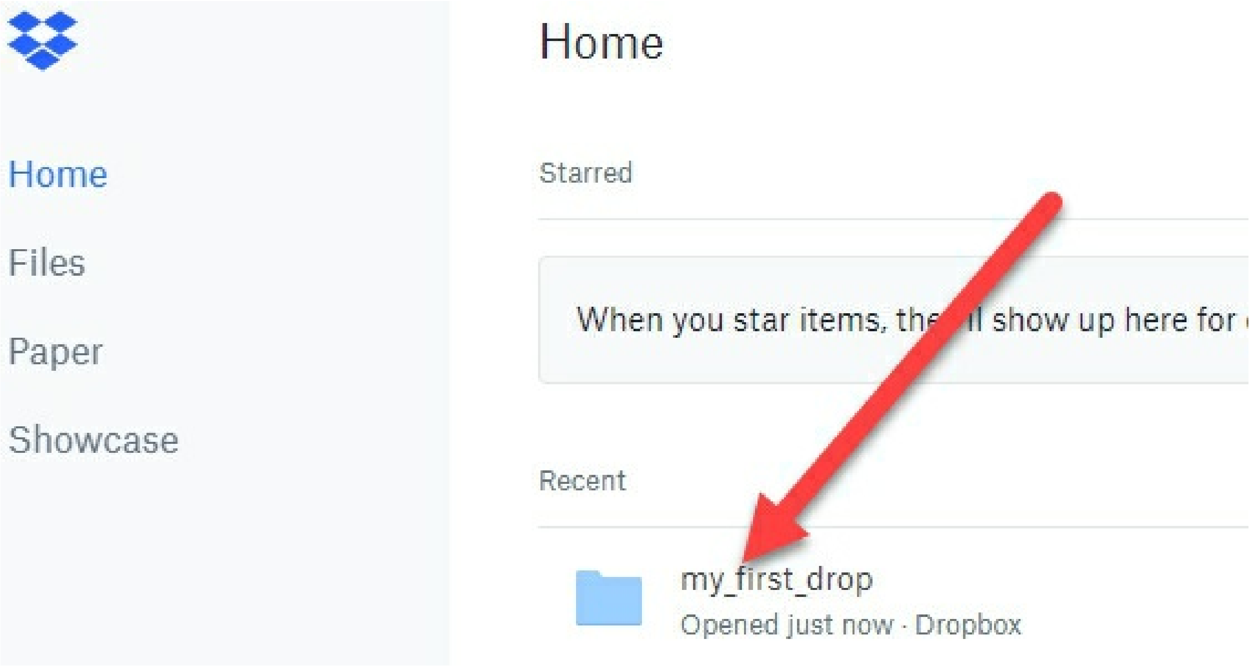
```
drop_create('my_first_drop')
```

Output:



```
> drop_create('my_first_drop')
Folder /my_first_drop created successfully
```

In DropBox


Home
Files
Paper
Showcase
Home
Starred
When you star items, the ll show up here for
Recent
my_first_drop
Opened just now · Dropbox

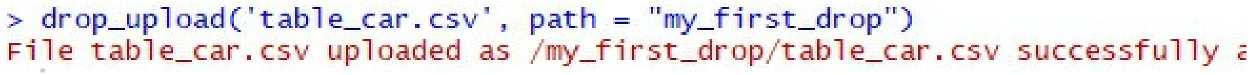
To upload the .csv file into your Dropbox, use the function drop_upload().

Basic syntax:

```
drop_upload(file, path = NULL, mode = "overwrite")
arguments:
- file: local path
- path: Path on Dropbox
- mode = "overwrite":  By default, overwrite an existing file.
If set to `add`, the upload is not completed.
```

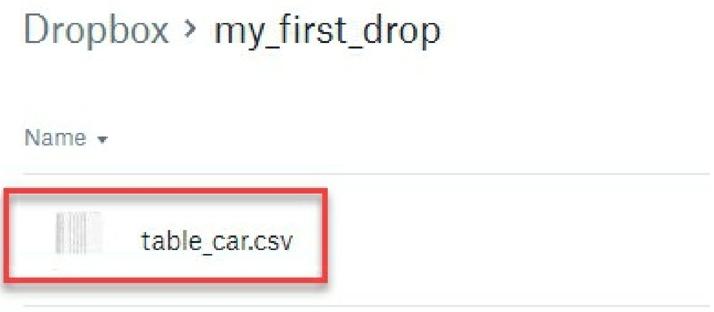
```
drop_upload('table_car.csv', path = "my_first_drop")
```

Output:



```
> drop_upload('table_car.csv', path = "my_first_drop")
File table_car.csv uploaded as /my_first_drop/table_car.csv successfully a
```

At DropBox



You can read the csv file from Dropbox with the function drop_read_csv()

```
dropbox_table_car <-drop_read_csv("my_first_drop/table_car.csv")
dropbox_table_car
```

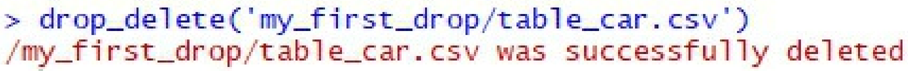
Output:

```
##   X gear mean_mpg mean_disp
## 1 1    3 16.10667  326.3000
## 2 2    4 24.53333  123.0167
## 3 3    5 21.38000  202.4800
```

When you are done using the file and want to delete it. You need to write the path of the file in the function drop_delete()

```
drop_delete('my_first_drop/table_car.csv')
```

Output:

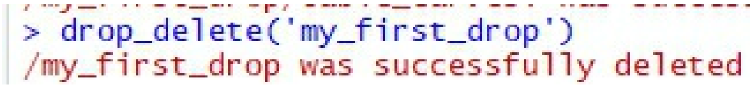


```
> drop_delete('my_first_drop/table_car.csv')
/my_first_drop/table_car.csv was successfully deleted
```

It is also possible to delete a folder

```
drop_delete('my_first_drop')
```

Output:



```
> drop_delete('my_first_drop')
/my_first_drop was successfully deleted
```

Summary

We can summarize all the functions in the table below

Library	**Objective**	**Function**
base	Export csv	write.csv()
xlsx	Export excel	write.xlsx()
haven	Export spss	write_sav()
haven	Export sas	write_sas()
haven	Export stata	write_dta()
base	Export R	save()
googledrive	Upload Google Drive	drive_upload()
googledrive	Open in Google Drive	drive_browse()
googledrive	Retrieve file ID	drive_get(as_id())
googledrive	Dowload from Google Drive	download_google()
googledrive	Remove file from Google Drive	drive_rm()

rdrop2	Authentification	drop_auth()
rdrop2	Create a folder	drop_create()
rdrop2	Upload to Dropbox	drop_upload()
rdrop2	Read csv from Dropbox	drop_read_csv
rdrop2	Delete file from Dropbox	drop_delete()

Chapter 19: Correlation in R: Pearson & Spearman with Matrix Example

A bivariate relationship describes a relationship -or correlation- between two variables, and . In this tutorial, we discuss the concept of **correlation** and show how it can be used to measure the relationship between any two variables.

There are two primary methods to compute the correlation between two variables.

- Pearson: Parametric correlation
- Spearman: Non-parametric correlation

Pearson Correlation

The Pearson correlation method is usually used as a primary check for the relationship between two variables.

The **coefficient of correlation**, , is a measure of the strength of the **linear** relationship between two variables and . It is computed as follow:

$$r = \frac{Cov(x,y)}{\sigma_x \sigma_y}$$

with

- $\sigma_x = \sum(x - \overline{x})^2$, i.e. standard deviation of
- $\sigma_y = \sum(y - \overline{y})^2$, i.e. standard deviation of

The correlation ranges between -1 and 1.

- A value of near or equal to 0 implies little or no linear relationship between and .
- In contrast, the closer comes to 1 or -1, the stronger the linear relationship.

We can compute the t-test as follow and check the distribution table with a degree of freedom equals to :

$$t = \frac{r}{\sqrt{1 - r^2}} \sqrt{n - 2}$$

Spearman Rank Correlation

A rank correlation sorts the observations by rank and computes the level of similarity between the rank. A rank correlation has the advantage of being robust to outliers and is not linked to the distribution of the data. Note that, a rank correlation is suitable for the ordinal variable.

Spearman's rank correlation, , is always between -1 and 1 with a value close to the extremity indicates strong relationship. It is computed as follow:

$$\rho = \frac{Cov(rg_x, rg_y)}{\sigma_{rg_x} \sigma_{rg_y}}$$

with stated the covariances between rank and . The denominator calculates the standard deviations.

In R, we can use the cor() function. It takes three arguments, , and the method.

```
cor(x, y, method)
```

Arguments:

- x: First vector
- y: Second vector
- method: The formula used to compute the correlation. Three string values:
  - "pearson"
  - "kendall"
  - "spearman"

An optional argument can be added if the vectors contain missing value: use = "complete.obs"

We will use the BudgetUK dataset. This dataset reports the budget allocation of British households between 1980 and 1982. There are 1519 observations with ten features, among them:

- wfood: share food share spend
- wfuel: share fuel spend
- wcloth: budget share for clothing spend
- walc: share alcohol spend
- wtrans: share transport spend
- wother: share of other goods spend
- totexp: total household spend in pound
- income total net household income
- age: age of household
- children: number of children

Example

```
library(dplyr)
```

```
PATH <-"https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/british_household.csv"
data <-read.csv(PATH)
  filter(income < 500)
  mutate(log_income = log(income),
         log_totexp = log(totexp),
         children_fac = factor(children, order = TRUE, labels =
c("No", "Yes")))
  select(-c(X,X.1, children, totexp, income))
glimpse(data)
```

Code Explanation

- We first import the data and have a look with the glimpse() function from the dplyr library.
- Three points are above 500K, so we decided to exclude them.
- It is a common practice to convert a monetary variable in log. It helps to reduce the impact of outliers and decreases the skewness in the dataset.

Output:

```
## Observations: 1,516## Variables: 10
## $ wfood        <dbl> 0.4272, 0.3739, 0.1941, 0.4438, 0.3331,
0.3752, 0...
## $ wfuel        <dbl> 0.1342, 0.1686, 0.4056, 0.1258, 0.0824,
0.0481, 0...
## $ wcloth       <dbl> 0.0000, 0.0091, 0.0012, 0.0539, 0.0399,
0.1170, 0...
## $ walc         <dbl> 0.0106, 0.0825, 0.0513, 0.0397, 0.1571,
0.0210, 0...
## $ wtrans       <dbl> 0.1458, 0.1215, 0.2063, 0.0652, 0.2403,
0.0955, 0...
## $ wother       <dbl> 0.2822, 0.2444, 0.1415, 0.2716, 0.1473,
0.3431, 0...
## $ age          <int> 25, 39, 47, 33, 31, 24, 46, 25, 30, 41,
48, 24, 2...
## $ log_income   <dbl> 4.867534, 5.010635, 5.438079, 4.605170,
4.605170,...
## $ log_totexp   <dbl> 3.912023, 4.499810, 5.192957, 4.382027,
4.499810,...
## $ children_fac <ord> Yes, Yes, Yes, Yes, No, No, No, No, No,
No, Yes, ...
```

We can compute the correlation coefficient between income and wfood variables with the "pearson" and "spearman" methods.

```
cor(data$log_income, data$wfood, method = "pearson")
```

output:

```
## [1] -0.2466986
```

```
cor(data$log_income, data$wfood, method = "spearman")
```

Output:

```
## [1] -0.2501252
```

Correlation Matrix

The bivariate correlation is a good start, but we can get a broader picture with multivariate analysis. A correlation with many variables is pictured inside a **correlation matrix**. A correlation matrix is a matrix that represents the pair correlation of all the variables.

The cor() function returns a correlation matrix. The only difference with the bivariate correlation is we don't need to specify which variables. By default, R computes the correlation between all the variables.

Note that, a correlation cannot be computed for factor variable. We need to make sure we drop categorical feature before we pass the data frame inside cor().

A correlation matrix is symmetrical which means the values above the diagonal have the same values as the one below. It is more visual to show half of the matrix.

We exclude children_fac because it is a factor level variable. cor does not perform correlation on a categorical variable.

```
# the last column of data is a factor level. We don't include it
in the code
mat_1 <-as.dist(round(cor(data[,1:9]),2))
mat_1
```

Code Explanation

- cor(data): Display the correlation matrix
- round(data, 2): Round the correlation matrix with two decimals
- as.dist(): Shows the second half only

Output:

```
##            wfood wfuel wcloth  walc wtrans wother   age
log_income
##
wfuel       0.11
## wcloth     -0.33
-0.25
## walc       -0.12
-0.13  -0.09
## wtrans     -0.34 -0.16  -0.19
-0.22
## wother     -0.35 -0.14  -0.22
-0.12  -0.29
## age         0.02 -0.05   0.04
-0.14   0.03   0.02
## log_income -0.25
-0.12   0.10  0.04   0.06   0.13  0.23
## log_totexp -0.50
-0.36   0.34  0.12   0.15   0.15  0.21       0.49
```

Significance level

The significance level is useful in some situations when we use the pearson or spearman method. The function rcorr() from the library Hmisc computes for us the p-value. We can download the library from conda and copy the code to paste it in the terminal:

```
conda install -c r r-hmisc
```

The rcorr() requires a data frame to be stored as a matrix. We can convert our data into a matrix before to compute the correlation matrix with the p-value.

```
library("Hmisc")
data_rcorr <-as.matrix(data[, 1: 9])

mat_2 <-rcorr(data_rcorr)
# mat_2 <-rcorr(as.matrix(data)) returns the same output
```

The list object mat_2 contains three elements:

- r: Output of the correlation matrix
- n: Number of observation
- P: p-value

We are interested in the third element, the p-value. It is common to show the correlation matrix with the p-value instead of the coefficient of correlation.

```
p_value <-round(mat_2[["P"]], 3)
p_value
```

Code Explanation

- mat_2[["P"]]: The p-values are stored in the element called P
- round(mat_2[["P"]], 3): Round the elements with three digits

Output:

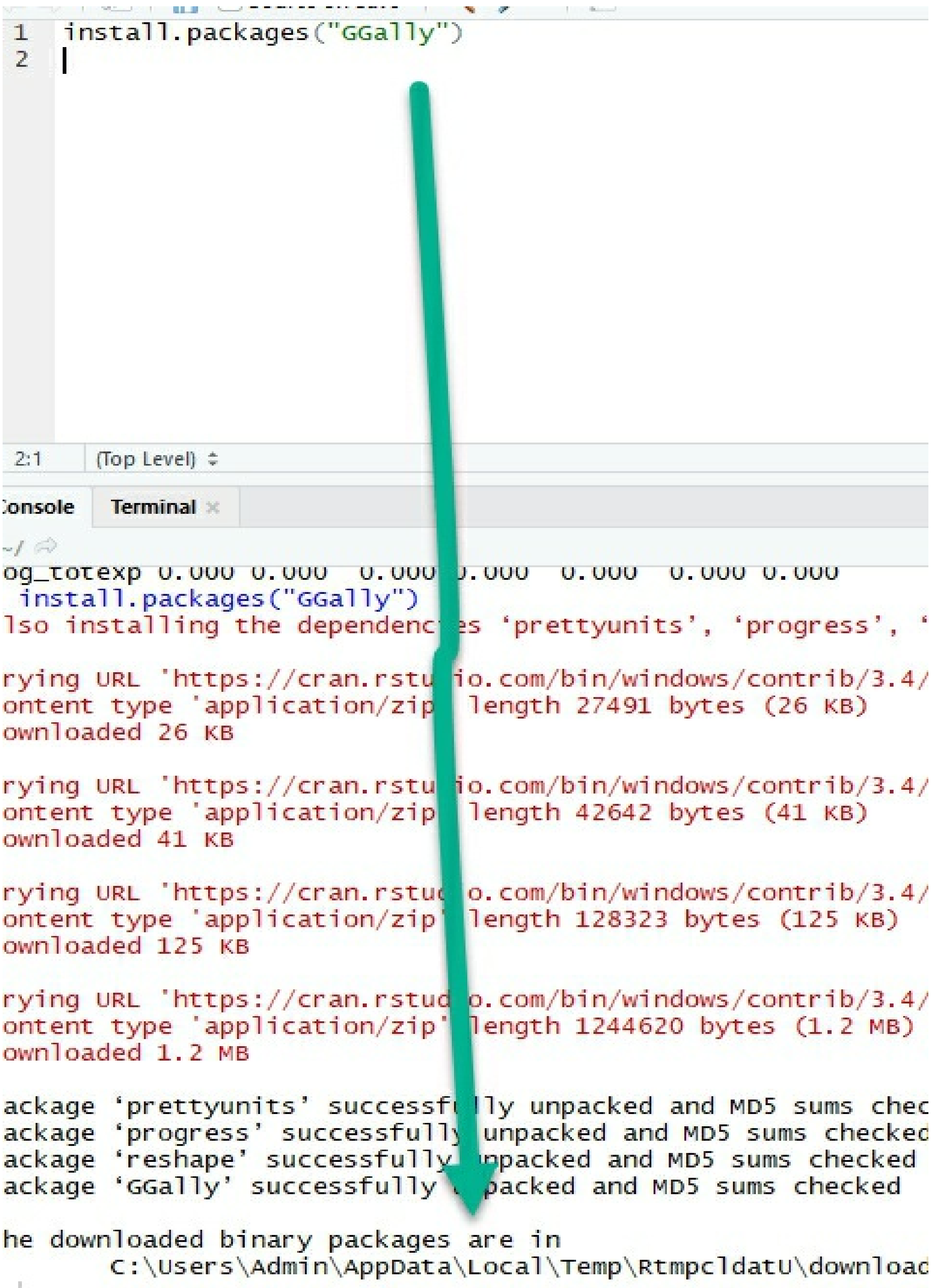
```
           wfood wfuel wcloth  walc wtrans wother   age
log_income log_totexp
wfood         NA 0.000  0.000 0.000  0.000  0.000
0.365      0.000          0
wfuel      0.000    NA  0.000 0.000  0.000  0.000
0.076      0.000          0
wcloth     0.000 0.000     NA 0.001  0.000  0.000
0.160      0.000          0
walc       0.000 0.000  0.001    NA  0.000  0.000
0.000      0.105          0
wtrans     0.000 0.000  0.000 0.000     NA  0.000
0.259      0.020          0
```

```
wother     0.000 0.000  0.000 0.000  0.000      NA
0.355      0.000          0
age        0.365 0.076  0.160
0.000  0.259  0.355    NA      0.000          0
log_income 0.000 0.000  0.000 0.105  0.020  0.000
0.000         NA          0
log_totexp 0.000 0.000  0.000 0.000  0.000  0.000
0.000      0.000         NA
```

Visualize Correlation Matrix

A heat map is another way to show a correlation matrix. The GGally library is an extension of ggplot2. Currently, it is not available in the conda library. We can install directly in the console.

```
install.packages("GGally")
```



```
install.packages("GGally")
```

```
og_totexp 0.000 0.000  0.000 0.000  0.000  0.000 0.000
 install.packages("GGally")
lso installing the dependencies ‘prettyunits’, ‘progress’, ‘

rying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/
ontent type 'application/zip' length 27491 bytes (26 KB)
ownloaded 26 KB

rying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/
ontent type 'application/zip' length 42642 bytes (41 KB)
ownloaded 41 KB

rying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/
ontent type 'application/zip' length 128323 bytes (125 KB)
ownloaded 125 KB

rying URL 'https://cran.rstudio.com/bin/windows/contrib/3.4/
ontent type 'application/zip' length 1244620 bytes (1.2 MB)
ownloaded 1.2 MB

ackage ‘prettyunits’ successfully unpacked and MD5 sums chec
ackage ‘progress’ successfully unpacked and MD5 sums checked
ackage ‘reshape’ successfully unpacked and MD5 sums checked
ackage ‘GGally’ successfully unpacked and MD5 sums checked

he downloaded binary packages are in
       C:\Users\Admin\AppData\Local\Temp\RtmpcldatU\download
```

The library includes different functions to show the summary statistics such as the correlation and distribution of all the variables in a matrix.

The ggcorr() function has lots of arguments. We will introduce only the arguments we will use in the tutorial:

The function ggcorr

```
ggcorr(df, method = c("pairwise", "pearson"),
  nbreaks = NULL, digits = 2, low = "#3B9AB2",
  mid = "#EEEEEE", high = "#F21A00",
  geom = "tile", label = FALSE,
  label_alpha = FALSE)
```

Arguments:

- **df**: Dataset used
- **method**: Formula to compute the correlation. By default, pairwise and Pearson are computed
- **nbreaks**: Return a categorical range for the coloration of the coefficients. By default, no break and the color gradient is continuous
- **digits**: Round the correlation coefficient. By default, set to 2
- **low**: Control the lower level of the coloration
- **mid**: Control the middle level of the coloration
- **high**: Control the high level of the coloration
- **geom**: Control the shape of the geometric argument. By default, "tile"
- **label**: Boolean value. Display or not the label. By default, set to \`FALSE\`

Basic heat map

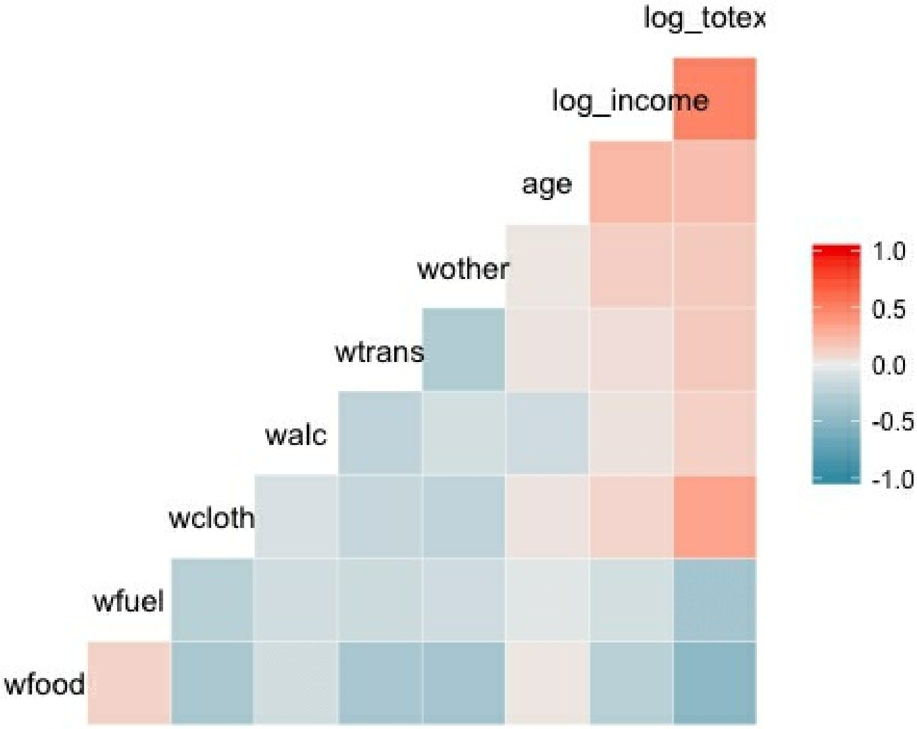
The most basic plot of the package is a heat map. The legend of the graph shows a gradient color from - 1 to 1, with hot color indicating strong positive correlation and cold color, a negative correlation.

```
library(GGally)
ggcorr(data)
```

Code Explanation

- ggcorr(data): Only one argument is needed, which is the data frame name. Factor level variables are not included in the plot.

Output:



Add control to the heat map

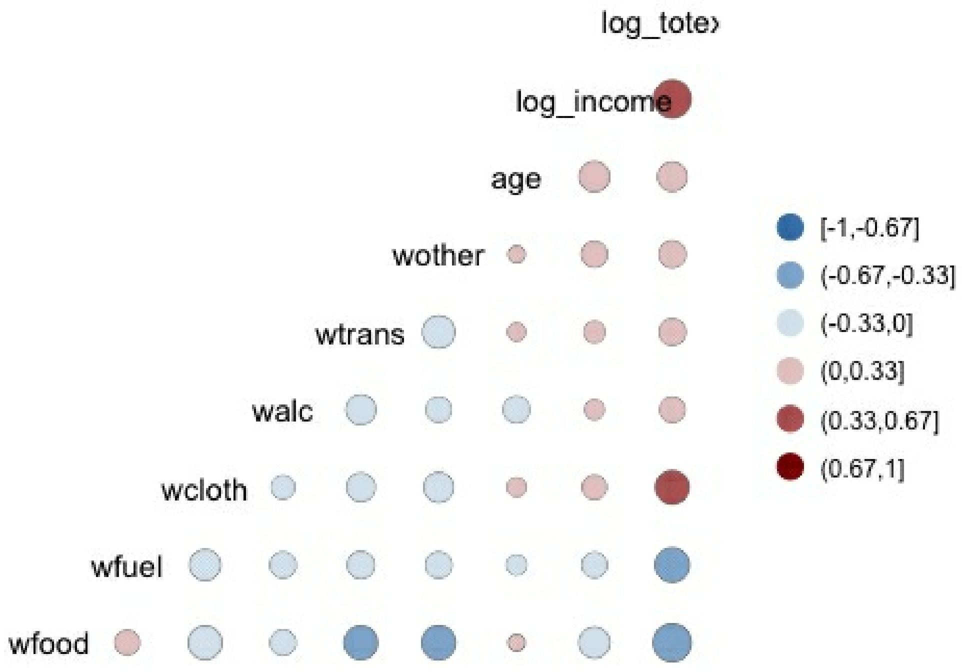
We can add more controls to the graph.

```
ggcorr(data,
    nbreaks = 6,
    low = "steelblue",
    mid = "white",
    high = "darkred",
    geom = "circle")
```

Code Explanation

- nbreaks=6: break the legend with 6 ranks.
- low = "steelblue": Use lighter colors for negative correlation
- mid = "white": Use white colors for middle ranges correlation
- high = "darkred": Use dark colors for positive correlation
- geom = "circle": Use circle as the shape of the windows in the heat map. The size of the circle is proportional to the absolute value of the correlation.

Output:



Add label to the heat map

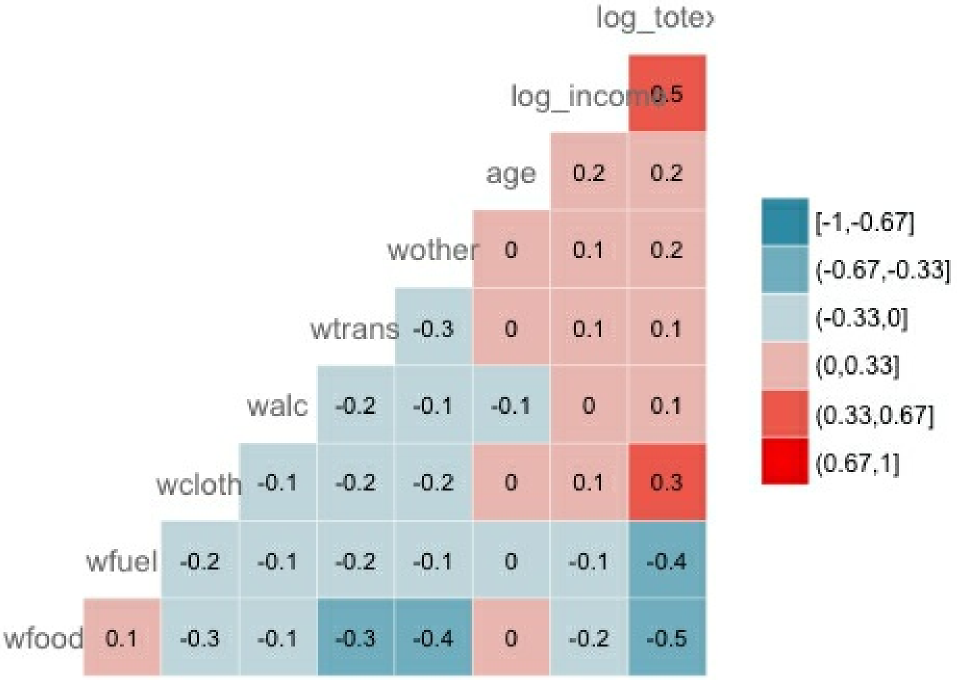
GGally allows us to add a label inside the windows.

```
ggcorr(data,
    nbreaks = 6,
    label = TRUE,
    label_size = 3,
    color = "grey50")
```

Code Explanation

- label = TRUE: Add the values of the coefficients of correlation inside the heat map.
- color = "grey50": Choose the color, i.e. grey
- label_size = 3: Set the size of the label equals to 3

Output:



ggpairs

Finally, we introduce another function from the GGaly library. Ggpair. It produces a graph in a matrix format. We can display three kinds of computation within one graph. The matrix is a dimension, with equals the number of observations. The upper/lower part displays windows and in the diagonal. We can control what information we want to show in each part of the matrix. The formula for ggpair is:

```
ggpair(df, columns = 1: ncol(df), title = NULL,
    upper = list(continuous = "cor"),
    lower = list(continuous = "smooth"),
    mapping = NULL)
```

Arguments:

- **df**: Dataset used
- **columns**: Select the columns to draw the plot
- **title**: Include a title
- **upper**: Control the boxes above the diagonal of the plot. Need to supply the type of computations or graph to return. If continuous = "cor", we ask R to compute the correlation. Note that, the argument needs to be a list. Other arguments can be used, see the [vignette]("http://ggobi.github.io/ggally/#custom_functions") for more information.
- **Lower**: Control the boxes below the diagonal.
- **Mapping**: Indicates the aesthetic of the graph. For instance, we can compute the graph for different groups.

Bivariate analysis with ggpair with grouping

The next graph plots three information:

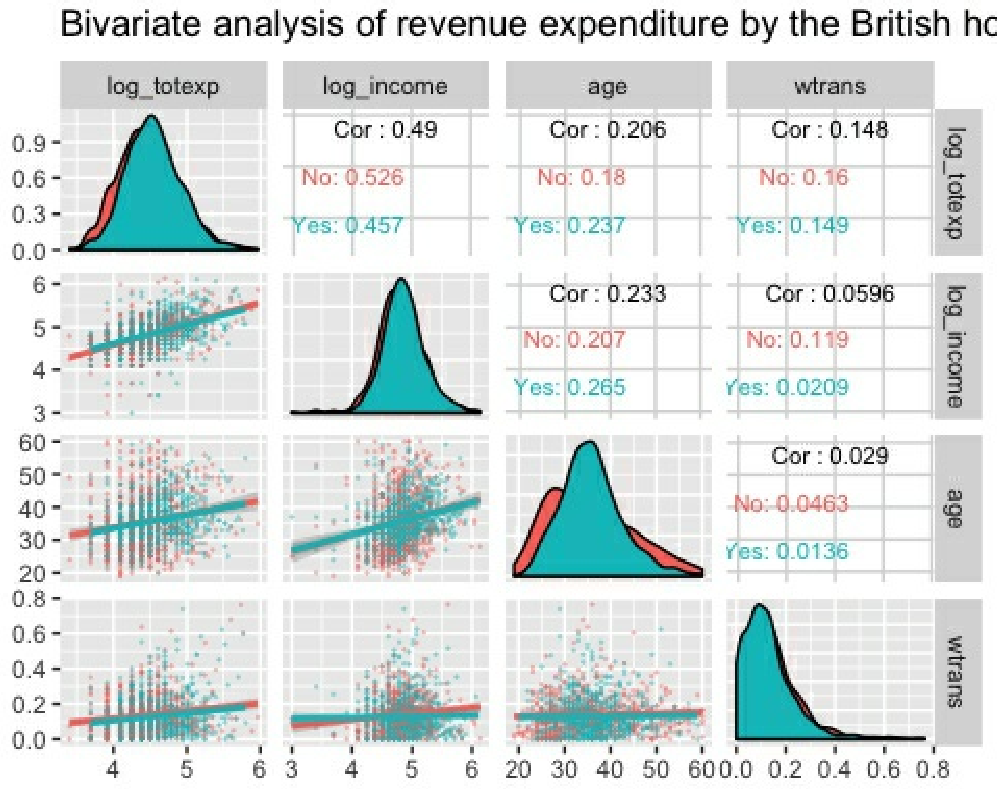
- The correlation matrix between log_totexp, log_income, age and wtrans variable grouped by whether the household has a kid or not.
- Plot the distribution of each variable by group
- Display the scatter plot with the trend by group

```
library(ggplot2)
ggpairs(data, columns = c("log_totexp", "log_income", "age",
"wtrans"), title = "Bivariate analysis of revenue expenditure by
the British household", upper = list(continuous = wrap("cor",
        size = 3)),
    lower = list(continuous = wrap("smooth",
        alpha = 0.3,
        size = 0.1)),
    mapping = aes(color = children_fac))
```

Code Explanation

- columns = c("log_totexp", "log_income", "age", "wtrans"): Choose the variables to show in the graph
- title = "Bivariate analysis of revenue expenditure by the British household": Add a title
- upper = list(): Control the upper part of the graph. I.e. Above the diagonal
- continuous = wrap("cor", size = 3)): Compute the coefficient of correlation. We wrap the argument continuous inside the wrap() function to control for the aesthetic of the graph (i.e. size = 3) - lower = list(): Control the lower part of the graph. I.e. Below the diagonal.
- continuous = wrap("smooth",alpha = 0.3,size=0.1): Add a scatter plot with a linear trend. We wrap the argument continuous inside the wrap() function to control for the aesthetic of the graph (i.e. size=0.1, alpha=0.3)
- mapping = aes(color = children_fac): We want each part of the graph to be stacked by the variable children_fac, which is a categorical variable taking the value of 1 if the household does not have kids and 2 otherwise

Output:



Bivariate analysis with ggpair with partial grouping

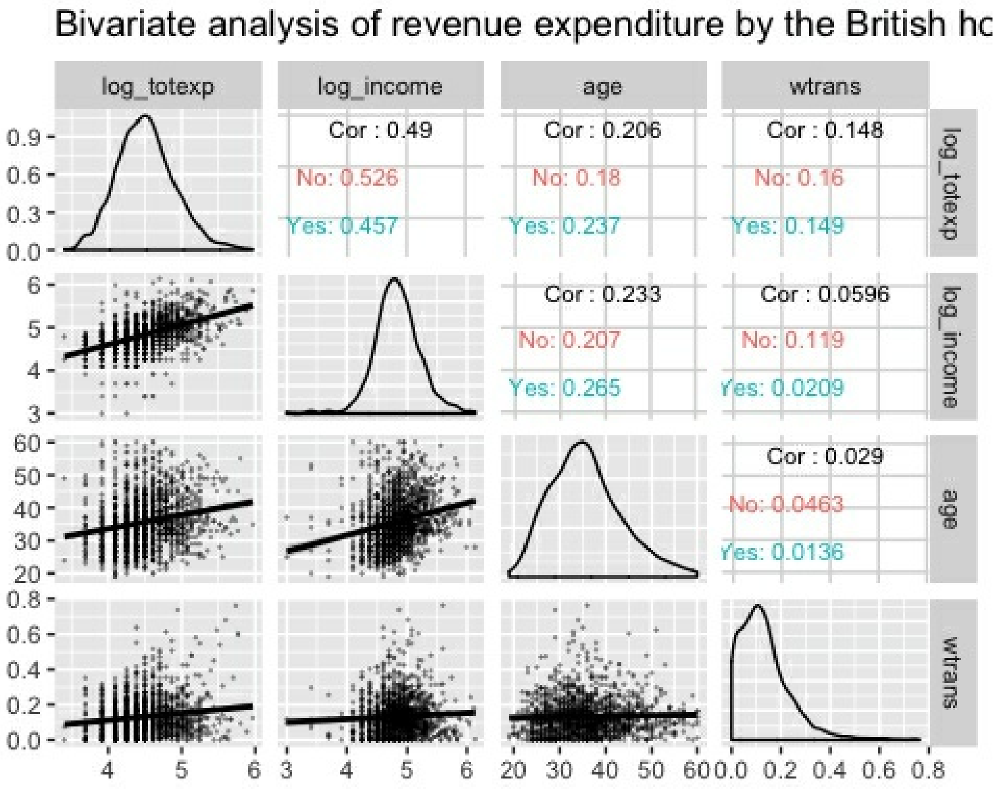
The graph below is a little bit different. We change the position of the mapping inside the upper argument.

```
ggpairs(data, columns = c("log_totexp", "log_income", "age",
"wtrans"),
    title = "Bivariate analysis of revenue expenditure by the
British household",
    upper = list(continuous = wrap("cor",
            size = 3),
        mapping = aes(color = children_fac)),
    lower = list(
        continuous = wrap("smooth",
            alpha = 0.3,
            size = 0.1))
)
```

Code Explanation

- Exact same code as previous example except for:
- mapping = aes(color = children_fac): Move the list in upper = list(). We only want the computation stacked by group in the upper part of the graph.

Output:



Summary

We can summarize the function in the table below:

library	Objective	method	code
Base	bivariate correlation	Pearson	`cor(dfx2, method = "pearson")`
Base	bivariate correlation	Spearman	`cor(dfx2, method = "spearman")`

Base	Multivariate correlation	pearson	`cor(df, method = "pearson")`
Base	Multivariate correlation	Spearman	`cor(df, method = "spearman")`
Hmisc	P value		`rcorr(as.matrix(data[,1:9]))[["P"]]`
Ggally	heat map		`ggcorr(df)`
	Multivariate plots		`cf code below`

Chapter 20: R Aggregate Function: Summarise & Group_by() Example

Summary of a variable is important to have an idea about the data. Although, summarizing a variable by group gives better information on the distribution of the data.

In this tutorial, you will learn how summarize a dataset by group with the dplyr library.

For this tutorial, you will use the batting dataset. The original dataset contains 102816 observations and 22 variables. You will only use 20 percent of this dataset and use the following variables:

- playerID: Player ID code. Factor
- yearID: Year. Factor
- teamID: Team. factor
- lgID: League. Factor: AA AL FL NL PL UA
- AB: At bats. Numeric
- G: Games: number of games by a player. Numeric
- R: Runs. Numeric
- HR: Homeruns. Numeric
- SH: Sacrifice hits. Numeric

Before you perform summary, you will do the following steps to prepare the data:

- Step 1: Import the data
- Step 2: Select the relevant variables
- Step 3: Sort the data

```
library(dplyr)
```

```

# Step 1
data <- read.csv("https://raw.githubusercontent.com/guru99-
edu/R-Programming/master/lahman-batting.csv") % > %

# Step 2
select(c(playerID, yearID, AB, teamID, lgID, G, R, HR, SH))  % >
%

# Step 3
arrange(playerID, teamID, yearID)
```

A good practice when you import a dataset is to use the glimpse() function to have an idea about the structure of the dataset.

```
# Structure of the data
glimpse(data)
```

Output:

```
Observations: 104,324
Variables: 9
$ playerID <fctr> aardsda01, aardsda01, aardsda01, aardsda01,
aardsda01, a...
$ yearID   <int> 2015, 2008, 2007, 2006, 2012, 2013, 2009, 2010,
2004, 196...
$ AB       <int> 1, 1, 0, 2, 0, 0, 0, 0, 0, 603, 600, 606, 547,
516, 495, ...
$ teamID   <fctr> ATL, BOS, CHA, CHN, NYA, NYN, SEA, SEA, SFN,
ATL, ATL, A...
$ lgID     <fctr> NL, AL, AL, NL, AL, NL, AL, AL, NL, NL, NL,
NL, NL, NL, ...
$ G        <int> 33, 47, 25, 45, 1, 43, 73, 53, 11, 158, 155,
160, 147, 15...
$ R        <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 117, 113, 84, 100,
103, 95, 75...
$ HR       <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 44, 39, 29, 44, 38,
47, 34, 40...
$ SH       <int> 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0, 1, 6, ...
```

Summarise()

The syntax of summarise() is basic and consistent with the other verbs included in the dplyr library.

```
summarise(df, variable_name=condition)
arguments:
- `df`: Dataset used to construct the summary statistics
- `variable_name=condition`: Formula to create the new variable
```

Look at the code below:

```
summarise(data, mean_run =mean(R))
```

Code Explanation

- summarise(data, mean_run = mean(R)): Creates a variable named mean_run which is the average of the column run from the dataset data.

Output:

```
##   mean_run
## 1 19.20114
```

You can add as many variables as you want. You return the average games played and the average sacrifice hits.

```
summarise(data, mean_games = mean(G),
    mean_SH = mean(SH, na.rm = TRUE))
```

Code Explanation

- mean_SH = mean(SH, na.rm = TRUE): Summarize a second variable. You set na.rm = TRUE because the column SH contains missing observations.

Output:

```
##   mean_games  mean_SH
## 1   51.98361 2.340085
```

Group_by vs no group_by

The function summerise() without group_by() does not make any sense. It creates summary statistic by group. The library dplyr applies a function automatically to the group you passed inside the verb group_by.

Note that, group_by works perfectly with all the other verbs (i.e. mutate(), filter(), arrange(), ...).

It is convenient to use the pipeline operator when you have more than one step. You can compute the average homerun by baseball league.

```
data % > %
        group_by(lgID) % > %
        summarise(mean_run = mean(HR))
```

Code Explanation

- data: Dataset used to construct the summary statistics
- group_by(lgID): Compute the summary by grouping the variable `lgID
- summarise(mean_run = mean(HR)): Compute the average homerun

Output:

```
##
# A tibble: 7 x 2
##     lgID  mean_run
##   <fctr>     <dbl>
## 1     AA 0.9166667
## 2     AL 3.1270988
## 3     FL 1.3131313
## 4     NL 2.8595953
## 5     PL 2.5789474
## 6     UA 0.6216216
## 7   <NA> 0.2867133
```

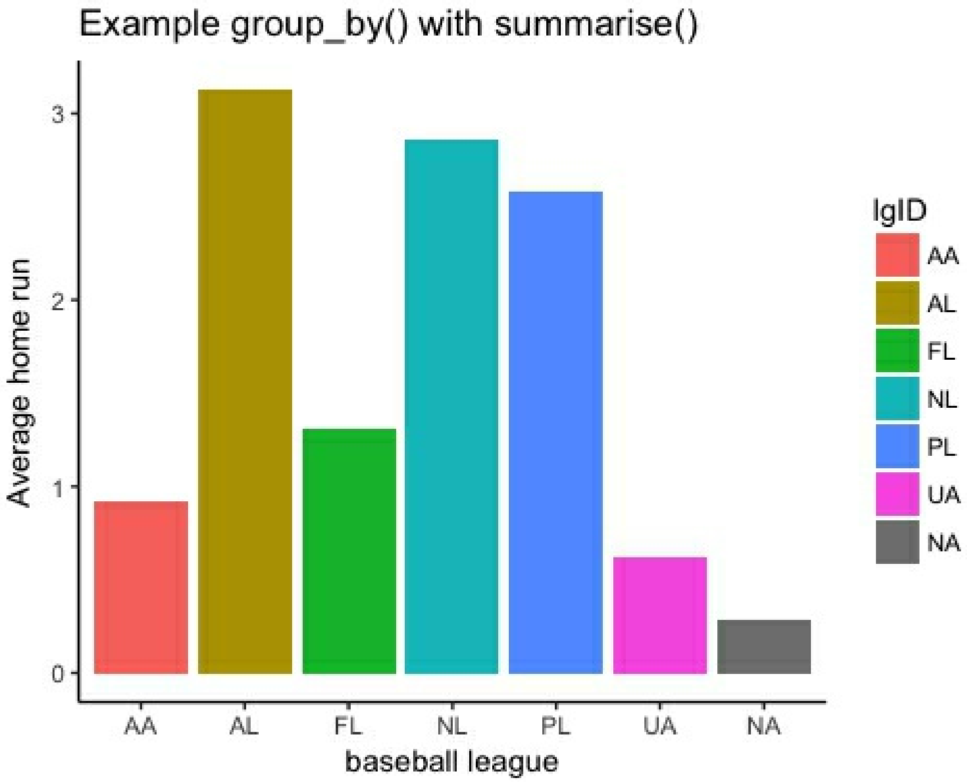
The pipe operator works with ggplot() as well. You can easily show the summary statistic with a graph. All the steps are pushed inside the pipeline until the grap is plot. It seems more visual to see the average homerun by league with a bar char. The code below demonstrates the power of combining group_by(), summarise() and ggplot() together.

You will do the following step:

- Step 1: Select data frame
- Step 2: Group data
- Step 3: Summarize the data
- Step 4: Plot the summary statistics

```
library(ggplot2)
# Step 1
data % > %
#Step 2
group_by(lgID) % > %
#Step 3
summarise(mean_home_run = mean(HR)) % > %
#Step 4
ggplot(aes(x = lgID, y = mean_home_run, fill = lgID)) +
    geom_bar(stat = "identity") +
    theme_classic() +
    labs(
        x = "baseball league",
        y = "Average home run",
        title = paste(
            "Example group_by() with summarise()"
        )
    )
```

Output:



Function in summarise()

The verb summarise() is compatible with almost all the functions in R. Here is a short list of useful functions you can use together with summarise():

Objective	Function	Description
Basic	mean()	Average of vector x
	median()	Median of vector x
	sum()	Sum of vector x
variation	sd()	standard deviation of vector x
	IQR()	Interquartile of vector x
Range	min()	Minimum of vector x
	max()	Maximum of vector x
	quantile()	Quantile of vector x
Position	first()	Use with group_by() First observation of the group
	last()	Use with group_by(). Last observation of the group
	nth()	Use with group_by(). nth observation of the group

Count	n()	Use with group_by(). Count the number of rows
	n_distinct()	Use with group_by(). Count the number of distinct observations

We will see examples for every functions of table 1.

Basic function

In the previous example, you didn't store the summary statistic in a data frame.

You can proceed in two steps to generate a date frame from a summary:

- Step 1: Store the data frame for further use
- Step 2: Use the dataset to create a line plot

Step 1) You compute the average number of games played by year.

```
## Mean
ex1 <- data % > %
        group_by(yearID) % > %
        summarise(mean_game_year = mean(G))
head(ex1)
```

Code Explanation

- The summary statistic of batting dataset is stored in the data frame ex1.

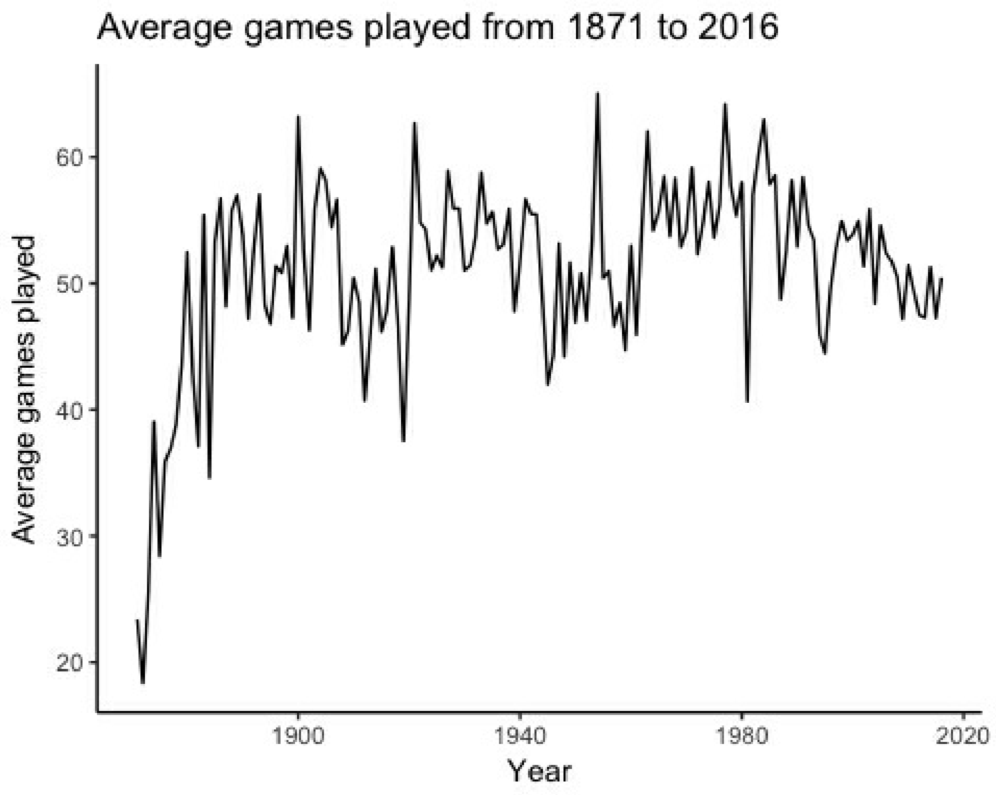
Output:

```
## # A tibble: 6 x 2
##   yearID mean_game_year
##    <int>          <dbl>
## 1   1871       23.42308
## 2   1872       18.37931
## 3   1873       25.61538
## 4   1874       39.05263
## 5   1875       28.39535
## 6   1876       35.90625
```

Step 2) You show the summary statistic with a line plot and see the trend.

```
# Plot the graph
ggplot(ex1, aes(x = yearID, y = mean_game_year)) +
    geom_line() +
    theme_classic() +
    labs(
        x = "Year",
        y = "Average games played",
        title = paste(
            "Average games played from 1871 to 2016"
        )
    )
```

Output:



Subsetting

The function summarise() is compatible with subsetting.

```
## Subsetting + Median
data % > %
group_by(lgID) % > %
summarise(median_at_bat_league = median(AB),
        #Compute the median without the zero
        median_at_bat_league_no_zero = median(AB[AB > 0]))
```

Code Explanation

- median_at_bat_league_no_zero = median(AB[AB > 0]): The variable AB contains lots of 0. You can compare the median of the **at bat** variable with and without 0.

Output:

```
## # A tibble: 7 x 3
##     lgID median_at_bat_league median_at_bat_league_no_zero
##   <fctr>                <dbl>                        <dbl>
## 1     AA                  130                          131
## 2     AL                   38                           85
## 3     FL                   88                           97
## 4     NL                   56                           67
## 5     PL                  238                          238
## 6     UA                   35                           35
##
7   <NA>                  101                          101
```

Sum

Another useful function to aggregate the variable is sum().

You can check which leagues have the more homeruns.

```
## Sum
data % > %
        group_by(lgID) % > %
        summarise(sum_homerun_league = sum(HR))
```

Output:

```
## # A tibble: 7 x 2
##     lgID sum_homerun_league
##   <fctr>              <int>
## 1     AA                341
## 2     AL              29426
## 3     FL                130
## 4     NL              29817
## 5     PL                 98
## 6     UA                 46
## 7   <NA>                 41
```

Standard deviation

Spread in the data is computed with the standard deviation or sd() in R.

```
# Spread
data % > %
        group_by(teamID) % > %
        summarise(sd_at_bat_league = sd(HR))
```

Output:

```
## # A tibble: 148 x 2
##    teamID sd_at_bat_league
##    <fctr>            <dbl>
##  1    ALT               NA
##  2    ANA        8.7816395
##  3    ARI        6.0765503
##  4    ATL        8.5363863
##  5    BAL        7.7350173
##  6    BFN        1.3645163
##  7    BFP        0.4472136
##  8    BL1        0.6992059
##  9    BL2        1.7106757
## 10    BL3        1.0000000
## # ... with 138 more rows
```

There are lots of inequality in the quantity of homerun done by each team.

Minimum and maximum

You can access the minimum and the maximum of a vector with the function min() and max().

The code below returns the lowest and highest number of games in a season played by a player.

```
# Min and max
data % > %
        group_by(playerID) % > %
        summarise(min_G = min(G),
    max_G = max(G))
```

Output:

```
## # A tibble: 10,395 x 3
##     playerID min_G max_G
##       <fctr>       <int>
##  1 aardsda01    53    73
##  2 aaronha01   120   156
##  3  aasedo01    24    66
##  4  abadfe01    18    18
##  5 abadijo01    11    11
##  6 abbated01     3   153
##  7 abbeybe01    11    11
##  8 abbeych01    80   132
##  9 abbotgl01     5    23
## 10 abbotji01    13    29
## # ... with 10,385 more rows
```

Count

Count observations by group is always a good idea. With R, you can aggregate the the number of occurence with n().

For instance, the code below computes the number of years played by each player.

```
# count observations
```

```
data % > %
        group_by(playerID) % > %
        summarise(number_year = n()) % > %
        arrange(desc(number_year))
```

Output:

```
## # A tibble: 10,395 x 2
##     playerID number_year
##       <fctr>       <int>
##  1 pennohe01          11
##  2 joosted01          10
##  3 mcguide01          10
##  4  rosepe01          10
##  5 davisha01           9
##  6 johnssi01           9
##  7  kaatji01           9
##  8 keelewi01           9
##  9 marshmi01           9
## 10 quirkja01           9
## # ... with 10,385 more rows
```

First and last

You can select the first, last or nth position of a group.

For instance, you can find the first and last year of each player.

```
# first and last
data % > %
        group_by(playerID) % > %
        summarise(first_appearance = first(yearID),
                last_appearance = last(yearID))
```

Output:

```
## # A tibble: 10,395 x 3
##     playerID first_appearance last_appearance
##       <fctr>            <int>           <int>
##  1 aardsda01             2009            2010
##  2 aaronha01             1973            1975
##  3  aasedo01             1986            1990
##  4  abadfe01            2016            2016
##  5 abadijo01            1875            1875
##  6 abbated01            1905            1897
##  7 abbeybe01            1894            1894
##  8 abbeych01            1895            1897
##  9 abbotgl01            1973            1979
## 10 abbotji01            1992            1996
## # ... with 10,385 more rows
```

nth observation

The fonction nth() is complementary to first() and last(). You can access the nth observation within a group with the index to return.

For instance, you can filter only the second year that a team played.

```
# nth
data % > %
        group_by(teamID) % > %
        summarise(second_game = nth(yearID, 2)) % > %
        arrange(second_game)
```

Output:

```
## # A tibble: 148 x 2
##    teamID second_game
##    <fctr>       <int>
##  1    BS1        1871
##  2    CH1        1871
##  3    FW1        1871
##  4    NY2        1871
##  5    RC1        1871
##  6    BR1        1872
##  7    BR2        1872
##  8    CL1        1872
##  9    MID        1872
## 10    TRO        1872
## # ... with 138 more rows
```

Distinct number of observation

The function n() returns the number of observations in a current group. A closed function to n() is n_distinct(), which count the number of unique values.

In the next example, you add up the total of players a team recruited during the all periods.

```
# distinct values
data % > %
        group_by(teamID) % > %
        summarise(number_player = n_distinct(playerID)) % > %
        arrange(desc(number_player))
```

Code Explanation

- group_by(teamID): Group by year **and** team
- summarise(number_player = **n_distinct**(playerID)): Count the distinct number of players by team
- arrange(desc(number_player)): Sort the data by the number of player

Output:

```
## # A tibble: 148 x 2
##    teamID number_player
##    <fctr>         <int>
##  1    CHN           751
##  2    SLN           729
##  3    PHI           699
##  4    PIT           683
##  5    CIN           679
##  6    BOS           647
##  7    CLE           646
##  8    CHA           636
##  9    DET           623
## 10    NYA           612
## # ... with 138 more rows
```

Multiple groups

A summary statistic can be realized among multiple groups.

```
# Multiple groups
data % > %
        group_by(yearID, teamID) % > %
        summarise(mean_games = mean(G)) % > %
        arrange(desc(teamID, yearID))
```

Code Explanation

- group_by(yearID, teamID): Group by year **and** team
- summarise(mean_games = mean(G)): Summarize the number of game player
- arrange(desc(teamID, yearID)): Sort the data by team and year

Output:

```
## # A tibble: 2,829 x 3
## # Groups:   yearID [146]
##    yearID teamID mean_games
##     <int> <fctr>      <dbl>
##  1   1884    WSU   20.41667
##  2   1891    WS9   46.33333
##  3   1886    WS8   22.00000
##  4   1887    WS8   51.00000
##  5   1888    WS8   27.00000
##  6   1889    WS8   52.42857
##  7   1884    WS7    8.00000
##  8   1875    WS6   14.80000
##  9   1873    WS5   16.62500
## 10   1872    WS4    4.20000
## # ... with 2,819 more rows
```

Filter

Before you intend to do an operation, you can filter the dataset. The dataset starts in 1871, and the analysis does not need the years prior to 1980.

```
# Filter
data % > %
```

```
        filter(yearID > 1980) % > %
        group_by(yearID) % > %
        summarise(mean_game_year = mean(G))
```

Code Explanation

- filter(yearID > 1980): Filter the data to show only the relevant years (i.e. after 1980)
- group_by(yearID): Group by year
- summarise(mean_game_year = mean(G)): Summarize the data

Output:

```
## # A tibble: 36 x 2
##    yearID mean_game_year
##     <int>          <dbl>
##  1   1981       40.64583
##  2   1982       56.97790
##  3   1983       60.25128
##  4   1984       62.97436
##  5   1985       57.82828
##  6   1986       58.55340
##  7   1987       48.74752
##  8   1988       52.57282
##  9   1989       58.16425
## 10   1990       52.91556
## # ... with 26 more rows
```

Ungroup

Last but not least, you need to remove the grouping before you want to change the level of the computation.

```
# Ungroup the data
data % > %
        filter(HR > 0) % > %
        group_by(playerID) % > %
        summarise(average_HR_game = sum(HR) / sum(G)) % > %
        ungroup() % > %
        summarise(total_average_homerun = mean(average_HR_game))
```

Code Explanation

- filter(HR >0) : Exclude zero homerun
- group_by(playerID): group by player
- summarise(average_HR_game = sum(HR)/sum(G)): Compute average homerun by player
- ungroup(): remove the grouping
- summarise(total_average_homerun = mean(average_HR_game)): Summarize the data

Output:

```
## # A tibble: 1 x 1
##   total_average_homerun
##                   <dbl>
## 1            0.06882226
```

Summary

When you want to return a summary by group, you can use:

```
# group by X1, X2, X3
group(df, X1, X2, X3)
```

you need to ungroup the data with:

```
ungroup(df)
```

The table below summarizes the function you learnt with summarise()

method	**function**	**code**
mean	mean	`summarise(df,mean_x1 = mean(x1))`
median	median	`summarise(df,median_x1 = median(x1))`

sum	sum	`summarise(df,sum_x1 = sum(x1))`
standard deviation	sd	`summarise(df,sd_x1 = sd(x1))`
interquartile	IQR	`summarise(df,interquartile_x1 = IQR(x1))`
minimum	min	`summarise(df,minimum_x1 = min(x1))`
maximum	max	`summarise(df,maximum_x1 = max(x1))`
quantile	quantile	`summarise(df,quantile_x1 = quantile(x1))`
first observation	first	`summarise(df,first_x1 = first(x1))`
last observation	last	`summarise(df,last_x1 = last(x1))`
nth observation	nth	`summarise(df,nth_x1 = nth(x1, 2))`
number of occurrence	n	`summarise(df,n_x1 = n(x1))`
number of distinct occurrence	n_distinct	`summarise(df,n_distinct _x1 = n_distinct(x1))`

Chapter 21: R Select(), Filter(), Arrange(), Pipeline with Example

The library called dplyr contains valuable verbs to navigate inside the dataset. Through this tutorial, you will use the Travel times dataset. The dataset collects information on the trip leads by a driver between his home and his workplace. There are fourteen variables in the dataset, including:

- DayOfWeek: Identify the day of the week the driver uses his car
- Distance: The total distance of the journey
- MaxSpeed: The maximum speed of the journey
- TotalTime: The length in minutes of the journey

The dataset has around 200 observations in the dataset, and the rides occurred between Monday to Friday.

First of all, you need to:

- load the dataset
- check the structure of the data.

One handy feature with dplyr is the glimpse() function. This is an improvement over str(). We can use glimpse() to see the structure of the dataset and decide what manipulation is required.

```
library(dplyr)
PATH <- "https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/travel_times.csv"
df <- read.csv(PATH)
glimpse(df)
```

Output:

```
## Observations: 205
## Variables: 14
## $ X              <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12,
13, 14, ...
## $ Date           <fctr> 1/6/2012, 1/6/2012, 1/4/2012,
1/4/2012, 1/3/20...
## $ StartTime      <fctr> 16:37, 08:20, 16:17, 07:53, 18:57,
07:57, 17:3...
## $ DayOfWeek      <fctr> Friday, Friday, Wednesday, Wednesday,
Tuesday,...
## $ GoingTo        <fctr> Home, GSK, Home, GSK, Home, GSK,
Home, GSK, GS...
## $ Distance       <dbl> 51.29, 51.63, 51.27, 49.17, 51.15,
51.80, 51.37...
## $ MaxSpeed       <dbl> 127.4, 130.3, 127.4, 132.3, 136.2,
135.8, 123.2...
## $ AvgSpeed       <dbl> 78.3, 81.8, 82.0, 74.2, 83.4, 84.5,
82.9, 77.5,...
## $ AvgMovingSpeed <dbl> 84.8, 88.9, 85.8, 82.9, 88.1, 88.8,
87.3, 85.9,...
## $ FuelEconomy    <fctr> , , , , , , -, -, 8.89, 8.89, 8.89,
8.89, 8.89...
## $ TotalTime      <dbl> 39.3, 37.9, 37.5, 39.8, 36.8, 36.8,
37.2, 37.9,...
## $ MovingTime     <dbl> 36.3, 34.9, 35.9, 35.6, 34.8, 35.0,
35.3, 34.3,...
## $ Take407All     <fctr> No, No, No, No, No, No, No, No, No,
No, No, No...
## $ Comments       <fctr> , , , , , , , , , , , , , , , Put
snow tires o...
```

This is obvious that the variable Comments needs further diagnostic. The first observations of the Comments variable are only missing values.

```
sum(df$Comments =="")
```

Code Explanation

- sum(df$Comments ==""): Sum the observations equalts to "" in the column comments from df

Output:

```
## [1] 181
```

select()

We will begin with the select() verb. We don't necessarily need all the variables, and a good practice is to select only the variables you find relevant.

We have 181 missing observations, almost 90 percent of the dataset. If you decide to exclude them, you won't be able to carry on the analysis.

The other possibility is to drop the variable Comment with the select() verb.

We can select variables in different ways with select(). Note that, the first argument is the dataset.

```
- `select(df, A, B ,C)`: Select the variables A, B and C from df
dataset.
- `select(df, A:C)`: Select all variables from A to C from df
dataset.
- `select(df, -C)`: Exclude C from the dataset from df dataset.
```

You can use the third way to exclude the Comments variable.

```
step_1_df <- select(df, -Comments)
dim(df)
```

Output:

```
## [1] 205  14
```

```
dim(step_1_df)
```

Output:

```
## [1] 205  13
```

The original dataset has 14 features while the step_1_df has 13.

Filter()

The filter() verb helps to keep the observations following a criteria. The filter() works exactly like select(), you pass the data frame first and then a condition separated by a comma:

```
filter(df, condition)
arguments:
- df: dataset used to filter the data
- condition:  Condition used to filter the data
```

One criteria

First of all, you can count the number of observations within each level of a factor variable.

```
table(step_1_df$GoingTo)
```

Code Explanation

- table(): Count the number of observations by level. Note, only factor level variable are accepted
- table(step_1_df$GoingTo): Count the number of of trips toward the final destination.

Output:

```
##
##  GSK Home
##  105  100
```

The function table() indicates 105 rides are going to GSK and 100 to Home.

We can filter the data to return one dataset with 105 observations and another one with 100 observations.

```
# Select observations
```

```
if GoingTo == Home
select_home <- filter(df, GoingTo == "Home")
dim(select_home)
```

Output:

```
## [1] 100  14
```

```
# Select observations
if GoingTo == Work
select_work <- filter(df, GoingTo == "GSK")
dim(select_work)
```

Output:

```
## [1] 105  14
```

Multiple criterions

We can filter a dataset with more than one criteria. For instance, you can extract the observations where the destination is Home and occured on a Wednesday.

```
select_home_wed <- filter(df, GoingTo == "Home" & DayOfWeek ==
"Wednesday")
dim(select_home_wed)
```

Output:

```
## [1] 23 14
```

23 observations matched this criterion.

Pipeline

The creation of a dataset requires a lot of operations, such as:

- importing

- merging
- selecting
- filtering
- and so on

The dplyr library comes with a practical operator, %>%, called the **pipeline**. The pipeline feature makes the manipulation clean, fast and less prompt to error.

This operator is a code which performs steps without saving intermediate steps to the hard drive. If you are back to our example from above, you can select the variables of interest and filter them. We have three steps:

- Step 1: Import data: Import the gps data
- Step 2: Select data: Select GoingTo and DayOfWeek
- Step 3: Filter data: Return only Home and Wednesday

We can use the hard way to do it:

```
# Step 1
step_1 <- read.csv(PATH)

# Step 2
step_2 <- select(step_1, GoingTo, DayOfWeek)

# Step 3
step_3 <- filter(step_2, GoingTo == "Home", DayOfWeek ==
"Wednesday")

head(step_3)
```

Output:

```
##   GoingTo DayOfWeek
## 1    Home Wednesday
## 2    Home Wednesday
## 3    Home Wednesday
## 4    Home Wednesday
## 5    Home Wednesday
## 6    Home Wednesday
```

That is not a convenient way to perform many operations, especially in a situation with lots of steps. The environment ends up with a lot of objects stored.

Let's use the pipeline operator %>% instead. We only need to define the data frame used at the beginning and all the process will flow from it.

Basic syntax of pipeline

```
New_df <- df %>%
step 1 %>%
step 2 %>%
...
arguments
- New_df: Name of the new data frame
- df: Data frame used to compute the step
- step: Instruction for each step
- Note: The last instruction does not need the pipe operator
`%`, you don't have instructions to pipe anymore
Note: Create a new variable is optional. If not included, the
output will be displayed in the console.
```

You can create your first pipe following the steps enumerated above.

```
# Create the data frame filter_home_wed.It will be the object
return at the end of the pipeline
filter_home_wed <-

#Step 1
read.csv(PATH) % > %

#Step 2
select(GoingTo, DayOfWeek) % > %

#Step 3
filter(GoingTo == "Home",DayOfWeek == "Wednesday")
identical(step_3, filter_home_wed)
```

Output:

```
## [1] TRUE
```

We are ready to create a stunning dataset with the pipeline operator.

arrange()

In the previous tutorial, you learn how to sort the values with the function sort(). The library dplyr has its sorting function. It works like a charm with the pipeline. The arrange() verb can reorder one or many rows, either ascending (default) or descending.

```
- `arrange(A)`: Ascending sort of variable A
- `arrange(A, B)`: Ascending sort of variable A and B
- `arrange(desc(A), B)`: Descending sort of variable A and
ascending sort of B
```

We can sort the distance by destination.

```
# Sort by destination and distance
step_2_df <-step_1_df %>%
        arrange(GoingTo, Distance)
head<step_2_df)
```

Output:

```
##     X       Date StartTime DayOfWeek GoingTo Distance
MaxSpeed AvgSpeed
## 1
193  7/25/2011     08:06    Monday     GSK    48.32    121.2
## 2
196  7/21/2011     07:59  Thursday     GSK    48.35    129.3
## 3 198  7/20/2011     08:24
Wednesday     GSK    48.50    125.8     75.7
## 4 189  7/27/2011     08:15
Wednesday     GSK    48.82    124.5     70.4
## 5  95
10/11/2011     08:25   Tuesday     GSK    48.94    130.8     85.7
## 6 171  8/10/2011     08:13
Wednesday     GSK    48.98    124.8     72.8
##   AvgMovingSpeed FuelEconomy TotalTime MovingTime Take407All
## 1           78.4        8.45      45.7       37.0          No
## 2           89.0        8.28      35.6       32.6         Yes
## 3           87.3        7.89      38.5       33.3         Yes
## 4            77.8         8.45      41.6        37.6           No
## 5            93.2         7.81      34.3        31.5          Yes
## 6            78.8         8.54      40.4        37.3           No
```

Summary

In the table below, you summarize all the operations you learnt during the tutorial.

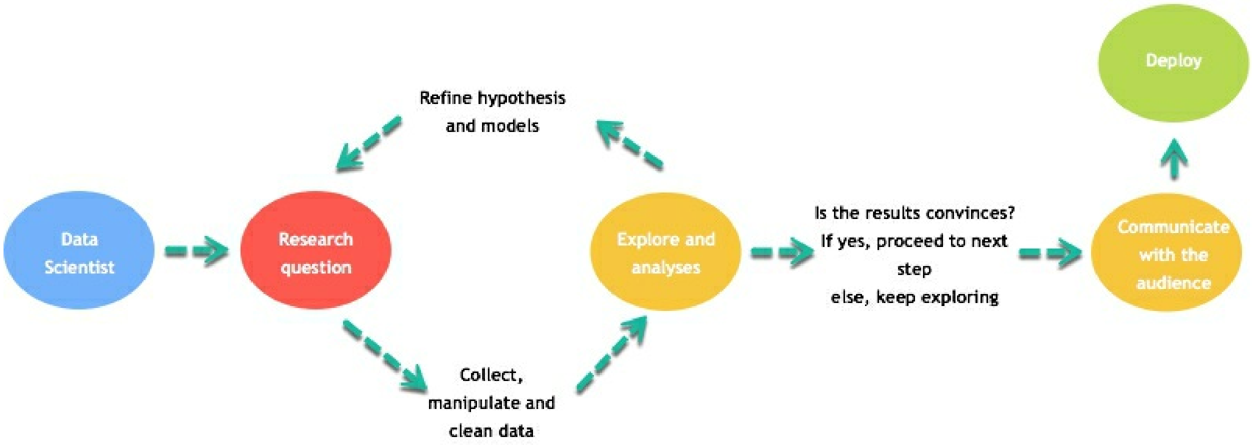
Verb	Objective	Code	Explanation
glimpse	check the structure of a df	`glimpse(df)`	Identical to str()
select()	Select/exclude the variables	`select(df, A, B ,C)`	Select the variables A, B and C
		`select(df, A:C)`	Select all variables from A to C
		`select(df, -C)`	Exclude C
filter()	Filter the df based a one or many conditions	`filter(df, condition1)`	One condition
		`filter(df, condition1`	ondition2)
arrange()	Sort the dataset with one or many variables	`arrange(A)`	Ascending sort of variable A
		`arrange(A, B)`	Ascending sort of variable A and B
		`arrange(desc(A), B)`	Descending sort of variable A and ascending sort of B
%>%	Create a pipeline between each step	`step 1 %>% step 2 %>% step 3`	

Chapter 22: Scatter Plot in R using ggplot2 (with Example)

Graphs are the third part of the process of data analysis. The first part is about **data extraction**, the second part deals with **cleaning and manipulating the data**. At last, the data scientist may need to **communicate his results graphically**.

The job of the data scientist can be reviewed in the following picture

- The first task of a data scientist is to define a research question. This research question depends on the objectives and goals of the project.
- After that, one of the most prominent tasks is the feature engineering. The data scientist needs to collect, manipulate and clean the data
- When this step is completed, he can start to explore the dataset. Sometimes, it is necessary to refine and change the original hypothesis due to a new discovery.


Data Scientist
Research question
Refine hypothesis and models
Collect, manipulate and clean data
Explore and analyses
Is the results convinces? If yes, proceed to next step else, keep exploring
Communicate with the audience
Deploy

- When the **explanatory** analysis is achieved, the data scientist has to consider the capacity of the reader to **understand the underlying concepts and models**.

- His results should be presented in a format that all stakeholders can understand. One of the best methods to **communicate** the results is through a **graph**.
- Graphs are an incredible tool to simplify complex analysis.

ggplot2 package

This part of the tutorial focuses on how to make graphs/charts with R.

In this tutorial, you are going to use ggplot2 package. This package is built upon the consistent underlying of the book Grammar of graphics written by Wilkinson, 2005. ggplot2 is very flexible, incorporates many themes and plot specification at a high level of abstraction. With ggplot2, you can't plot 3-dimensional graphics and create interactive graphics.

In ggplot2, a graph is composed of the following arguments:

- data
- aesthetic mapping
- geometric object
- statistical transformations
- scales
- coordinate system
- position adjustments
- faceting

You will learn how to control those arguments in the tutorial.

The basic syntax of ggplot2 is:

```
ggplot(data, mapping=aes()) +
geometric object

arguments:
data: Dataset used to plot the graph
mapping: Control the x and y-axis
geometric object: The type of plot you want to show. The most
```

```
common object are:

- Point: `geom_point()`
- Bar: `geom_bar()`
- Line: `geom_line()`
- Histogram: `geom_histogram()`
```

Scatterplot

Let's see how ggplot works with the mtcars dataset. You start by plotting a scatterplot of the mpg variable and drat variable.

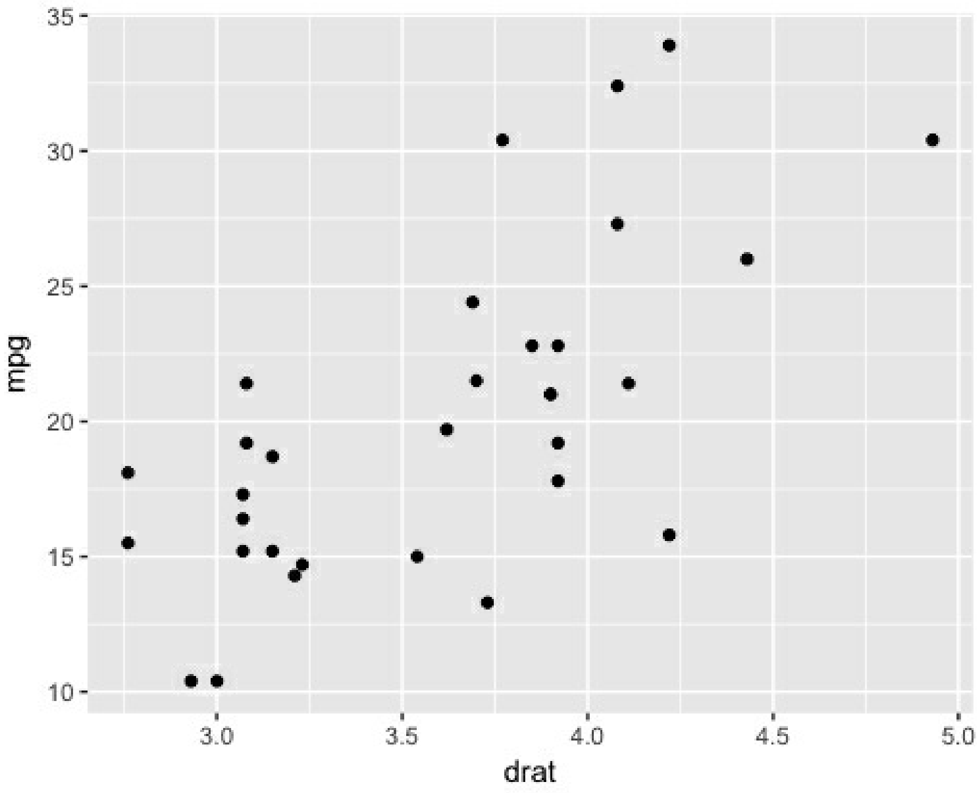
Basic scatter plot

```
library(ggplot2)
ggplot(mtcars, aes(x = drat, y = mpg)) +
    geom_point()
```

Code Explanation

- You first pass the dataset mtcars to ggplot.
- Inside the aes() argument, you add the x-axis and y-axis.
- The + sign means you want R to keep reading the code. It makes the code more readable by breaking it.
- Use geom_point() for the geometric object.

Output:



Scatter plot with groups

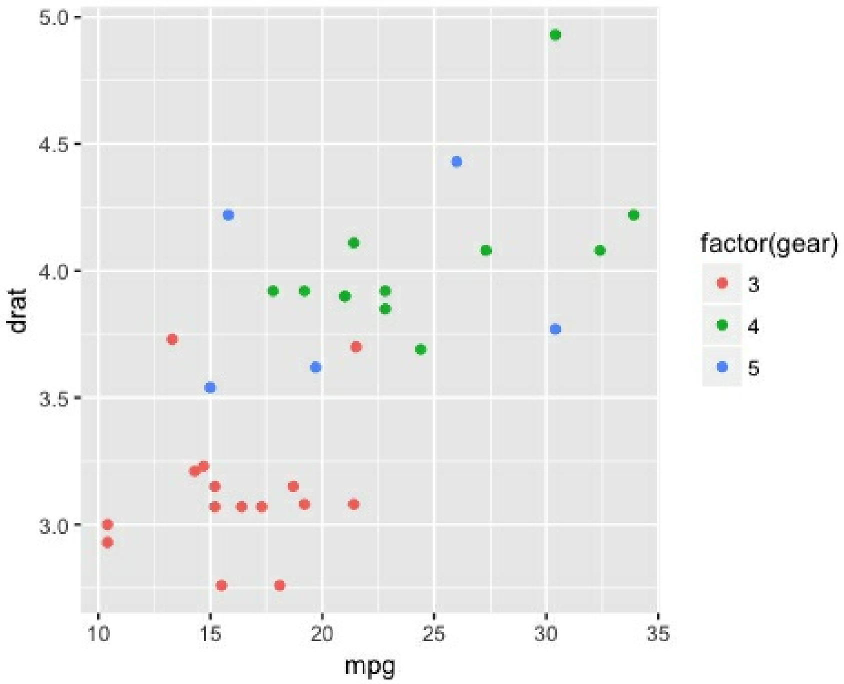
Sometimes, it can be interesting to distinguish the values by a group of data (i.e. factor level data).

```
ggplot(mtcars, aes(x = mpg, y = drat)) +
    geom_point(aes(color = factor(gear)))
```

Code Explanation

- The aes() inside the geom_point() controls the color of the group. The group should be a factor variable. Thus, you convert the variable gear in a factor.
- Altogether, you have the code aes(color = factor(gear)) that change the color of the dots.

Output:



Change axis

Rescale the data is a big part of the data scientist job. In rare occasion data comes in a nice bell shape. One solution to make your data less sensitive to outliers is to rescale them.

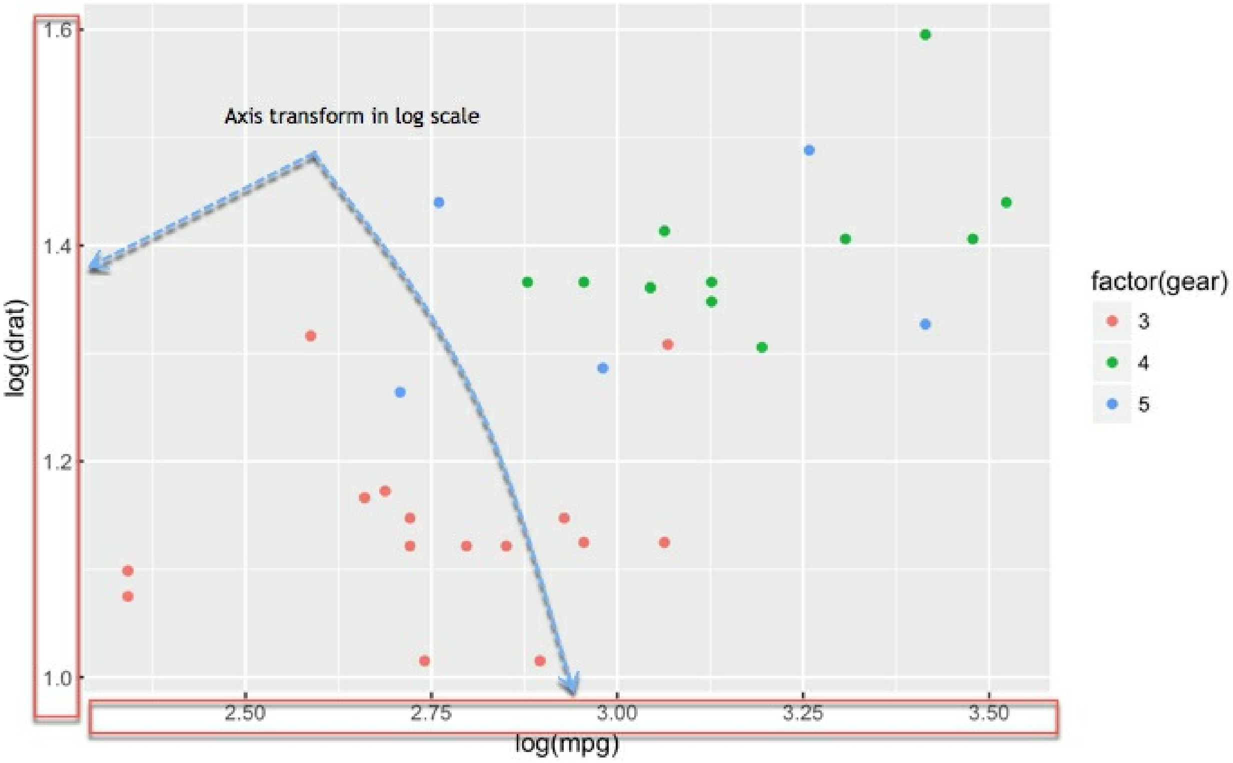
```
ggplot(mtcars, aes(x = log(mpg), y = log(drat))) +
    geom_point(aes(color = factor(gear)))
```

Code Explanation

- You transform the x and y variables in log() directly inside the aes() mapping.

Note that any other transformation can be applied such as standardization or normalization.

Output:



Scatter plot with fitted values

You can add another level of information to the graph. You can plot the fitted value of a linear regression.

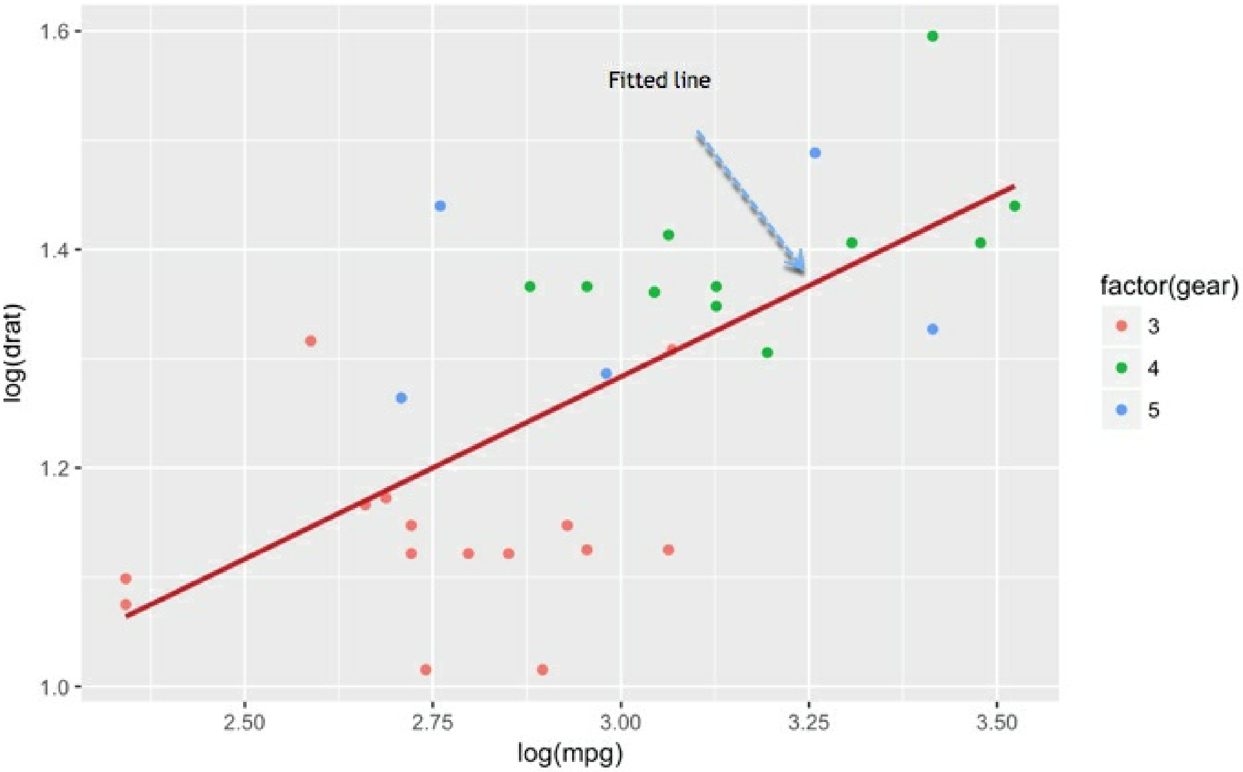
```
my_graph <- ggplot(mtcars, aes(x = log(mpg), y = log(drat))) +
    geom_point(aes(color = factor(gear))) +
    stat_smooth(method = "lm",
        col = "#C42126",
        se = FALSE,
        size = 1)
my_graph
```

Code Explanation

- graph: You store your graph into the variable graph. It is helpful for further use or avoid too complex line of codes
- The argument stat_smooth() controls for the smoothing method
- method = "lm": Linear regression

- col = "#C42126": Code for the red color of the line
- se = FALSE: Don't display the standard error
- size = 1: the size of the line is 1

Output:



Note that other smoothing methods are available

- glm
- gam
- loess: default value
- rim

Add information to the graph

So far, we haven't added information in the graphs. Graphs need to be informative. The reader should see the story behind the data analysis just by looking at the graph without referring additional documentation. Hence, graphs need good labels. You can add labels with labs()function.

The basic syntax for lab() is :

```
lab(title = "Hello Guru99")
argument:
- title: Control the title. It is possible to change or add
title with:
- subtitle: Add subtitle below title
- caption: Add caption below the graph
- x: rename x-axis
- y: rename y-axis
Example:lab(title = "Hello Guru99", subtitle = "My first plot")
```

Add a title

One mandatory information to add is obviously a title.

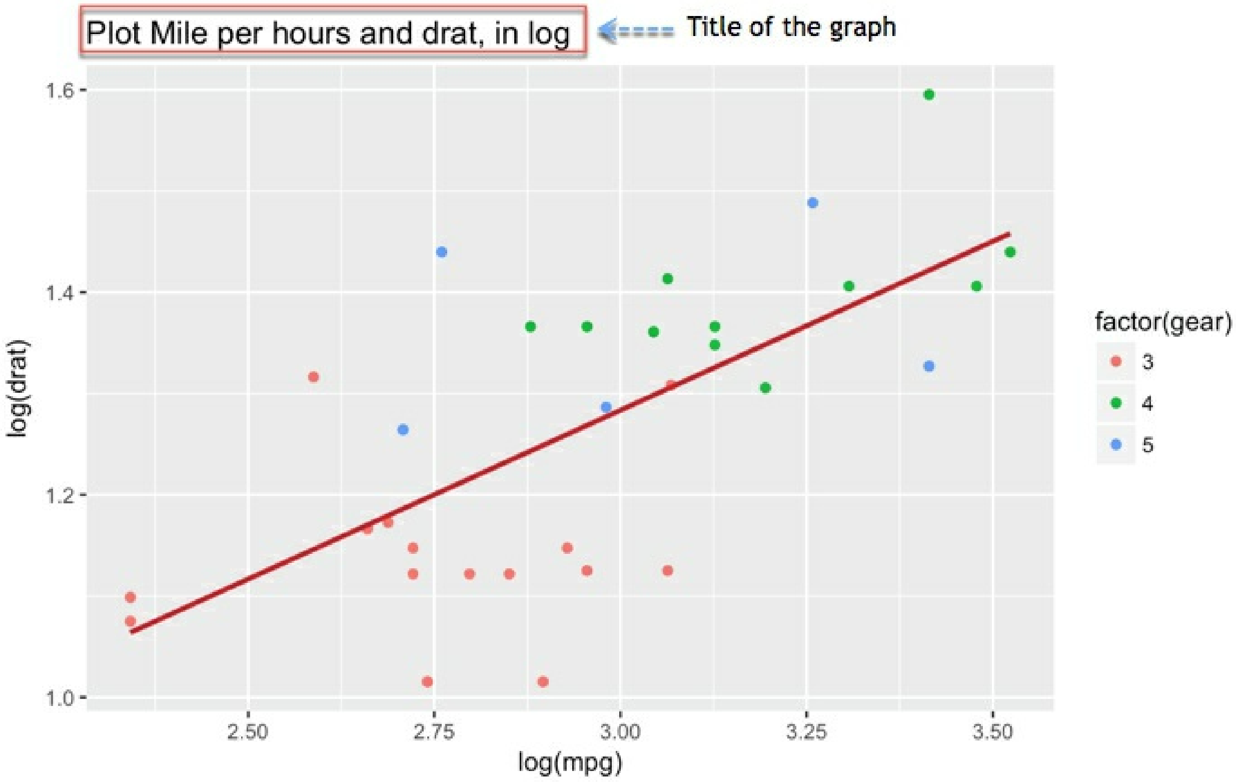
```
my_graph +
    labs(
        title = "Plot Mile per hours and drat, in log"
         )
```

Code Explanation

- my_graph: You use the graph you stored. It avoids rewriting all the codes each time you add new information to the graph.
- You wrap the title inside the lab().

- Code for the red color of the line
- se = FALSE: Don't display the standard error
- size = 1: the size of the line is 1

Output:



Add a title with a dynamic name

A dynamic title is helpful to add more precise information in the title.

You can use the paste() function to print static text and dynamic text. The basic syntax of paste() is:

```
paste("This is a text", A)
arguments
- " ": Text inside the quotation marks are the static text
- A: Display the variable stored in A
- Note you can add as much static text and variable as you want.
You need to separate them with a comma
```

Example:

```
A <-2010
paste("The first year is", A)
```

Output:

```
## [1] "The first year is 2010"
```

```
B <-2018

paste("The first year is", A, "and the last year is", B)
```

Output:

```
## [1] "The first year is 2010 and the last year is
2018"
```

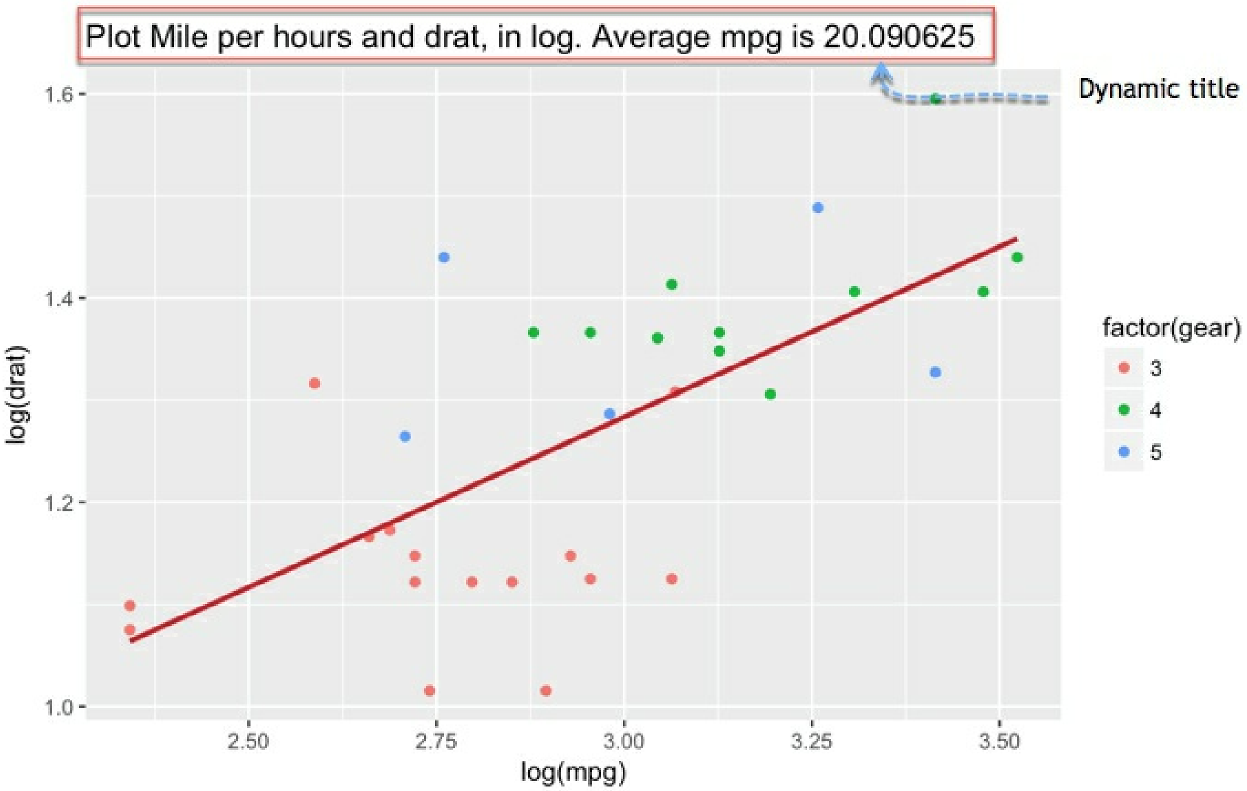
You can add a dynamic name to our graph, namely the average of mpg.

```
mean_mpg <- mean(mtcars$mpg)
my_graph + labs(
    title = paste("Plot Mile per hours and drat, in log. Average
mpg is", mean_mpg)
)
```

Code Explanation

- You create the average of mpg with mean(mtcars$mpg) stored in mean_mpg variable
- You use the paste() with mean_mpg to create a dynamic title returning the mean value of mpg

Output:



Add a subtitle

Two additional detail can make your graph more explicit. You are talking about the subtitle and the caption. The subtitle goes right below the title. The caption can inform about who did the computation and the source of the data.

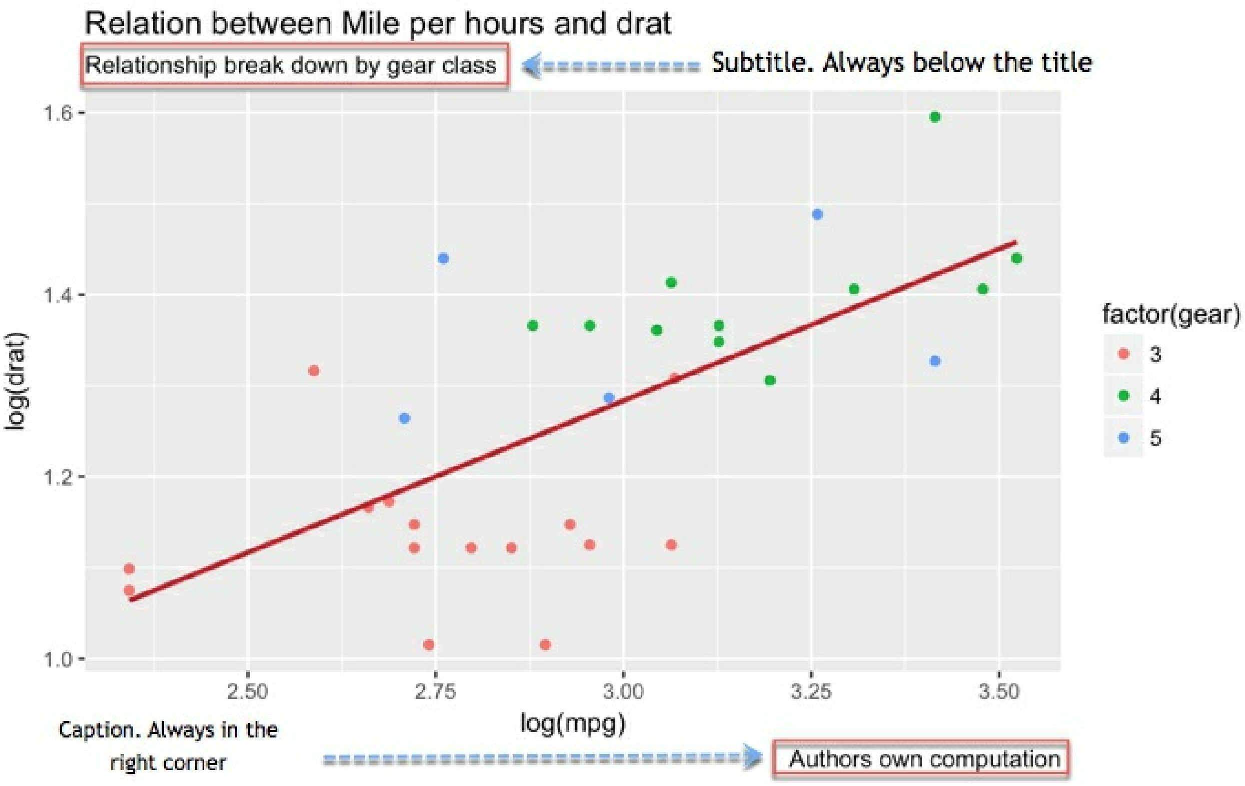
```
my_graph +
    labs(
        title =
        "Relation between Mile per hours and drat",
        subtitle =
        "Relationship break down by gear class",
        caption = "Authors own computation"
    )
```

Code Explanation

- Inside the lab(), you added:

    - title = "Relation between Mile per hours and drat": Add title
    - subtitle = "Relationship break down by gear class": Add subtitle
    - caption = "Authors own computation: Add caption
    - You separate each new information with a comma, ,
- Note that you break the lines of code. It is not compulsory, and it only helps to read the code more easily

Output:



Rename x-axis and y-axis

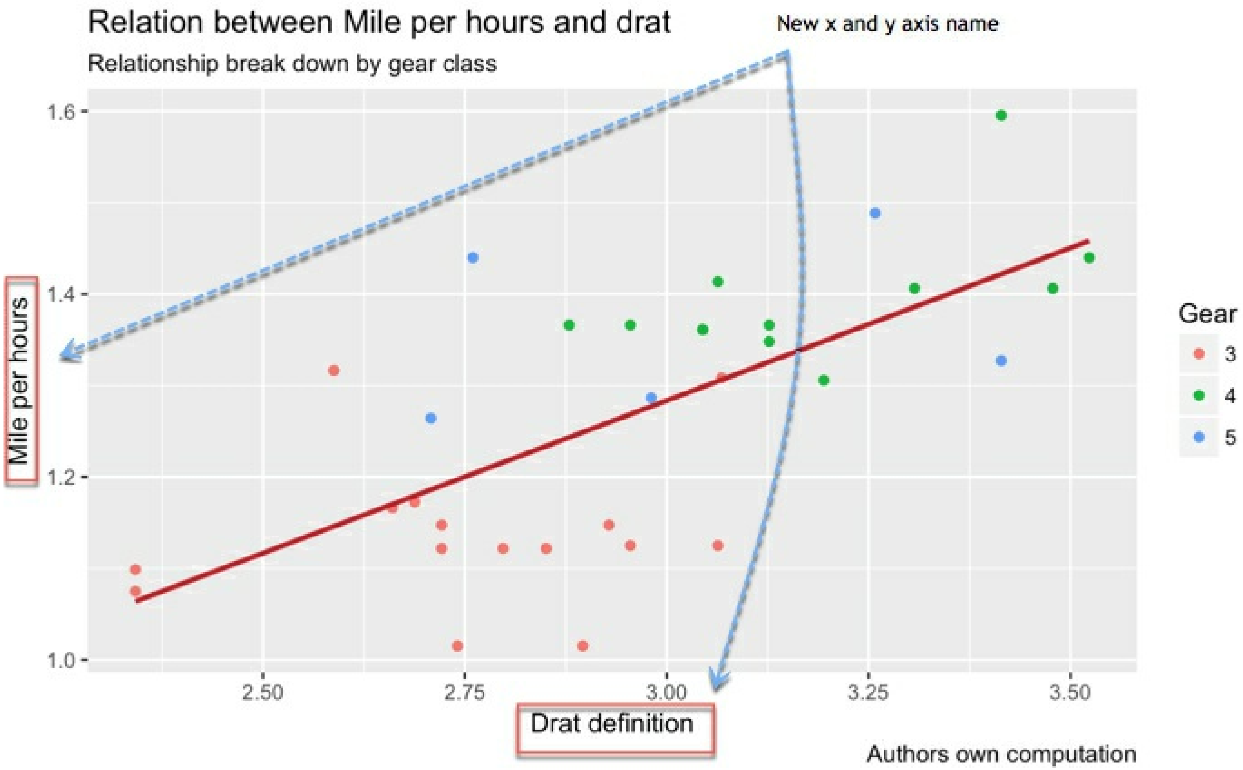
Variables itself in the dataset might not always be explicit or by convention use the _ when there are multiple words (i.e. GDP_CAP). You don't want such name appear in your graph. It is important to change the name or add more details, like the units.

```
my_graph +
    labs(
        x = "Drat definition",
        y = "Mile per hours",
        color = "Gear",
        title = "Relation between Mile per hours and drat",
        subtitle = "Relationship break down by gear class",
        caption = "Authors own computation"
    )
```

Code Explanation

- Inside the lab(), you added:
  - x = "Drat definition": Change the name of x-axis
  - y = "Mile per hours": Change the name of y-axis

Output:



Control the scales

You can control the scale of the axis.

The function seq() is convenient when you need to create a sequence of number. The basic syntax is:

```
seq(begin, last, by = x)
arguments:
- begin: First number of the sequence
- last: Last number of the sequence
- by= x: The step. For instance, if x is 2, the code adds 2 to
`begin-1` until it reaches `last`
```

For instance, if you want to create a range from 0 to 12 with a step of 3, you will have four numbers, 0 4 8 12

```
seq(0, 12,4)
```

Output:

```
## [1]  0  4  8 12
```

You can control the scale of the x-axis and y-axis as below

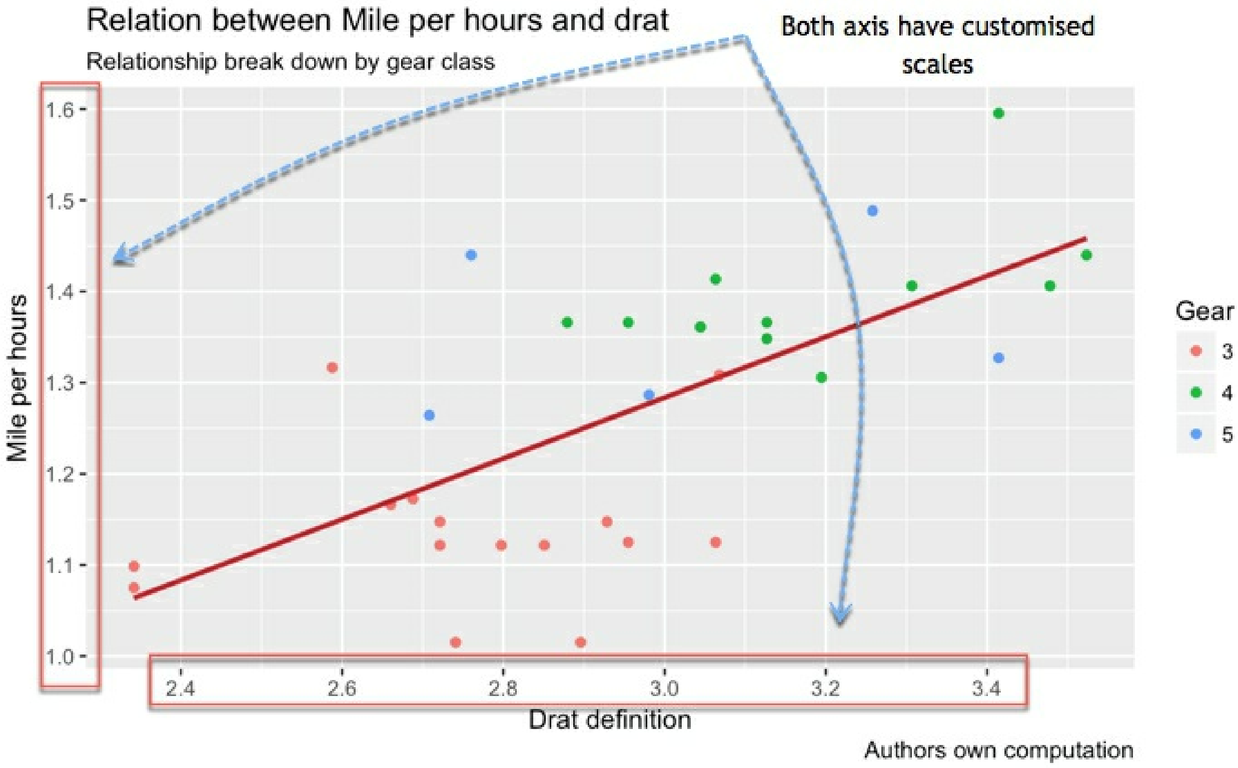
```
my_graph +
    scale_x_continuous(breaks = seq(1, 3.6, by = 0.2)) +
    scale_y_continuous(breaks = seq(1, 1.6, by = 0.1)) +
    labs(
        x = "Drat definition",
        y = "Mile per hours",
        color = "Gear",
        title = "Relation between Mile per hours and drat",
        subtitle = "Relationship break down by gear class",
        caption = "Authors own computation"
    )
```

Code Explanation

- The function scale_y_continuous() controls the **y-axis**
- The function scale_x_continuous() controls the **x-axis**.
- The parameter breaks controls the split of the axis. You can manually add the sequence of number or use the seq()function:
    - seq(1, 3.6, by = 0.2): Create six numbers from 2.4 to 3.4 with

a step of 3
  - seq(1, 1.6, by = 0.1): Create seven numbers from 1 to 1.6 with a step of 1

Output:



Theme

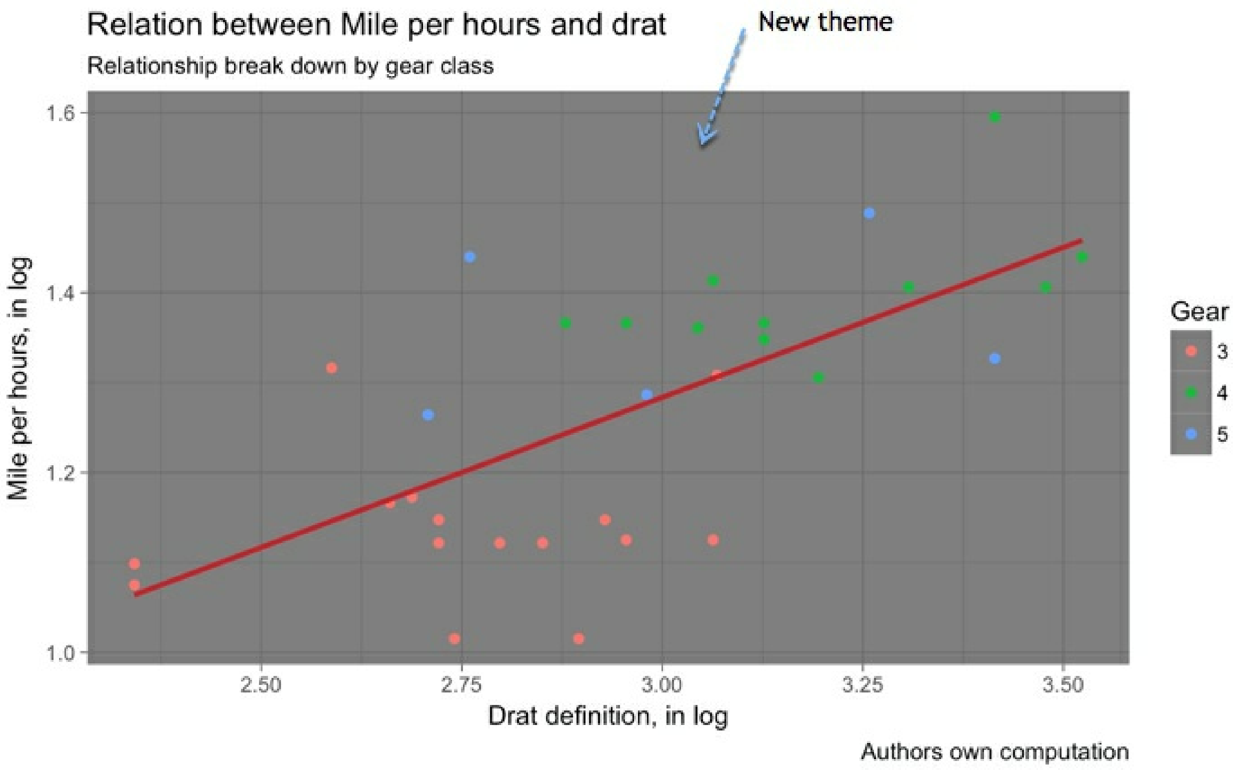
Finally, R allows us to customize out plot with different themes. The library ggplot2 includes eights themes:

- theme_bw()
- theme_light()
- theme_classis()
- theme_linedraw()
- theme_dark()
- theme_minimal()
- theme_gray()

- theme_void()

```
my_graph +
    theme_dark() +
    labs(
        x = "Drat definition, in log",
        y = "Mile per hours, in log",
        color = "Gear",
        title = "Relation between Mile per hours and drat",
        subtitle = "Relationship break down by gear class",
        caption = "Authors own computation"
    )
```

Output:



Save Plots

After all these steps, it is time to save and share your graph. You add ggsave('NAME OF THE FILE) right after you plot the graph and it will be stored on the hard drive.

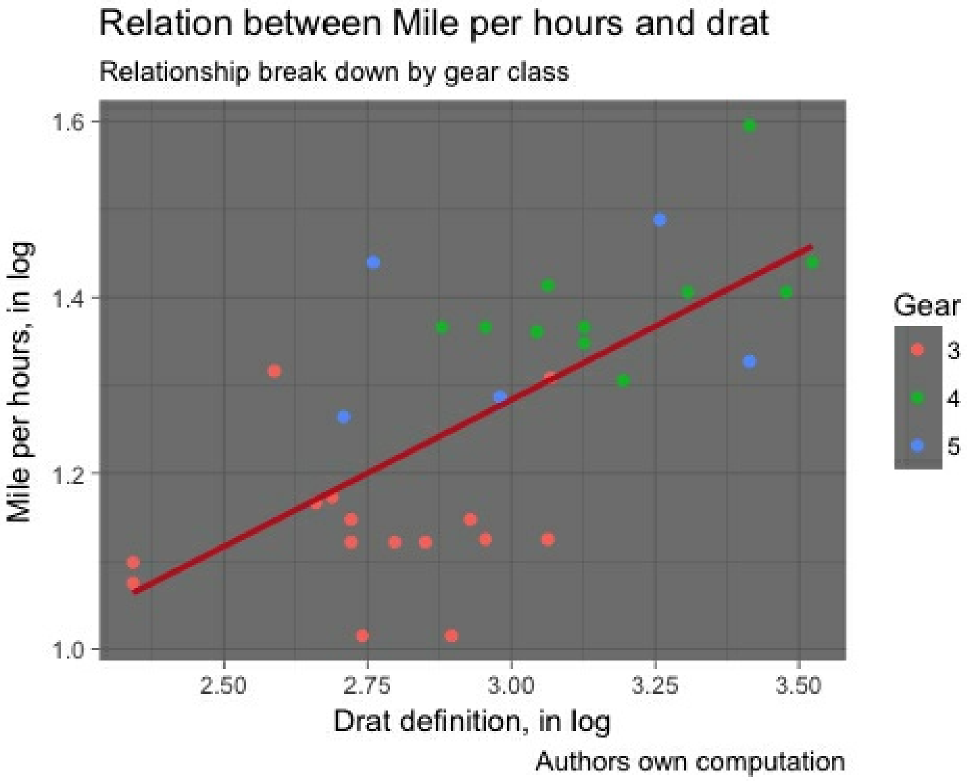
The graph is saved in the working directory. To check the working directory, you can run this code:

```
directory <-getwd()
directory
```

Let's plot your fantastic graph, saves it and check the location

```
my_graph +
    theme_dark() +
    labs(
        x = "Drat definition, in log",
        y = "Mile per hours, in log",
        color = "Gear",
        title = "Relation between Mile per hours and drat",
        subtitle = "Relationship break down by gear class",
        caption = "Authors own computation"
    )
```

Output:



```
ggsave("my_fantastic_plot.png")
```

Output:

```
## Saving 5 x 4 in image
```

Note: For pedagogical purpose only, we created a function called open_folder() to open the directory folder for you. You just need to run the code below and see where the picture is stored. You should see a file names my_fantastic_plot.png.

```
# Run this code to create the
function
open_folder <- function(dir) {
    if (.Platform['OS.type'] == "windows") {
        shell.exec(dir)
    } else {
        system(paste(Sys.getenv("R_BROWSER"), dir))
    }
}

# Call the
function to open the folder open_folder(directory)
```

Summary

You can summarize the arguments to create a scatter plot in the table below:

Objective	**Code**

Basic scatter plot	`ggplot(df, aes(x = x1, y = y)) +`
	`geom_point()`

Scatter plot with color group	`ggplot(df, aes(x = x1, y = y)) +`
	`geom_point(aes(color = factor(x1)) +`
	`stat_smooth(method = "lm")`

Add fitted values	`ggplot(df, aes(x = x1, y = y)) +`
	`geom_point(aes(color = factor(x1))`

	`ggplot(df, aes(x = x1, y = y)) +`

Add title	geom_point() + labs(title = paste("Hello Guru99"))
Add subtitle	ggplot(df, aes(x = x1, y = y)) + geom_point() + labs(subtitle = paste("Hello Guru99"))
Rename x	ggplot(df, aes(x = x1, y = y)) + geom_point() + labs(x = "X1")
Rename y	ggplot(df, aes(x = x1, y = y)) + geom_point() + labs(y = "y1")
Control the scale	ggplot(df, aes(x = x1, y = y)) + geom_point() + scale_y_continuous(breaks = seq(10, 35, by = 10)) + scale_x_continuous(breaks = seq(2, 5, by = 1)
Create logs	ggplot(df, aes(x =log(x1), y = log(y))) + geom_point()
Theme	ggplot(df, aes(x = x1, y = y)) + geom_point() + theme_classic()
Save	ggsave("my_fantastic_plot.png")

Chapter 23: How to make Boxplot in R (with EXAMPLE)

You can use the geometric object geom_boxplot() from ggplot2 library to draw a box plot. Box plot helps to **visualize the distribution of the data by quartile and detect the presence of outliers.**

We will use the airquality dataset to introduce box plot with ggplot. This dataset measures the airquality of New York from May to September 1973. The dataset contains 154 observations. We will use the following variables:

- Ozone: Numerical variable
- Wind: Numerical variable
- Month: May to September. Numerical variable

Create Box Plot

Before you start to create your first box plot, you need to manipulate the data as follow:

- Step 1: Import the data
- Step 2: Drop unnecessary variables
- Step 3: Convert Month in factor level
- Step 4: Create a new categorical variable dividing the month with three level: begin, middle and end.
- Step 5: Remove missing observations

All these steps are done with dplyr and the pipeline operator %>%.

```
library(dplyr)
library(ggplot2)
# Step 1
data_air <- airquality % > %
```

```
#Step 2
select(-c(Solar.R, Temp)) % > %

#Step 3
mutate(Month = factor(Month, order = TRUE, labels = c("May",
"June", "July", "August", "September")),

#Step 4
day_cat = factor(ifelse(Day < 10, "Begin", ifelse(Day < 20,
"Middle", "End"))))
```

A good practice is to check the structure of the data with the function glimpse().

```
glimpse(data_air)
```

Output:

```
## Observations: 153
## Variables: 5
## $ Ozone   <int> 41, 36, 12, 18, NA, 28, 23, 19, 8, NA, 7, 16,
11, 14, ...
## $ Wind    <dbl> 7.4, 8.0, 12.6, 11.5, 14.3, 14.9, 8.6, 13.8,
20.1, 8.6...
## $ Month   <ord> May, May, May, May, May, May, May, May, May,
May, May,...
## $ Day     <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,
14, 15, 16,...
## $ day_cat <fctr> Begin, Begin, Begin, Begin, Begin, Begin,
Begin, Begi...
```

There are NA's in the dataset. Removing them is wise.

```
# Step 5
data_air_nona <-data_air %>% na.omit()
```

Basic box plot

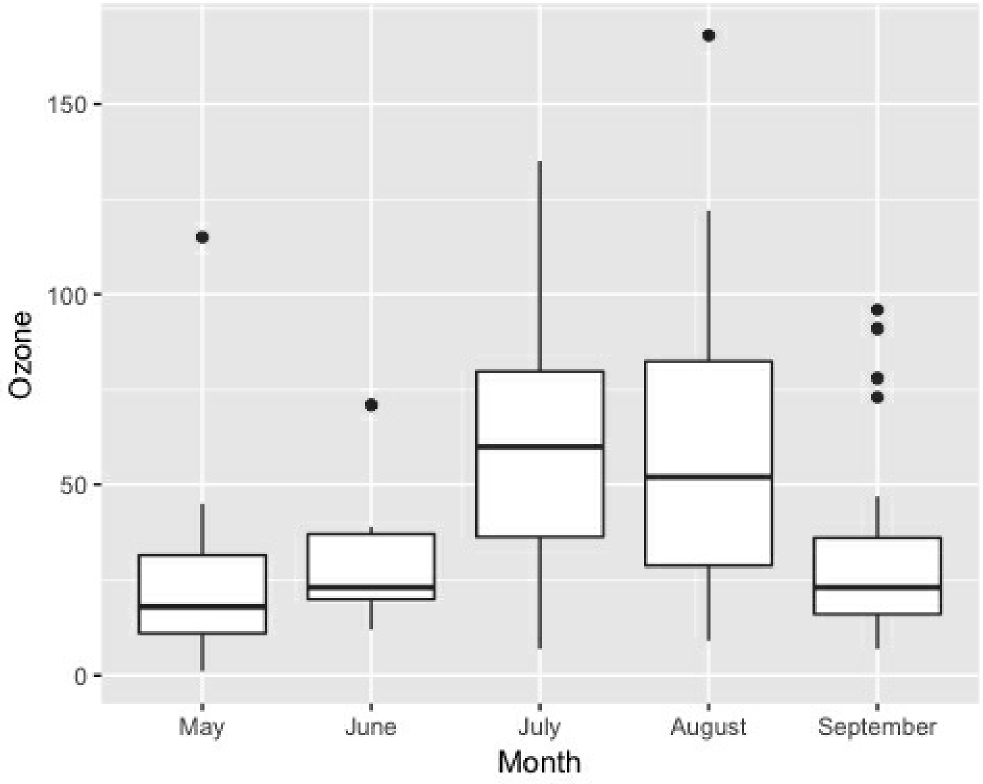
Let's plot the basic box plot with the distribution of ozone by month.

```
# Store the graph
box_plot <- ggplot(data_air_nona, aes(x = Month, y = Ozone))
# Add the geometric object box plot
box_plot +
    geom_boxplot()
```

Code Explanation

- Store the graph for further use
    - box_plot: You store the graph into the variable box_plot It is helpful for further use or avoid too complex line of codes
- Add the geometric object box plot
    - You pass the dataset data_air_nona to ggplot.
    - Inside the aes() argument, you add the x-axis and y-axis.
    - The + sign means you want R to keep reading the code. It makes the code more readable by breaking it.
    - Use geom_boxplot() to create a box plot

Output:



Change side of the graph

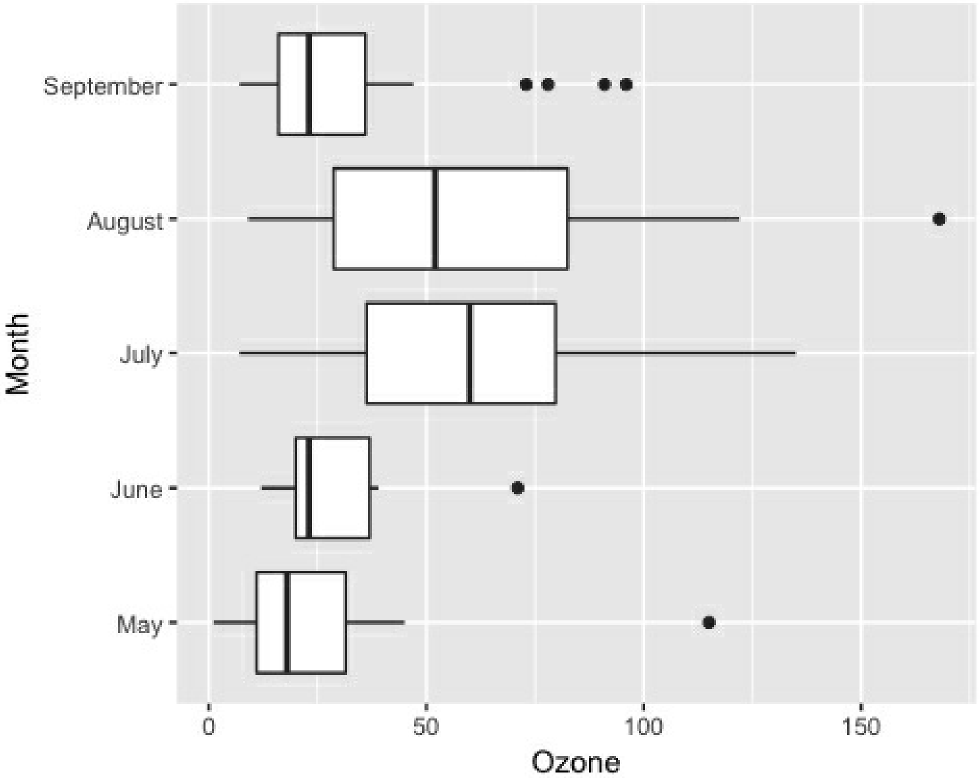
You can flip the side of the graph.

```
box_plot +
  geom_boxplot()+
  coord_flip()
```

Code Explanation

- box_plot: You use the graph you stored. It avoids rewriting all the codes each time you add new information to the graph.
- geom_boxplot(): Create the box plot
- coord_flip(): Flip the side of the graph

Output:



Change color of outlier

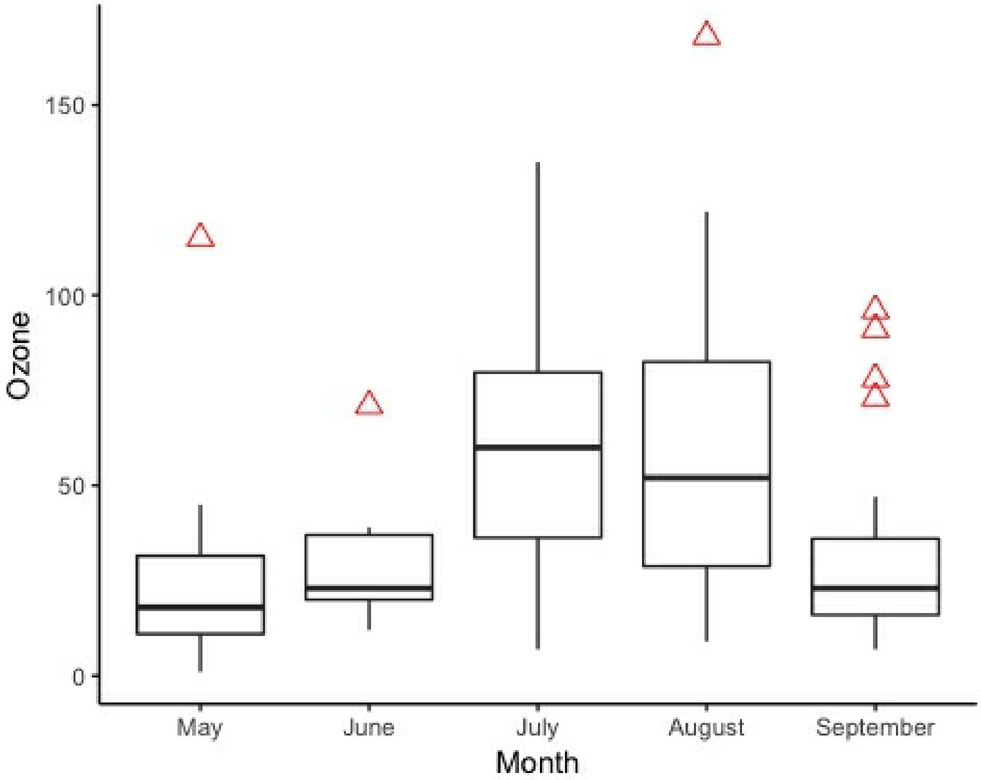
You can change the color, shape and size of the outliers.

```
box_plot +
    geom_boxplot(outlier.colour = "red",
        outlier.shape = 2,
        outlier.size = 3) +
    theme_classic()
```

Code Explanation

- outlier.colour="red": Control the color of the outliers
- outlier.shape=2: Change the shape of the outlier. 2 refers to triangle
- outlier.size=3: Change the size of the triangle. The size is proportional to the number.

Output:



Add a summary statistic

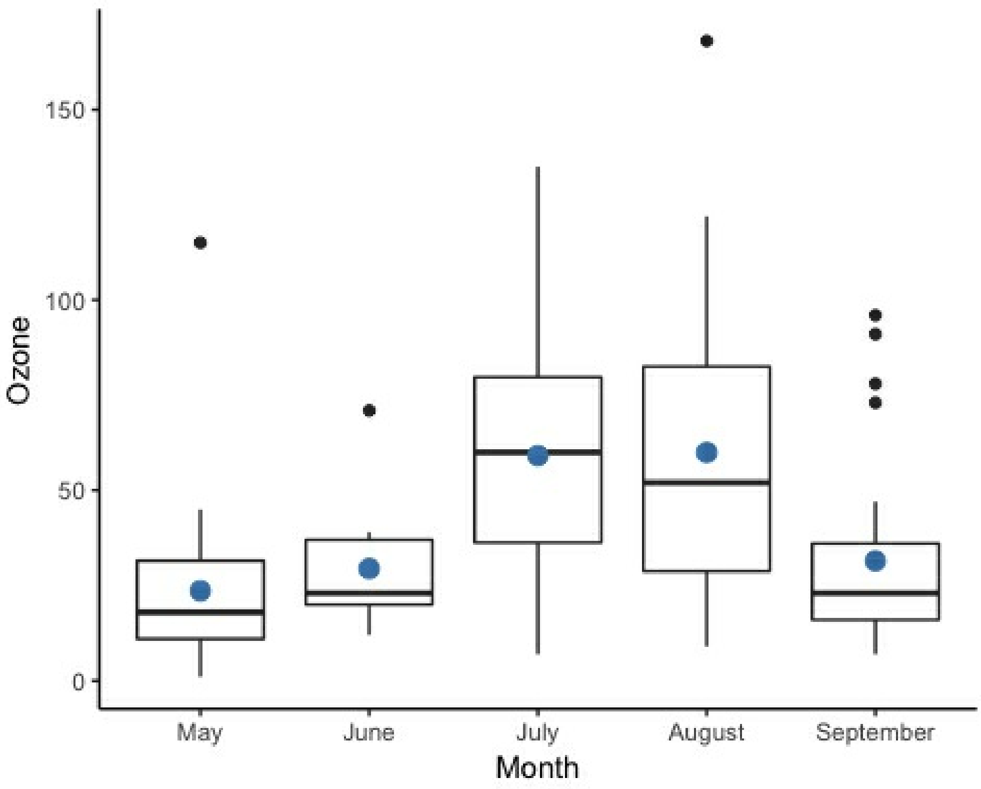
You can add a summary statistic to the box plot.

```
box_plot +
    geom_boxplot() +
    stat_summary(fun.y = mean,
        geom = "point",
        size = 3,
        color = "steelblue") +
    theme_classic()
```

Code Explanation

- stat_summary() allows adding a summary to the box plot
- The argument fun.y controls the statistics returned. You will use mean
- Note: Other statistics are available such as min and max. More than one statistics can be exhibited in the same graph
- geom = "point": Plot the average with a point
- size=3: Size of the point
- color ="steelblue": Color of the points

Output:



Box Plot with Dots

In the next plot, you add the dot plot layers. Each dot represents an observation.

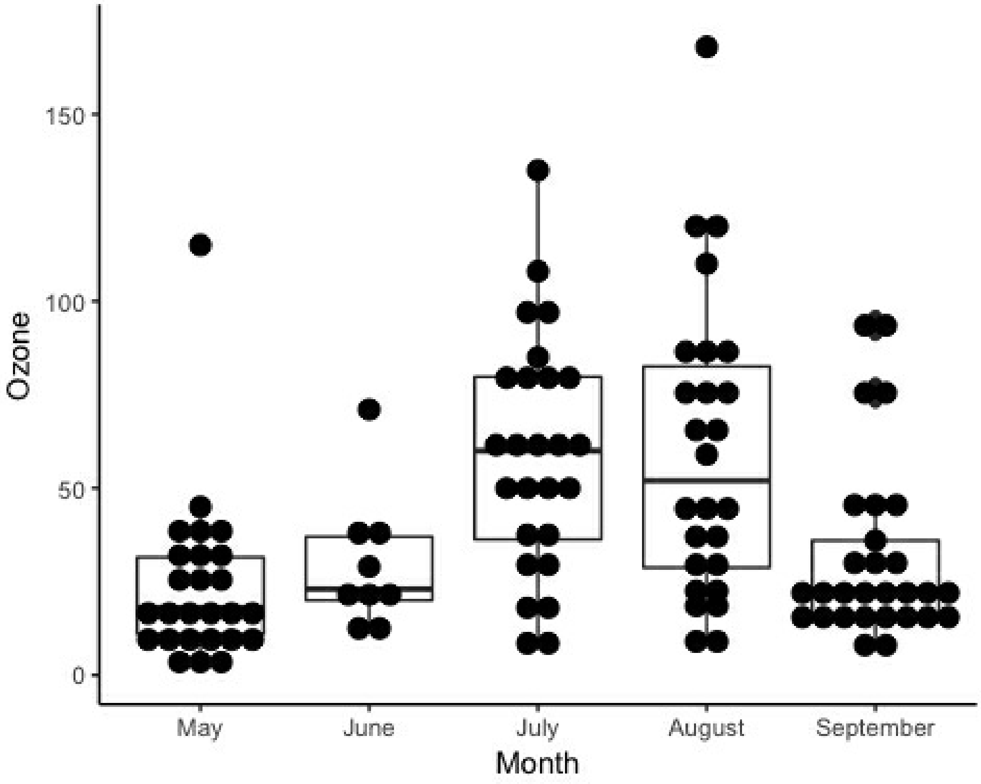
```
box_plot +
    geom_boxplot() +
    geom_dotplot(binaxis = 'y',
        dotsize = 1,
        stackdir = 'center') +
    theme_classic()
```

Code Explanation

- geom_dotplot() allows adding dot to the bin width
- binaxis='y': Change the position of the dots along the y-axis. By default, x-axis
- dotsize=1: Size of the dots
- stackdir='center': Way to stack the dots: Four values:

    - "up" (default),
    - "down"
    - "center"
    - "centerwhole"

Output:



Control Aesthetic of the Box Plot

Change the color of the box

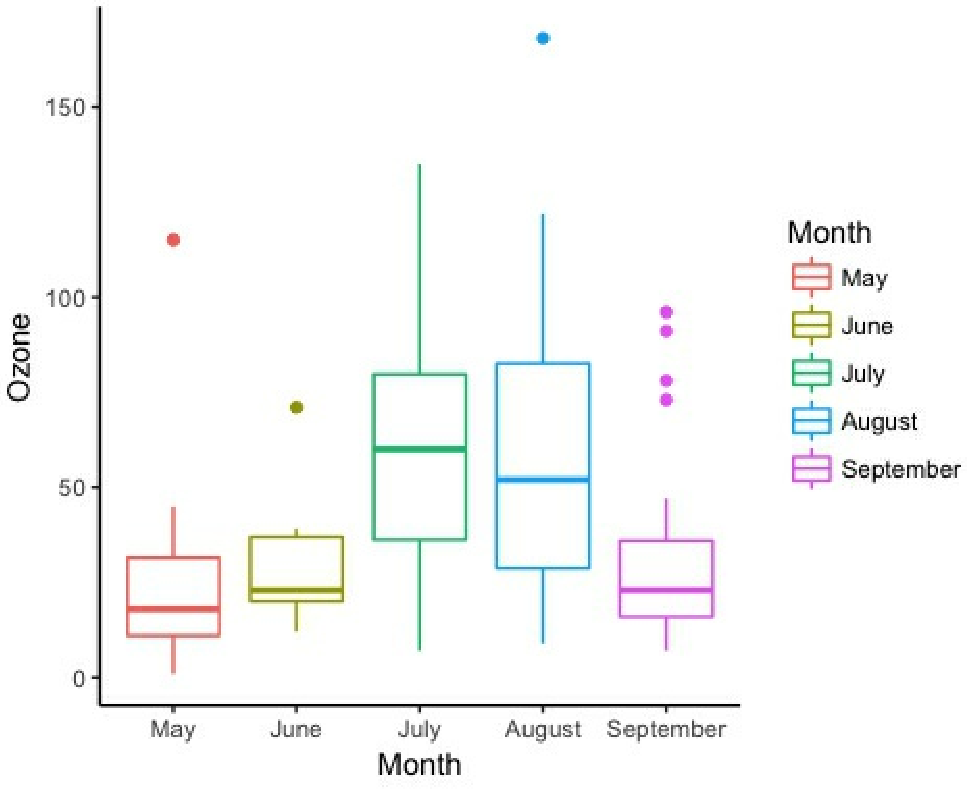
You can change the colors of the group.

```
ggplot(data_air_nona, aes(x = Month, y = Ozone, color = Month))
+
    geom_boxplot() +
    theme_classic()
```

Code Explanation

- The colors of the groups are controlled in the aes() mapping. You can use color= Month to change the color of the box according to the months

Output:



Box plot with multiple groups

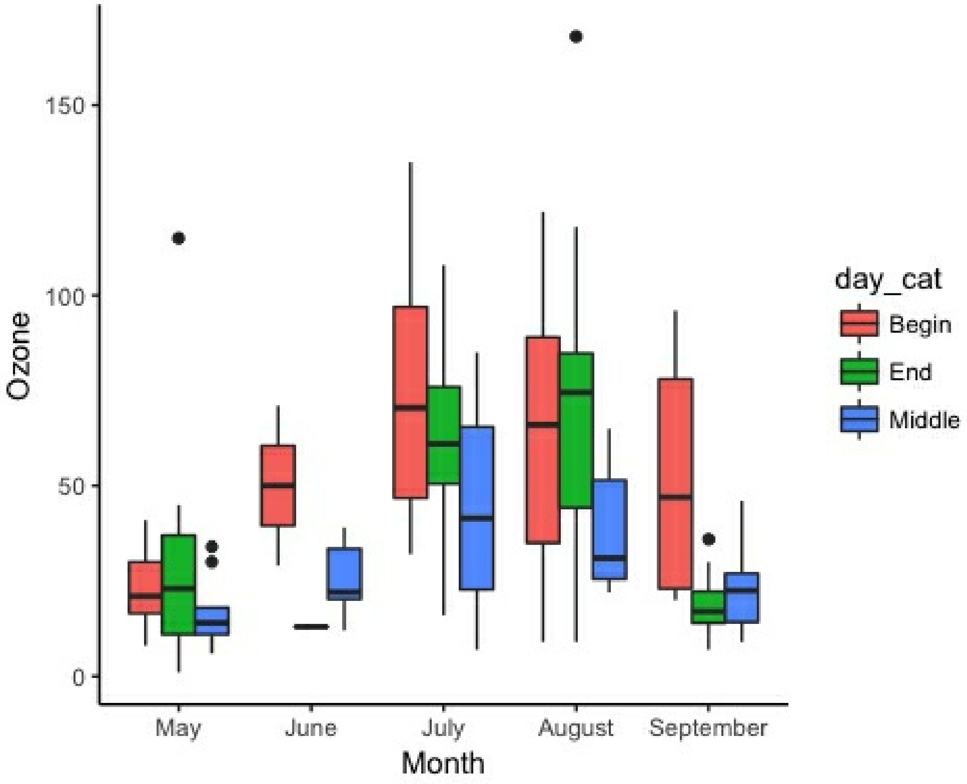
It is also possible to add multiple groups. You can visualize the difference in the air quality according to the day of the measure.

```
ggplot(data_air_nona, aes(Month, Ozone)) +
    geom_boxplot(aes(fill = day_cat)) +
    theme_classic()
```

Code Explanation

- The aes() mapping of the geometric object controls the groups to display (this variable has to be a factor)
- aes(fill= day_cat) allows creating three boxes for each month in the x-axis

Output:



Box Plot with Jittered Dots

Another way to show the dot is with jittered points. It is a convenient way to visualize points with a categorical variable.

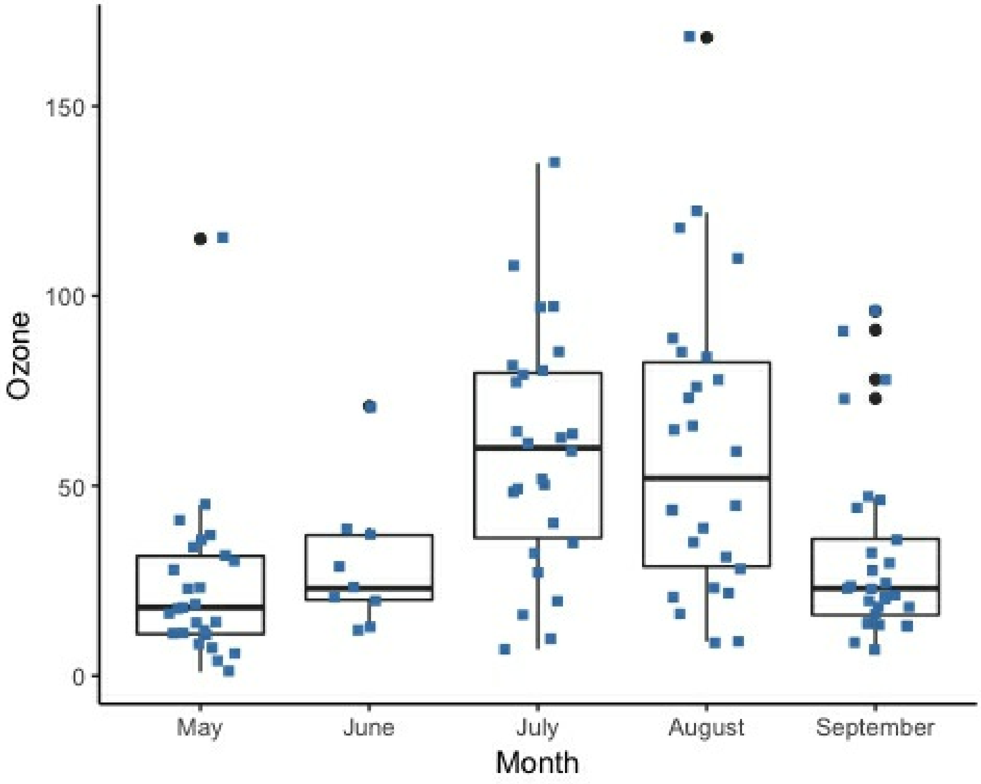
This method avoids the overlapping of the discrete data.

```
box_plot +
    geom_boxplot() +
    geom_jitter(shape = 15,
        color = "steelblue",
        position = position_jitter(width = 0.21)) +
    theme_classic()
```

Code Explanation

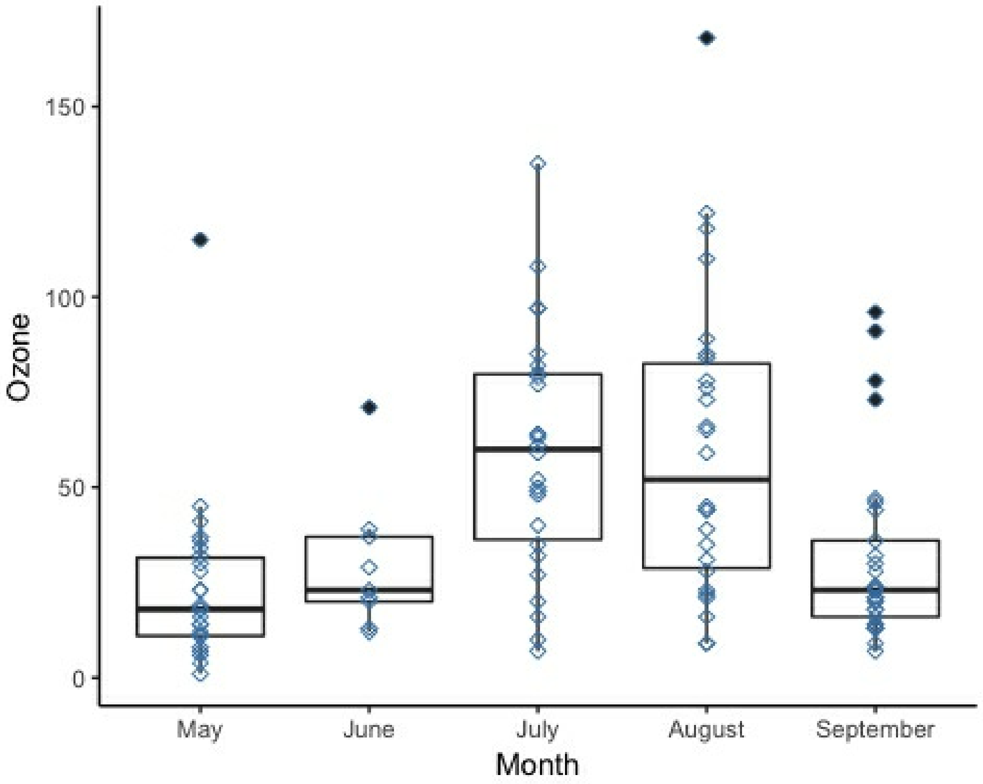
- geom_jitter() adds a little decay to each point.
- shape=15 changes the shape of the points. 15 represents the squares
- color = "steelblue": Change the color of the point
- position=position_jitter(width = 0.21): Way to place the overlapping points. position_jitter(width = 0.21) means you move the points by 20 percent from the x-axis. By default, 40 percent.

Output:



You can see the difference between the first graph with the jitter method and the second with the point method.

```
box_plot +
    geom_boxplot() +
    geom_point(shape = 5,
        color = "steelblue") +
    theme_classic()
```



Notched Box Plot

An interesting feature of geom_boxplot(), is a notched box plot. The notch plot narrows the box around the median. The main purpose of a notched box plot is to compare the significance of the median between groups. There is strong evidence two groups have different medians when the notches do not overlap. A notch is computed as follow:

$$median \pm 1.57 * \frac{IQR}{\sqrt{n}}$$

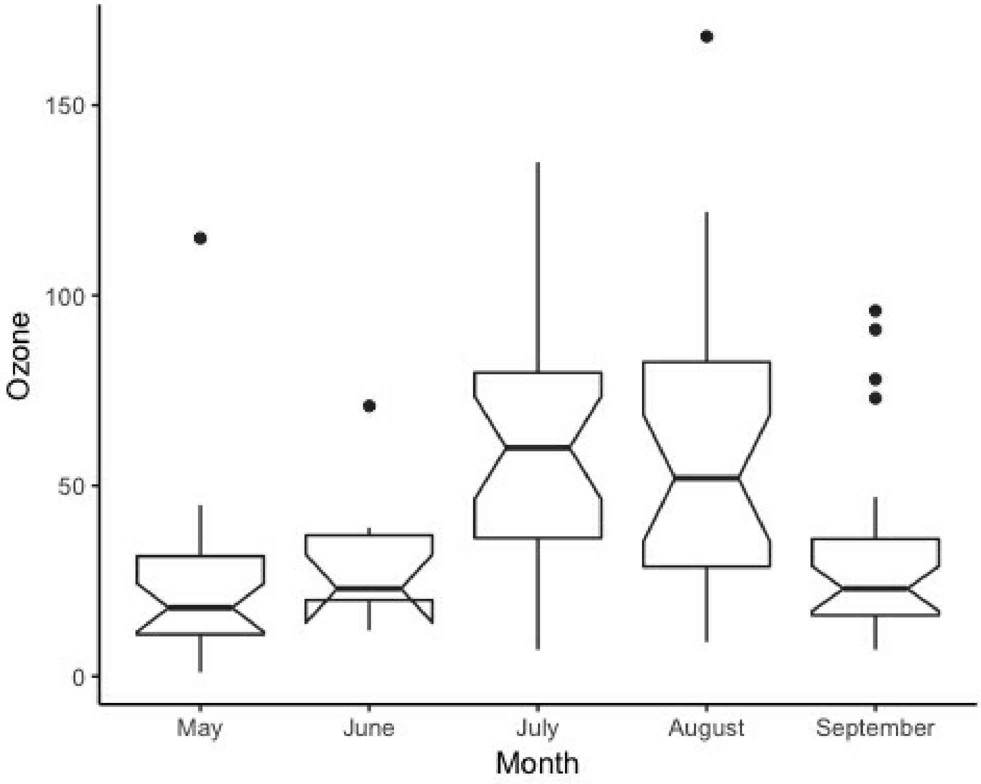
with is the interquartile and number of observations.

```
box_plot +
    geom_boxplot(notch = TRUE) +
    theme_classic()
```

Code Explanation

- geom_boxplot(notch=TRUE): Create a notched box plot

Output:



Summary

We can summarize the different types of box plot in the table below:

Objective	**Code**
Basic box plot	`ggplot(df, aes( x = x1, y =y)) + geom_boxplot()`

flip the side	`ggplot(df, aes( x = x1, y =y)) + geom_boxplot() + coord_flip()`
Notched box plot	`ggplot(df, aes( x = x1, y =y)) + geom_boxplot(notch=TRUE)`
Box plot with jittered dots	`ggplot(df, aes( x = x1, y =y)) + geom_boxplot() + geom_jitter(position = position_jitter(0.21))`

Chapter 24: Bar Chart & Histogram in R (with Example)

A bar chart is a great way to display categorical variables in the x-axis. This type of graph denotes two aspects in the y-axis.

1. The first one counts the number of occurrence between groups.
2. The second one shows a summary statistic (min, max, average, and so on) of a variable in the y-axis.

You will use the mtcars dataset with has the following variables:

- cyl: Number of the cylinder in the car. Numeric variable
- am: Type of transmission. 0 for automatic and 1 for manual. Numeric variable
- mpg: Miles per gallon. Numeric variable

How to create Bar Chart

To create graph in R, you can use the library ggplot which creates ready-for-publication graphs. The basic syntax of this library is:

```
ggplot(data, mapping = aes()) +
geometric object

arguments:
data: dataset used to plot the graph
mapping: Control the x and y-axis
geometric object: The type of plot you want to show. The most
common objects are:

- Point: `geom_point()`
- Bar: `geom_bar()`
- Line: `geom_line()`
- Histogram: `geom_histogram()`
```

In this tutorial, you are interested in the geometric object geom_bar() that create the bar chart.

Bar chart: count

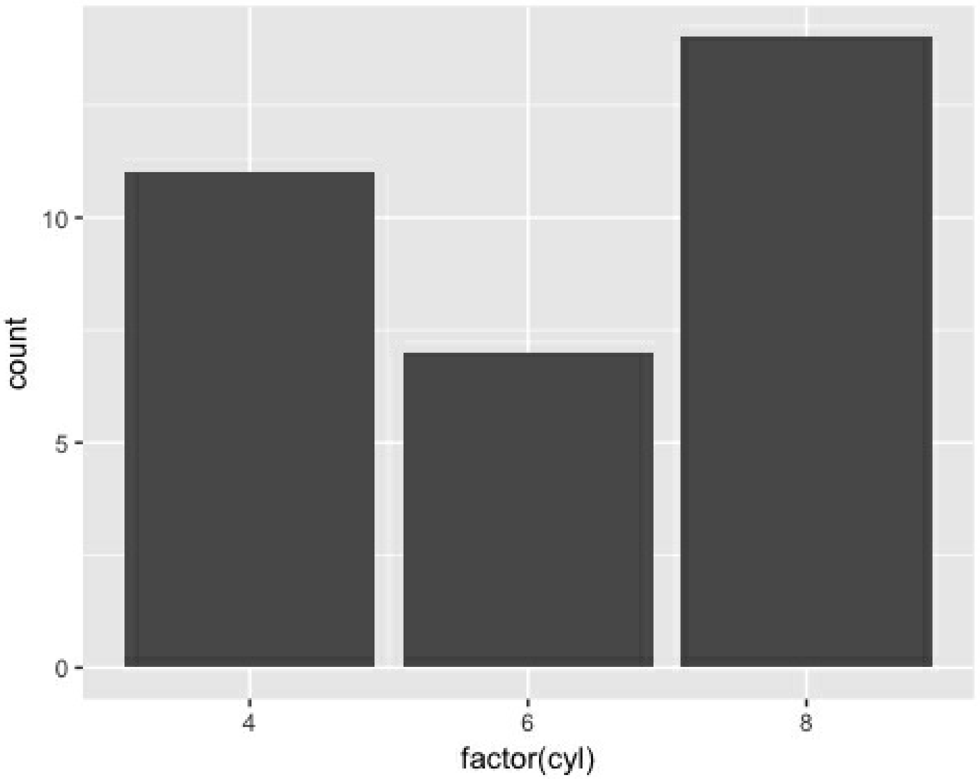
Your first graph shows the frequency of cylinder with geom_bar(). The code below is the most basic syntax.

```
library(ggplot2)
# Most basic bar chart
ggplot(mtcars, aes(x = factor(cyl))) +
    geom_bar()
```

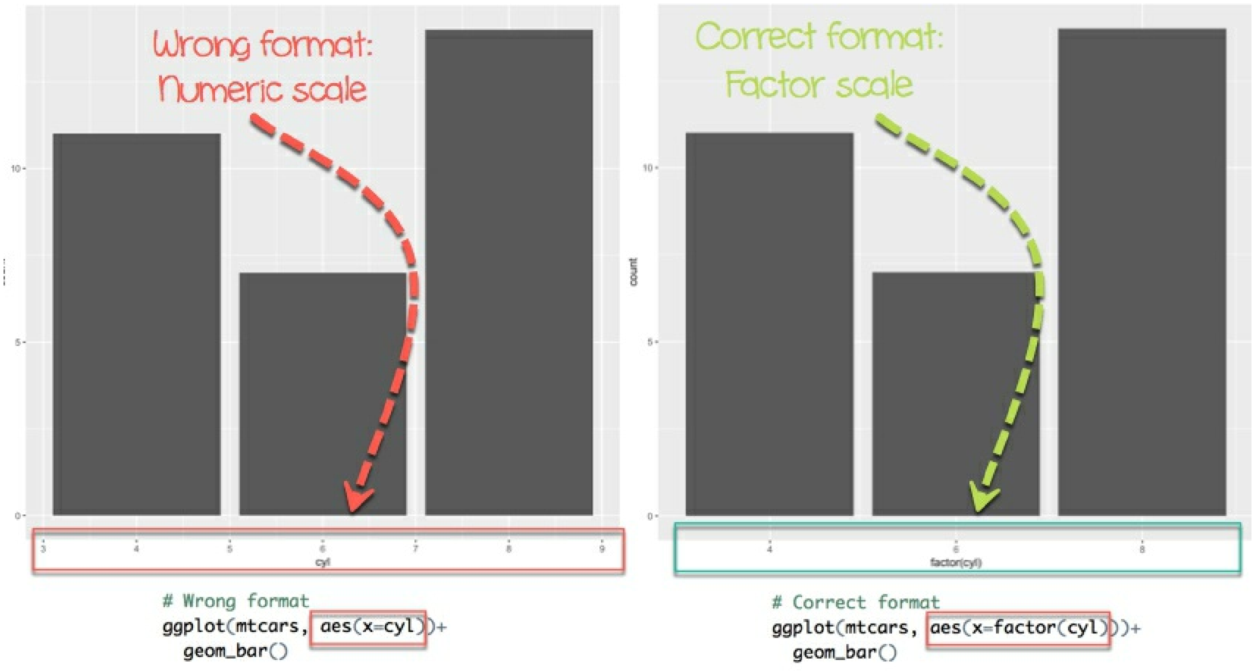
Code Explanation

- You pass the dataset mtcars to ggplot.
- Inside the aes() argument, you add the x-axis as a factor variable(cyl)
- The + sign means you want R to keep reading the code. It makes the code more readable by breaking it.
- Use geom_bar() for the geometric object.

Output:



Note: make sure you convert the variables into a factor otherwise R treats the variables as numeric. See the example below.



```
# Wrong format
ggplot(mtcars, aes(x=cyl))+
  geom_bar()
```

```
# Correct format
ggplot(mtcars, aes(x=factor(cyl)))+
  geom_bar()
```

Customize the graph

Four arguments can be passed to customize the graph:

```
- `stat`: Control the type of formatting. By default, `bin` to
plot a count in the y-axis. For continuous value, pass `stat =
"identity"`
- `alpha`: Control density of the color
- `fill`: Change the color of the bar
- `size`: Control the size the bar
```

Change the color of the bars

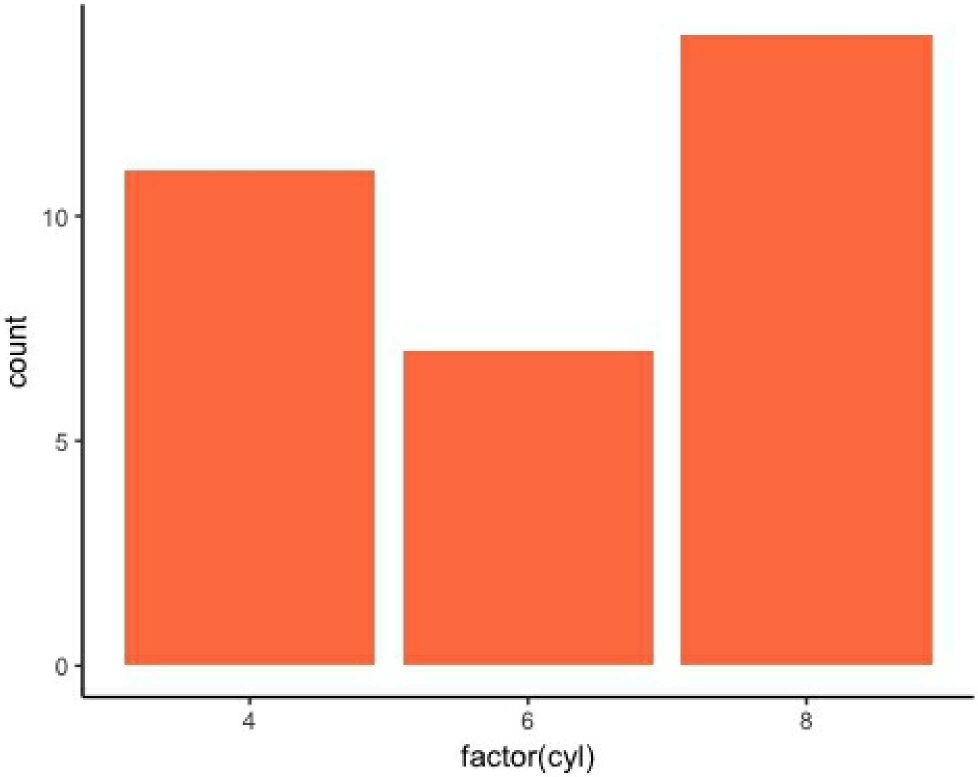
You can change the color of the bars. Note that the colors of the bars are all similar.

```
# Change the color of the bars
ggplot(mtcars, aes(x = factor(cyl))) +
    geom_bar(fill = "coral") +
    theme_classic()
```

Code Explanation

- The colors of the bars are controlled by the aes() mapping inside the geometric object (i.e. not in the ggplot()). You can change the color with the fill arguments. Here, you choose the coral color.

Output:



You can use this code:

```
grDevices::colors()
```

to see all the colors available in R. There are around 650 colors.

Change the intensity

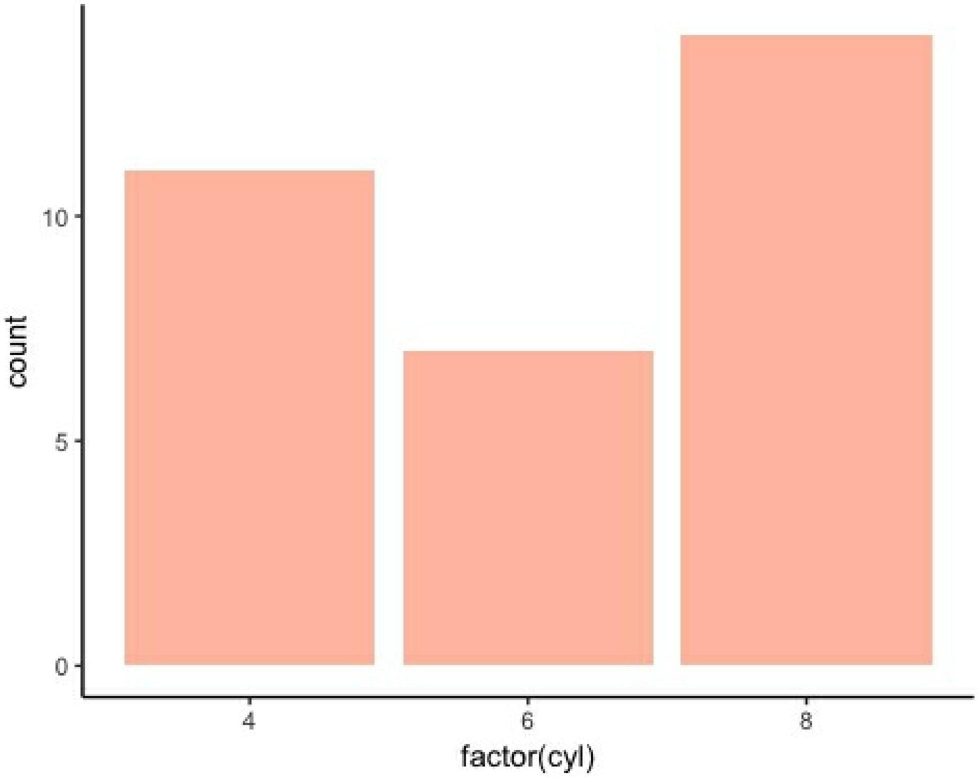
You can increase or decrease the intensity of the bars' color

```
# Change intensity
ggplot(mtcars,
        aes(factor(cyl))) +
    geom_bar(fill = "coral",
        alpha = 0.5) +
    theme_classic()
```

Code Explanation

- To increase/decrease the intensity of the bar, you can change the value of the alpha. A large alpha increases the intensity, and low alpha reduces the intensity. alpha ranges from 0 to 1. If 1, then the color is the same as the palette. If 0, color is white. You choose alpha = 0.1.

Output:



Color by groups

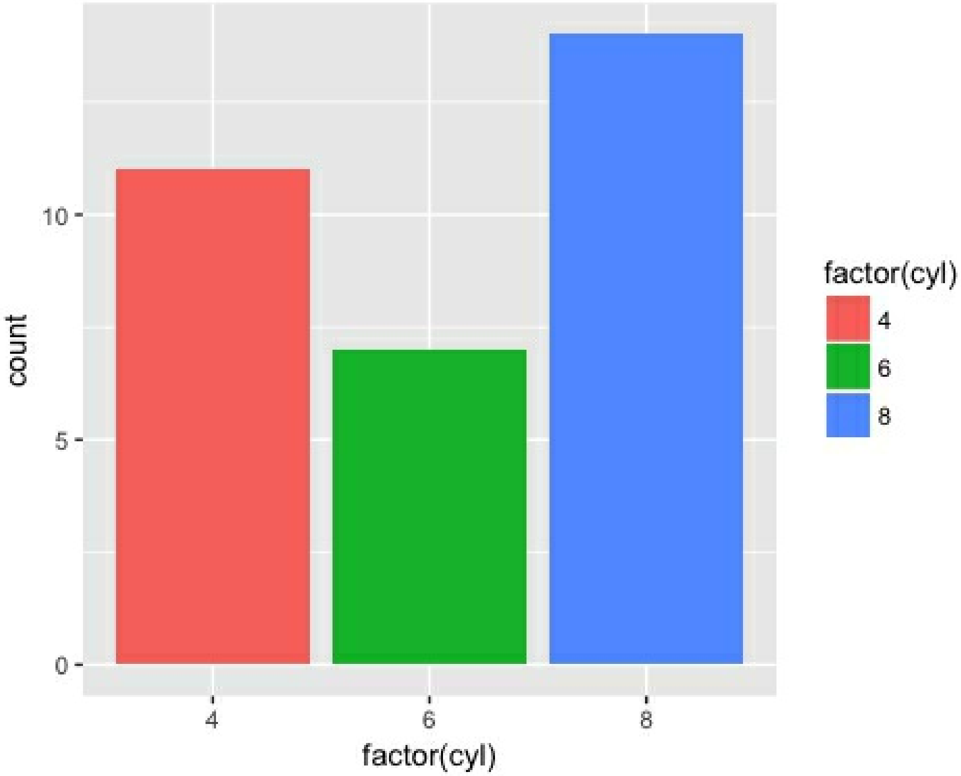
You can change the colors of the bars, meaning one different color for each group. For instance, cyl variable has three levels, then you can plot the bar chart with three colors.

```
# Color by group
ggplot(mtcars, aes(factor(cyl),
        fill = factor(cyl))) +
    geom_bar()
```

Code Explanation

- The argument fill inside the aes() allows changing the color of the bar. You change the color by setting fill = x-axis variable. In your example, the x-axis variable is cyl; fill = factor(cyl)

Output:



Add a group in the bars

You can further split the y-axis based on another factor level. For instance, you can count the number of automatic and manual transmission based on the cylinder type.

You will proceed as follow:

- Step 1: Create the data frame with mtcars dataset
- Step 2: Label the am variable with auto for automatic transmission and man for manual transmission. Convert am and cyl as a factor so that you don't need to use factor() in the ggplot()

function.

- Step 3: Plot the bar chart to count the number of transmission by cylinder

```
library(dplyr)
# Step 1
data <- mtcars % > %
#Step 2
mutate(am = factor(am, labels = c("auto", "man")),
    cyl = factor(cyl))
```

You have the dataset ready, you can plot the graph;

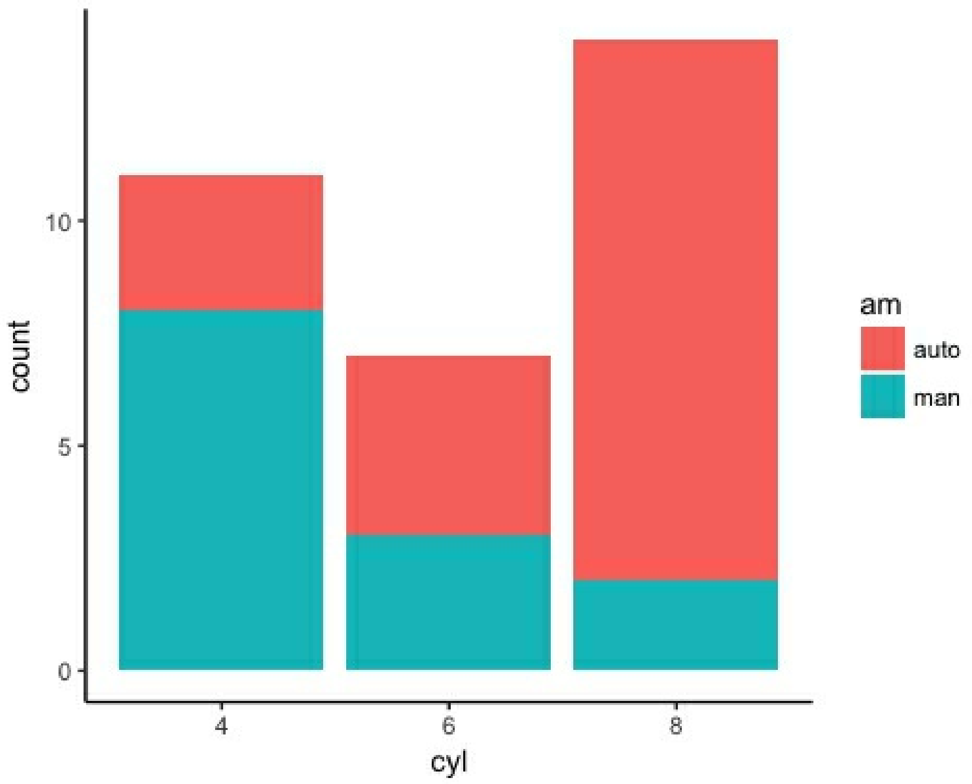
# Step 3

```
ggplot(data, aes(x = cyl, fill = am)) +
    geom_bar() +
    theme_classic()
```

Code Explanation

- The ggpplot() contains the dataset data and the aes().
- In the aes() you include the variable x-axis and which variable is required to fill the bar (i.e. am)
- geom_bar(): Create the bar chart

Output:



The mapping will fill the bar with two colors, one for each level. It is effortless to change the group by choosing other factor variables in the dataset.

## Bar chart in percentage

You can visualize the bar in percentage instead of the raw count.

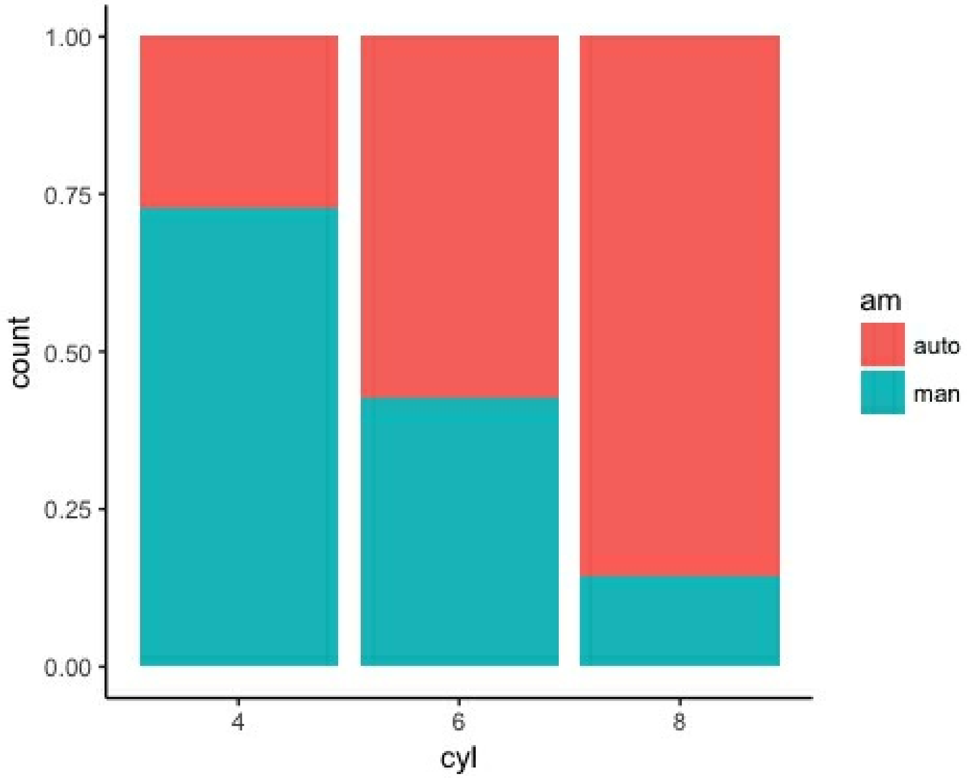
# Bar chart in percentage

```
ggplot(data, aes(x = cyl, fill = am)) +
    geom_bar(position = "fill") +
    theme_classic()
```

Code Explanation

- Use position = "fill" in the geom_bar() argument to create a graphic with percentage in the y-axis.

Output:



Side by side bars

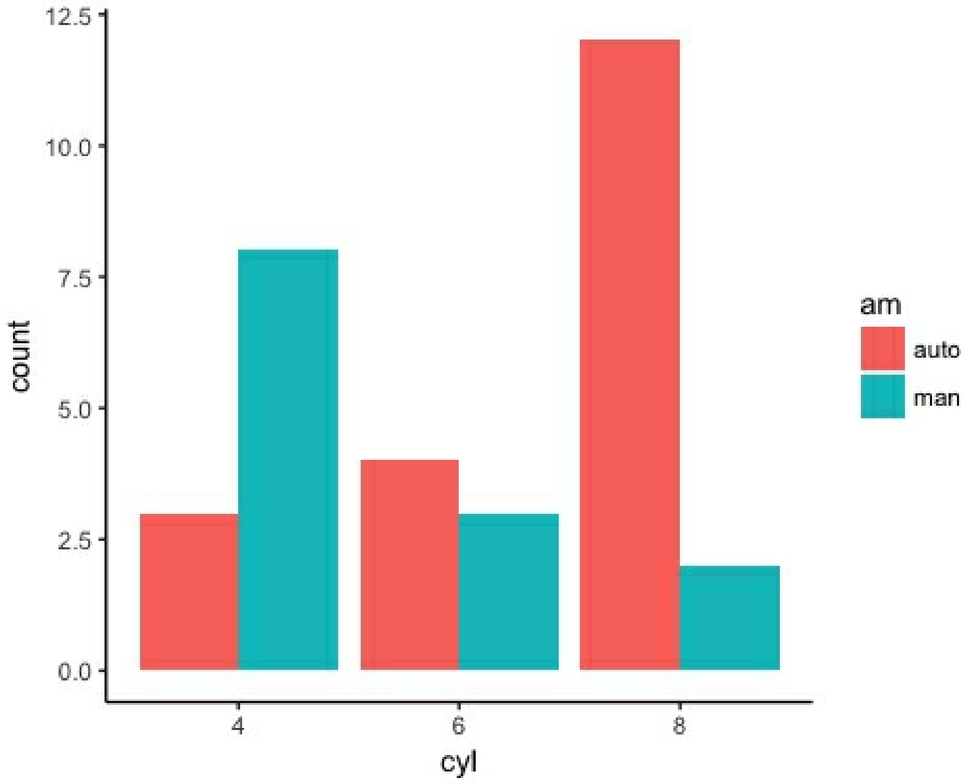
It is easy to plot the bar chart with the group variable side by side.

```
# Bar chart side by side
ggplot(data, aes(x = cyl, fill = am)) +
    geom_bar(position = position_dodge()) +
    theme_classic()
```

Code Explanation

- position=position_dodge(): Explicitly tells how to arrange the bars

Output:



Histogram

In the second part of the bar chart tutorial, you can represent the group of variables with values in the y-axis.

Your objective is to create a graph with the average mile per gallon for each type of cylinder. To draw an informative graph, you will follow these steps:

- Step 1: Create a new variable with the average mile per gallon by cylinder
- Step 2: Create a basic histogram
- Step 3: Change the orientation
- Step 4: Change the color
- Step 5: Change the size
- Step 6: Add labels to the graph

Step 1) Create a new variable

You create a data frame named data_histogram which simply returns the average miles per gallon by the number of cylinders in the car. You call this new variable mean_mpg, and you round the mean with two decimals.

# Step 1

```
data_histogram <- mtcars % > %
mutate(cyl = factor(cyl)) % > %
group_by(cyl) % > %
summarize(mean_mpg = round(mean(mpg), 2))
```

Step 2) Create a basic histogram

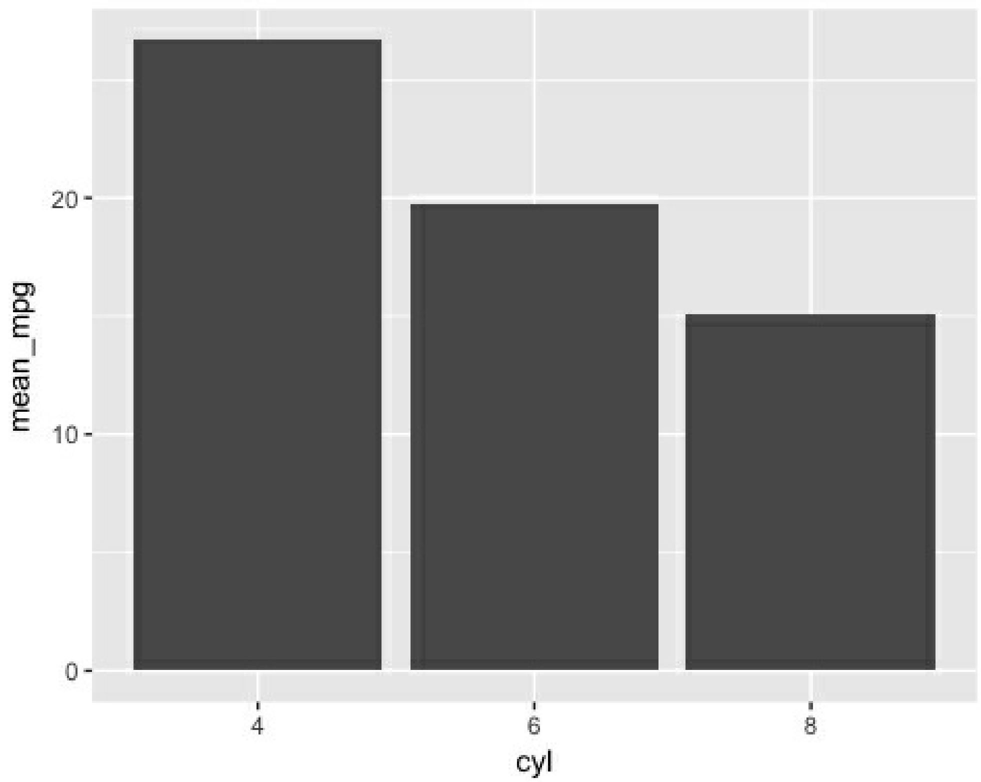
You can plot the histogram. It is not ready to communicate to be delivered to client but gives us an intuition about the trend.

```
ggplot(data_histogram, aes(x = cyl, y = mean_mpg)) +
    geom_bar(stat = "identity")
```

Code Explanation

- The aes() has now two variables. The cyl variable refers to the x-axis, and the mean_mpg is the y-axis.
- You need to pass the argument stat="identity" to refer the variable in the y-axis as a numerical value. geom_bar uses stat="bin" as default value.

Output:



Step 3) Change the orientation

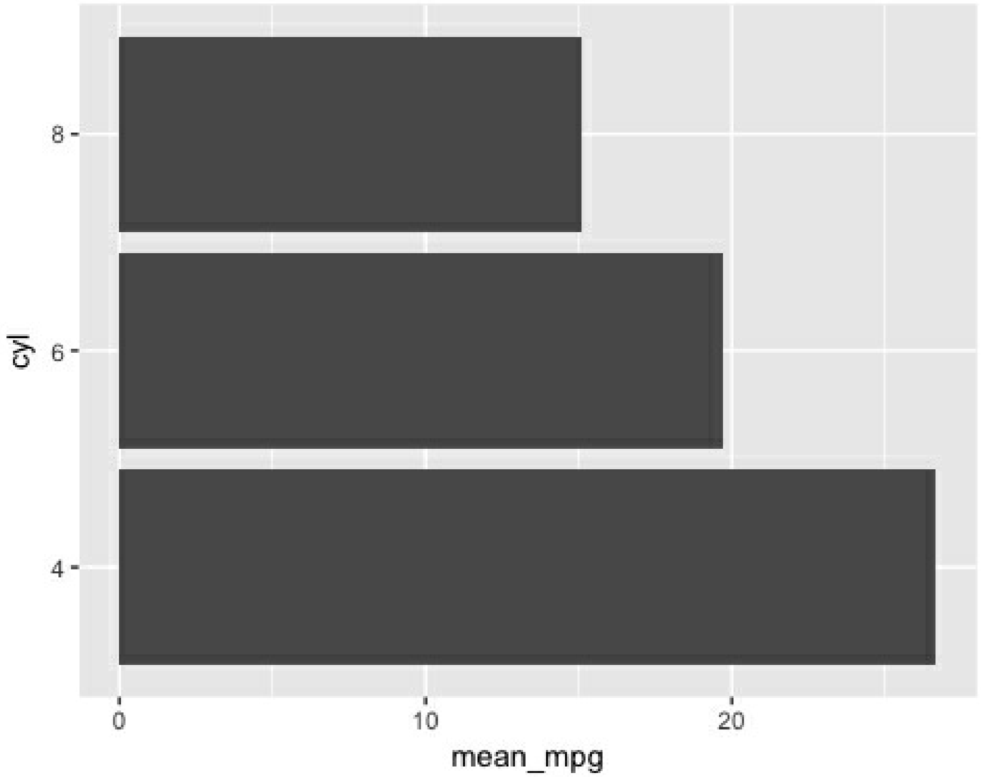
You change the orientation of the graph from vertical to horizontal.

```
ggplot(data_histogram, aes(x = cyl, y = mean_mpg)) +
    geom_bar(stat = "identity") +
    coord_flip()
```

Code Explanation

- You can control the orientation of the graph with coord_flip().

Output:



Step 4) Change the color

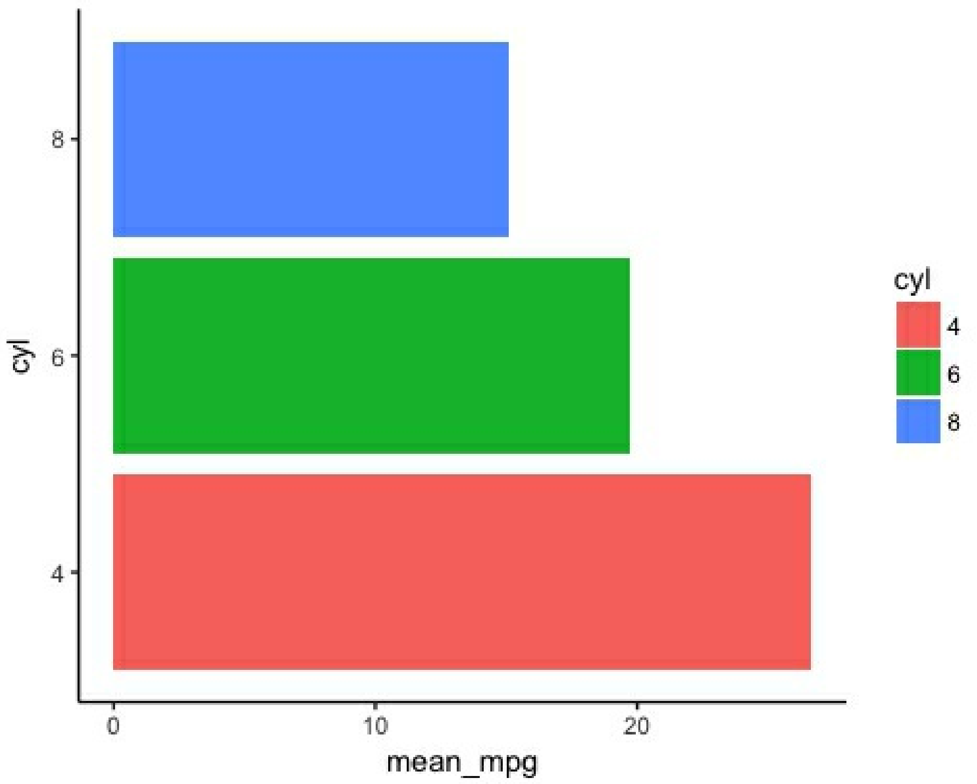
You can differentiate the colors of the bars according to the factor level of the x-axis variable.

```
ggplot(data_histogram, aes(x = cyl, y = mean_mpg, fill = cyl)) +
    geom_bar(stat = "identity") +
    coord_flip() +
    theme_classic()
```

Code Explanation

- You can plot the graph by groups with the fill= cyl mapping. R takes care automatically of the colors based on the levels of cyl variable

Output:



Step 5) Change the size

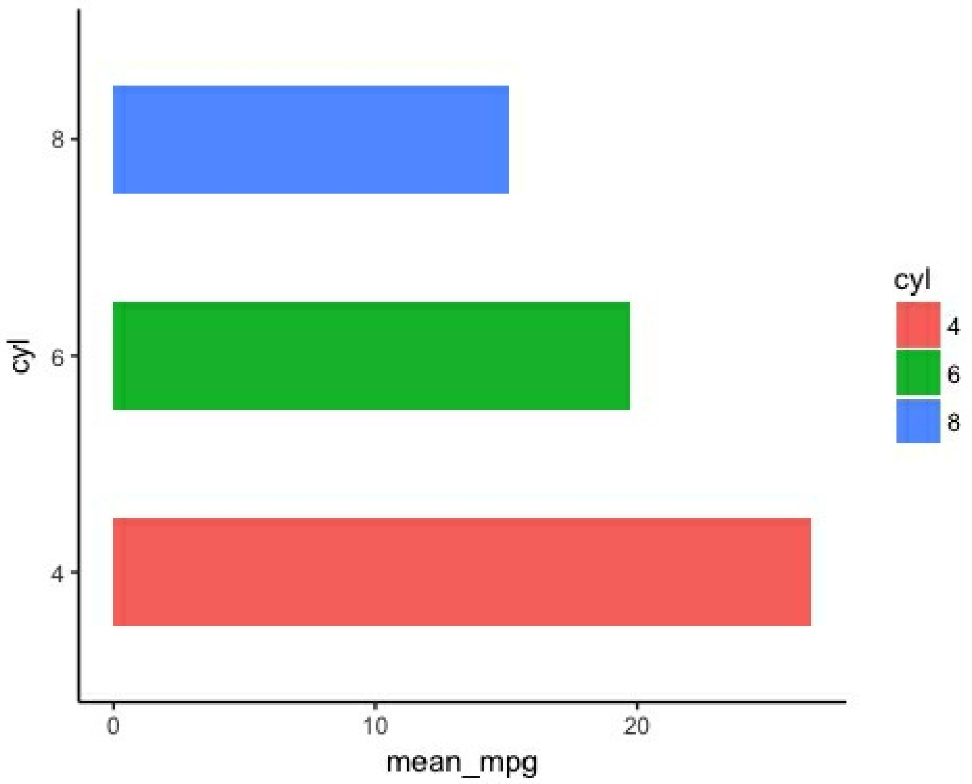
To make the graph looks prettier, you reduce the width of the bar.

```
graph <- ggplot(data_histogram, aes(x = cyl, y = mean_mpg, fill
= cyl)) +
    geom_bar(stat = "identity",
        width = 0.5) +
    coord_flip() +
    theme_classic()
```

Code Explanation

- The width argument inside the geom_bar() controls the size of the bar. Larger value increases the width.
- Note, you store the graph in the variable graph. You do so because the next step will not change the code of the variable graph. It improves the readability of the code.

Output:



Step 6) Add labels to the graph

The last step consists to add the value of the variable mean_mpg in the label.

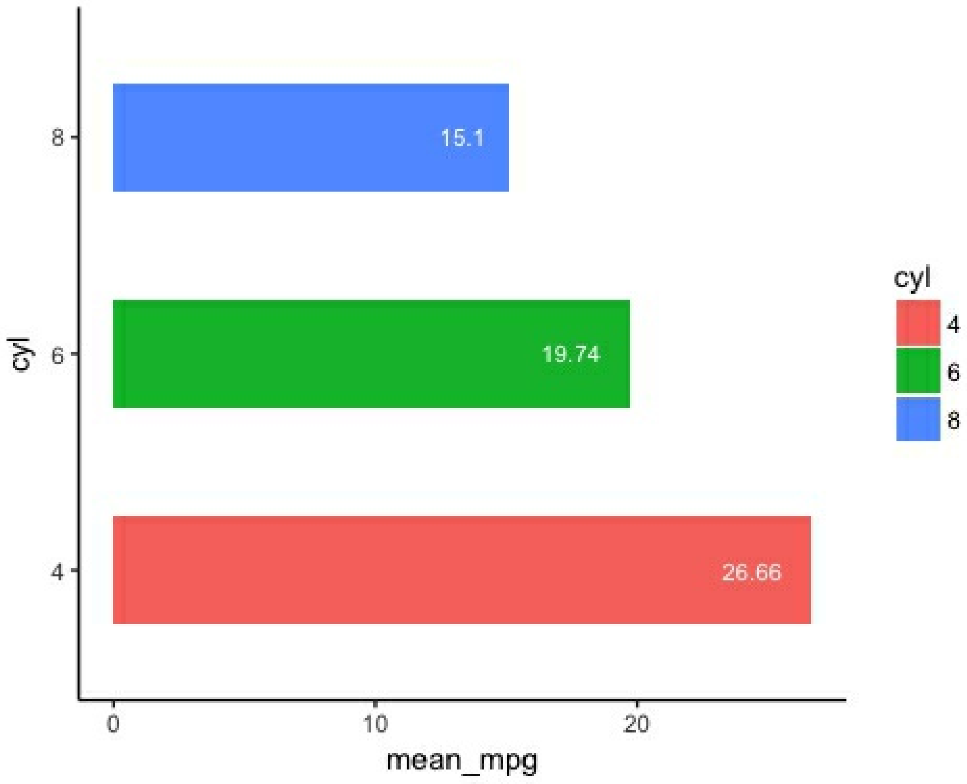
```
graph +
    geom_text(aes(label = mean_mpg),
        hjust = 1.5,
        color = "white",
        size = 3) +
    theme_classic()
```

Code Explanation

- The function geom_text() is useful to control the aesthetic of the text.
  - label=: Add a label inside the bars
  - mean_mpg: Use the variable mean_mpg for the label
- hjust controls the location of the label. Values closed to 1 displays the label at the top of the bar, and higher values bring the label to

the bottom. If the orientation of the graph is vertical, change hjust to vjust.
- color="white": Change the color of the text. Here you use the white color.
- size=3: Set the size of the text.

Output:



Summary

A bar chart is useful when the x-axis is a categorical variable. The y-axis can be either a count or a summary statistic. The table below summarizes how to control bar chart with ggplot2:

Objective	**code**
Count	`ggplot(df, eas(x= factor(x1)) + geom_bar()`

Count with different color of fill	`ggplot(df, eas(x= factor(x1), fill = factor(x1))) + geom_bar()`
Count with groups, stacked	`ggplot(df, eas(x= factor(x1), fill = factor(x2))) + geom_bar(position=position_dodge())`
Count with groups, side by side	`ggplot(df, eas(x= factor(x1), fill = factor(x2))) + geom_bar()`
Count with groups, stacked in %	`ggplot(df, eas(x= factor(x1), fill = factor(x2))) + geom_bar(position=position_dodge())`
Values	`ggplot(df, eas(x= factor(x1)+ y = x2) + geom_bar(stat="identity")`

Chapter 25: T Test in R: One Sample and Paired (with Example)

What is Statistical Inference?

Stastitical inference is the art of generating conclusions about the distribution of the data. A data scientist is often exposed to question that can only be answered scientifically. Therefore, statistical inference is a strategy to test whether a hypothesis is true, i.e. validated by the data.

A common strategy to assess hypothesis is to conduct a t-test. A t-test can tell whether two groups have the same mean. A t-test is also called a **Student Test**. A t-test can be estimated for:

1. A single vector (i.e., one-sample t-test)
2. Two vectors from the same sample group (i.e., paired t-test).

You assume that both vectors are randomly sampled, independent and come from a normally distributed population with unknown but equal variances.

What is t-test?

The basic idea behind a t-test is to use statistic to evaluate two contrary hypotheses:

- H0: NULL hypothesis: The average is the same as the sample used

- H3: True hypothesis: The average is different from the sample used

The t-test is commonly used with small sample sizes. To perform a t-test, you need to assume normality of the data.

The basic syntax for t.test() is:

```
t.test(x, y = NULL,
       mu = 0, var.equal = FALSE)
arguments:
- x : A vector to compute the one-sample t-test
- y: A second vector to compute the two sample t-test
- mu: Mean of the population- var.equal: Specify if the variance
of the two vectors are equal. By default, set to `FALSE`
```

One-sample t-test

The t-test, or student's test, compares the mean of a vector against a theoretical mean, μ. The formula used to compute the t-test is:

$$t = \frac{m - \mu}{\frac{s}{\sqrt{n}}}$$

Here

- m refers to the mean
- μ to the theoretical mean
- s is the standard deviation
- n the number of observations.

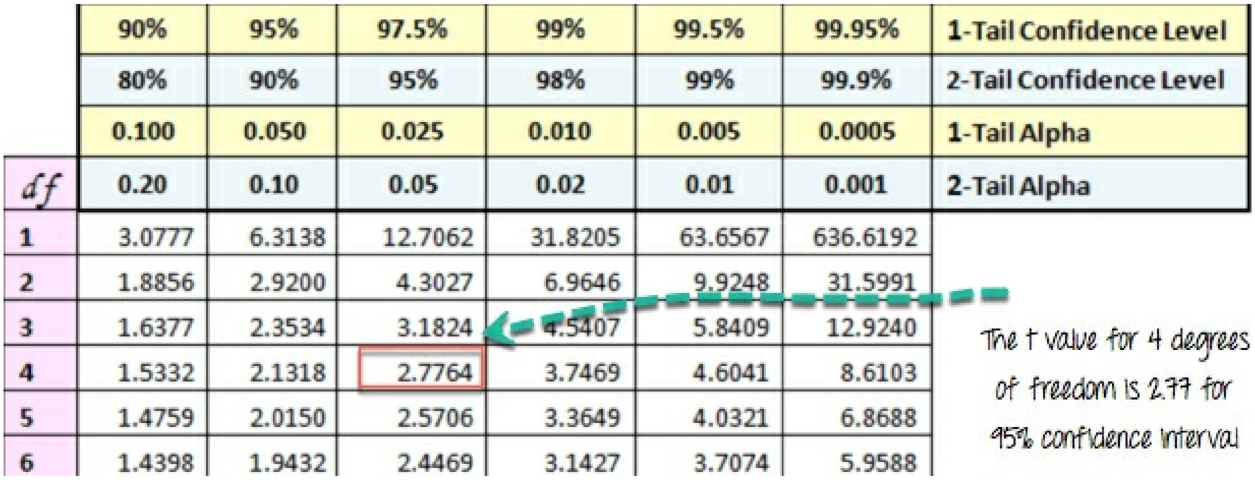
To evaluate the statistical significance of the t-test, you need to compute the **p-value**. The **p-value** ranges from 0 to 1, and is interpreted as follow:

- A p-value lower than 0.05 means you are strongly confident to reject the null hypothesis, thus H3 is accepted.
- A p-value higher than 0.05 indicates that you don't have enough evidences to reject the null hypothesis.

You can construct the pvalue by looking at the corresponding absolute value of the t-test in the Student distribution with a degrees of freedom equals to $df = n - 1.$

For instance, if you have 5 observations, you need to compare our t-value with the t-value in the Student distribution with 4 degrees of freedom and at 95 percent confidence interval. To reject the null hypothesesis, the t-value should be higher than 2.77.

Cf table below:



	90%	95%	97.5%	99%	99.5%	99.95%	1-Tail Confidence Level
	80%	90%	95%	98%	99%	99.9%	2-Tail Confidence Level
	0.100	0.050	0.025	0.010	0.005	0.0005	1-Tail Alpha
df	0.20	0.10	0.05	0.02	0.01	0.001	2-Tail Alpha
1	3.0777	6.3138	12.7062	31.8205	63.6567	636.6192	
2	1.8856	2.9200	4.3027	6.9646	9.9248	31.5991	
3	1.6377	2.3534	3.1824	4.5407	5.8409	12.9240	
4	1.5332	2.1318	2.7764	3.7469	4.6041	8.6103	
5	1.4759	2.0150	2.5706	3.3649	4.0321	6.8688	
6	1.4398	1.9432	2.4469	3.1427	3.7074	5.9588	

The t value for 4 degrees of freedom is 2.77 for 95% confidence interval

Example:

Suppose you are a company producing cookies. Each cookie is supposed to contain 10 grams of sugar. The cookies are produced by a machine that adds the sugar in a bowl before mixing everything. You believe the machine does not add 10 grams of sugar for each cookie. If your assumption is true, the machine needs to be fixed. You stored the level of sugar of thirty cookies.

Note: You can create a randomized vector with the function rnorm().

This function generates normally distributed values. The basic syntax is:

```
rnorm(n, mean, sd)
arguments
- n: Number of observations to generate
- mean: The mean of the distribution. Optional
- sd: The standard deviation of the distribution. Optional
```

You can create a distribution with 30 observations with a mean of 9.99 and a standard deviation of 0.04.

```
set.seed(123) sugar_cookie <- rnorm(30, mean = 9.99, sd = 0.04)
head(sugar_cookie)
```

Output:

```
## [1]  9.967581  9.980793 10.052348  9.992820  9.995172
10.058603
```

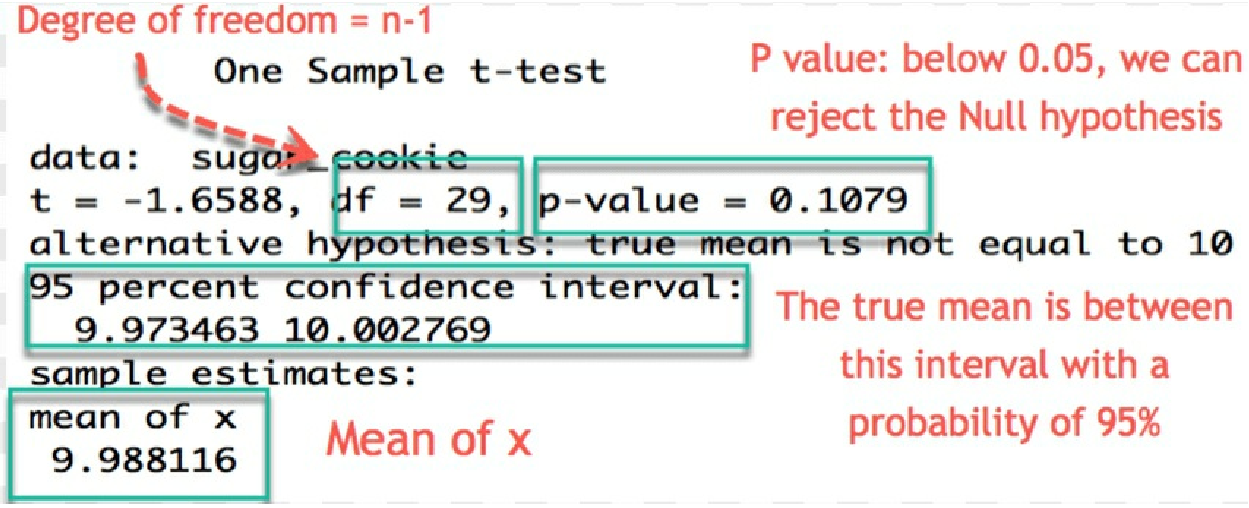
You can use a one-sample t-test to check whether the level of sugar is different than the recipe. You can draw a hypothesis test:

- H0: The average level of sugar is equal to 10
- H3: The average level of sugar is different than 10

You use a significance level of 0.05.

```
# H0 : mu = 10
t.test(sugar_cookie, mu = 10)
```

Here is the output



```
        One Sample t-test

data:   sugar_cookie
t = -1.6588, df = 29, p-value = 0.1079
alternative hypothesis: true mean is not equal to 10
95 percent confidence interval:
  9.973463 10.002769
sample estimates:
mean of x
 9.988116
```

Degree of freedom = n-1
P value: below 0.05, we can reject the Null hypothesis
The true mean is between this interval with a probability of 95%
Mean of x

The p-value of the one sample t-test is 0.1079 and above 0.05. You can be confident at 95% that the amount of sugar added by the machine is between 9.973 and 10.002 grams. You cannot reject the null (H0) hypothesis. There is not enough evidence that amount of sugar added by the machine does not follow the recipe.

Paired t-test

The paired t-test, or dependant sample t-test, is used when the mean of the treated group is computed twice. The basic application of the paired t-test is:

- A/B testing: Compare two variants
- Case control studies: Before/after treatment

Example:

A beverage company is interested in knowing the performance of a discount program on the sales. The company decided to follow the daily sales of one of its shops where the program is being promoted. At the end of the program, the company wants to know if there is a statistical difference between the average sales of the shop before and after the program.

- The company tracked the sales everyday before the program started. This is our first vector.

- The program is promoted for one week and the sales are recorded every day. This is our second vector.
- You will perform the t-test to judge the effectiveness of the program. This is called a paired t-test because the values of both vectors come from the same distribution (i.e., the same shop).

The hypothesis testing is:

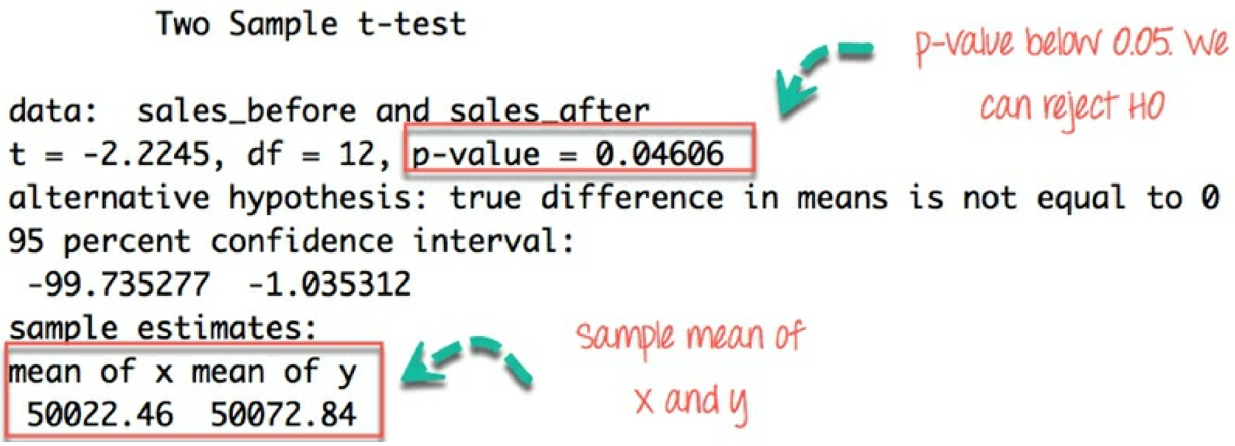
- H0: No difference in mean
- H3: The two means are different

Remember, one assumption in the t-test is an unknown but equal variance. In reality, the data barely have equal mean, and it leads to incorrect results for the t-test.

One solution to relax the equal variance assumption is to use the Welch's test. R assumes the two variances are not equal by default. In your dataset, both vectors have the same variance, you can set var.equal= TRUE.

You create two random vectors from a Gaussian distribution with a higher mean for the sales after the program.

```
set.seed(123)
# sales before the program
sales_before <- rnorm(7, mean = 50000, sd = 50)
# sales after the program.This has higher mean
sales_after <- rnorm(7, mean = 50075, sd = 50)
# draw the distribution
t.test(sales_before, sales_after,var.equal = TRUE)
```



```
        Two Sample t-test

data:  sales_before and sales_after
t = -2.2245, df = 12, p-value = 0.04606
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -99.735277  -1.035312
sample estimates:
mean of x mean of y 
 50022.46  50072.84 
```

You obtained a p-value of 0.04606, lower than the threshold of 0.05. You conclude the averages of the two groups are significantly different. The program improves the sales of shops.

Summary

The t-test belongs to the family of inferential statistics. It is commonly employed to find out if there is a statistical difference between the means of two groups.

We can summarize the t-test is the table below:

test	**Hypothesis to test**	**p-value**	**code**	**optional argument**
one-sample t-test	Mean of a vector is different from the theoretical mean	0.05	`t.test(x, mu = mean)`	
paired sample t-test	Mean A is different from mean B for the same group	0.06	`t.test(A,B, mu = mean)`	`var.equal= TRUE`

If we assume the variances are equal, we need to change the parameter var.equal= TRUE.

Chapter 26: R ANOVA Tutorial: One way & Two way (with Examples)

What is ANOVA?

Analysis of Variance(ANOVA) helps you test differences between two or more group means. ANOVA test is centered around the different sources of variation (variation between and within group) in a typical variable. A primarily ANOVA test provides evidence of the existence of the mean equality between the group. This statistical method is an extension of the t-test. It is used in a situation where the factor variable has more than one group.

One-way ANOVA

There are many situations where you need to compare the mean between multiple groups. For instance, the marketing department wants to know if three teams have the same sales performance.

- Team: 3 level factor: A, B, and C
- Sale: A measure of performance

The ANOVA test can tell if the three groups have similar performances.

To clarify if the data comes from the same population, you can perform a **one-way analysis of variance** (one-way ANOVA hereafter). This test, like any other statistical tests, gives evidence whether the H0 hypothesis can be accepted or rejected.

Hypothesis in one-way ANOVA test:

- H0: The means between groups are identical
- H3: At least, the mean of one group is different

In other words, the H0 hypothesis implies that there is not enough evidence to prove the mean of the group (factor) are different from another.

This test is similar to the t-test, although ANOVA test is recommended in situation with more than 2 groups. Except that, the t-test and ANOVA provide similar results.

Assumptions

We assume that each factor is randomly sampled, independent and comes from a normally distributed population with unknown but equal variances.

Interpret ANOVA test

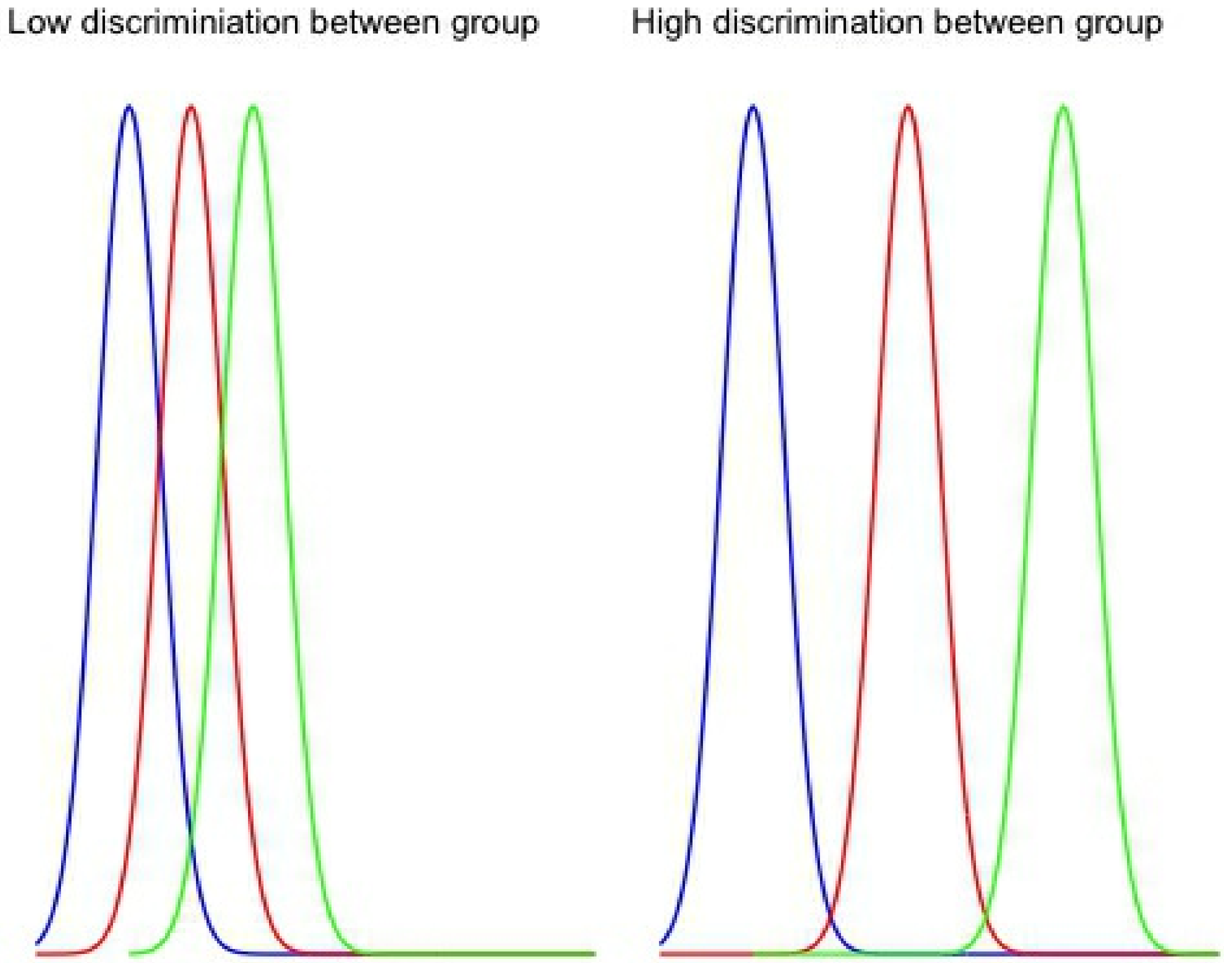
The F-statistic is used to test if the data are from significantly different populations, i.e., different sample means.

To compute the F-statistic, you need to divide the **between-group variability** over the **within-group variability**.

The **between-group** variability reflects the differences between the groups inside all of the population. Look at the two graphs below to understand the concept of between-group variance.

The left graph shows very little variation between the three group, and it is very likely that the three means tends to the **overall** mean (i.e., mean for the three groups).

The right graph plots three distributions far apart, and none of them overlap. There is a high chance the difference between the total mean and the groups mean will be large.

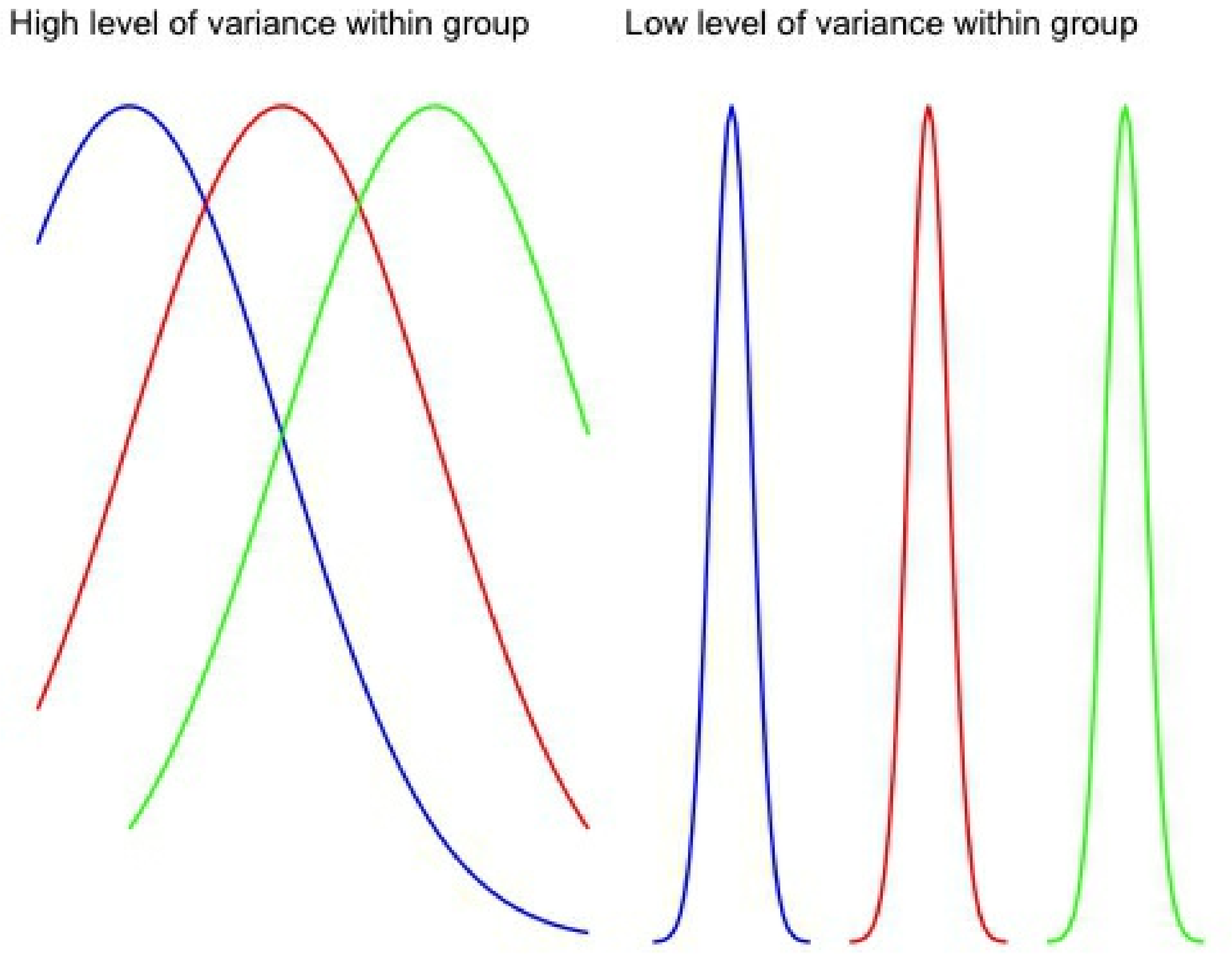


The **within group** variability considers the difference between the groups. The variation comes from the individual observations; some points might be totally different than the group means. The **within group** variability picks up this effect and refer to the sampling error.

To understand visually the concept of within group variability, look at the graph below.

The left part plots the distribution of three different groups. You increased the spread of each sample and it is clear the individual variance is large. The F-test will decrease, meaning you tend to accept the null hypothesis

The right part shows exactly the same samples (identical mean) but with lower variability. It leads to an increase of the F-test and tends in favor of the alternative hypothesis.


High level of variance within group
Low level of variance within group

You can use both measures to construct the F-statistics. It is very intuitive to understand the F-statistic. If the numerator increases, it means the between-group variability is high, and it is likely the groups in the sample are drawn from completely different distributions.

In other words, a low F-statistic indicates little or no significant difference between the group's average.

Example One way ANOVA Test

You will use the poison dataset to implement the one-way ANOVA test. The dataset contains 48 rows and 3 variables:

- Time: Survival time of the animal
- poison: Type of poison used: factor level: 1,2 and 3
- treat: Type of treatment used: factor level: 1,2 and 3

Before you start to compute the ANOVA test, you need to prepare the data as follow:

- Step 1: Import the data
- Step 2: Remove unnecessary variable
- Step 3: Convert the variable poison as ordered level

```
library(dplyr)
PATH <- "https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/poisons.csv"
df <- read.csv(PATH) %>%
select(-X) %>%
mutate(poison = factor(poison, ordered = TRUE))
glimpse(df)
```

Output:

```
## Observations: 48
## Variables: 3
## $ time   <dbl> 0.31, 0.45, 0.46, 0.43, 0.36, 0.29, 0.40,
0.23, 0.22, 0...
## $ poison <ord> 1, 1, 1, 1, 2, 2, 2, 2, 3, 3, 3, 3, 1, 1, 1,
1, 2, 2, 2...
## $ treat  <fctr> A, A, A, A, A, A, A, A, A, A, A, A, B, B, B,
B, B, B, ...
```

Our objective is to test the following assumption:

- H0: There is no difference in survival time average between group
- H3: The survival time average is different for at least one group.

In other words, you want to know if there is a statistical difference between the mean of the survival time according to the type of poison given to the Guinea pig.

You will proceed as follow:

- Step 1: Check the format of the variable poison
- Step 2: Print the summary statistic: count, mean and standard deviation
- Step 3: Plot a box plot
- Step 4: Compute the one-way ANOVA test
- Step 5: Run a pairwise t-test

Step 1) You can check the level of the poison with the following code. You should see three character values because you convert them in factor with the mutate verb.

```
levels(df$poison)
```

Output:

```
## [1] "1" "2" "3"
```

Step 2) You compute the mean and standard deviation.

```
df % > %
        group_by(poison) % > %
        summarise(
                count_poison = n(),
                mean_time = mean(time, na.rm = TRUE),
                sd_time = sd(time, na.rm = TRUE)
        )
```

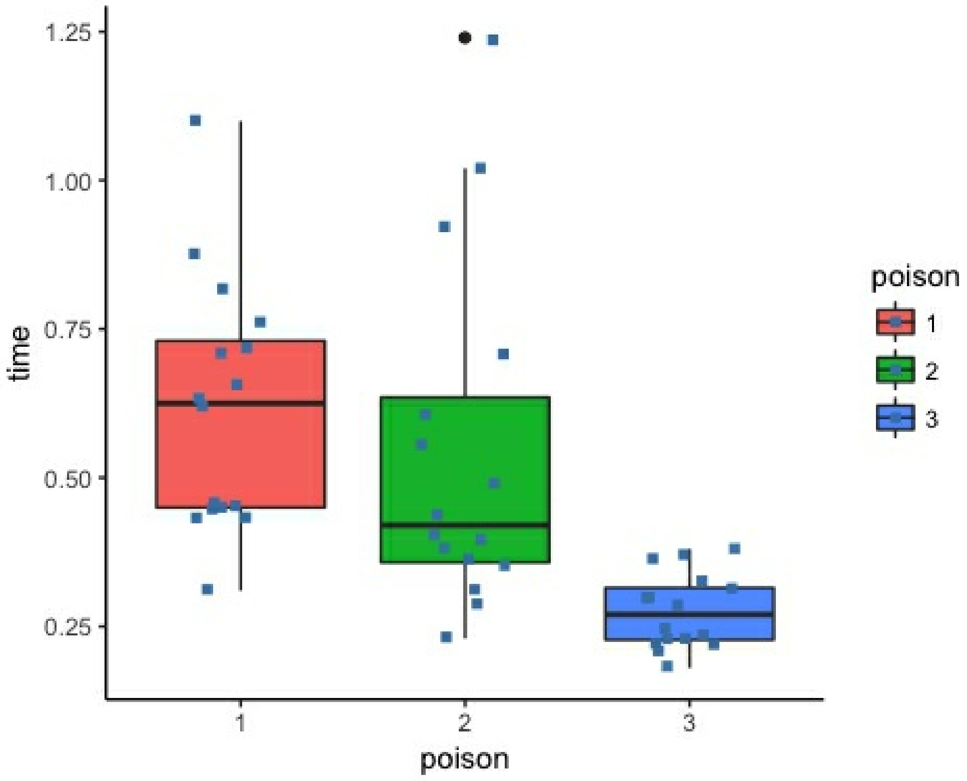
Output:

```
##
# A tibble: 3 x 4
##   poison count_poison mean_time    sd_time
##    <ord>        <int>     <dbl>      <dbl>
## 1      1           16  0.617500 0.20942779
## 2      2           16  0.544375 0.28936641
## 3      3           16  0.276250 0.06227627
```

Step 3) In step three, you can graphically check if there is a difference between the distribution. Note that you include the jittered dot.

```
ggplot(df, aes(x = poison, y = time, fill = poison)) +
    geom_boxplot() +
    geom_jitter(shape = 15,
        color = "steelblue",
        position = position_jitter(0.21)) +
    theme_classic()
```

Output:



Step 4) You can run the one-way ANOVA test with the command aov. The basic syntax for an ANOVA test is:

```
aov(formula, data)
Arguments:
- formula: The equation you want to estimate
- data: The dataset used
```

The syntax of the formula is:

```
y ~ X1+ X2+...+Xn # X1 +  X2 +... refers to the independent
variables
y ~ . # use all the remaining variables as independent variables
```

You can answer our question: Is there any difference in the survival time between the Guinea pig, knowing the type of poison given.

Note that, it is advised to store the model and use the function summary() to get a better print of the results.

```
anova_one_way <- aov(time~poison, data = df)
summary(anova_one_way)
```

Code Explanation

- aov(time ~ poison, data = df): Run the ANOVA test with the following formula
- summary(anova_one_way): Print the summary of the test

Output:

```
##             Df Sum Sq Mean Sq F value   Pr(>F)    
## poison       2  1.033  0.5165   11.79 7.66e-05 ***
## Residuals   45  1.972  0.0438                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 
1
```

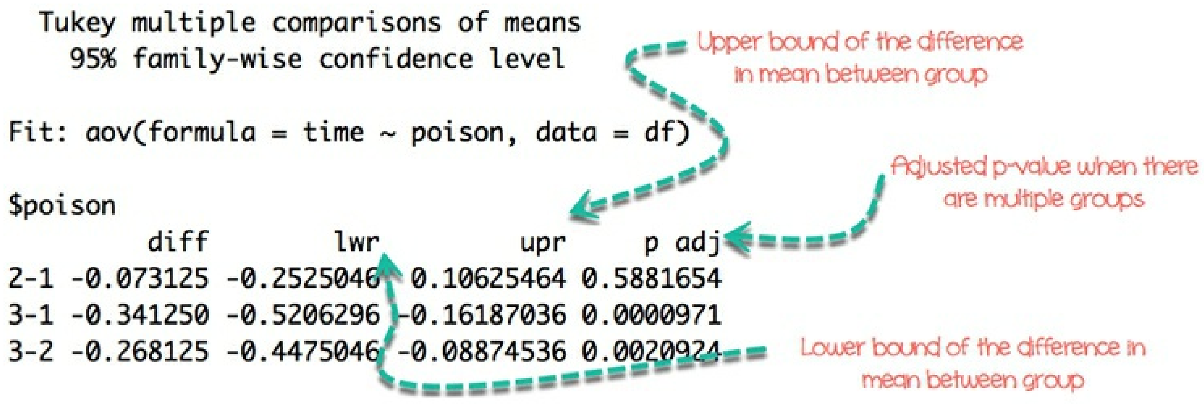
The p-value is lower than the usual threshold of 0.05. You are confident to say there is a statistical difference between the groups, indicated by the "*".

Pairwise comparison

The one-way ANOVA test does not inform which group has a different mean. Instead, you can perform a Tukey test with the function TukeyHSD().

```
TukeyHSD(anova_one_way)
```

Output:



```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = time ~ poison, data = df)

$poison
         diff        lwr         upr     p adj
2-1 -0.073125 -0.2525046  0.10625464 0.5881654
3-1 -0.341250 -0.5206296 -0.16187036 0.0000971
3-2 -0.268125 -0.4475046 -0.08874536 0.0020924
```

Upper bound of the difference in mean between group

Adjusted p-value when there are multiple groups

Lower bound of the difference in mean between group

Two-way ANOVA

A two-way ANOVA test adds another group variable to the formula. It is identical to the one-way ANOVA test, though the formula changes slightly:

$$y=x1+x2$$

with is a quantitative variable and and are categorical variables.

Hypothesis in two-way ANOVA test:

- H0: The means are equal for both variables (i.e., factor variable)
- H3: The means are different for both variables

You add treat variable to our model. This variable indicates the treatment given to the Guinea pig. You are interested to see if there is a statistical dependence between the poison and treatment given to the Guinea pig.

We adjust our code by adding treat with the other independent variable.

```
anova_two_way <- aov(time~poison + treat, data = df)
summary(anova_two_way)
```

Output:

```
##             Df Sum Sq Mean Sq F value  Pr(>F)    
## poison       2 1.0330  0.5165   20.64 5.7e-07 ***
## treat        3 0.9212  0.3071   12.27 6.7e-06 ***
## Residuals   42 1.0509  0.0250                    
## ---
```

You can conclude that both poison and treat are statistically different from 0. You can reject the NULL hypothesis and confirm that changing the treatment or the poison impact the time of survival.

Summary

We can summarize the test in the table below:

Test	**code**	**hypothesis**	**p-value**
One way ANOVA	`aov(y ~ X, data = df)`	H3: Average is different for at least one group	0.05
Pairwise	`TukeyHSD(ANOVA summary)`		0.05
Two way ANOVA	`aov(y ~ X1 + X2, data = df)`	H3: Average is different for both group	0.05

Chapter 27: R Simple, Multiple Linear and Stepwise Regression [with Example]

Simple Linear regression

Linear regression answers a simple question: Can you measure an exact relationship between one target variables and a set of predictors?

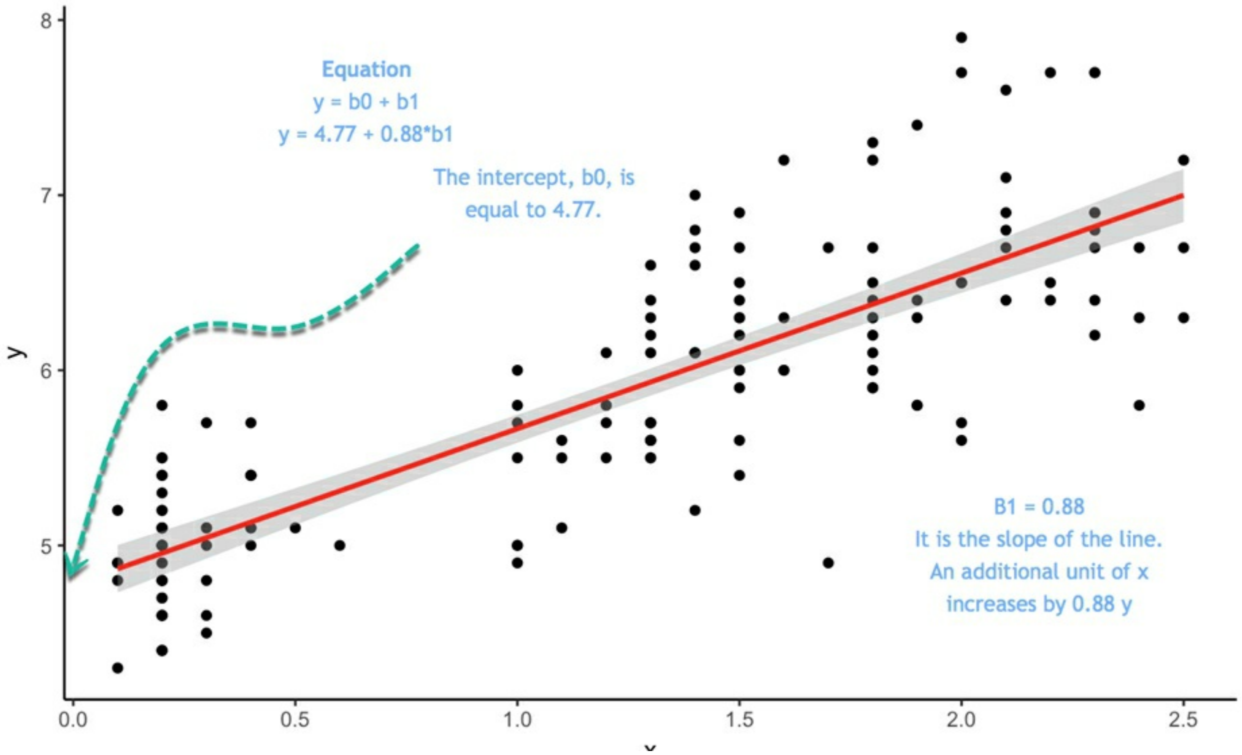
The simplest of probabilistic models is the straight line model:

$$y = \beta_0 + \beta_1 x + \varepsilon$$

where

- y = Dependent variable
- x = Independent variable
- ε = random error component
- β_0 = intercept
- β_1 = Coefficient of x

Consider the following plot:



The equation is $y = \beta_0 + \beta_1 x + \varepsilon$. β_0 is the intercept. If x equals to 0, y will be equal to the intercept, 4.77. is the slope of the line. It tells in which proportion y varies when x varies.

To estimate the optimal values of β_0 and β_1 , you use a method called **Ordinary Least Squares (OLS)**. This method tries to find the parameters that minimize the sum of the squared errors, that is the vertical distance between the predicted y values and the actual y values. The difference is known as the **error term**.

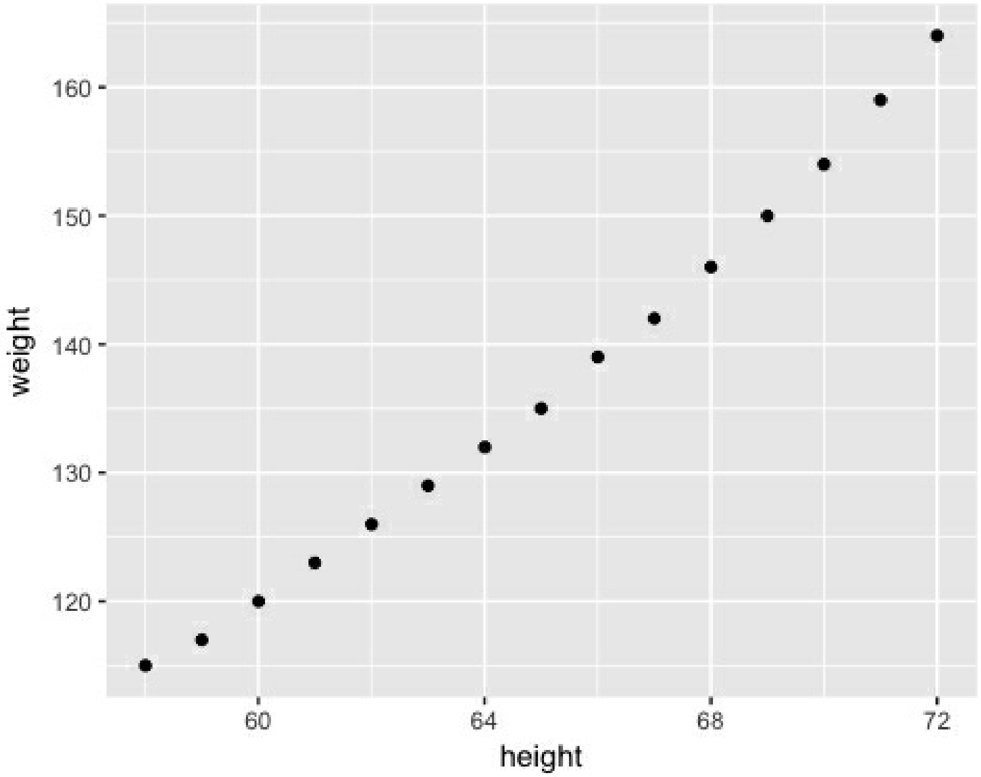
Before you estimate the model, you can determine whether a linear relationship between y and x is plausible by plotting a scatterplot.

Scatterplot

We will use a very simple dataset to explain the concept of simple linear regression. We will import the Average Heights and weights for American Women. The dataset contains 15 observations. You want to measure whether Heights are positively correlated with weights.

```
library(ggplot2)
path <- 'https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/women.csv'
df <-read.csv(path)
ggplot(df,aes(x=height, y =  weight))+
geom_point()
```

Output:



The scatterplot suggests a general tendency for y to increase as x increases. In the next step, you will measure by how much increases for each additional .

Least Squares Estimates

In a simple OLS regression, the computation of α_0 and β_0 is straightforward. The goal is not to show the derivation in this tutorial.

You will only write the formula.

You want to estimate: $y = \beta_0 + \beta_1 x + \varepsilon$

The goal of the OLS regression is to minimize the following equation:

$$\Sigma(y_i - \hat{y}_i)^2 = \Sigma e_i^2$$

where

y_i is the actual value and $\hat{y}_i$ is the predicted value.

The solution for β_0 is $\beta_0 = \overline{y} - \beta_1 \overline{x}$

Note that $\overline{x}$ means the average value of x

The solution for β is $\beta = \frac{Cov(x,y)}{Var(x)}$

In R, you can use the cov()and var()function to estimate β and you can use the mean() function to estimate α

```
beta <- cov(df$height, df$weight) / var (df$height)
beta
```

Output:

```
##[1] 3.45
```

```
alpha <- mean(df$weight) - beta * mean(df$height)
alpha
```

Output:

```
## [1] -87.51667
```

The beta coefficient implies that for each additional height, the weight increases by 3.45.

Estimating simple linear equation manually is not ideal. R provides a suitable function to estimate these parameters. You will see this function shortly. Before that, we will introduce how to compute by hand a simple linear regression model. In your journey of data scientist, you will barely or never estimate a simple linear model. In most situation, regression tasks are performed on a lot of estimators.

Multiple Linear regression

More practical applications of regression analysis employ models that are more complex than the simple straight-line model. The probabilistic model that includes more than one independent variable is called **multiple regression models**. The general form of this model is:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_k x_k + \varepsilon$$

In matrix notation, you can rewrite the model:

- $Y = \beta X + \varepsilon$

The dependent variable y is now a function of k independent variables. The value of the coefficient β_i determines the contribution of the independent variable x_i and β_0.

We briefly introduce the assumption we made about the random error ε of the OLS:

- Mean equal to 0

- Variance equal to σ^2
- Normal distribution
- Random errors are independent (in a probabilistic sense)

You need to solve for β , the vector of regression coefficients that minimise the sum of the squared errors between the predicted and actual y values.

The closed-form solution is:

$$\beta = (X^T X)^{-1} X^T Y$$

with:

- indicates the **transpose** of the matrix X
- $(X^T X)^{-1}$ indicates the **invertible matrix**

We use the mtcars dataset. You are already familiar with the dataset. Our goal is to predict the mile per gallon over a set of features.

Continuous variables

For now, you will only use the continuous variables and put aside categorical features. The variable am is a binary variable taking the value of 1 if the transmission is manual and 0 for automatic cars; vs is also a binary variable.

```
library(dplyr)
df <- mtcars % > %
select(-c(am, vs, cyl, gear, carb))
glimpse(df)
```

Output:

```
## Observations: 32
## Variables: 6
## $ mpg  <dbl> 21.0, 21.0, 22.8, 21.4, 18.7, 18.1, 14.3, 24.4,
22.8, 19....
## $ disp <dbl> 160.0, 160.0, 108.0, 258.0, 360.0, 225.0, 360.0,
146.7, 1...
## $ hp   <dbl> 110, 110, 93, 110, 175, 105, 245, 62, 95, 123,
123, 180, ...
## $ drat <dbl> 3.90, 3.90, 3.85, 3.08, 3.15, 2.76, 3.21, 3.69,
3.92, 3.9...
## $ wt   <dbl> 2.620, 2.875, 2.320, 3.215, 3.440, 3.460, 3.570,
3.190, 3...
## $ qsec <dbl> 16.46, 17.02, 18.61, 19.44, 17.02, 20.22, 15.84,
20.00, 2...
```

You can use the lm() function to compute the parameters. The basic syntax of this function is:

```
lm(formula, data, subset)
Arguments:
        -formula: The equation you want to estimate
        -data: The dataset used
        -subset: Estimate the model on a subset of the dataset
```

Remember an equation is of the following form

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_k x_k + \varepsilon$$

in R

- The symbol = is replaced by ~
- Each x is replaced by the variable name
- If you want to drop the constant, add -1 at the end of the formula

Example:

You want to estimate the weight of individuals based on their height and revenue. The equation is

$$weigh = \beta_0 + \beta_1 height_1 + \beta_2 revenue_2 + \varepsilon$$

The equation in R is written as follow:

y ~ X1+ X2+...+Xn # With intercept

So for our example:

- Weigh ~ height + revenue

Your objective is to estimate the mile per gallon based on a set of variables. The equation to estimate is:

$$mpg = \beta_0 + \beta_1 disp_1 + \beta_2 hp_2 + \beta_3 drat_3 + \beta_4 wt_4 + \varepsilon$$

You will estimate your first linear regression and store the result in the fit object.

```
model <- mpg~.disp + hp + drat + wt
fit <- lm(model, df)
fit
```

Code Explanation

- model <- mpg **~**. disp + hp + drat+ wt: Store the model to estimate
- **lm**(model, df): Estimate the model with the data frame df

```
##
## Call:
## lm(formula = model, data = df)
##
## Coefficients:
##
(Intercept)         disp           hp         drat           wt
##    16.53357      0.00872     -0.02060      2.01577     -4.3854
##        qsec
##     0.64015
```

The output does not provide enough information about the quality of the fit. You can access more details such as the significance of the coefficients, the degree of freedom and the shape of the residuals with the summary() function.

```
summary(fit)
```

Output:

```
## return the p-value and coefficient
##
## Call:
## lm(formula = model, data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5404 -1.6701 -0.4264  1.1320  5.4996
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 16.53357   10.96423   1.508  0.14362
## disp         0.00872    0.01119   0.779  0.44281
## hp          -0.02060    0.01528  -1.348  0.18936
## drat         2.01578    1.30946   1.539  0.13579
## wt          -4.38546    1.24343  -3.527  0.00158 **
## qsec         0.64015    0.45934   1.394  0.17523
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '
1
##
## Residual standard error: 2.558 on 26 degrees of freedom
## Multiple R-squared:  0.8489, Adjusted R-squared:  0.8199
## F-statistic: 29.22 on 5 and 26 DF, p-value: 6.892e-10
```

Inference from the above table output

- The above table proves that there is a strong negative relationship between wt and mileage and positive relationship with drat.
- Only the variable wt has a statistical impact on mpg. Remember, to test a hypothesis in statistic, we use:
  - H0: No statistical impact
  - H3: The predictor has a meaningful impact on y
  - If the p value is lower than 0.05, it indicates the variable is statistically significant
- Adjusted R-squared: Variance explained by the model. In your model, the model explained 82 percent of the variance of y. R squared is always between 0 and 1. The higher the better

You can run the ANOVA test to estimate the effect of each feature on the variances with the anova() function.

```
anova(fit)
```

Output:

```
## Analysis of Variance Table
##
## Response: mpg
##           Df Sum Sq Mean Sq  F value   Pr(>F)
## disp       1 808.89  808.89 123.6185 2.23e-11 ***
## hp         1  33.67   33.67   5.1449 0.031854 *
## drat       1  30.15   30.15   4.6073 0.041340 *
## wt         1  70.51   70.51  10.7754 0.002933 **
## qsec       1  12.71   12.71   1.9422 0.175233
## Residuals 26 170.13    6.54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '
1
```

A more conventional way to estimate the model performance is to display the residual against different measures.

You can use the plot() function to show four graphs:

- Residuals vs Fitted values

- Normal Q-Q plot: Theoretical Quartile vs Standardized residuals

- Scale-Location: Fitted values vs Square roots of the standardised residuals

- Residuals vs Leverage: Leverage vs Standardized residuals

You add the code par(mfrow=c(2,2)) before plot(fit). If you don't add this line of code, R prompts you to hit the enter command to display the next graph.

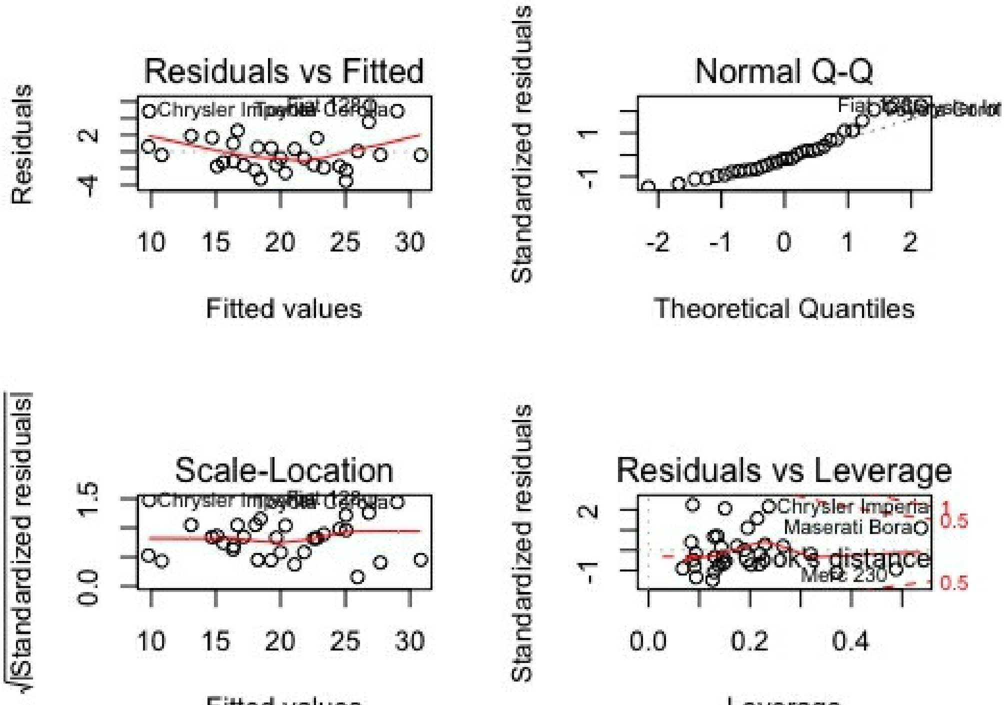
```
par(mfrow=(2,2))
```

Code Explanation

- (mfrow=c(2,2)): return a window with the four graphs side by side.
- The first 2 adds the number of rows
- The second 2 adds the number of columns.
- If you write (mfrow=c(3,2)): you will create a 3 rows 2 columns window

```
plot(fit)
```

Output:



The lm() formula returns a list containing a lot of useful information. You can access them with the fit object you have created, followed by the $ sign and the information you want to extract.

- coefficients: `fit$coefficients`

- residuals: `fit$residuals`

- fitted value: `fit$fitted.values`

Factors regression

In the last model estimation, you regress mpg on continuous variables only. It is straightforward to add factor variables to the model. You add the variable am to your model. It is important to be sure the variable is a factor level and not continuous.

```
df <- mtcars % > %
mutate(cyl = factor(cyl),
    vs = factor(vs),
    am = factor(am),
    gear = factor(gear),
    carb = factor(carb))
summary(lm(model, df))
```

Output:

```
##
## Call:
## lm(formula = model, data = df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5087 -1.3584 -0.0948  0.7745  4.6251
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 23.87913   20.06582   1.190   0.2525
## cyl6        -2.64870    3.04089  -0.871   0.3975
## cyl8        -0.33616    7.15954  -0.047   0.9632
## disp         0.03555    0.03190   1.114   0.2827
## hp          -0.07051    0.03943  -1.788   0.0939 .
## drat         1.18283    2.48348   0.476   0.6407
## wt          -4.52978    2.53875  -1.784   0.0946 .
## qsec         0.36784    0.93540   0.393   0.6997
## vs1          1.93085    2.87126   0.672   0.5115
## am1          1.21212    3.21355   0.377   0.7113
## gear4        1.11435    3.79952   0.293   0.7733
## gear5        2.52840    3.73636   0.677   0.5089
## carb2       -0.97935    2.31797  -0.423   0.6787
## carb3        2.99964    4.29355   0.699   0.4955
## carb4        1.09142    4.44962   0.245   0.8096
## carb6        4.47757    6.38406   0.701   0.4938
## carb8        7.25041    8.36057   0.867   0.3995
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '
1
##
## Residual standard error: 2.833 on 15 degrees of freedom
## Multiple R-squared:  0.8931, Adjusted R-squared:  0.779
## F-statistic:  7.83 on 16 and 15 DF,  p-value: 0.000124
```

R uses the first factor level as a base group. You need to compare the coefficients of the other group against the base group.

Stepwise regression

The last part of this tutorial deals with the **stepwise regression** algorithm. The purpose of this algorithm is to add and remove potential candidates in the models and keep those who have a significant impact on the dependent variable. This algorithm is meaningful when the dataset contains a large list of predictors. You don't need to manually add and remove the independent variables. The stepwise regression is built to select the best candidates to fit the model.

Let's see in action how it works. You use the mtcars dataset with the continuous variables only for pedagogical illustration. Before you begin analysis, its good to establish variations between the data with a correlation matrix. The GGally library is an extension of ggplot2.

The library includes different functions to show summary statistics such as correlation and distribution of all the variables in a matrix. We will use the ggscatmat function, but you can refer to the vignette for more information about the GGally library.

The basic syntax for ggscatmat() is:

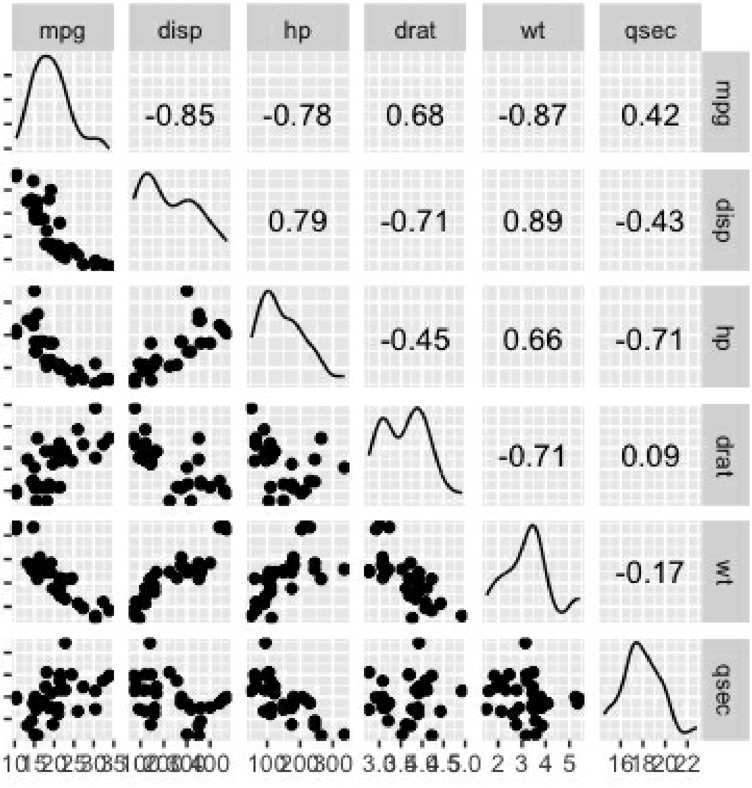
```
ggscatmat(df, columns = 1:ncol(df), corMethod = "pearson")
arguments:
-df:  A matrix of continuous variables
-columns: Pick up the columns to use in the function. By
```

```
default, all columns are used
-corMethod: Define the function to compute the correlation
between variable. By default, the algorithm uses the Pearson
formula
```

You display the correlation for all your variables and decides which one will be the best candidates for the first step of the stepwise regression. There are some strong correlations between your variables and the dependent variable, mpg.

```
library(GGally)
df <- mtcars % > %
        select(-c(am, vs, cyl, gear, carb))
ggscatmat(df, columns = 1: ncol(df))
```

Output:



Stepwise regression

Variables selection is an important part to fit a model. The stepwise regression will perform the searching process automatically. To estimate how many possible choices there are in the dataset, you compute 2^k with k is the number of predictors. The amount of possibilities grows bigger with the number of independent variables. That's why you need to have an automatic search.

You need to install the olsrr package from CRAN. The package is not available yet in Anaconda. Hence, you install it directly from the command line:

```
install.packages("olsrr")
```

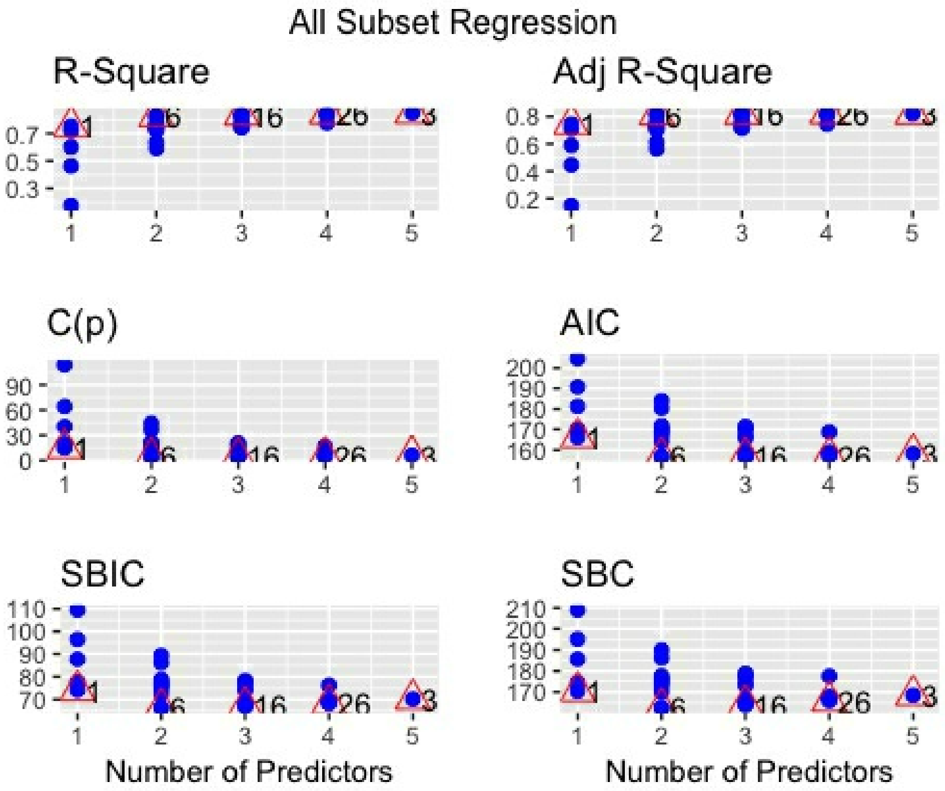
You can plot all the subsets of possibilities with the fit criteria (i.e. R-square, Adjusted R-square, Bayesian criteria). The model with the lowest AIC criteria will be the final model.

```
library(olsrr)
model <- mpg~.
fit <- lm(model, df)
test <- ols_all_subset(fit)
plot(test)
```

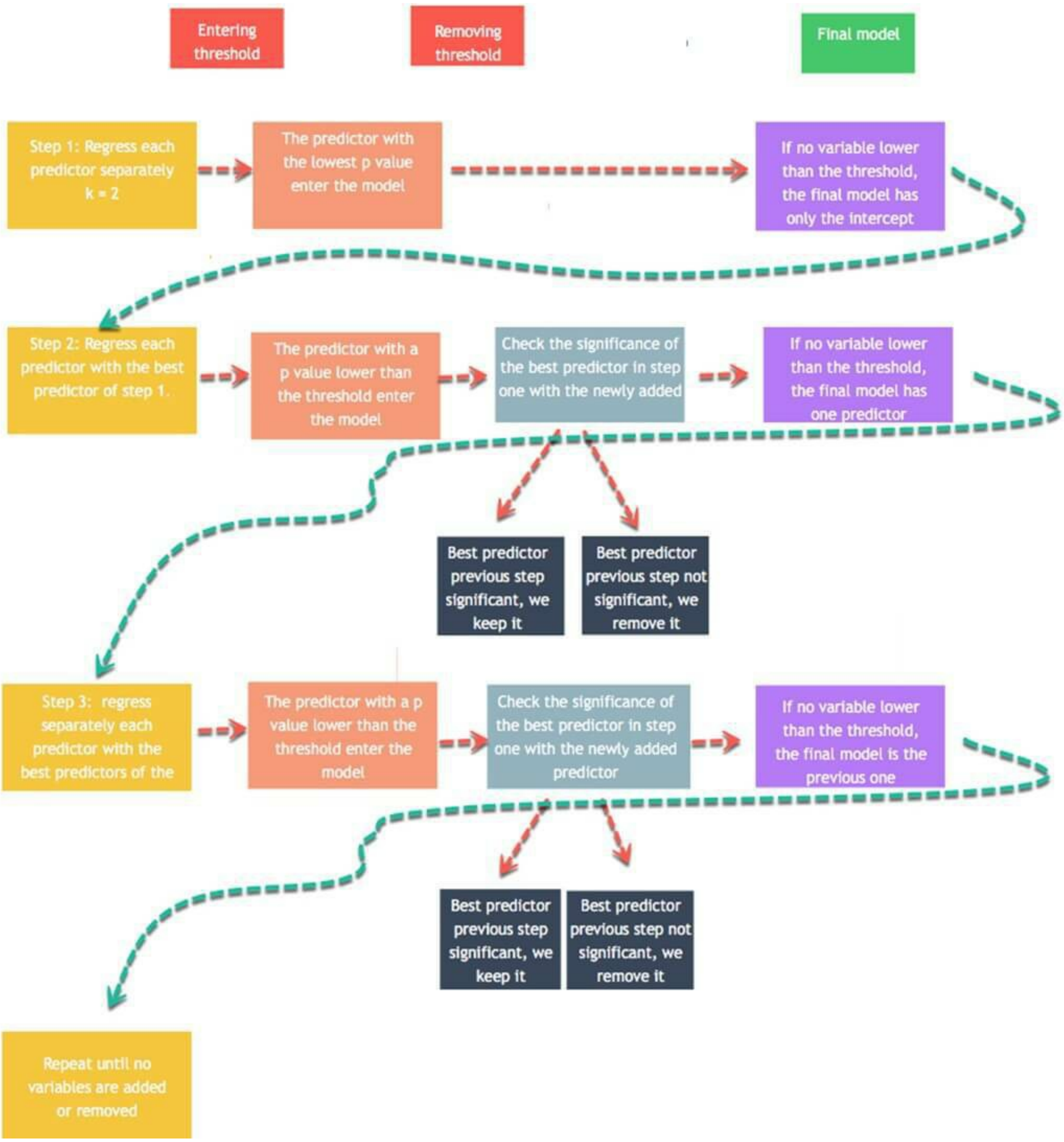
Code Explanation

- mpg ~.: Construct the model to estimate
- **lm**(model, df): Run the OLS model
- **ols_all_subset**(fit): Construct the graphs with the relevant statistical information
- **plot(test):** Plot the graphs

Output:



Linear regression models use the **t-test** to estimate the statistical impact of an independent variable on the dependent variable. Researchers set the maximum threshold at 10 percent, with lower values indicates a stronger statistical link. The strategy of the stepwise regression is constructed around this test to add and remove potential candidates. The algorithm works as follow:


Entering threshold
Removing threshold
Final model
Step 1: Regress each predictor separately k = 2
The predictor with the lowest p value enter the model
If no variable lower than the threshold, the final model has only the intercept
Step 2: Regress each predictor with the best predictor of step 1.
The predictor with a p value lower than the threshold enter the model
Check the significance of the best predictor in step one with the newly added
If no variable lower than the threshold, the final model has one predictor
Best predictor previous step significant, we keep it
Best predictor previous step not significant, we remove it
Step 3: regress separately each predictor with the best predictors of the
The predictor with a p value lower than the threshold enter the model
Check the significance of the best predictor in step one with the newly added predictor
If no variable lower than the threshold, the final model is the previous one
Best predictor previous step significant, we keep it
Best predictor previous step not significant, we remove it
Repeat until no variables are added or removed

- Step 1: Regress each predictor on y separately. Namely, regress x_1 on y, x_2 on y to x_n. Store the **p-value** and keep the regressor with a p-value lower than a defined threshold (0.1 by default). The predictors with a significance lower than the threshold will be added to the final model. If no variable has a p-value lower than the entering threshold, then the algorithm stops, and you have your final model with a constant only.
- Step 2: Use the predictor with the lowest p-value and adds

separately one variable. You regress a constant, the best predictor of step one and a third variable. You add to the stepwise model, the new predictors with a value lower than the entering threshold. If no variable has a p-value lower than 0.1, then the algorithm stops, and you have your final model with one predictor only. You regress the stepwise model to check the significance of the step 1 best predictors. If it is higher than the removing threshold, you keep it in the stepwise model. Otherwise, you exclude it.

- Step 3: You replicate step 2 on the new best stepwise model. The algorithm adds predictors to the stepwise model based on the entering values and excludes predictor from the stepwise model if it does not satisfy the excluding threshold.
- The algorithm keeps on going until no variable can be added or excluded.

You can perform the algorithm with the function ols_stepwise() from the olsrr package.

```
ols_stepwise(fit, pent = 0.1, prem = 0.3, details = FALSE)

arguments:
-fit:  Model to fit. Need to use `lm()`before to run
`ols_stepwise()
-pent: Threshold of the p-value used to enter a variable into
the stepwise model. By default, 0.1
-prem: Threshold of the p-value used to exclude a variable into
the stepwise model. By default, 0.3
-details: Print the details of each step
```

Before that, we show you the steps of the algorithm. Below is a table with the dependent and independent variables:

Dependent variable	**Independent variables**
mpg	disp
	hp

	drat
	wt
	qsec

Start

To begin with, the algorithm starts by running the model on each independent variable separately. The table shows the p-value for each model.

```
## [[1]]
##  (Intercept)         disp
## 3.576586e-21 9.380327e-10
##
## [[2]]
##  (Intercept)           hp
## 6.642736e-18 1.787835e-07
##
## [[3]]
##  (Intercept)         drat
## 0.1796390847 0.0000177624
##
## [[4]]
##  (Intercept)           wt
## 8.241799e-19 1.293959e-10
##
## [[5]
## (Intercept)        qsec
##  0.61385436  0.01708199
```

To enter the model, the algorithm keeps the variable with the lowest p-value. From the above output, it is wt

Step 1

In the first step, the algorithm runs mpg on wt and the other variables independently.

```
## [[1]]
##  (Intercept)           wt         disp
## 4.910746e-16 7.430725e-03 6.361981e-02
##
## [[2]]
##  (Intercept)           wt           hp
## 2.565459e-20 1.119647e-06 1.451229e-03
##
## [[3]]
##  (Intercept)           wt         drat
## 2.737824e-04 1.589075e-06 3.308544e-01
##
## [[4]]
##  (Intercept)           wt         qsec
## 7.650466e-04 2.518948e-11 1.499883e-03
```

Each variable is a potential candidate to enter the final model. However, the algorithm keeps only the variable with the lower p-value. It turns out hp has a slighlty lower p-value than qsec. Therefore, hp enters the final model

Step 2

The algorithm repeats the first step but this time with two independent variables in the final model.

```
## [[1]]
##  (Intercept)           wt           hp         disp
## 1.161936e-16 1.330991e-03 1.097103e-02 9.285070e-01
##
## [[2]]
##  (Intercept)           wt           hp         drat
## 5.133678e-05 3.642961e-04 1.178415e-03 1.987554e-01
##
## [[3]]
##  (Intercept)           wt           hp         qsec
## 2.784556e-03 3.217222e-06 2.441762e-01 2.546284e-01
```

None of the variables that entered the final model has a p-value sufficiently low. The algorithm stops here; we have the final model:

```
##
## Call:
```

```
## lm(formula = mpg ~ wt + hp, data = df)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -3.941 -1.600 -0.182  1.050  5.854
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 37.22727    1.59879  23.285  < 2e-16 ***
## wt          -3.87783    0.63273  -6.129 1.12e-06 ***
## hp          -0.03177    0.00903  -3.519  0.00145 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '
1
##
## Residual standard error: 2.593 on 29 degrees of freedom
## Multiple R-squared:  0.8268, Adjusted R-squared:  0.8148
## F-statistic: 69.21 on 2 and 29 DF,  p-value: 9.109e-
12
```

You can use the function ols_stepwise() to compare the results.

```
stp_s <-ols_stepwise(fit, details=TRUE)
```

Output:

The algorithm founds a solution after 2 steps, and return the same output as we had before.

At the end, you can say the models is explained by two variables and an intercept. Mile per gallon is negatively correlated with Gross horsepower and Weight

```
## You are selecting variables based on p value...
## 1 variable(s) added....
## Variable Selection Procedure
##  Dependent Variable: mpg
##
##  Stepwise Selection: Step 1
##
##  Variable wt Entered
##
##                          Model
```

```
Summary
## -------------------------------------------------------------
-
## R                        0.868       RMSE                3.046
## R-Squared                0.753       Coef. Var          15.161
## Adj. R-Squared           0.745       MSE                 9.277
## Pred R-Squared           0.709       MAE                 2.341
## -------------------------------------------------------------
-
##  RMSE: Root Mean Square Error
##  MSE: Mean Square Error
##  MAE: Mean Absolute Error
##               ANOVA
## -------------------------------------------------------------
-------
##                 Sum
of
##                Squares        DF    Mean
Square      F         Sig.
## -------------------------------------------------------------
-------
##
Regression     847.725         1        847.725    91.375    0.00
##
Residual       278.322        30          9.277
##
Total         1126.047        31
## -------------------------------------------------------------
-------
##
##                                     Parameter
Estimates
## -------------------------------------------------------------
---------------------------
##       model      Beta    Std. Error    Std.
Beta      t         Sig      lower     upper
## -------------------------------------------------------------
---------------------------
##
(Intercept)    37.285         1.878                 19.858    0.0
##          wt    -5.344         0.559       -0.868    -9.559
## -------------------------------------------------------------
---------------------------
## 1 variable(s) added...
## Stepwise Selection: Step 2
```

```
##
##  Variable hp Entered
##
##                         Model
Summary
## -------------------------------------------------------------
-
## R                       0.909       RMSE                2.593
## R-Squared               0.827       Coef. Var          12.909
## Adj. R-Squared          0.815       MSE                 6.726
## Pred R-Squared          0.781       MAE                 1.901
## -------------------------------------------------------------
-
##  RMSE: Root Mean Square Error
##  MSE: Mean Square Error
##  MAE: Mean Absolute Error
##                      ANOVA
## -------------------------------------------------------------
-------
##                 Sum
of
##                Squares        DF    Mean
Square      F         Sig.
## -------------------------------------------------------------
-------
##
Regression     930.999         2        465.500    69.211    0.00
##
Residual       195.048        29          6.726
##
Total         1126.047        31
## -------------------------------------------------------------
-------
##
##                                   Parameter
Estimates
## -------------------------------------------------------------
---------------------------
##       model      Beta    Std. Error    Std.
Beta      t        Sig      lower     upper
## -------------------------------------------------------------
---------------------------
##
(Intercept)    37.227         1.599                 23.285    0.0
##          wt    -3.878         0.633       -0.630    -6.129
##          hp    -0.032         0.009       -0.361    -3.519
## -------------------------------------------------------------
---------------------------
## No more variables to be added or removed.
```

Machine learning

Machine learning is becoming widespread among data scientist and is deployed in hundreds of products you use daily. One of the first ML application was **spam filter**.

Following are other application of Machine Learning-

- Identification of unwanted spam messages in email
- Segmentation of customer behavior for targeted advertising
- Reduction of fraudulent credit card transactions
- Optimization of energy use in home and office building
- Facial recognition

Supervised learning

In **supervised learning**, the training data you feed to the algorithm includes a label.

Classification is probably the most used supervised learning technique. One of the first classification task researchers tackled was the spam filter. The objective of the learning is to predict whether an email is classified as spam or ham (good email). The machine, after the training step, can detect the class of email.

Regressions are commonly used in the machine learning field to predict continuous value. Regression task can predict the value of a **dependent variable** based on a set of **independent variables** (also called predictors or regressors). For instance, linear regressions can predict a stock price, weather forecast, sales and so on.

Here is the list of some fundamental supervised learning algorithms.

- Linear regression
- Logistic regression
- Nearest Neighbors
- Support Vector Machine (SVM)
- Decision trees and Random Forest
- Neural Networks

Unsupervised learning

In **unsupervised learning**, the training data is unlabeled. The system tries to learn without a reference. Below is a list of unsupervised learning algorithms.

- K-mean
- Hierarchical Cluster Analysis
- Expectation Maximization
- Visualization and dimensionality reduction
- Principal Component Analysis
- Kernel PCA
- Locally-Linear Embedding

Summary

Ordinary least squared regression can be summarized in the table below:

Library	Objective	Function	Arguments
base	Compute a linear regression	lm()	formula, data
base	Summarize model	summarize()	fit

base	Exctract coefficients	lm()$coefficient	
base	Exctract residuals	lm()$residuals	
base	Exctract fitted value	lm()$fitted.values	
olsrr	Run stepwise regression	ols_stepwise()	fit, pent = 0.1, prem = 0.3, details = FALSE

Note: Remember to transform categorical variable in factor before to fit the model.

Chapter 28: Decision Tree in R with Example

What are Decision Trees?

Decision trees are versatile Machine Learning algorithm that can perform both classification and regression tasks. They are very powerful algorithms, capable of fitting complex datasets. Besides, decision trees are fundamental components of random forests, which are among the most potent Machine Learning algorithms available today.

Training and Visualizing a decision trees

To build your first decision trees, we will proceed as follow:

Step 1) Import the data

If you are curious about the fate of the titanic, you can watch this video on Youtube. The purpose of this dataset is to predict which people are more likely to survive after the collision with the iceberg. The dataset contains 13 variables and 1309 observations. The dataset is ordered by the variable X.

```
set.seed(678)
path <- 'https://raw.githubusercontent.com/guru99-edu/R-Programming/master/titanic_data.csv'
titanic <-read.csv(path)
head(titanic)
```

Output:

```
##   X pclass
survived                                            name    sex
## 1 1      1        1                   Allen, Miss. Elisabeth
Walton female
## 2 2      1        1                  Allison, Master. Hudson
Trevor   male
## 3 3      1        0                    Allison, Miss. Helen
Loraine female
## 4 4      1        0            Allison, Mr. Hudson Joshua
Creighton   male
## 5 5      1        0 Allison, Mrs. Hudson J C (Bessie Waldo
Daniels) female
## 6 6      1        1                             Anderson, Mr.
Harry   male
##       age sibsp parch ticket     fare   cabin embarked
## 1 29.0000     0     0  24160 211.3375      B5        S
## 2  0.9167     1     2 113781 151.5500 C22 C26        S
## 3  2.0000     1     2 113781 151.5500 C22 C26        S
## 4 30.0000     1     2 113781 151.5500 C22 C26        S
## 5 25.0000     1     2 113781 151.5500 C22 C26        S
## 6 48.0000     0     0  19952  26.5500     E12        S
##                         home.dest
## 1                    St Louis, MO
## 2 Montreal, PQ / Chesterville, ON
## 3 Montreal, PQ / Chesterville, ON
## 4 Montreal, PQ / Chesterville, ON
## 5 Montreal, PQ / Chesterville, ON
## 6                    New York, NY
```

```
tail(titanic)
```

Output:

```
##         X pclass
survived                      name    sex  age sibsp
## 1304 1304      3        0     Yousseff, Mr.
Gerious   male   NA     0
## 1305 1305      3        0      Zabour, Miss. Hileni female
14.5     1
## 1306 1306      3        0     Zabour, Miss. Thamine
female   NA     1
## 1307 1307      3        0 Zakarian, Mr. Mapriededer   male
26.5     0
## 1308 1308      3        0       Zakarian, Mr. Ortin   male
27.0     0
```

```
## 1309 1309      3        0        Zimmerman, Mr. Leo   male
29.0     0
##      parch ticket    fare cabin embarked home.dest
## 1304     0   2627 14.4583             C
## 1305     0   2665 14.4542             C
## 1306     0   2665 14.4542             C
## 1307     0   2656  7.2250             C
## 1308     0   2670  7.2250             C
## 1309     0 315082  7.8750             S
```

From the head and tail output, you can notice the data is not shuffled. This is a big issue! When you will split your data between a train set and test set, you will select **only** the passenger from class 1 and 2 (No passenger from class 3 are in the top 80 percent of the observations), which means the algorithm will never see the features of passenger of class 3. This mistake will lead to poor prediction.

To overcome this issue, you can use the function sample().

```
shuffle_index <- sample(1:nrow(titanic))
head(shuffle_index)
```

Code Explanation

- sample(1:nrow(titanic)): Generate a random list of index from 1 to 1309 (i.e. the maximum number of rows).

Output:

```
## [1]  288  874 1078  633  887  992
```

You will use this index to shuffle the titanic dataset.

```
titanic <- titanic[shuffle_index, ]
head(titanic)
```

Output:

```
##         X pclass survived
## 288   288      1        0
## 874   874      3        0
## 1078 1078      3        1
## 633   633      3        0
## 887   887      3        1
## 992   992      3        1
##                                                           name
age
## 288                                      Sutton, Mr.
Frederick   male  61
## 874                   Humblen, Mr. Adolf Mathias Nicolai
Olsen   male  42
## 1078                                 O'Driscoll, Miss.
Bridget female  NA
## 633  Andersson, Mrs. Anders Johan (Alfrida Konstantia
Brogren) female  39
## 887                                        Jermyn, Miss.
Annie female  NA
## 992                                           Mamee, Mr.
Hanna   male  NA
##      sibsp parch ticket    fare cabin
embarked           home.dest## 288      0     0  36963
32.3208   D50        S     Haddenfield, NJ
## 874      0     0 348121  7.6500 F
G63        S
##
1078     0     0  14311  7.7500              Q
## 633      1     5 347082 31.2750              S Sweden
Winnipeg, MN
##
887      0     0  14313  7.7500              Q
## 992      0     0   2677  7.2292              C
```

Step 2) Clean the dataset

The structure of the data shows some variables have NA's. Data clean up to be done as follows

- Drop variables home.dest,cabin, name, X and ticket
- Create factor variables for pclass and survived
- Drop the NA

```
library(dplyr)
# Drop variables
clean_titanic <- titanic % > %
```

```
select(-c(home.dest, cabin, name, X, ticket)) % > %
#Convert to factor level
        mutate(pclass = factor(pclass, levels = c(1, 2, 3),
labels = c('Upper', 'Middle', 'Lower')),
        survived = factor(survived, levels = c(0, 1), labels =
c('No', 'Yes'))) % > %
na.omit()
glimpse(clean_titanic)
```

Code Explanation

- select(-c(home.dest, cabin, name, X, ticket)): Drop unnecessary variables
- pclass = factor(pclass, levels = c(1,2,3), labels= c('Upper', 'Middle', 'Lower')): Add label to the variable pclass. 1 becomes Upper, 2 becomes MIddle and 3 becomes lower
- factor(survived, levels = c(0,1), labels = c('No', 'Yes')): Add label to the variable survived. 1 Becomes No and 2 becomes Yes
- na.omit(): Remove the NA observations

Output:

```
## Observations: 1,045
## Variables: 8
## $ pclass   <fctr> Upper, Lower, Lower, Upper, Middle, Upper,
Middle, U...
## $ survived <fctr> No, No, No, Yes, No, Yes, Yes, No, No, No,
No, No, Y...
## $ sex      <fctr> male, male, female, female, male, male,
female, male...
## $ age      <dbl> 61.0, 42.0, 39.0, 49.0, 29.0, 37.0, 20.0,
54.0, 2.0, ...
## $ sibsp    <int> 0, 0, 1, 0, 0, 1, 0, 0, 4, 0, 0, 1, 1, 0, 0,
0, 1, 1,...
## $ parch    <int> 0, 0, 5, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 2,
0, 4, 0,...
## $ fare     <dbl> 32.3208, 7.6500, 31.2750, 25.9292, 10.5000,
52.5542, ...
## $ embarked <fctr> S, S, S, S, S, S, S, S, S, C, S, S, S, Q,
C, S, S, C...
```

Step 3) Create train/test set

Before you train your model, you need to perform two steps:

- Create a train and test set: You train the model on the train set and test the prediction on the test set (i.e. unseen data)
- Install rpart.plot from the console

The common practice is to split the data 80/20, 80 percent of the data serves to train the model, and 20 percent to make predictions. You need to create two separate data frames. You don't want to touch the test set until you finish building your model. You can create a function name create_train_test() that takes three arguments.

```
create_train_test(df, size = 0.8, train = TRUE)
arguments:
-df: Dataset used to train the model.
-size: Size of the split. By default, 0.8. Numerical value
-train: If set to `TRUE`, the function creates the train set,
otherwise the test set. Default value sets to `TRUE`. Boolean
value.You need to add a Boolean parameter because R does not
allow to return two data frames simultaneously.
```

```
create_train_test & lt;- function(data, size = 0.8, train =
TRUE) {
    n_row = nrow(data)
    total_row = size * n_row
    train_sample & lt; - 1: total_row
    if (train == TRUE) {
        return (data[train_sample, ])
    } else {
        return (data[-train_sample, ])
    }
}
```

Code Explanation

- function(data, size=0.8, train = TRUE): Add the arguments in the function
- n_row = nrow(data): Count number of rows in the dataset

- total_row = size*n_row: Return the nth row to construct the train set
- train_sample <- 1:total_row: Select the first row to the nth rows
- if (train ==TRUE){ } else { }: If condition sets to true, return the train set, else the test set.

You can test your function and check the dimension.

```
data_train <- create_train_test(clean_titanic, 0.8, train =
TRUE)
data_test <- create_train_test(clean_titanic, 0.8, train =
FALSE)
dim(data_train)
```

Output:

```
## [1] 836   8
```

```
dim(data_test)
```

Output:

```
## [1] 209   8
```

The train dataset has 1046 rows while the test dataset has 262 rows.

You use the function prop.table() combined with table() to verify if the randomization process is correct.

```
prop.table(table(data_train$survived))
```

Output:

```
##
##        No       Yes
## 0.5944976 0.4055024
```

```
prop.table(table(data_test$survived))
```

Output:

```
##
```

```
##        No       Yes
## 0.5789474 0.4210526
```

In both dataset, the amount of survivors is the same, about 40 percent.

Install rpart.plot

rpart.plot is not available from conda libraries. You can install it from the console:

```
install.packages("rpart.plot")
```

Step 4) Build the model

You are ready to build the model. The syntax for Rpart() function is:

```
rpart(formula, data=, method='')
arguments:
- formula: The function to predict
- data: Specifies the data frame- method:
- "class" for a classification tree
- "anova" for a regression tree
```

You use the class method because you predict a class.

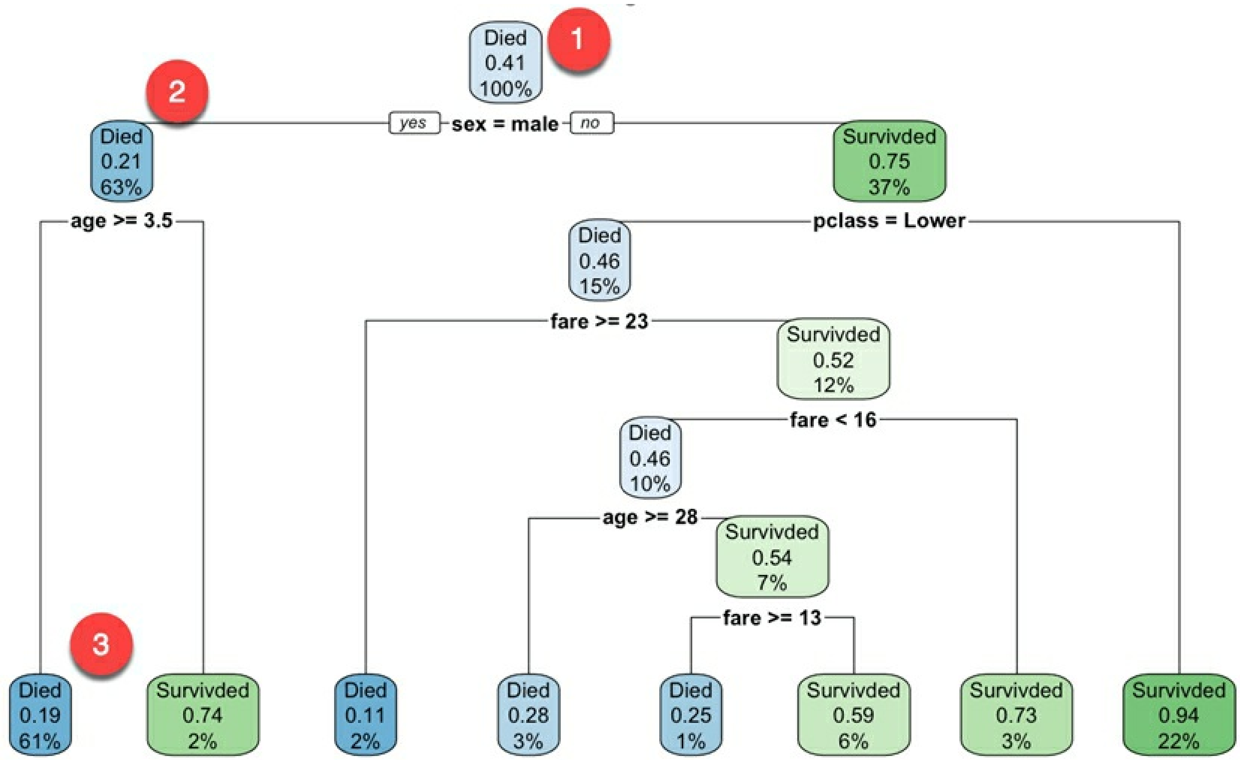
```
library(rpart)
library(rpart.plot)
fit <- rpart(survived~., data = data_train, method = 'class')
rpart.plot(fit, extra = 106
```

Code Explanation

- rpart(): Function to fit the model. The arguments are:
    - survived ~.: Formula of the Decision Trees
    - data = data_train: Dataset
    - method = 'class': Fit a binary model
- rpart.plot(fit, extra= 106): Plot the tree. The extra features are set to 101 to display the probability of the 2nd class (useful for binary

responses). You can refer to the vignette for more information about the other choices.

Output:



You start at the root node (depth 0 over 3, the top of the graph):

1. At the top, it is the overall probability of survival. It shows the proportion of passenger that survived the crash. 41 percent of passenger survived.
2. This node asks whether the gender of the passenger is male. If yes, then you go down to the root's left child node (depth 2). 63 percent are males with a survival probability of 21 percent.
3. In the second node, you ask if the male passenger is above 3.5 years old. If yes, then the chance of survival is 19 percent.
4. You keep on going like that to understand what features impact the likelihood of survival.

Note that, one of the many qualities of Decision Trees is that they require very little data preparation. In particular, they don't require feature scaling or centering.

By default, rpart() function uses the **Gini** impurity measure to split the note. The higher the Gini coefficient, the more different instances within the node.

Step 5) Make a prediction

You can predict your test dataset. To make a prediction, you can use the predict() function. The basic syntax of predict for decision trees is:

```
predict(fitted_model, df, type = 'class')
arguments:
- fitted_model: This is the object stored after model
estimation.
- df: Data frame used to make the prediction
- type: Type of prediction
    - 'class': for classification
    - 'prob': to compute the probability of each
class
    - 'vector': Predict the mean response at the node level
```

You want to predict which passengers are more likely to survive after the collision from the test set. It means, you will know among those 209 passengers, which one will survive or not.

```
predict_unseen <-predict(fit, data_test, type = 'class')
```

Code Explanation

- predict(fit, data_test, type = 'class'): Predict the class (0/1) of the test set

Testing the passenger who didn't make it and those who did.

```
table_mat <- table(data_test$survived, predict_unseen)
table_mat
```

Code Explanation

- table(data_test$survived, predict_unseen): Create a table to count how many passengers are classified as survivors and passed away compare to the correct classification

Output:

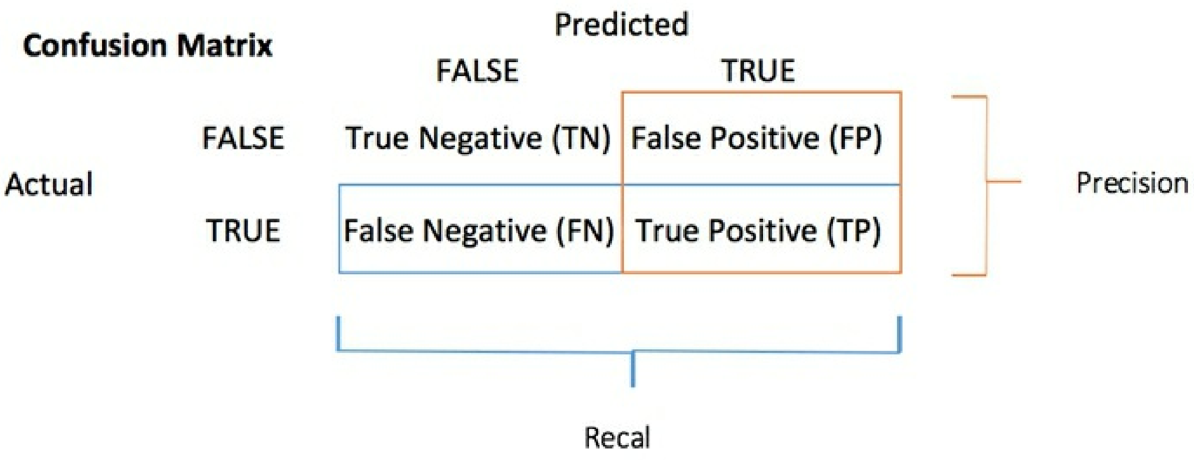
```
##      predict_unseen
##        No Yes
##   No  106  15
##   Yes  30  58
```

The model correctly predicted 106 dead passengers but classified 15 survivors as dead. By analogy, the model misclassified 30 passengers as survivors while they turned out to be dead.

Step 6) Measure performance

You can compute an accuracy measure for classification task with the **confusion matrix**:

The **confusion matrix** is a better choice to evaluate the classification performance. The general idea is to count the number of times True instances are classified are False.



Each row in a confusion matrix represents an actual target, while each column represents a predicted target. The first row of this matrix considers dead passengers (the False class): 106 were correctly classified as dead (**True negative**), while the remaining one was wrongly classified as a survivor (**False positive**). The second row considers the survivors, the positive class were 58 (**True positive**), while the **True negative** was 30.

You can compute the **accuracy test** from the confusion matrix:

$$accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

It is the proportion of true positive and true negative over the sum of the matrix. With R, you can code as follow:

```
accuracy_Test <- sum(diag(table_mat)) / sum(table_mat)
```

Code Explanation

- sum(diag(table_mat)): Sum of the diagonal
- sum(table_mat): Sum of the matrix.

You can print the accuracy of the test set:

```
print(paste('Accuracy for test', accuracy_Test))
```

Output:

```
## [1] "Accuracy for test 0.784688995215311"
```

You have a score of 78 percent for the test set. You can replicate the same exercise with the training dataset.

Step 7) Tune the hyper-parameters

Decision tree has various parameters that control aspects of the fit. In rpart library, you can control the parameters using the rpart.control()

function. In the following code, you introduce the parameters you will tune. You can refer to the vignette for other parameters.

```
rpart.control(minsplit = 20, minbucket = round(minsplit/3),
maxdepth = 30)
Arguments:
-minsplit: Set the minimum number of observations in the node
before the algorithm perform a split
-minbucket:  Set the minimum number of observations in the final
note i.e. the leaf
-maxdepth: Set the maximum depth of any node of the final tree.
The root node is treated a depth 0
```

We will proceed as follow:

- Construct function to return accuracy
- Tune the maximum depth
- Tune the minimum number of sample a node must have before it can split
- Tune the minimum number of sample a leaf node must have

You can write a function to display the accuracy. You simply wrap the code you used before:

1. predict: predict_unseen <- predict(fit, data_test, type = 'class')
2. Produce table: table_mat <- table(data_test$survived, predict_unseen)
3. Compute accuracy: accuracy_Test <- sum(diag(table_mat))/sum(table_mat)

```
accuracy_tune <- function(fit) {
    predict_unseen <- predict(fit, data_test, type = 'class')
    table_mat <- table(data_test$survived, predict_unseen)
    accuracy_Test <- sum(diag(table_mat)) / sum(table_mat)
    accuracy_Test
}
```

You can try to tune the parameters and see if you can improve the model over the default value. As a reminder, you need to get an accuracy higher than 0.78

```
control <- rpart.control(minsplit = 4,
    minbucket = round(5 / 3),
    maxdepth = 3,
    cp = 0)
tune_fit <- rpart(survived~., data = data_train, method =
'class', control = control)
accuracy_tune(tune_fit)
```

Output:

```
## [1] 0.7990431
```

With the following parameter:

```
minsplit = 4
minbucket= round(5/3)
maxdepth = 3cp=0
```

You get a higher performance than the previous model. Congratulation!

Summary

We can summarize the functions to train a decision trees algorithm.

Library	Objective	function	class	parameters	details
rpart	Train classification trees	rpart()	class	formula, df, method	
rpart	Train regression tree	rpart()	anova	formula, df, method	
rpart	Plot the trees	rpart.plot()		fitted model	
				fitted model,	

base	predict	predict()	class	type	
base	predict	predict()	prob	fitted model, type	
base	predict	predict()	vector	fitted model, type	
rpart	Control parameters	rpart.control()		minsplit	Set the minimum number of observations in the node before the algorithm perform a split
				minbucket	Set the minimum number of observations in the final note i.e. the leaf
				maxdepth	Set the maximum depth of any node of the final tree. The root node is treated a depth 0
rpart	Train model with control parameter	rpart()		formula, df, method, control	

Note : Train the model on a training data and test the performance on an unseen dataset, i.e. test set.

Chapter 29: R Random Forest Tutorial with Example

What is Random Forest in R?

Random forests are based on a simple idea: 'the wisdom of the crowd'. Aggregate of the results of multiple predictors gives a better prediction than the best individual predictor. A group of predictors is called an **ensemble**. Thus, this technique is called **Ensemble Learning**.

In earlier tutorial, you learned how to use **Decision trees** to make a binary prediction. To improve our technique, we can train a group of **Decision Tree classifiers**, each on a different random subset of the train set. To make a prediction, we just obtain the predictions of all individuals trees, then predict the class that gets the most votes. This technique is called **Random Forest**.

We will proceed as follow to train the Random Forest:

Step 1) Import the data

To make sure you have the same dataset as in the tutorial for decision trees, the train test and test set are stored on the internet. You can import them without make any change.

```
library(dplyr)
data_train <-
read.csv("https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/train.csv")
glimpse(data_train)
data_test <- read.csv("https://raw.githubusercontent.com/guru99-
edu/R-Programming/master/test.csv")
glimpse(data_test)
```

Step 2) Train the model

One way to evaluate the performance of a model is to train it on a number of different smaller datasets and evaluate them over the other smaller testing set. This is called the **F-fold cross-validation** feature. R has a function to randomly split number of datasets of almost the same size. For example, if k=9, the model is evaluated over the nine folder and tested on the remaining test set. This process is repeated until all the subsets have been evaluated. This technique is widely used for model selection, especially when the model has parameters to tune.

Now that we have a way to evaluate our model, we need to figure out how to choose the parameters that generalized best the data.

Random forest chooses a random subset of features and builds many Decision Trees. The model averages out all the predictions of the Decisions trees.

Random forest has some parameters that can be changed to improve the generalization of the prediction. You will use the function RandomForest() to train the model.

Syntax for Randon Forest is

```
RandomForest(formula, ntree=n, mtry=FALSE, maxnodes = NULL)
Arguments:
- Formula: Formula of the fitted model
- ntree: number of trees in the forest
- mtry: Number of candidates draw to feed the algorithm. By
default, it is the square of the number of columns.
- maxnodes: Set the maximum amount of terminal nodes in the
forest
- importance=TRUE: Whether independent variables importance in
the random forest be assessed
```

Note: Random forest can be trained on more parameters. You can refer to the vignette to see the different parameters.

Tuning a model is very tedious work. There are lot of combination possible between the parameters. You don't necessarily have the time to try all of them. A good alternative is to let the machine find the best combination for you. There are two methods available:

- Random Search
- Grid Search

We will define both methods but during the tutorial, we will train the model using grid search

Grid Search definition

The grid search method is simple, the model will be evaluated over all the combination you pass in the function, using cross-validation.

For instance, you want to try the model with 10, 20, 30 number of trees and each tree will be tested over a number of mtry equals to 1, 2, 3, 4, 5. Then the machine will test 15 different models:

```
   .mtry ntrees
1      1     10
2      2     10
3      3     10
4      4     10
5      5     10
6      1     20
7      2     20
8      3     20
9      4     20
10     5     20
11     1     30
12     2     30
13     3     30
14     4     30
15     5     30
```

The algorithm will evaluate:

```
RandomForest(formula, ntree=10, mtry=1)
RandomForest(formula, ntree=10, mtry=2)
RandomForest(formula, ntree=10, mtry=3)
RandomForest(formula, ntree=20, mtry=2)
...
```

Each time, the random forest experiments with a cross-validation. One shortcoming of the grid search is the number of experimentations. It can become very easily explosive when the number of combination is high. To overcome this issue, you can use the random search

Random Search definition

The big difference between random search and grid search is, random search will not evaluate all the combination of hyperparameter in the searching space. Instead, it will randomly choose combination at every iteration. The advantage is it lower the computational cost.

Set the control parameter

You will proceed as follow to construct and evaluate the model:

- Evaluate the model with the default setting
- Find the best number of mtry
- Find the best number of maxnodes
- Find the best number of ntrees
- Evaluate the model on the test dataset

Before you begin with the parameters exploration, you need to install two libraries.

- caret: R machine learning library. If you have install R with r-essential. It is already in the library
    - Anaconda: conda install -c r r-caret
- e1071: R machine learning library.
    - Anaconda: conda install -c r r-e1071

You can import them along with RandomForest

```
library(randomForest)
library(caret)
library(e1071)
```

Default setting

K-fold cross validation is controlled by the trainControl() function

```
trainControl(method = "cv", number = n, search ="grid")
arguments
- method = "cv": The method used to resample the dataset.
- number = n: Number of folders to create
- search = "grid": Use the search grid method. For randomized
method, use "grid"
Note: You can refer to the vignette to see the other arguments
of the function.
```

You can try to run the model with the default parameters and see the accuracy score.

Note: You will use the same controls during all the tutorial.

```
# Define the control
trControl <- trainControl(method = "cv",
    number = 10,
    search = "grid")
```

You will use caret library to evaluate your model. The library has one function called train() to evaluate almost all machine learning algorithm. Say differently, you can use this function to train other algorithms.

The basic syntax is:

```
train(formula, df, method = "rf", metric= "Accuracy", trControl
= trainControl(), tuneGrid = NULL)
argument
- `formula`: Define the formula of the algorithm
- `method`: Define which model to train. Note, at the end of the
```

```
tutorial, there is a list of all the models that can be trained
- `metric` = "Accuracy": Define how to select the optimal model
- `trControl = trainControl()`: Define the control parameters
- `tuneGrid = NULL`: Return a data frame with all the possible
combination
```

Let's try the build the model with the default values.

```
set.seed(1234)
# Run the model
rf_default <- train(survived~.,
    data = data_train,
    method = "rf",
    metric = "Accuracy",
    trControl = trControl)
# Print the results
print(rf_default)
```

Code Explanation

- trainControl(method="cv", number=10, search="grid"): Evaluate the model with a grid search of 10 folder
- train(...): Train a random forest model. Best model is chosen with the accuracy measure.

Output:

```
## Random Forest
##
## 836 samples
##   7 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 753, 752, 753, 752, 752, 752, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##    2    0.7919248  0.5536486
##    6    0.7811245  0.5391611
##   10    0.7572002  0.4939620
##
```

```
## Accuracy was used to select the optimal model using  the
largest value.
## The final value used for the model was mtry = 2.
```

The algorithm uses 500 trees and tested three different values of mtry: 2, 6, 10.

The final value used for the model was mtry = 2 with an accuracy of 0.78. Let's try to get a higher score.

Step 2) Search best mtry

You can test the model with values of mtry from 1 to 10

```
set.seed(1234)
tuneGrid <- expand.grid(.mtry = c(1: 10))
rf_mtry <- train(survived~.,
    data = data_train,
    method = "rf",
    metric = "Accuracy",
    tuneGrid = tuneGrid,
    trControl = trControl,
    importance = TRUE,
    nodesize = 14,
    ntree = 300)
print(rf_mtry)
```

Code Explanation

- tuneGrid <- expand.grid(.mtry=c(3:10)): Construct a vector with value from 3:10

The final value used for the model was mtry = 4.

Output:

```
## Random Forest
##
## 836 samples
##   7 predictor
##   2 classes: 'No', 'Yes'
##
```

```
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 753, 752, 753, 752, 752, 752, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##    1    0.7572576  0.4647368
##    2    0.7979346  0.5662364
##    3    0.8075158  0.5884815
##    4    0.8110729  0.5970664
##    5    0.8074727  0.5900030
##    6    0.8099111  0.5949342
##    7    0.8050918  0.5866415
##    8    0.8050918  0.5855399
##    9    0.8050631  0.5855035
##   10    0.7978916  0.5707336
##
## Accuracy was used to select the optimal model using  the
largest value.
## The final value used for the model was mtry = 4.
```

The best value of mtry is stored in:

```
rf_mtry$bestTune$mtry
```

You can store it and use it when you need to tune the other parameters.

```
max(rf_mtry$results$Accuracy)
```

Output:

```
## [1] 0.8110729
```

```
best_mtry <- rf_mtry$bestTune$mtry
best_mtry
```

Output:

```
## [1] 4
```

Step 3) Search the best maxnodes

You need to create a loop to evaluate the different values of maxnodes. In the following code, you will:

- Create a list
- Create a variable with the best value of the parameter mtry; Compulsory
- Create the loop
- Store the current value of maxnode
- Summarize the results

```
store_maxnode <- list()
tuneGrid <- expand.grid(.mtry = best_mtry)
for (maxnodes in c(5: 15)) {
    set.seed(1234)
    rf_maxnode <- train(survived~.,
        data = data_train,
        method = "rf",
        metric = "Accuracy",
        tuneGrid = tuneGrid,
        trControl = trControl,
        importance = TRUE,
        nodesize = 14,
        maxnodes = maxnodes,
        ntree = 300)
    current_iteration <- toString(maxnodes)
    store_maxnode[[current_iteration]] <- rf_maxnode
}
results_mtry <- resamples(store_maxnode)
summary(results_mtry)
```

Code explanation:

- store_maxnode <- list(): The results of the model will be stored in this list
- expand.grid(.mtry=best_mtry): Use the best value of mtry
- for (maxnodes in c(15:25)) { ... }: Compute the model with values of maxnodes starting from 15 to 25.
- maxnodes=maxnodes: For each iteration, maxnodes is equal to the current value of maxnodes. i.e 15, 16, 17, ...
- key <- toString(maxnodes): Store as a string variable the value of maxnode.

- store_maxnode[[key]] <- rf_maxnode: Save the result of the model in the list.
- resamples(store_maxnode): Arrange the results of the model
- summary(results_mtry): Print the summary of all the combination.

Output:

```
##
## Call:
## summary.resamples(object = results_mtry)
##
## Models: 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15
## Number of resamples: 10
##
## Accuracy
##         Min.   1st Qu.    Median      Mean   3rd
Qu.      Max. NA's
## 5  0.6785714 0.7529762 0.7903758 0.7799771 0.8168388
0.8433735    0
## 6  0.6904762 0.7648810 0.7784710 0.7811962 0.8125000
0.8313253    0
## 7  0.6904762 0.7619048 0.7738095 0.7788009 0.8102410
0.8333333    0
## 8  0.6904762 0.7627295 0.7844234 0.7847820 0.8184524
0.8433735    0
## 9  0.7261905 0.7747418 0.8083764 0.7955250 0.8258749
0.8333333    0
## 10 0.6904762 0.7837780 0.7904475 0.7895869 0.8214286
0.8433735    0
## 11 0.7023810 0.7791523 0.8024240 0.7943775 0.8184524
0.8433735    0
## 12 0.7380952 0.7910929 0.8144005 0.8051205 0.8288511
0.8452381    0
## 13 0.7142857 0.8005952 0.8192771 0.8075158 0.8403614
0.8452381    0
## 14 0.7380952 0.7941050 0.8203528 0.8098967 0.8403614
0.8452381    0
## 15 0.7142857 0.8000215 0.8203528 0.8075301 0.8378873
0.8554217    0
##
## Kappa
##         Min.   1st Qu.    Median      Mean   3rd
Qu.      Max. NA's
```

```
## 5  0.3297872 0.4640436 0.5459706 0.5270773 0.6068751
0.6717371    0
## 6  0.3576471 0.4981484 0.5248805 0.5366310 0.6031287
0.6480921    0
## 7  0.3576471 0.4927448 0.5192771 0.5297159 0.5996437
0.6508314    0
## 8  0.3576471 0.4848320 0.5408159 0.5427127 0.6200253
0.6717371    0
## 9  0.4236277 0.5074421 0.5859472 0.5601687 0.6228626
0.6480921    0
## 10 0.3576471 0.5255698 0.5527057 0.5497490 0.6204819
0.6717371    0
## 11 0.3794326 0.5235007 0.5783191 0.5600467 0.6126720
0.6717371    0
## 12 0.4460432 0.5480930 0.5999072 0.5808134 0.6296780
0.6717371    0
## 13 0.4014252 0.5725752 0.6087279 0.5875305 0.6576219
0.6678832    0
## 14 0.4460432 0.5585005 0.6117973 0.5911995 0.6590982
0.6717371    0
## 15 0.4014252 0.5689401 0.6117973 0.5867010 0.6507194
0.6955990    0
```

The last value of maxnode has the highest accuracy. You can try with higher values to see if you can get a higher score.

```
store_maxnode <- list()
tuneGrid <- expand.grid(.mtry = best_mtry)
for (maxnodes in c(20: 30)) {
    set.seed(1234)
    rf_maxnode <- train(survived~.,
        data = data_train,
        method = "rf",
        metric = "Accuracy",
        tuneGrid = tuneGrid,
        trControl = trControl,
        importance = TRUE,
        nodesize = 14,
        maxnodes = maxnodes,
        ntree = 300)
    key <- toString(maxnodes)
    store_maxnode[[key]] <- rf_maxnode
}
```

```
results_node <- resamples(store_maxnode)
summary(results_node)
```

Output:

```
##
## Call:
## summary.resamples(object = results_node)
##
## Models: 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30
## Number of resamples: 10
##
## Accuracy
##         Min.   1st Qu.    Median      Mean   3rd
Qu.      Max. NA's
## 20 0.7142857 0.7821644 0.8144005 0.8075301 0.8447719
0.8571429    0
## 21 0.7142857 0.8000215 0.8144005 0.8075014 0.8403614
0.8571429    0
## 22 0.7023810 0.7941050 0.8263769 0.8099254 0.8328313
0.8690476    0
## 23 0.7023810 0.7941050 0.8263769 0.8111302 0.8447719
0.8571429    0
## 24 0.7142857 0.7946429 0.8313253 0.8135112 0.8417599
0.8690476    0
## 25 0.7142857 0.7916667 0.8313253 0.8099398 0.8408635
0.8690476    0
## 26 0.7142857 0.7941050 0.8203528 0.8123207 0.8528758
0.8571429    0
## 27 0.7023810 0.8060456 0.8313253 0.8135112 0.8333333
0.8690476    0
## 28 0.7261905 0.7941050 0.8203528 0.8111015 0.8328313
0.8690476    0
## 29 0.7142857 0.7910929 0.8313253 0.8087063 0.8333333
0.8571429    0
## 30 0.6785714 0.7910929 0.8263769 0.8063253 0.8403614
0.8690476    0
##
## Kappa
##         Min.   1st Qu.    Median      Mean   3rd
Qu.      Max. NA's
## 20 0.3956835 0.5316120 0.5961830 0.5854366 0.6661120
0.6955990    0
## 21 0.3956835 0.5699332 0.5960343 0.5853247 0.6590982
0.6919315    0
```

```
## 22 0.3735084 0.5560661 0.6221836 0.5914492 0.6422128
0.7189781    0
## 23 0.3735084 0.5594228 0.6228827 0.5939786 0.6657372
0.6955990    0
## 24 0.3956835 0.5600352 0.6337821 0.5992188 0.6604703
0.7189781    0
## 25 0.3956835 0.5530760 0.6354875 0.5912239 0.6554912
0.7189781    0
## 26 0.3956835 0.5589331 0.6136074 0.5969142 0.6822128
0.6955990    0
## 27 0.3735084 0.5852459 0.6368425 0.5998148 0.6426088
0.7189781    0
## 28 0.4290780 0.5589331 0.6154905 0.5946859 0.6356141
0.7189781    0
## 29 0.4070588 0.5534173 0.6337821 0.5901173 0.6423101
0.6919315    0
## 30 0.3297872 0.5534173 0.6202632 0.5843432 0.6590982
0.7189781    0
```

The highest accuracy score is obtained with a value of maxnode equals to 22.

Step 4) Search the best ntrees

Now that you have the best value of mtry and maxnode, you can tune the number of trees. The method is exactly the same as maxnode.

```
store_maxtrees <- list()
for (ntree in c(250, 300, 350, 400, 450, 500, 550, 600, 800,
1000, 2000)) {
    set.seed(5678)
    rf_maxtrees <- train(survived~.,
        data = data_train,
        method = "rf",
        metric = "Accuracy",
        tuneGrid = tuneGrid,
        trControl = trControl,
        importance = TRUE,
        nodesize = 14,
        maxnodes = 24,
        ntree = ntree)
    key <- toString(ntree)
    store_maxtrees[[key]] <- rf_maxtrees
}
results_tree <- resamples(store_maxtrees)
summary(results_tree)
```

Output:

```
##
## Call:
## summary.resamples(object = results_tree)
##
## Models: 250, 300, 350, 400, 450, 500, 550, 600, 800, 1000,
2000
## Number of resamples: 10
##
## Accuracy
##           Min.   1st Qu.    Median      Mean   3rd
Qu.      Max. NA's
## 250  0.7380952 0.7976190 0.8083764 0.8087010 0.8292683
0.8674699    0
## 300  0.7500000 0.7886905 0.8024240 0.8027199 0.8203397
0.8452381    0
## 350  0.7500000 0.7886905 0.8024240 0.8027056 0.8277623
0.8452381    0
## 400  0.7500000 0.7886905 0.8083764 0.8051009 0.8292683
0.8452381    0
## 450  0.7500000 0.7886905 0.8024240 0.8039104 0.8292683
0.8452381    0
## 500  0.7619048 0.7886905 0.8024240 0.8062914 0.8292683
0.8571429    0
## 550  0.7619048 0.7886905 0.8083764 0.8099062 0.8323171
0.8571429    0
## 600  0.7619048 0.7886905 0.8083764 0.8099205 0.8323171
0.8674699    0
## 800  0.7619048 0.7976190 0.8083764 0.8110820 0.8292683
0.8674699    0
## 1000 0.7619048 0.7976190 0.8121510 0.8086723 0.8303571
0.8452381    0
## 2000 0.7619048 0.7886905 0.8121510 0.8086723 0.8333333
0.8452381    0
##
## Kappa
##           Min.   1st Qu.    Median      Mean   3rd
Qu.      Max. NA's
## 250  0.4061697 0.5667400 0.5836013 0.5856103 0.6335363
```

```
0.7196807    0
## 300  0.4302326 0.5449376 0.5780349 0.5723307 0.6130767
0.6710843    0
## 350  0.4302326 0.5449376 0.5780349 0.5723185 0.6291592
0.6710843    0
## 400  0.4302326 0.5482030 0.5836013 0.5774782 0.6335363
0.6710843    0
## 450  0.4302326 0.5449376 0.5780349 0.5750587 0.6335363
0.6710843    0
## 500  0.4601542 0.5449376 0.5780349 0.5804340 0.6335363
0.6949153    0
## 550  0.4601542 0.5482030 0.5857118 0.5884507 0.6396872
0.6949153    0
## 600  0.4601542 0.5482030 0.5857118 0.5884374 0.6396872
0.7196807    0
## 800  0.4601542 0.5667400 0.5836013 0.5910088 0.6335363
0.7196807    0
## 1000 0.4601542 0.5667400 0.5961590 0.5857446 0.6343666
0.6678832    0
## 2000 0.4601542 0.5482030 0.5961590 0.5862151 0.6440678
0.6656337    0
```

You have your final model. You can train the random forest with the following parameters:

- ntree =800: 800 trees will be trained
- mtry=4: 4 features is chosen for each iteration
- maxnodes = 24: Maximum 24 nodes in the terminal nodes (leaves)

```
fit_rf <- train(survived~.,
    data_train,
    method = "rf",
    metric = "Accuracy",
    tuneGrid = tuneGrid,
    trControl = trControl,
    importance = TRUE,
    nodesize = 14,
    ntree = 800,
    maxnodes = 24)
```

Step 5) Evaluate the model

The library caret has a function to make prediction.

```
predict(model, newdata= df)
argument
- `model`: Define the model evaluated before.
- `newdata`: Define the dataset to make prediction
```

```
prediction <-predict(fit_rf, data_test)
```

You can use the prediction to compute the confusion matrix and see the accuracy score

```
confusionMatrix(prediction, data_test$survived)
```

Output:

```
## Confusion Matrix and Statistics
## 
##           Reference
## Prediction  No Yes
##        No  110  32
##        Yes  11  56
##                                           
##                Accuracy : 0.7943          
##                  95% CI : (0.733, 0.8469)
##     No Information Rate : 0.5789          
##     P-Value [Acc > NIR] : 3.959e-11       
##                                           
##                   Kappa : 0.5638          
##  Mcnemar's Test P-Value : 0.002289        
##                                           
##             Sensitivity : 0.9091          
##             Specificity : 0.6364          
##          Pos Pred Value : 0.7746          
##          Neg Pred Value : 0.8358          
##              Prevalence : 0.5789          
##          Detection Rate : 0.5263          
##    Detection Prevalence : 0.6794          
##       Balanced Accuracy : 0.7727          
##                                           
##        'Positive' Class : No              
## 
```

You have an accuracy of 0.7943 percent, which is higher than the default value

Step 6) Visualize Result

Lastly, you can look at the feature importance with the function varImp(). It seems that the most important features are the sex and age. That is not surprising because the important features are likely to appear closer to the root of the tree, while less important features will often appear closed to the leaves.

```
varImpPlot(fit_rf)
```

Output:

```
varImp(fit_rf)
## rf variable importance
##
##              Importance
## sexmale         100.000
## age              28.014
## pclassMiddle     27.016
## fare             21.557
## pclassUpper      16.324
## sibsp            11.246
## parch             5.522
## embarkedC         4.908
## embarkedQ         1.420
## embarkedS         0.000
```

Summary

We can summarize how to train and evaluate a random forest with the table below:

Library	Objective	function	parameter
randomForest	Create a Random forest	RandomForest()	formula, ntree=n, mtry=FALSE, maxnodes = NULL
	Create K folder		method = "cv", number = n, search

caret	cross validation	trainControl()	="grid"
caret	Train a Random Forest	train()	formula, df, method = "rf", metric= "Accuracy", trControl = trainControl(), tuneGrid = NULL
caret	Predict out of sample	predict	model, newdata= df
caret	Confusion Matrix and Statistics	confusionMatrix()	model, y test
caret	variable importance	cvarImp()	model

Appendix

List of model used in caret

```
names>(getModelInfo())
```

Output:

```
##   [1]
"ada"                 "AdaBag"              "AdaBoost.M1"
"adaboost"            "amdai"               "ANFIS"
"avNNet"              "awnb"                "awtan"
"bag"                 "bagEarth"            "bagEarthGCV"
"bagFDA"              "bagFDAGCV"           "bam"
"bartMachine"         "bayesglm"            "binda"
"blackboost"          "blasso"              "blassoAveraged"
"bridge"              "brnn"                "BstLm"
"bstSm"               "bstTree"             "C5.0"
"C5.0Cost"            "C5.0Rules"           "C5.0Tree"
"cforest"             "chaid"               "CSimca"
"ctree"               "ctree2"              "cubist"
"dda"                 "deepboost"           "DENFIS"
"dnn"                 "dwdLinear"           "dwdPoly"
"dwdRadial"           "earth"               "elm"
"enet"                "evtree"              "extraTrees"
"fda"                 "FH.GBML"             "FIR.DM"
"foba"                "FRBCS.CHI"           "FRBCS.W"
"FS.HGD"              "gam"                 "gamboost"
"gamLoess"            "gamSpline"           "gaussprLinear"
```

```
"gaussprPoly"          "gaussprRadial"        "gbm_h3o"
"gbm"                  "gcvEarth"             "GFS.FR.MOGUL"
"GFS.GCCL"             "GFS.LT.RS"            "GFS.THRIFT"
"glm.nb"               "glm"                  "glmboost"
"glmnet_h3o"           "glmnet"               "glmStepAIC"
"gpls"                 "hda"                  "hdda"
"hdrda"                "HYFIS"                "icr"
"J48"                  "JRip"                 "kernelpls"
"kknn"                 "knn"                  "krlsPoly"
"krlsRadial"           "lars"                 "lars2"
"lasso"                "lda"                  "lda2"
"leapBackward"         "leapForward"          "leapSeq"
"Linda"                "lm"                   "lmStepAIC"
[100]
"LMT"                  "loclda"               "logicBag"
[103]
"LogitBoost"           "logreg"               "lssvmLinear"
[106]
"lssvmPoly"            "lssvmRadial"          "lvq"
[109]
"M5"                   "M5Rules"              "manb"
[112]
"mda"                  "Mlda"                 "mlp"
[115]
"mlpKerasDecay"        "mlpKerasDecayCost"    "mlpKerasDropout"
[118] "mlpKerasDropoutCost"
"mlpML"                "mlpSGD"              ## [121]
"mlpWeightDecay"       "mlpWeightDecayML"     "monmlp"
[124]
"msaenet"              "multinom"             "mxnet"
[127]
"mxnetAdam"            "naive_bayes"          "nb"
[130]
"nbDiscrete"           "nbSearch"             "neuralnet"
[133]
"nnet"                 "nnls"                 "nodeHarvest"
[136]
"null"                 "OneR"                 "ordinalNet"
[139]
"ORFlog"               "ORFpls"               "ORFridge"
[142]
"ORFsvm"               "ownn"                 "pam"
[145]
"parRF"                "PART"                 "partDSA"
[148]
```

```
"pcaNNet"             "pcr"                 "pda"
[151]
"pda2"                "penalized"           "PenalizedLDA"
[154]
"plr"                 "pls"                 "plsRglm"
[157]
"polr"                "ppr"                 "PRIM"
[160]
"protoclass"          "pythonKnnReg"        "qda"
[163]
"QdaCov"              "qrf"                 "qrnn"
[166]
"randomGLM"           "ranger"              "rbf"
[169]
"rbfDDA"              "Rborist"             "rda"
[172]
"regLogistic"         "relaxo"              "rf"
[175]
"rFerns"              "RFlda"               "rfRules"
[178]
"ridge"               "rlda"                "rlm"
[181]
"rmda"                "rocc"                "rotationForest"
[184]
"rotationForestCp"    "rpart"               "rpart1SE"
[187]
"rpart2"              "rpartCost"           "rpartScore"
[190]
"rqlasso"             "rqnc"                "RRF"
[193]
"RRFglobal"           "rrlda"               "RSimca"
[196]
"rvmLinear"           "rvmPoly"             "rvmRadial"
[199]
"SBC"                 "sda"                 "sdwd"
[202]
"simpls"              "SLAVE"               "slda"
[205]
"smda"                "snn"                 "sparseLDA"
[208]
"spikeslab"           "spls"                "stepLDA"
[211]
"stepQDA"             "superpc"             "svmBoundrangeString"
[214]
"svmExpoString"       "svmLinear"           "svmLinear2"
```

```
[217]
"svmLinear3"          "svmLinearWeights"    "svmLinearWeights2"
[220]
"svmPoly"             "svmRadial"           "svmRadialCost"
[223]
"svmRadialSigma"      "svmRadialWeights"    "svmSpectrumString"
[226]
"tan"                 "tanSearch"           "treebag"
[229]
"vbmpRadial"          "vglmAdjCat"          "vglmContRatio"
[232]
"vglmCumulative"      "widekernelpls"       "WM"
[235]
"wsrf"                "xgbLinear"           "xgbTree"
[238] "xyf"
```

Chapter 30: Generalized Linear Model (GLM) in R with Example

What is Logistic regression?

Logistic regression is used to predict a class, i.e., a probability. Logistic regression can predict a binary outcome accurately.

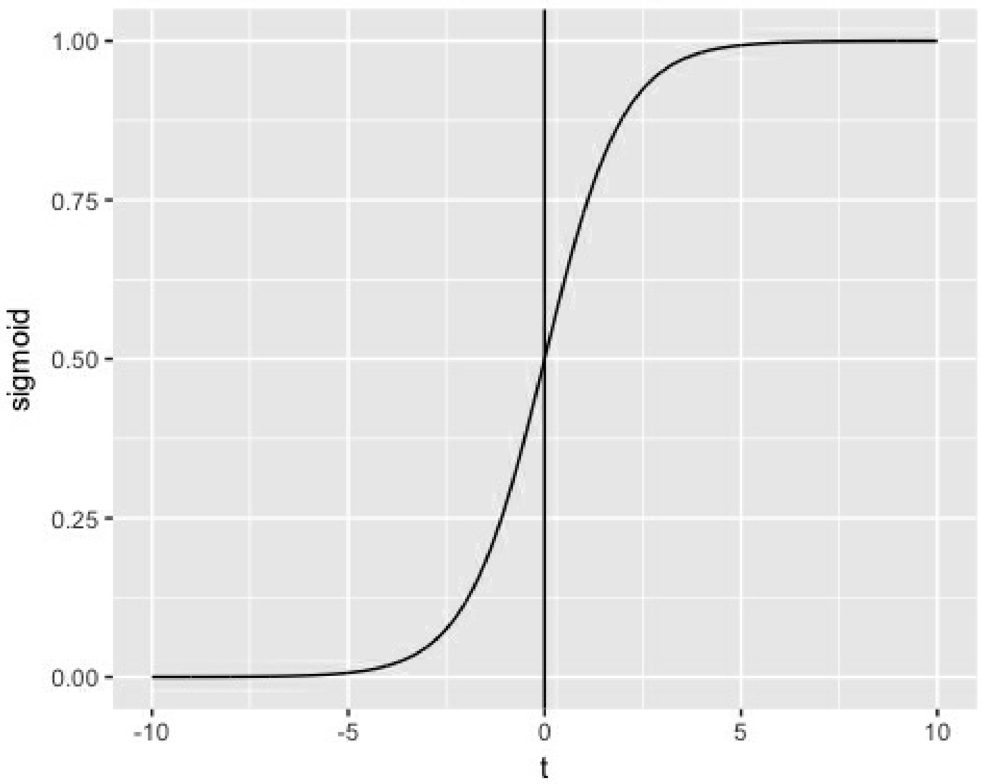
Imagine you want to predict whether a loan is denied/accepted based on many attributes. The logistic regression is of the form 0/1. y = 0 if a loan is rejected, y = 1 if accepted.

A logistic regression model differs from linear regression model in two ways.

- First of all, the logistic regression accepts only dichotomous (binary) input as a dependent variable (i.e., a vector of 0 and 1).
- Secondly, the outcome is measured by the following probabilistic link function called **sigmoid** due to its S-shaped.:

$$\sigma(t) = \frac{1}{1 + exp(-t)}$$

The output of the function is always between 0 and 1. Check Image below



The sigmoid function returns values from 0 to 1. For the classification task, we need a discrete output of 0 or 1.

To convert a continuous flow into discrete value, we can set a decision bound at 0.5. All values above this threshold are classified as 1

$$\hat{y} = \begin{cases} 0 & if \quad \hat{p} < .5 \\ 1 & if \quad \hat{p} \geq .5 \end{cases}$$

How to create Generalized Liner Model (GLM)

Let's use the **adult** data set to illustrate Logistic regression. The "adult" is a great dataset for the classification task. The objective is to predict whether the annual income in dollar of an individual will exceed 50.000. The dataset contains 46,033 observations and ten features:

- age: age of the individual. Numeric
- education: Educational level of the individual. Factor.
- marital.status: Marital status of the individual. Factor i.e. Never-married, Married-civ-spouse, ...
- gender: Gender of the individual. Factor, i.e. Male or Female
- income: Target variable. Income above or below 50K. Factor i.e. >50K, <=50K

amongst others

```
library(dplyr)
data_adult <-read.csv("https://raw.githubusercontent.com/guru99-
edu/R-Programming/master/adult.csv")
glimpse(data_adult)
```

Output:

```
Observations: 48,842
Variables: 10
$ x               <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12,
13, 14, 15,...
$ age             <int> 25, 38, 28, 44, 18, 34, 29, 63, 24, 55,
65, 36, 26...
$ workclass       <fctr> Private, Private, Local-gov, Private,
?, Private,...
$ education       <fctr> 11th, HS-grad, Assoc-acdm, Some-
college, Some-col...
$ educational.num <int> 7, 9, 12, 10, 10, 6, 9, 15, 10, 4, 9,
13, 9, 9, 9,...
$ marital.status  <fctr> Never-married, Married-civ-spouse,
Married-civ-sp...
$ race            <fctr> Black, White, White, Black, White,
White, Black, ...
$ gender          <fctr> Male, Male, Male, Male, Female, Male,
Male, Male,...
$ hours.per.week  <int> 40, 50, 40, 40, 30, 30, 40, 32, 40, 10,
40, 40, 39...
$ income          <fctr> <=50K, <=50K, >50K, >50K, <=50K, <=50K,
<=50K, >5...
```

We will proceed as follow:

- Step 1: Check continuous variables
- Step 2: Check factor variables
- Step 3: Feature engineering
- Step 4: Summary statistic
- Step 5: Train/test set
- Step 6: Build the model
- Step 7: Assess the performance of the model
- step 8: Improve the model

Your task is to predict which individual will have a revenue higher than 50K.

In this tutorial, each step will be detailed to perform an analysis on a real dataset.

Step 1) Check continuous variables

In the first step, you can see the distribution of the continuous variables.

```
continuous <-select_if(data_adult, is.numeric)
summary(continuous)
```

Code Explanation

- continuous <- select_if(data_adult, is.numeric): Use the function select_if() from the dplyr library to select only the numerical columns
- summary(continuous): Print the summary statistic

Output:

```
##        X              age        educational.num
hours.per.week
##  Min.   :    1   Min.   :17.00   Min.   : 1.00   Min.   :
1.00
##  1st Qu.:11509   1st Qu.:28.00   1st Qu.: 9.00   1st
Qu.:40.00
##  Median :23017   Median :37.00   Median :10.00   Median
```

```
:40.00
##  Mean   :23017   Mean   :38.56   Mean   :10.13   Mean   :40.95
##  3rd Qu.:34525   3rd Qu.:47.00   3rd Qu.:13.00   3rd
Qu.:45.00
##  Max.   :46033   Max.   :90.00   Max.   :16.00   Max.   :99.00
```

From the above table, you can see that the data have totally different scales and hours.per.weeks has large outliers (.i.e. look at the last quartile and maximum value).

You can deal with it following two steps:

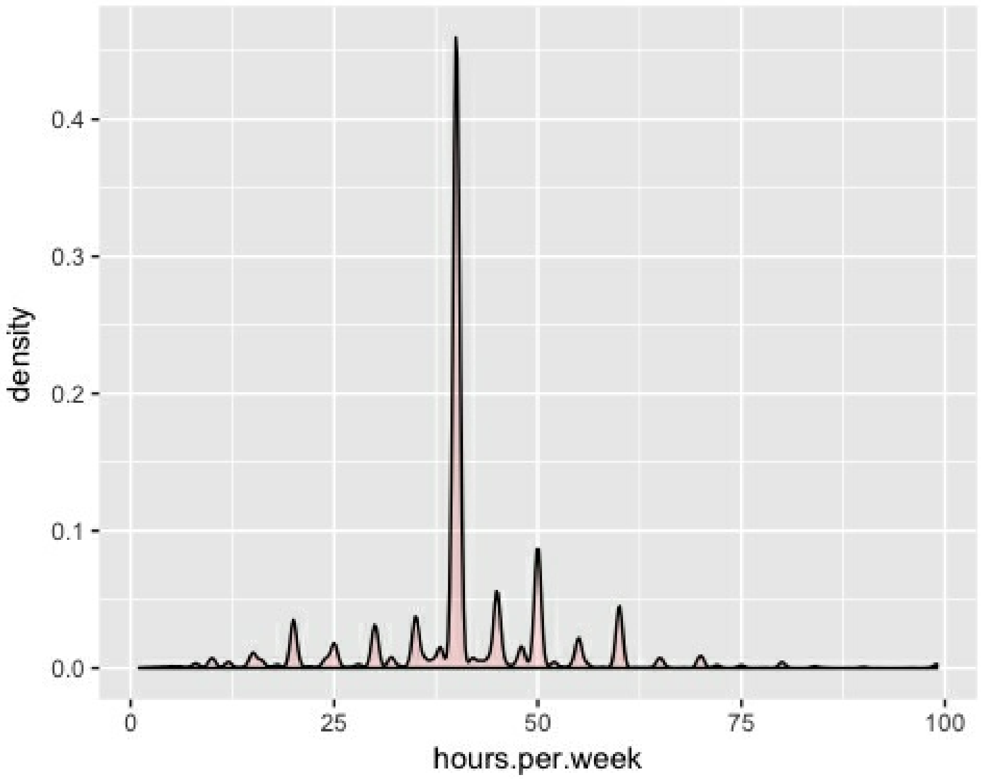
- 1: Plot the distribution of hours.per.week
- 2: Standardize the continuous variables

1. Plot the distribution

Let's look closer at the distribution of hours.per.week

```
# Histogram with kernel density curve
library(ggplot2)
ggplot(continuous, aes(x = hours.per.week)) +
    geom_density(alpha = .2, fill = "#FF6666")
```

Output:



The variable has lots of outliers and not well-defined distribution. You can partially tackle this problem by deleting the top 0.01 percent of the hours per week.

Basic syntax of quantile:

```
quantile(variable, percentile)
arguments:
-variable:  Select the variable in the data frame to compute the
percentile
-percentile:  Can be a single value between 0 and 1 or multiple
value. If multiple, use this format:  `c(A,B,C, ...)
- `A`,`B`,`C` and `...` are all integer from 0 to 1.
```

We compute the top 2 percent percentile

```
top_one_percent <- quantile(data_adult$hours.per.week, .99)
top_one_percent
```

Code Explanation

- quantile(data_adult$hours.per.week, .99): Compute the value of the 99 percent of the working time

Output:

```
## 99%
##  80
```

98 percent of the population works under 80 hours per week.

You can drop the observations above this threshold. You use the filter from the dplyr library.

```
data_adult_drop <-data_adult %>%
filter(hours.per.week<top_one_percent)
dim(data_adult_drop)
```

Output:

```
## [1] 45537    10
```

2. Standardize the continuous variables

You can standardize each column to improve the performance because your data do not have the same scale. You can use the function mutate_if from the dplyr library. The basic syntax is:

```
mutate_if(df, condition, funs(function))
arguments:
-`df`: Data frame used to compute the function
- `condition`: Statement used. Do not use parenthesis
- funs(function):  Return the function to apply. Do not use
parenthesis for the function
```

You can standardize the numeric columns as follow:

```
data_adult_rescale <- data_adult_drop % > %
        mutate_if(is.numeric, funs(as.numeric(scale(.))))
head(data_adult_rescale)
```

Code Explanation

- mutate_if(is.numeric, funs(scale)): The condition is only numeric column and the function is scale

Output:

```
##           X         age        workclass    education
educational.num
## 1 -1.732680
-1.02325949          Private         11th     -1.22106443
## 2 -1.732605 -0.03969284          Private      HS-
grad     -0.43998868
## 3 -1.732530 -0.79628257        Local-gov   Assoc-
acdm      0.73162494
## 4 -1.732455  0.41426100          Private Some-
college     -0.04945081
## 5 -1.732379
-0.34232873          Private         10th     -1.61160231
## 6 -1.732304  1.85178149 Self-emp-not-inc  Prof-
school      1.90323857
##       marital.status  race gender hours.per.week income
## 1      Never-married Black   Male    -0.03995944  <=50K
## 2 Married-civ-spouse White   Male     0.86863037  <=50K
## 3 Married-civ-spouse White   Male    -0.03995944   >50K
## 4 Married-civ-spouse Black   Male    -0.03995944   >50K
## 5      Never-married White   Male    -0.94854924  <=50K
## 6 Married-civ-spouse White   Male    -0.76683128   >50K
```

Step 2) Check factor variables

This step has two objectives:

- Check the level in each categorical column
- Define new levels

We will divide this step into three parts:

- Select the categorical columns
- Store the bar chart of each column in a list
- Print the graphs

We can select the factor columns with the code below:

```
# Select categorical column
factor <- data.frame(select_if(data_adult_rescale, is.factor))
        ncol(factor)
```

Code Explanation

- data.frame(select_if(data_adult, is.factor)): We store the factor columns in factor in a data frame type. The library ggplot2 requires a data frame object.

Output:

```
## [1] 6
```

The dataset contains 6 categorical variables

The second step is more skilled. You want to plot a bar chart for each column in the data frame factor. It is more convenient to automatize the process, especially in situation there are lots of columns.

```
library(ggplot2)
# Create graph for each column
graph <- lapply(names(factor),
    function(x)
        ggplot(factor, aes(get(x))) +
                geom_bar() +
                theme(axis.text.x = element_text(angle = 90)))
```

Code Explanation

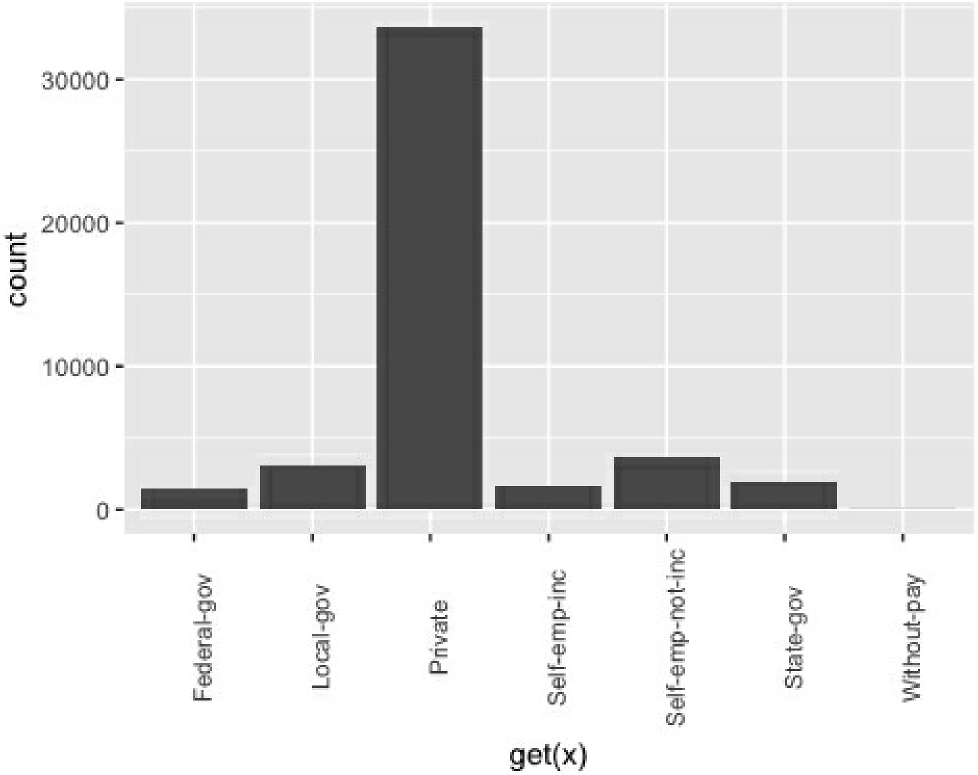
- lapply(): Use the function lapply() to pass a function in all the columns of the dataset. You store the output in a list
- function(x): The function will be processed for each x. Here x is the columns
- ggplot(factor, aes(get(x))) + geom_bar()+ theme(axis.text.x = element_text(angle = 90)): Create a bar char chart for each x element. Note, to return x as a column, you need to include it inside the get()

The last step is relatively easy. You want to print the 6 graphs.

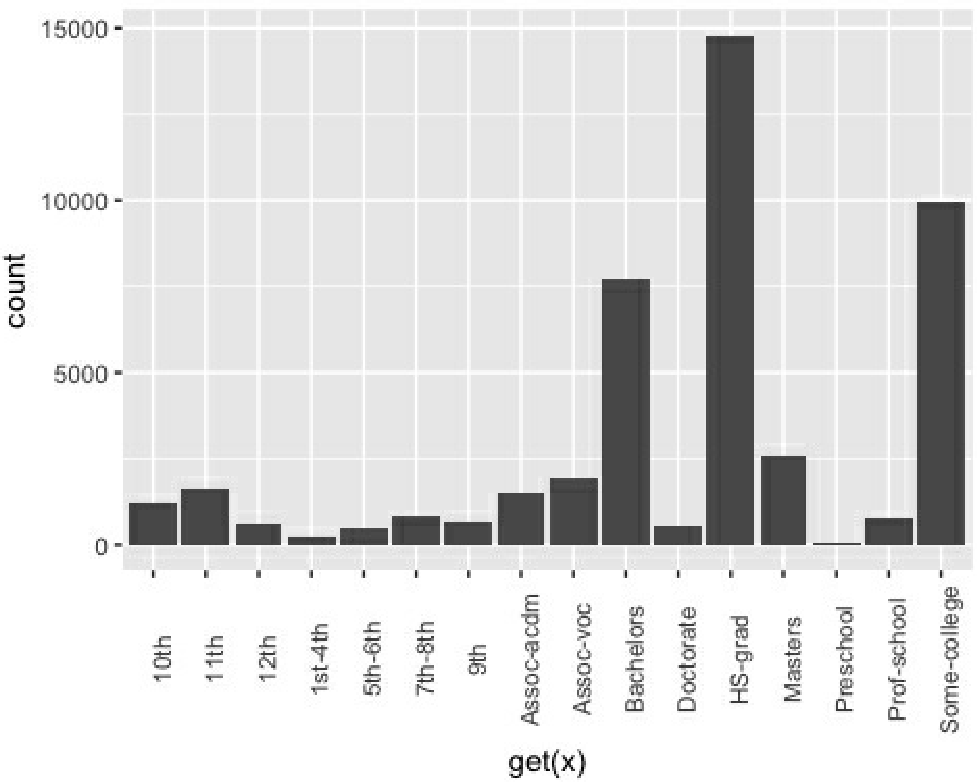
```
# Print the graph
graph
```

Output:

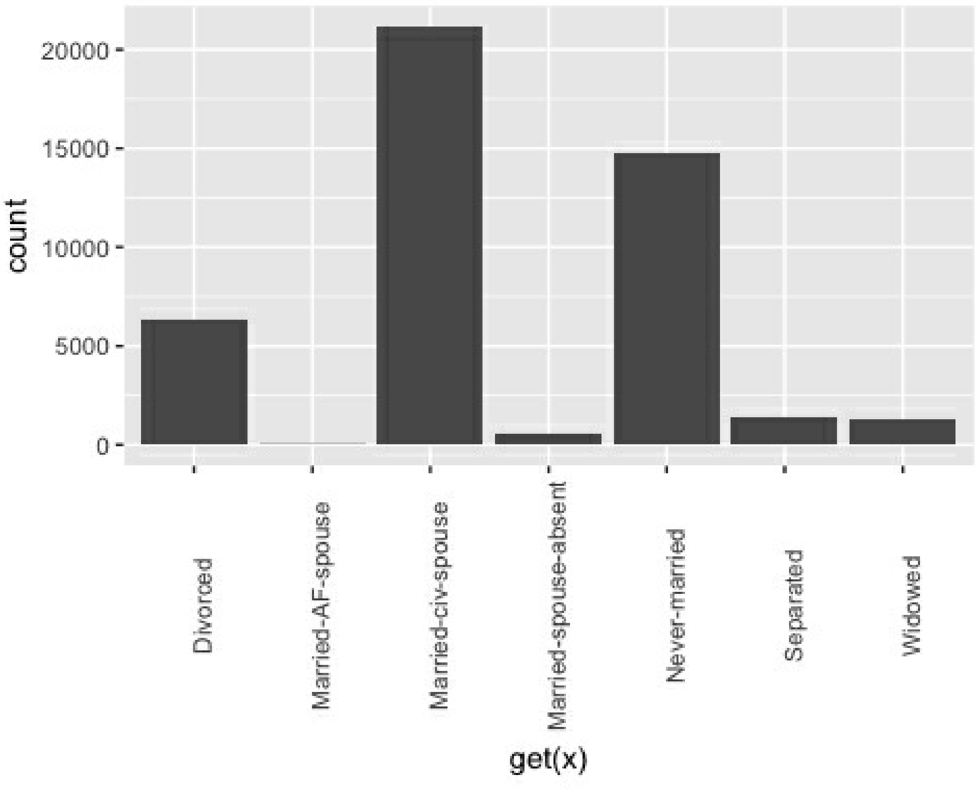
```
## [[1]]
```



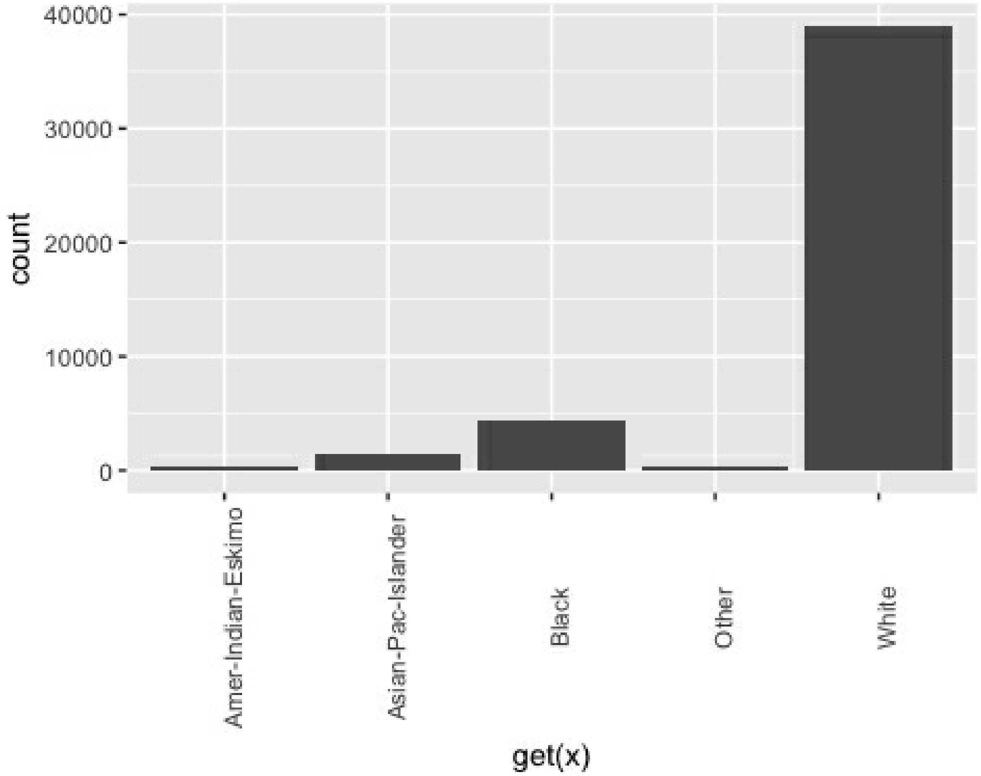
```
## ## [[2]]
```


15000
10000
5000
0
count
10th
11th
12th
1st-4th
5th-6th
7th-8th
9th
Assoc-acdm
Assoc-voc
Bachelors
Doctorate
HS-grad
Masters
Preschool
Prof-school
Some-college
get(x)

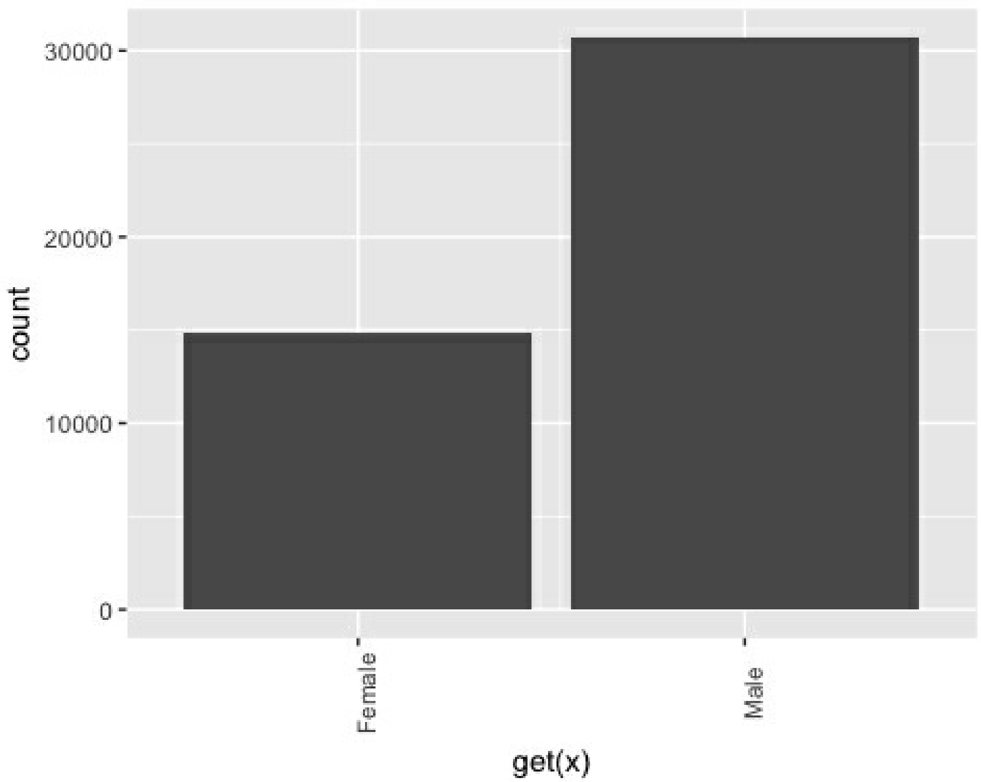
```
## ## [[3]]
```


20000
15000
10000
5000
0
count
Divorced
Married-AF-spouse
Married-civ-spouse
Married-spouse-absent
Never-married
Separated
Widowed
get(x)

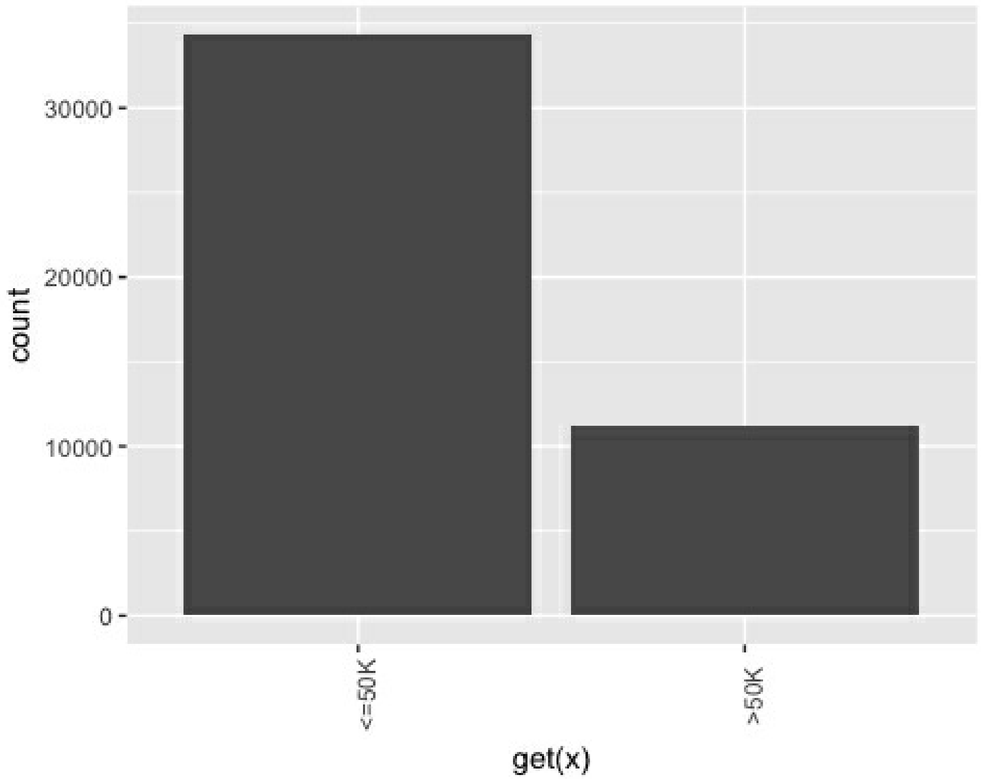
```
## ## [[4]]
```


40000
30000
20000
10000
0
count
Amer-Indian-Eskimo
Asian-Pac-Islander
Black
Other
White
get(x)

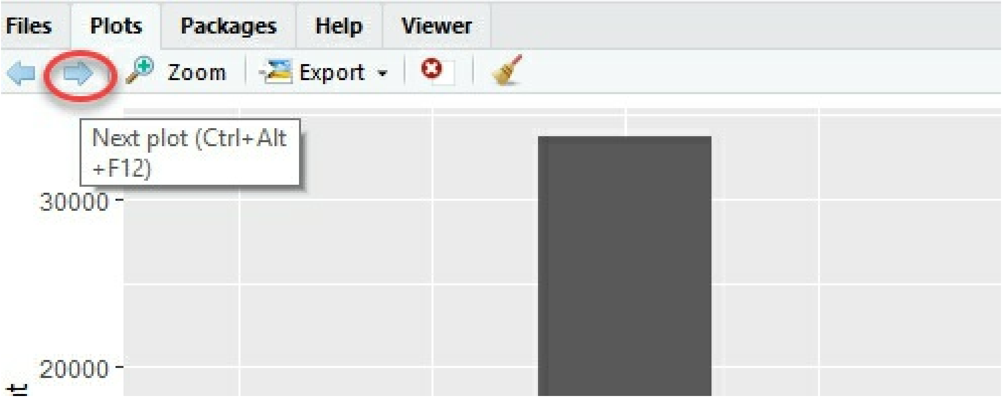
```
## ## [[5]]
```


30000
20000
10000
0
count
Female
Male
get(x)

```
## ## [[6]]
```


30000
20000
10000
0
count
<=50K
>50K
get(x)

Note: Use the next button to navigate to the next graph



Step 3) Feature engineering

Recast education

From the graph above, you can see that the variable education has 16 levels. This is substantial, and some levels have a relatively low number of observations. If you want to improve the amount of information you can get from this variable, you can recast it into higher level. Namely, you create larger groups with similar level of education. For instance, low level of education will be converted in dropout. Higher levels of education will be changed to master.

Here is the detail:

Old level	**New level**
Preschool	dropout
10th	Dropout
11th	Dropout

12th	Dropout
1st-4th	Dropout
5th-6th	Dropout
7th-8th	Dropout
9th	Dropout
HS-Grad	HighGrad
Some-college	Community
Assoc-acdm	Community
Assoc-voc	Community
Bachelors	Bachelors
Masters	Masters
Prof-school	Masters
Doctorate	PhD

```
recast_data <- data_adult_rescale % > %
        select(-X) % > %
        mutate(education = factor(ifelse(education ==
"Preschool" | education == "10th" | education == "11th" |
education == "12th" | education == "1st-4th" | education ==
"5th-6th" | education == "7th-8th" | education == "9th",
"dropout", ifelse(education == "HS-grad", "HighGrad",
ifelse(education == "Some-college" | education == "Assoc-acdm" | 
education == "Assoc-voc", "Community",
    ifelse(education == "Bachelors", "Bachelors",
        ifelse(education == "Masters" | education == "Prof-
school", "Master", "PhD")))))))
```

Code Explanation

- We use the verb mutate from dplyr library. We change the values of education with the statement ifelse

In the table below, you create a summary statistic to see, on average, how many years of education (z-value) it takes to reach the Bachelor, Master or PhD.

```
recast_data % > %
        group_by(education) % > %
        summarize(average_educ_year = mean(educational.num),
                count = n()) % > %
        arrange(average_educ_year)
```

Output:

```
## # A tibble: 6 x 3
## education average_educ_year count
##      <fctr>             <dbl> <int>
## 1   dropout       -1.76147258  5712
## 2  HighGrad       -0.43998868 14803
## 3 Community        0.09561361 13407
## 4 Bachelors        1.12216282  7720
## 5    Master        1.60337381  3338
## 6       PhD        2.29377644   557
```

Recast Marital-status

It is also possible to create lower levels for the marital status. In the following code you change the level as follow:

Old level	**New level**

Never-married	Not-married
Married-spouse-absent	Not-married
Married-AF-spouse	Married
Married-civ-spouse	
Separated	Separated
Divorced	
Widows	Widow

```
# Change level marry
recast_data <- recast_data % > %
        mutate(marital.status = factor(ifelse(marital.status ==
"Never-married" | marital.status == "Married-spouse-absent",
"Not_married", ifelse(marital.status == "Married-AF-spouse" |
marital.status == "Married-civ-spouse", "Married",
ifelse(marital.status == "Separated" | marital.status ==
"Divorced", "Separated", "Widow")))))
```

You can check the number of individuals within each group.

```
table(recast_data$marital.status)
```

Output:

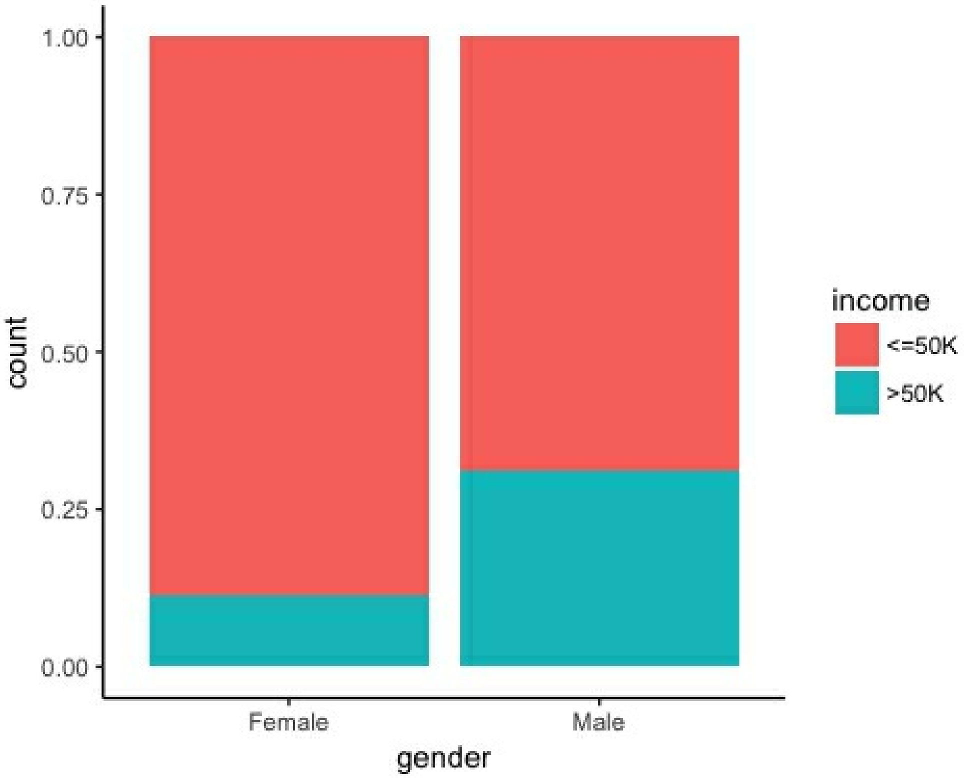
```
## ##     Married Not_married   Separated       Widow
##       21165       15359        7727        1286
```

Step 4) Summary Statistic

It is time to check some statistics about our target variables. In the graph below, you count the percentage of individuals earning more than 50k given their gender.

```
# Plot gender income
ggplot(recast_data, aes(x = gender, fill = income)) +
    geom_bar(position = "fill") +
    theme_classic()
```

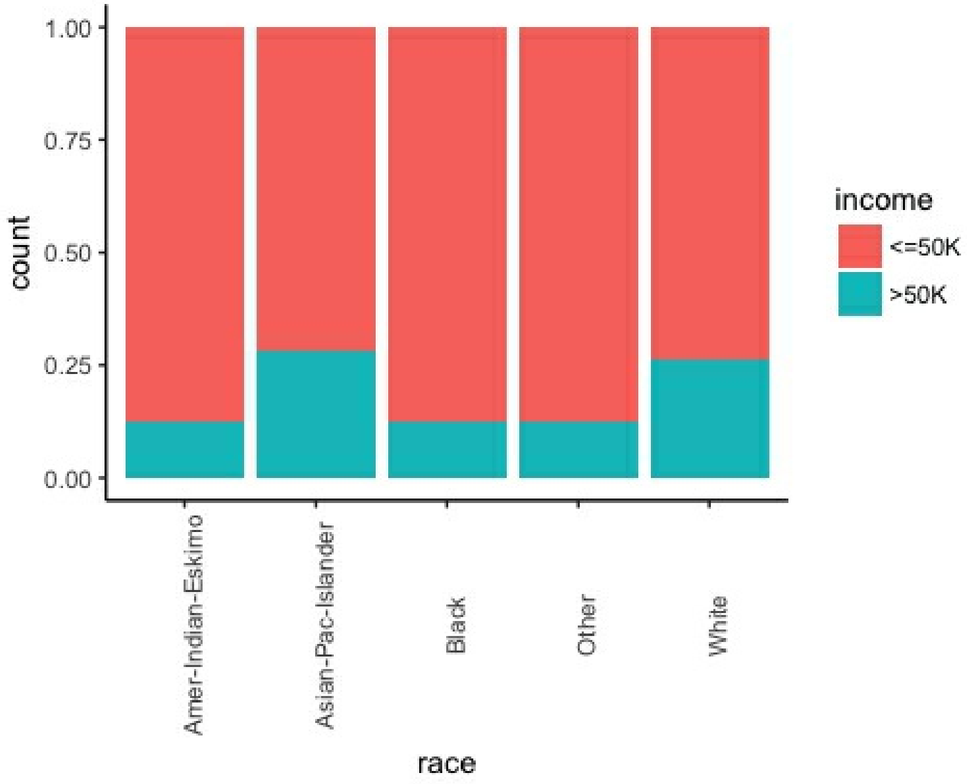
Output:



Next, check if the origin of the individual affects their earning.

```
# Plot origin income
ggplot(recast_data, aes(x = race, fill = income)) +
    geom_bar(position = "fill") +
    theme_classic() +
    theme(axis.text.x = element_text(angle = 90))
```

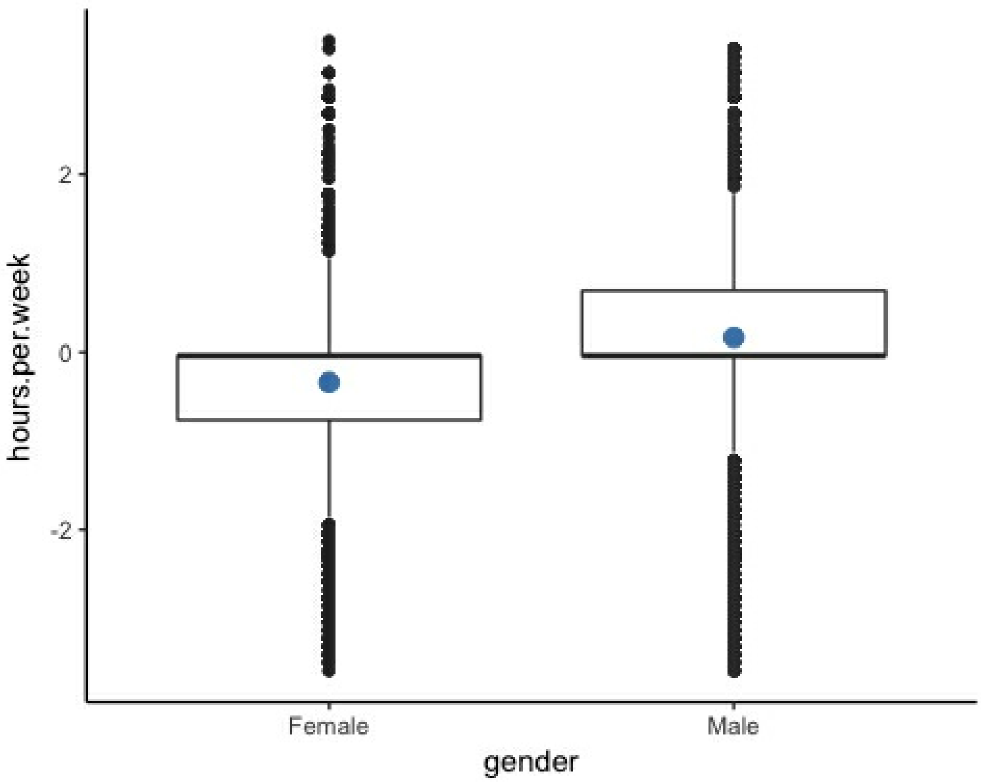
Output:



The number of hours work by gender.

```
# box plot gender working time
ggplot(recast_data, aes(x = gender, y = hours.per.week)) +
    geom_boxplot() +
    stat_summary(fun.y = mean,
        geom = "point",
        size = 3,
        color = "steelblue") +
    theme_classic()
```

Output:



The box plot confirms that the distribution of working time fits different groups. In the box plot, both genders do not have homogeneous observations.

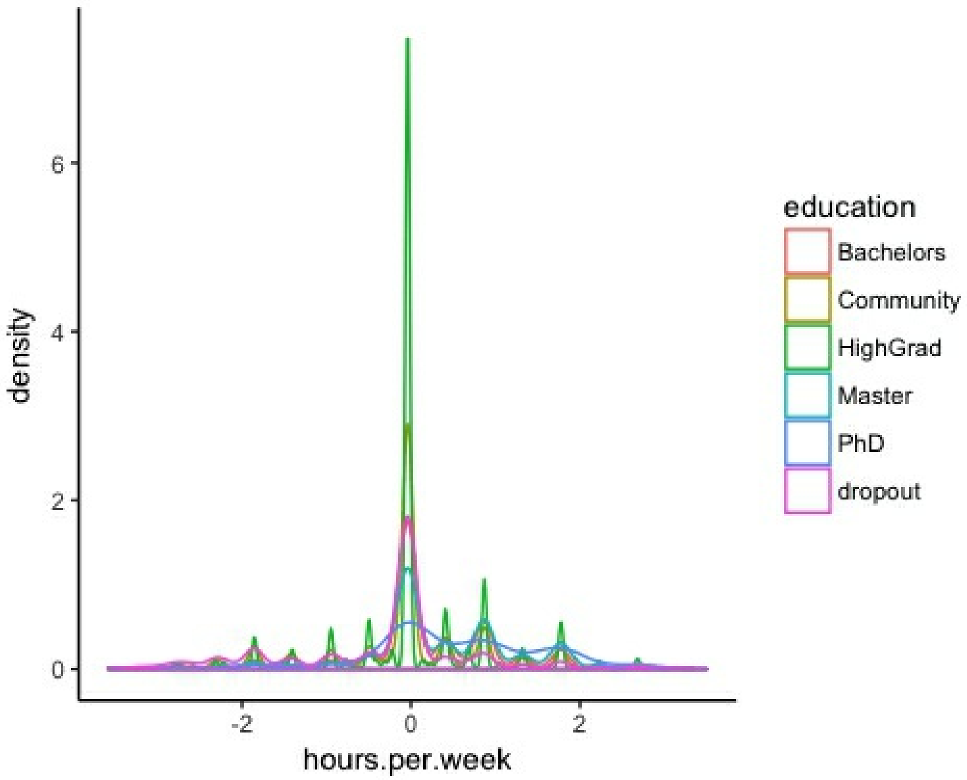
You can check the density of the weekly working time by type of education. The distributions have many distinct picks. It can probably be explained by the type of contract in the US.

```
# Plot distribution working time by education
ggplot(recast_data, aes(x = hours.per.week)) +
    geom_density(aes(color = education), alpha = 0.5) +
    theme_classic()
```

Code Explanation

- ggplot(recast_data, aes(x= hours.per.week)): A density plot only requires one variable
- geom_density(aes(color = education), alpha =0.5): The geometric object to control the density

Output:



To confirm your thoughts, you can perform a one-way ANOVA test:

```
anova <- aov(hours.per.week~education, recast_data)
summary(anova)
```

Output:

```
##                Df Sum Sq Mean Sq F value Pr(>F)    
## education       5   1552  310.31   321.2 <2e-16 ***
## Residuals   45531  43984    0.97                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 
1
```

The ANOVA test confirms the difference in average between groups.

Non-linearity

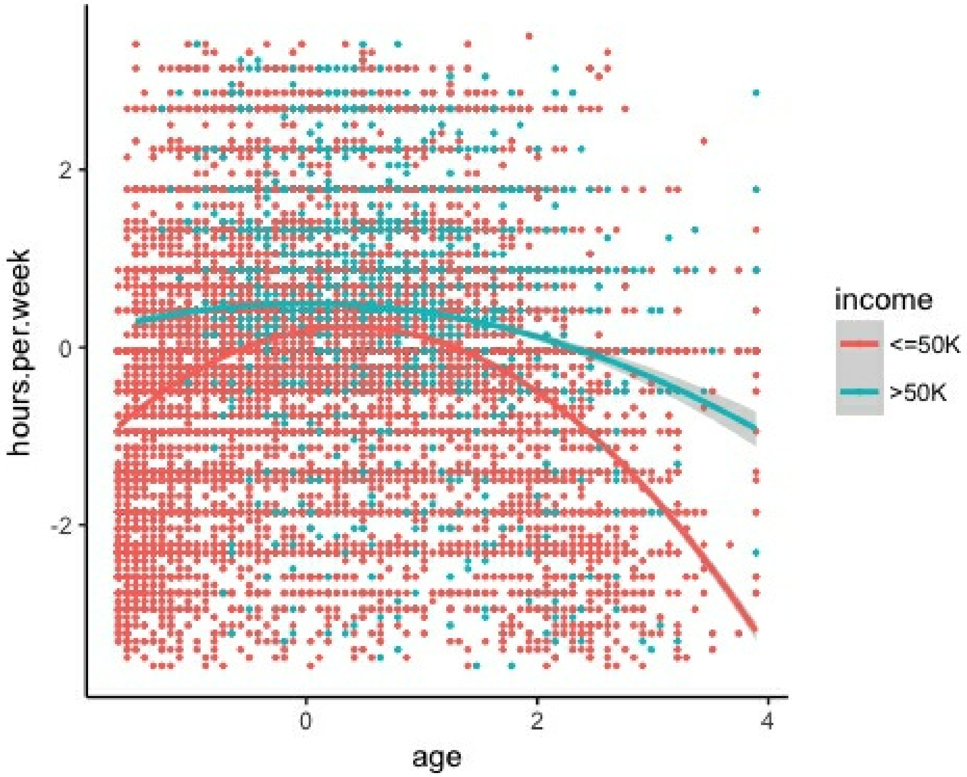
Before you run the model, you can see if the number of hours worked is related to age.

```
library(ggplot2)
ggplot(recast_data, aes(x = age, y = hours.per.week)) +
    geom_point(aes(color = income),
        size = 0.5) +
    stat_smooth(method = 'lm',
        formula = y~poly(x, 2),
        se = TRUE,
        aes(color = income)) +
    theme_classic()
```

Code Explanation

- ggplot(recast_data, aes(x = age, y = hours.per.week)): Set the aesthetic of the graph
- geom_point(aes(color= income), size =0.5): Construct the dot plot
- stat_smooth(): Add the trend line with the following arguments:
    - method='lm': Plot the fitted value if the linear regression
    - formula = y~poly(x,2): Fit a polynomial regression
    - se = TRUE: Add the standard error
    - aes(color= income): Break the model by income

Output:



In a nutshell, you can test interaction terms in the model to pick up the non-linearity effect between the weekly working time and other features. It is important to detect under which condition the working time differs.

Correlation

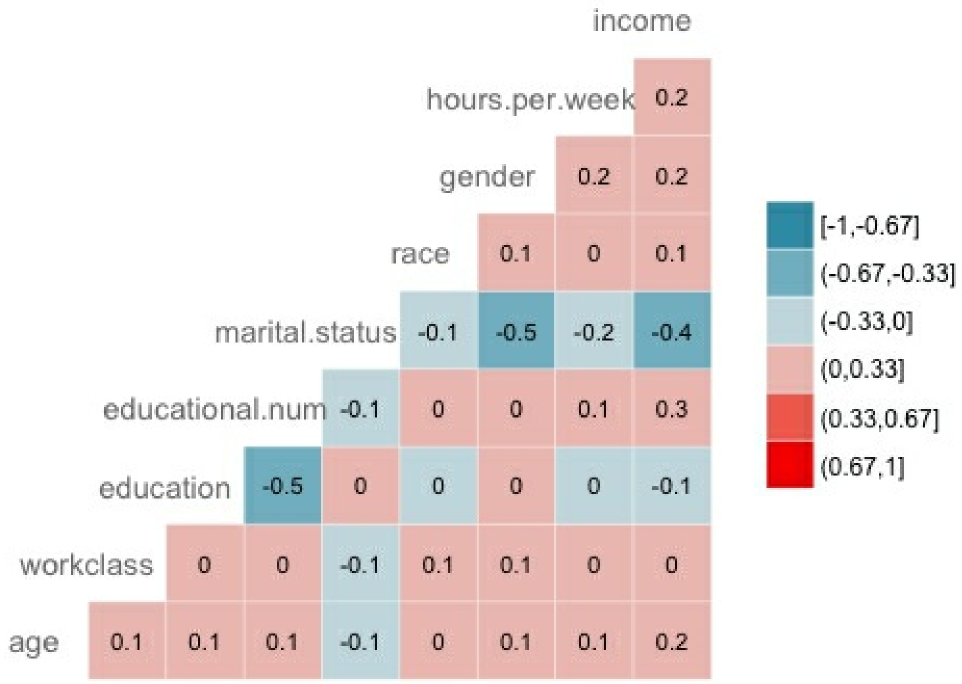
The next check is to visualize the correlation between the variables. You convert the factor level type to numeric so that you can plot a heat map containing the coefficient of correlation computed with the Spearman method.

```
library(GGally)
# Convert data to numeric
corr <- data.frame(lapply(recast_data, as.integer))
# Plot the graphggcorr(corr,
    method = c("pairwise", "spearman"),
    nbreaks = 6,
    hjust = 0.8,
    label = TRUE,
    label_size = 3,
    color = "grey50")
```

Code Explanation

- data.frame(lapply(recast_data,as.integer)): Convert data to numeric
- ggcorr() plot the heat map with the following arguments:
    - method: Method to compute the correlation
    - nbreaks = 6: Number of break
    - hjust = 0.8: Control position of the variable name in the plot
    - label = TRUE: Add labels in the center of the windows
    - label_size = 3: Size labels
    - color = "grey50"): Color of the label

Output:



Step 5) Train/test set

Any supervised machine learning task require to split the data between a train set and a test set. You can use the "function" you created in the other supervised learning tutorials to create a train/test set.

```
set.seed(1234)
create_train_test <- function(data, size = 0.8, train = TRUE) {
    n_row = nrow(data)
    total_row = size * n_row
    train_sample <- 1: total_row
    if (train == TRUE) {
        return (data[train_sample, ])
    } else {
        return (data[-train_sample, ])
    }
}
data_train <- create_train_test(recast_data, 0.8, train = TRUE)
data_test <- create_train_test(recast_data, 0.8, train = FALSE)
dim(data_train)
```

Output:

```
## [1] 36429     9
```

```
dim(data_test)
```

Output:

```
## [1] 9108    9
```

Step 6) Build the model

To see how the algorithm performs, you use the glm() package. The **Generalized Linear Model** is a collection of models. The basic syntax is:

```
glm(formula, data=data, family=linkfunction()
Argument:
```

```
- formula:  Equation used to fit the model- data: dataset used
- Family:     - binomial: (link = "logit")
- gaussian: (link = "identity")
- Gamma:    (link = "inverse")
- inverse.gaussian: (link = "1/mu^2")
- poisson:  (link = "log")
- quasi:    (link = "identity", variance =
"constant")
- quasibinomial:    (link = "logit")
- quasipoisson: (link = "log")
```

You are ready to estimate the logistic model to split the income level between a set of features.

```
formula <- income~.
logit <- glm(formula, data = data_train, family = 'binomial')
summary(logit)
```

Code Explanation

- formula <- income ~ .: Create the model to fit
- logit <- glm(formula, data = data_train, family = 'binomial'): Fit a logistic model (family = 'binomial') with the data_train data.
- summary(logit): Print the summary of the model

Output:

```
##
## Call:
## glm(formula = formula, family = "binomial", data =
data_train)
## ## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.6456  -0.5858  -0.2609  -0.0651   3.1982
##
## Coefficients:
##                            Estimate Std. Error z value
Pr(>|z|)
##
(Intercept)                0.07882    0.21726   0.363  0.71675
## age                        0.41119    0.01857  22.146  < 2e-
16 ***
## workclassLocal-gov        -0.64018    0.09396  -6.813 9.54e-
```

```
12 ***
## workclassPrivate          -0.53542    0.07886  -6.789 1.13e-
11 ***
## workclassSelf-emp-
inc     -0.07733    0.10350  -0.747  0.45499
## workclassSelf-emp-not-inc -1.09052    0.09140 -11.931  < 2e-
16 ***
## workclassState-gov        -0.80562    0.10617  -7.588 3.25e-
14 ***
## workclassWithout-
pay      -1.09765    0.86787  -1.265  0.20596
## educationCommunity        -0.44436    0.08267  -5.375 7.66e-
08 ***
## educationHighGrad         -0.67613    0.11827  -5.717 1.08e-
08 ***
## educationMaster            0.35651    0.06780   5.258 1.46e-
07 ***
##
educationPhD               0.46995    0.15772   2.980  0.00289
**
## educationdropout          -1.04974    0.21280  -4.933 8.10e-
07 ***
## educational.num            0.56908    0.07063   8.057 7.84e-
16 ***
## marital.statusNot_married -2.50346    0.05113 -48.966  < 2e-
16 ***
## marital.statusSeparated   -2.16177    0.05425 -39.846  < 2e-
16 ***
## marital.statusWidow       -2.22707    0.12522 -17.785  < 2e-
16 ***
## raceAsian-Pac-
Islander     0.08359    0.20344   0.411  0.68117
##
raceBlack                  0.07188    0.19330   0.372  0.71001
##
raceOther                  0.01370    0.27695   0.049  0.96054
##
raceWhite                  0.34830    0.18441   1.889  0.05894
.
##
genderMale                 0.08596    0.04289   2.004  0.04506
*
## hours.per.week             0.41942    0.01748  23.998  < 2e-
16 ***
## ---## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
```

```
0.1 ' ' 1
## ## (Dispersion parameter for binomial family taken to be 1)
## ##     Null deviance: 40601  on 36428  degrees of freedom
## Residual deviance: 27041  on 36406  degrees of freedom
## AIC: 27087
##
## Number of Fisher Scoring iterations: 6
```

The summary of our model reveals interesting information. The performance of a logistic regression is evaluated with specific key metrics.

- AIC (Akaike Information Criteria): This is the equivalent of **R2** in logistic regression. It measures the fit when a penalty is applied to the number of parameters. Smaller **AIC** values indicate the model is closer to the truth.
- Null deviance: Fits the model only with the intercept. The degree of freedom is n-1. We can interpret it as a Chi-square value (fitted value different from the actual value hypothesis testing).
- Residual Deviance: Model with all the variables. It is also interpreted as a Chi-square hypothesis testing.
- Number of Fisher Scoring iterations: Number of iterations before converging.

The output of the glm() function is stored in a list. The code below shows all the items available in the logit variable we constructed to evaluate the logistic regression.

# The list is very long, print only the first three elements

```
lapply(logit, class)[1:3]
```

Output:

```
## $coefficients
## [1] "numeric"
##
## $residuals
## [1] "numeric"
##
## $fitted.values
## [1] "numeric"
```

Each value can be extracted with the $ sign follow by the name of the metrics. For instance, you stored the model as logit. To extract the AIC criteria, you use:

```
logit$aic
```

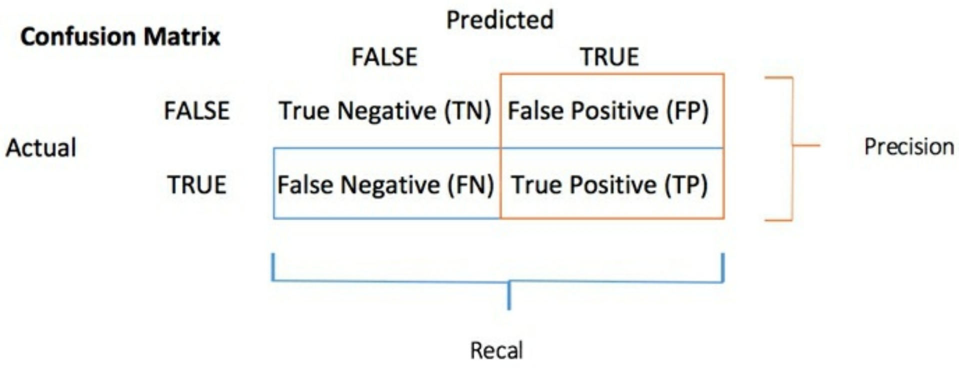
Output:

```
## [1] 27086.65
```

Step 7) Assess the performance of the model

Confusion Matrix

The **confusion matrix** is a better choice to evaluate the classification performance compared with the different metrics you saw before. The general idea is to count the number of times True instances are classified are False.



To compute the confusion matrix, you first need to have a set of predictions so that they can be compared to the actual targets.

```
predict <- predict(logit, data_test, type = 'response')
# confusion matrix
```

```
table_mat <- table(data_test$income, predict > 0.5)
table_mat
```

Code Explanation

- predict(logit,data_test, type = 'response'): Compute the prediction on the test set. Set type = 'response' to compute the response probability.
- table(data_test$income, predict > 0.5): Compute the confusion matrix. predict > 0.5 means it returns 1 if the predicted probabilities are above 0.5, else 0.

Output:

```
##
##         FALSE TRUE
##   <=50K  6310  495
##   >50K   1074 1229
```

Each row in a confusion matrix represents an actual target, while each column represents a predicted target. The first row of this matrix considers the income lower than 50k (the False class): 6241 were correctly classified as individuals with income lower than 50k (**True negative**), while the remaining one was wrongly classified as above 50k (**False positive**). The second row considers the income above 50k, the positive class were 1229 (**True positive**), while the **True negative** was 1074.

You can calculate the model **accuracy** by summing the true positive + true negative over the total observation

$$accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

```
accuracy_Test <- sum(diag(table_mat)) / sum(table_mat)
accuracy_Test
```

Code Explanation

- sum(diag(table_mat)): Sum of the diagonal
- sum(table_mat): Sum of the matrix.

Output:

```
## [1] 0.8277339
```

The model appears to suffer from one problem, it overestimates the number of false negatives. This is called the **accuracy test paradox**. We stated that the accuracy is the ratio of correct predictions to the total number of cases. We can have relatively high accuracy but a useless model. It happens when there is a dominant class. If you look back at the confusion matrix, you can see most of the cases are classified as true negative. Imagine now, the model classified all the classes as negative (i.e. lower than 50k). You would have an accuracy of 75 percent (6718/6718+2257). Your model performs better but struggles to distinguish the true positive with the true negative.

In such situation, it is preferable to have a more concise metric. We can look at:

- Precision=TP/(TP+FP)
- Recall=TP/(TP+FN)

Precision vs Recall

Precision looks at the accuracy of the positive prediction. **Recall** is the ratio of positive instances that are correctly detected by the classifier;

You can construct two functions to compute these two metrics

1. Construct precision

```
precision <- function(matrix) {
        # True positive
    tp <- matrix[2, 2]
        # false positive
    fp <- matrix[1, 2]
    return (tp / (tp + fp))
}
```

Code Explanation

- mat[1,1]: Return the first cell of the first column of the data frame, i.e. the true positive
- mat[1,2]; Return the first cell of the second column of the data frame, i.e. the false positive

```
recall <- function(matrix) {
# true positive
    tp <- matrix[2, 2]# false positive
    fn <- matrix[2, 1]
    return (tp / (tp + fn))
}
```

Code Explanation

- mat[1,1]: Return the first cell of the first column of the data frame, i.e. the true positive
- mat[2,1]; Return the second cell of the first column of the data frame, i.e. the false negative

You can test your functions

```
prec <- precision(table_mat)
prec
rec <- recall(table_mat)
rec
```

Output:

```
## [1] 0.712877
## [2] 0.5336518
```

When the model says it is an individual above 50k, it is correct in only 54 percent of the case, and can claim individuals above 50k in 72 percent of the case.

You can create the F_1 score based on the precision and recall. The F_1 is a harmonic mean of these two metrics, meaning it gives more weight to the lower values.

$$F_1 = 2 * \frac{precision * recall}{precision + recall}$$

```
f1 <- 2 * ((prec * rec) / (prec + rec))
f1
```

Output:

```
## [1] 0.6103799
```

Precision vs Recall tradeoff

It is impossible to have both a high precision and high recall.

If we increase the precision, the correct individual will be better predicted, but we would miss lots of them (lower recall). In some situation, we prefer higher precision than recall. There is a concave relationship between precision and recall.

- Imagine, you need to predict if a patient has a disease. You want to be as precise as possible.
- If you need to detect potential fraudulent people in the street through facial recognition, it would be better to catch many people labeled as fraudulent even though the precision is low. The police will be able to release the non-fraudulent individual.

The ROC curve

The **Receiver Operating Characteristic** curve is another common tool used with binary classification. It is very similar to the precision/recall curve, but instead of plotting precision versus recall, the ROC curve shows the true positive rate (i.e., recall) against the false positive rate. The false positive rate is the ratio of negative instances that are incorrectly classified as positive. It is equal to one minus the true negative rate. The true negative rate is also called **specificity**. Hence the ROC curve plots **sensitivity** (recall) versus 1-specificity

To plot the ROC curve, we need to install a library called RORC. We can find in the conda library. You can type the code:

```
conda install -c r r-rocr --yes
```

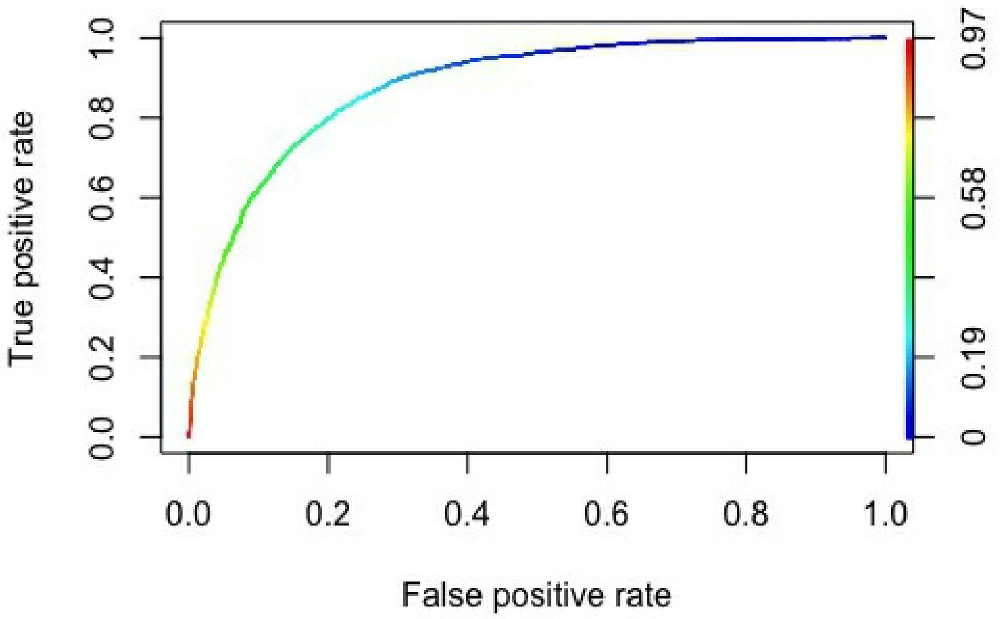
We can plot the ROC with the prediction() and performance() functions.

```
library(ROCR)
ROCRpred <- prediction(predict, data_test$income)
ROCRperf <- performance(ROCRpred, 'tpr', 'fpr')
plot(ROCRperf, colorize = TRUE, text.adj = c(-0.2, 1.7))
```

Code Explanation

- prediction(predict, data_test$income): The ROCR library needs to create a prediction object to transform the input data
- performance(ROCRpred, 'tpr','fpr'): Return the two combinations to produce in the graph. Here, tpr and fpr are constructed. Tot plot precision and recall together, use "prec", "rec".

Output:



Step 8) Improve the model

You can try to add non-linearity to the model with the interaction between

- age and hours.per.week
- gender and hours.per.week.

You need to use the score test to compare both model

```
formula_2 <- income~age: hours.per.week + gender: hours.per.week
+ .
logit_2 <- glm(formula_2, data = data_train, family =
'binomial')
predict_2 <- predict(logit_2, data_test, type = 'response')
table_mat_2 <- table(data_test$income, predict_2 > 0.5)
precision_2 <- precision(table_mat_2)
recall_2 <- recall(table_mat_2)
f1_2 <- 2 * ((precision_2 * recall_2) / (precision_2 +
recall_2))
f1_2
```

Output:

```
## [1] 0.6109181
```

The score is slightly higher than the previous one. You can keep working on the data a try to beat the score.

Summary

We can summarize the function to train a logistic regression in the table below:

Package	**Objective**	**function**	**argument**
-	Create train/test dataset	create_train_set()	data, size, train
glm	Train a Generalized Linear Model	glm()	formula, data, family*
glm	Summarize the model	summary()	fitted model
base	Make prediction	predict()	fitted model, dataset, type = 'response'
base	Create a confusion matrix	table()	y, predict()
base	Create accuracy score	sum(diag(table())/sum(table()	
ROCR	Create ROC : Step 1 Create prediction	prediction()	predict(), y
ROCR	Create ROC : Step 2 Create performance	performance()	prediction(), 'tpr', 'fpr'

ROCR	Create ROC : Step 3 Plot graph	plot()	performance()

The other **GLM** type of models are:

- binomial: (link = "logit")

- gaussian: (link = "identity")

- Gamma: (link = "inverse")

- inverse.gaussian: (link = "1/mu^2")

- poisson: (link = "log")

- quasi: (link = "identity", variance = "constant")

- quasibinomial: (link = "logit")

- quasipoisson: (link = "log")

Chapter 31: K-means Clustering in R with Example

What is Cluster analysis?

Cluster analysis is part of the **unsupervised learning**. A cluster is a group of data that share similar features. We can say, clustering analysis is more about discovery than a prediction. The machine searches for similarity in the data. For instance, you can use cluster analysis for the following application:

- Customer segmentation: Looks for similarity between groups of customers
- Stock Market clustering: Group stock based on performances
- Reduce dimensionality of a dataset by grouping observations with similar values

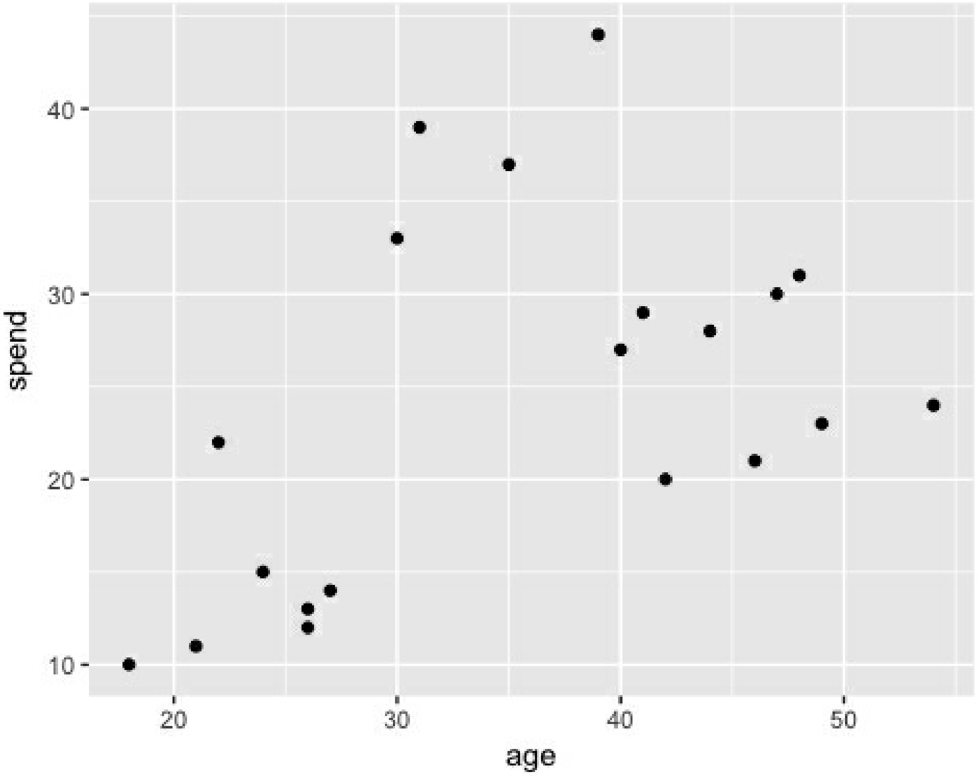
Clustering analysis is not too difficult to implement and is meaningful as well as actionable for business.

The most striking difference between supervised and unsupervised learning lies in the results. Unsupervised learning creates a new variable, the label, while supervised learning predicts an outcome. The machine helps the practitioner in the quest to label the data based on close relatedness. It is up to the analyst to make use of the groups and give a name to them.

Let's make an example to understand the concept of clustering. For simplicity, we work in two dimensions. You have data on the total spend of customers and their ages. To improve advertising, the marketing team wants to send more targeted emails to their customers.

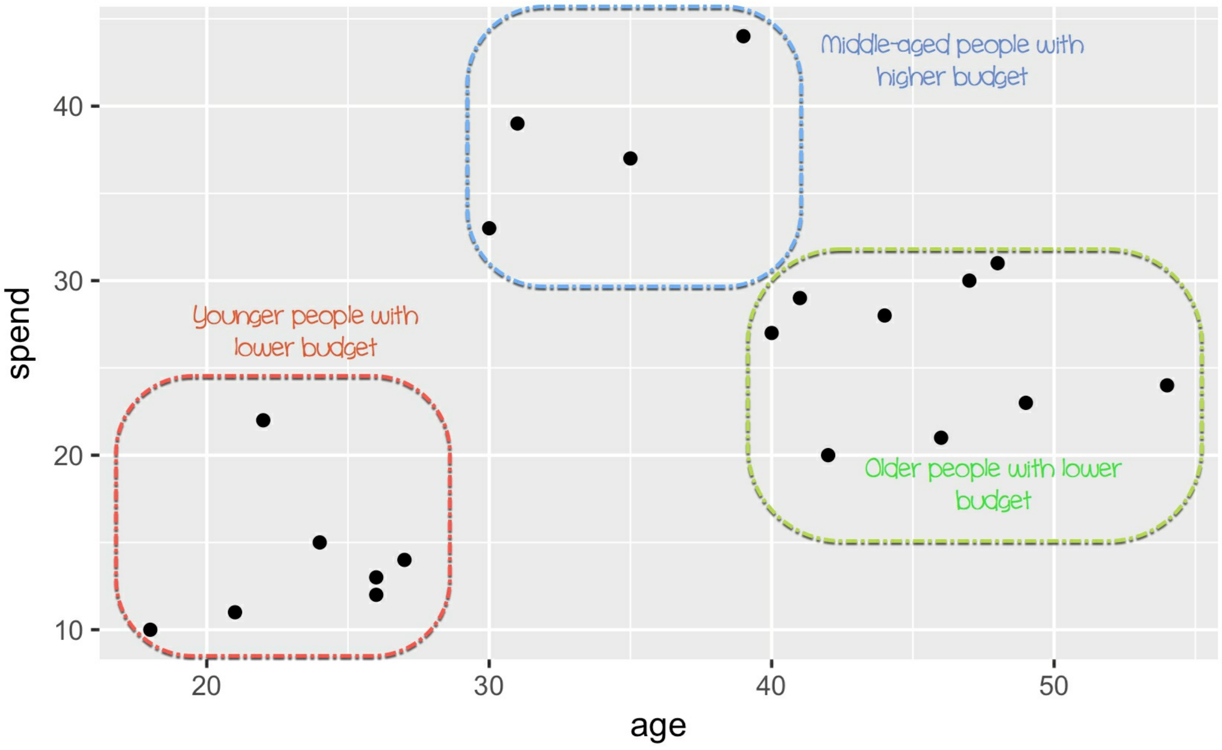
In the following graph, you plot the total spend and the age of the customers.

```
library(ggplot2)
df <- data.frame(age = c(18, 21, 22, 24, 26, 26, 27, 30, 31, 35,
39, 40, 41, 42, 44, 46, 47, 48, 49, 54),
    spend = c(10, 11, 22, 15, 12, 13, 14, 33, 39, 37, 44, 27,
29, 20, 28, 21, 30, 31, 23, 24)
)
ggplot(df, aes(x = age, y = spend)) +
    geom_point()
```



A pattern is visible at this point

1. At the bottom-left, you can see young people with a lower purchasing power
2. Upper-middle reflects people with a job that they can afford spend more
3. Finally, older people with a lower budget.



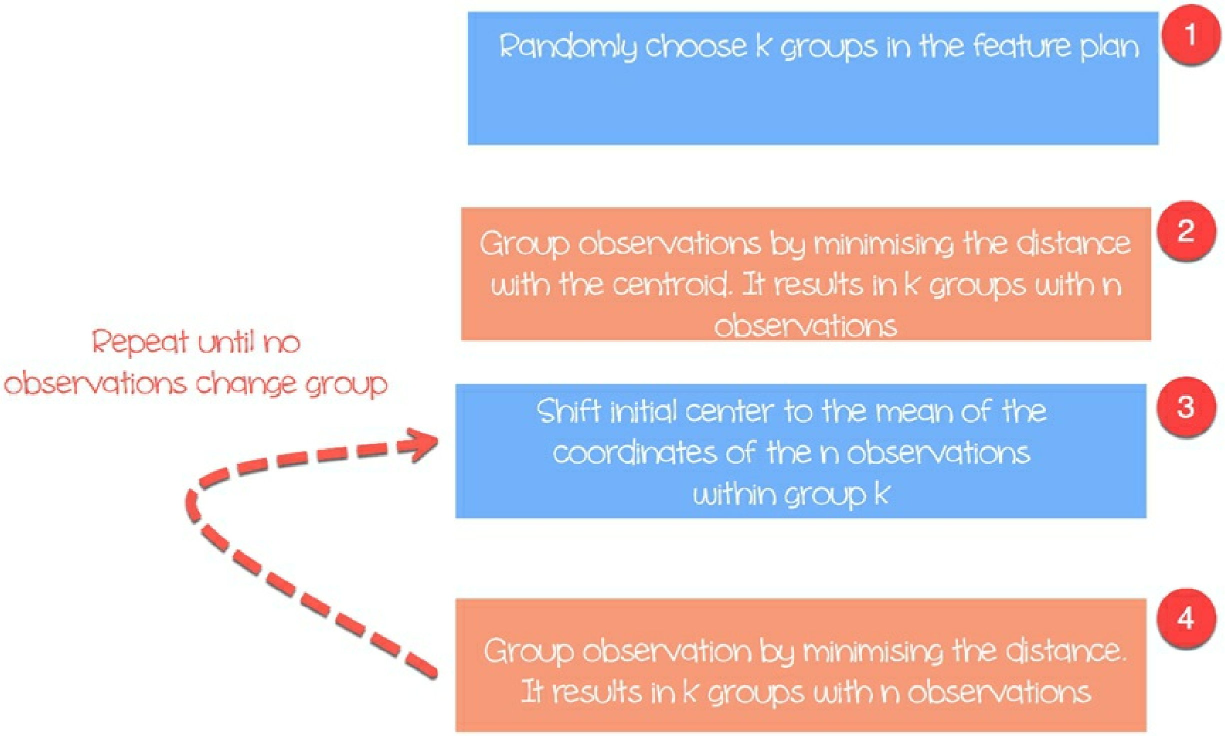
In the figure above, you cluster the observations by hand and define each of the three groups. This example is somewhat straightforward and highly visual. If new observations are appended to the data set, you can label them within the circles. You define the circle based on our judgment. Instead, you can use Machine Learning to group the data objectively.

In this tutorial, you will learn how to use the **k-means** algorithm.

K-means algorithm

K-mean is, without doubt, the most popular clustering method. Researchers released the algorithm decades ago, and lots of improvements have been done to k-means.

The algorithm tries to find groups by minimizing the distance between the observations, called **local optimal** solutions. The distances are measured based on the coordinates of the observations. For instance, in a two-dimensional space, the coordinates are simple and .


Randomly choose k groups in the feature plan
1
Group observations by minimising the distance with the centroid. It results in k groups with n observations
2
Repeat until no observations change group
Shift initial center to the mean of the coordinates of the n observations within group k
3
Group observation by minimising the distance. It results in k groups with n observations
4

The algorithm works as follow:

- Step 1: Choose groups in the feature plan randomly
- Step 2: Minimize the distance between the cluster center and the different observations (**centroid**). It results in groups with observations
- Step 3: Shift the initial centroid to the mean of the coordinates within a group.
- Step 4: Minimize the distance according to the new centroids. New boundaries are created. Thus, observations will move from one group to another
- Repeat until no observation changes groups

K-means usually takes the Euclidean distance between the feature and feature :

$$distance(x,y) = \sum_{i}^{n} (x_i - y_i)^2$$

Different measures are available such as the Manhattan distance or Minlowski distance. Note that, K-mean returns different groups each time you run the algorithm. Recall that the first initial guesses are random and compute the distances until the algorithm reaches a homogeneity within groups. That is, k-mean is very sensitive to the first choice, and unless the number of observations and groups are small, it is almost impossible to get the same clustering.

Select the number of clusters

Another difficulty found with k-mean is the choice of the number of clusters. You can set a high value of , i.e. a large number of groups, to improve stability but you might end up with **overfit** of data. Overfitting means the performance of the model decreases substantially for new coming data. The machine learnt the little details of the data set and struggle to generalize the overall pattern.

The number of clusters depends on the nature of the data set, the industry, business and so on. However, there is a rule of thumb to select the appropriate number of clusters:

$$cluster = \sqrt{2/n}$$

with equals to the number of observation in the dataset.

Generally speaking, it is interesting to spend times to search for the best value of to fit with the business need.

We will use the Prices of Personal Computers dataset to perform our clustering analysis. This dataset contains 6259 observations and 10 features. The dataset observes the price from 1993 to 1995 of 486 personal computers in the US. The variables are price, speed, ram, screen, cd among other.

You will proceed as follow:

- Import data
- Train the model
- Evaluate the model

Import data

K means is not suitable for factor variables because it is based on the distance and discrete values do not return meaningful values. You can delete the three categorical variables in our dataset. Besides, there are no missing values in this dataset.

```
library(dplyr)
PATH <-"https://raw.githubusercontent.com/guru99-edu/R-
Programming/master/computers.csv"
df <- read.csv(PATH) %>%
select(-c(X, cd, multi, premium))
glimpse(df)
```

Output

```
## Observations: 6, 259
## Variables: 7
## $ price < int > 1499, 1795, 1595, 1849, 3295, 3695, 1720,
1995, 2225, 2...
##$ speed < int > 25, 33, 25, 25, 33, 66, 25, 50, 50, 50, 33,
66, 50, 25, ...
##$ hd < int > 80, 85, 170, 170, 340, 340, 170, 85, 210, 210,
170, 210...
##$ ram < int > 4, 2, 4, 8, 16, 16, 4, 2, 8, 4, 8, 8, 4, 8, 8,
4, 2, 4, ...
##$ screen < int > 14, 14, 15, 14, 14, 14, 14, 14, 14, 15, 15,
14, 14, 14, ...
##$ ads < int > 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 94, 94,
94, 94, ...
## $ trend  <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, 1, 1...
```

From the summary statistics, you can see the data has large values. A good practice with k mean and distance calculation is to rescale the data so that the mean is equal to one and the standard deviation is equal to zero.

```
summary(df)
```

Output:

```
##      price          speed              hd              ram
##  Min.   : 949   Min.   : 25.00   Min.   :  80.0   Min.   :
2.000
##  1st Qu.:1794   1st Qu.: 33.00   1st Qu.: 214.0   1st Qu.:
4.000  `
##  Median :2144   Median : 50.00   Median : 340.0   Median :
8.000
##  Mean   :2220   Mean   : 52.01   Mean   : 416.6   Mean   :
8.287
##  3rd Qu.:2595   3rd Qu.: 66.00   3rd Qu.: 528.0   3rd Qu.:
8.000
##  Max.   :5399   Max.   :100.00   Max.   :2100.0   Max.   :32.0
##      screen           ads            trend
##  Min.   :14.00   Min.   : 39.0   Min.   : 1.00
##  1st Qu.:14.00   1st Qu.:162.5   1st Qu.:10.00
##  Median :14.00   Median :246.0   Median :16.00
##  Mean   :14.61   Mean   :221.3   Mean   :15.93
##  3rd Qu.:15.00   3rd Qu.:275.0   3rd Qu.:21.50
##  Max.   :17.00   Max.   :339.0   Max.   :35.00
```

You rescale the variables with the scale() function of the dplyr library. The transformation reduces the impact of outliers and allows to compare a sole observation against the mean. If a standardized value (or **z-score**) is high, you can be confident that this observation is indeed above the mean (a large z-score implies that this point is far away from the mean in term of standard deviation. A z-score of two indicates the value is 2 standard deviations away from the mean. Note, the z-score follows a Gaussian distribution and is symmetrical around the mean.

```
rescale_df <- df % > %
mutate(price_scal = scale(price),
    hd_scal = scale(hd),
    ram_scal = scale(ram),
    screen_scal = scale(screen),
    ads_scal = scale(ads),
    trend_scal = scale(trend)) % > %
select(-c(price, speed, hd, ram, screen, ads, trend))
```

R base has a function to run the k mean algorithm. The basic function of k mean is:

```
kmeans(df, k)
arguments:
-df: dataset used to run the algorithm
-k: Number of clusters
```

Train the model

In figure three, you detailed how the algorithm works. You can see each step graphically with the great package build by Yi Hui (also creator of Knit for Rmarkdown). The package animation is not available in the conda library. You can use the other way to install the package with install.packages("animation"). You can check if the package is installed in our Anaconda folder.

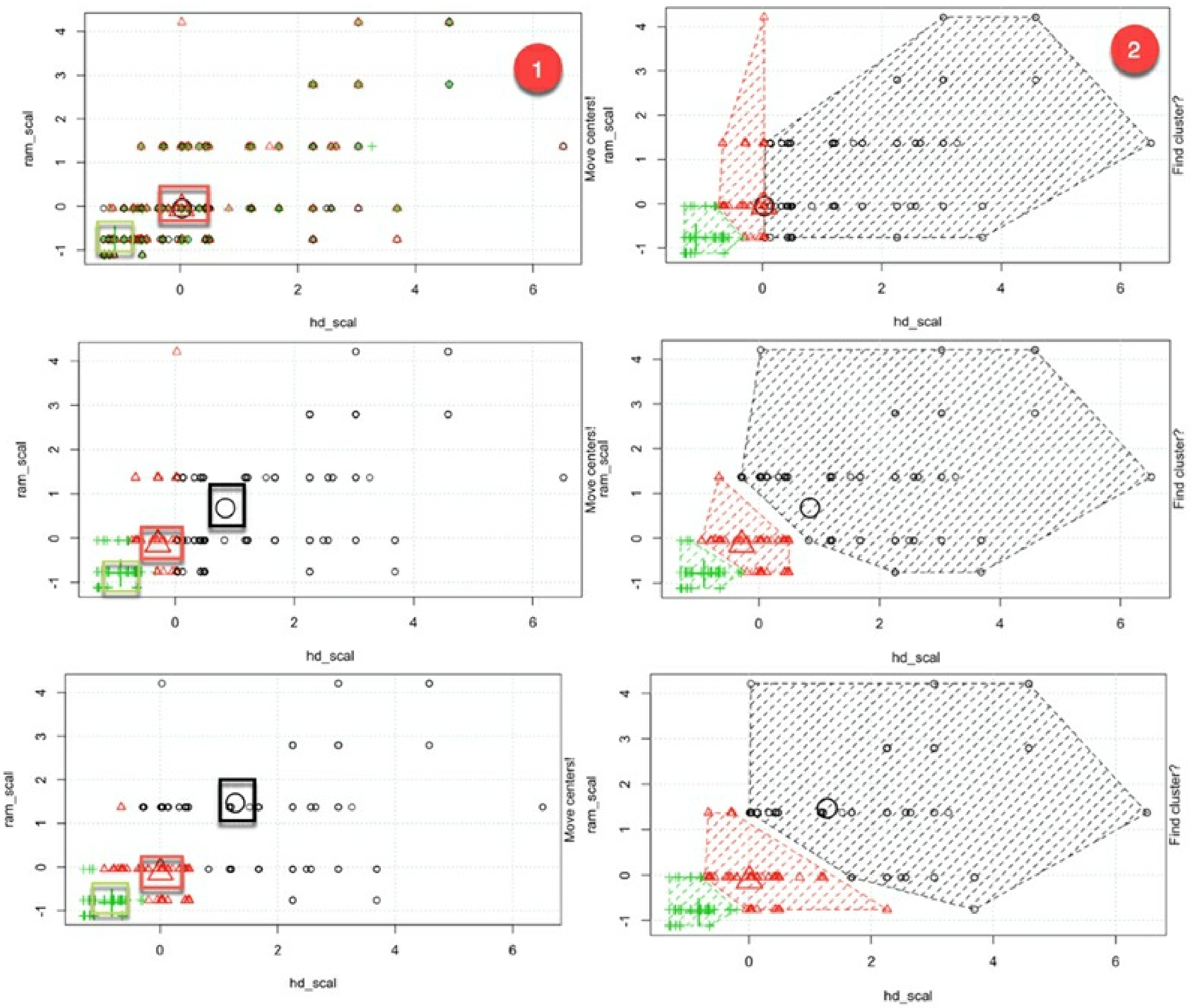
```
install.packages("animation")
```

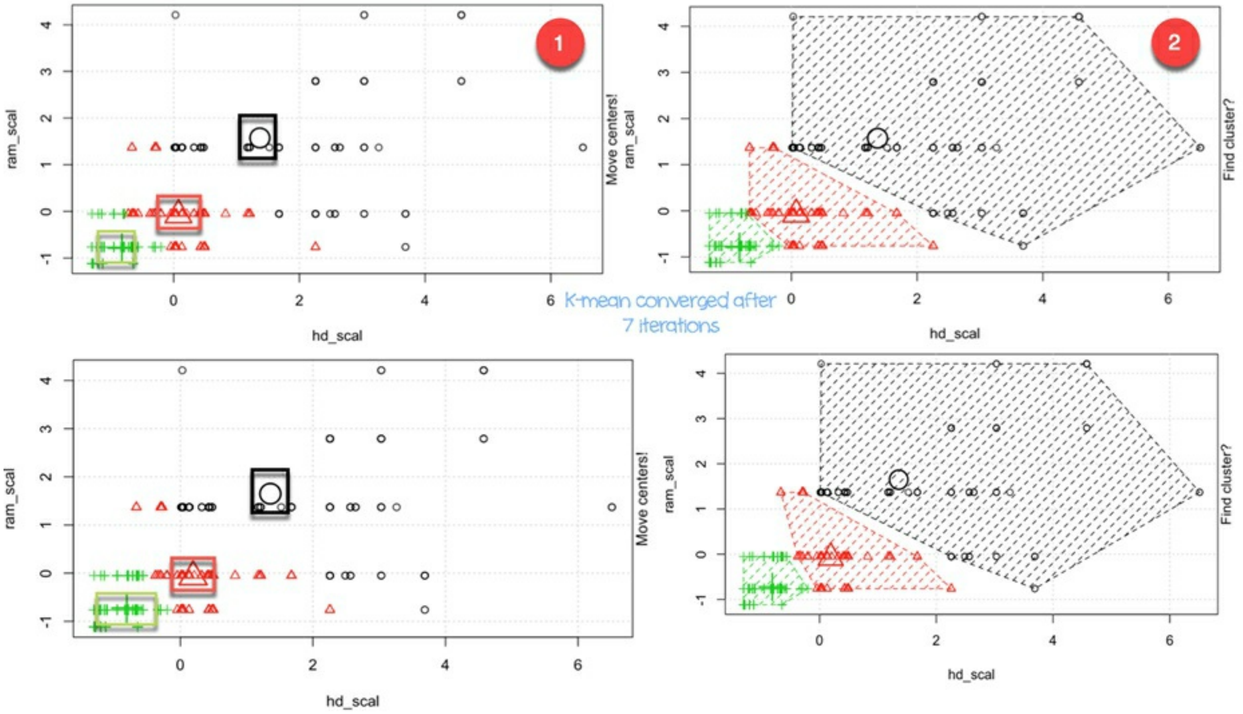
After you load the library, you add .ani after kmeans and R will plot all the steps. For illustration purpose, you only run the algorithm with the rescaled variables hd and ram with three clusters.

```
set.seed(2345)
library(animation)
kmeans.ani(rescale_df[2:3], 3)
```

Code Explanation

- kmeans.ani(rescale_df[2:3], 3): Select the columns 2 and 3 of rescale_df data set and run the algorithm with k sets to 3. Plot the animation.


1
2
ram_scal
hd_scal
Move centers!
Find cluster?
-1
0
1
2
3
4
6



You can interpret the animation as follow:

- Step 1: R randomly chooses three points
- Step 2: Compute the Euclidean distance and draw the clusters. You have one cluster in green at the bottom left, one large cluster colored in black at the right and a red one between them.
- Step 3: Compute the centroid, i.e. the mean of the clusters
- Repeat until no data changes cluster

The algorithm converged after seven iterations. You can run the k-mean algorithm in our dataset with five clusters and call it pc_cluster.

```
pc_cluster <-kmeans(rescale_df, 5)
```

- The list pc_cluster contains seven interesting elements:
- pc_cluster$cluster: Indicates the cluster of each observation
- pc_cluster$centers: The cluster centres
- pc_cluster$totss: The total sum of squares
- pc_cluster$withinss: Within sum of square. The number of components return is equal to `k`
- pc_cluster$tot.withinss: Sum of withinss

- pc_clusterbetweenss: Total sum of square minus Within sum of square
- pc_cluster$size: Number of observation within each cluster

You will use the sum of the within sum of square (i.e. tot.withinss) to compute the optimal number of clusters k. Finding k is indeed a substantial task.

Optimal k

One technique to choose the best k is called the **elbow method**. This method uses within-group homogeneity or within-group heterogeneity to evaluate the variability. In other words, you are interested in the percentage of the variance explained by each cluster. You can expect the variability to increase with the number of clusters, alternatively, heterogeneity decreases. Our challenge is to find the k that is beyond the diminishing returns. Adding a new cluster does not improve the variability in the data because very few information is left to explain.

In this tutorial, we find this point using the heterogeneity measure. The Total within clusters sum of squares is the tot.withinss in the list return by kmean().

You can construct the elbow graph and find the optimal k as follow:

- Step 1: Construct a function to compute the total within clusters sum of squares
- Step 2: Run the algorithm times
- Step 3: Create a data frame with the results of the algorithm
- Step 4: Plot the results

Step 1) Construct a function to compute the total within clusters sum of squares

You create the function that runs the k-mean algorithm and store the total within clusters sum of squares

```
kmean_withinss <- function(k) {
    cluster <- kmeans(rescale_df, k)
    return (cluster$tot.withinss)
}
```

Code Explanation

- function(k): Set the number of arguments in the function
- kmeans(rescale_df, k): Run the algorithm k times
- return(cluster$tot.withinss): Store the total within clusters sum of squares

You can test the function with equals 2.

Output:

```
## Try with 2 cluster
```

```
kmean_withinss(2)
```

Output:

```
## [1] 27087.07
```

Step 2) Run the algorithm n times

You will use the sapply() function to run the algorithm over a range of k. This technique is faster than creating a loop and store the value.

```
# Set maximum cluster
max_k <-20
# Run algorithm over a range of k
wss <- sapply(2:max_k, kmean_withinss)
```

Code Explanation

- max_k <-20: Set a maximum number of to 20
- sapply(2:max_k, kmean_withinss): Run the function kmean_withinss() over a range 2:max_k, i.e. 2 to 20.

Step 3) Create a data frame with the results of the algorithm

Post creation and testing our function, you can run the k-mean algorithm over a range from 2 to 20, store the tot.withinss values.

```
# Create a data frame to plot the graph
elbow <-data.frame(2:max_k, wss)
```

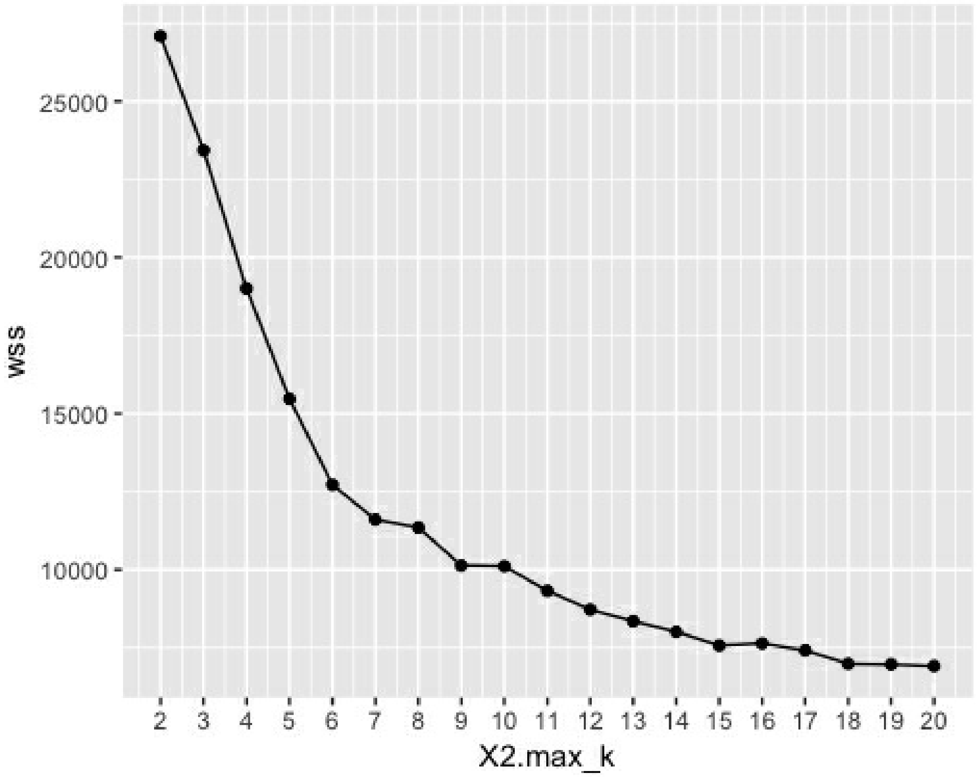
Code Explanation

- data.frame(2:max_k, wss): Create a data frame with the output of the algorithm store in wss

Step 4) Plot the results

You plot the graph to visualize where is the elbow point

```
# Plot the graph with gglop
ggplot(elbow, aes(x = X2.max_k, y = wss)) +
    geom_point() +
    geom_line() +
    scale_x_continuous(breaks = seq(1, 20, by = 1))
```



From the graph, you can see the optimal k is seven, where the curve is starting to have a diminishing return.

Once you have our optimal k, you re-run the algorithm with k equals to 7 and evaluate the clusters.

Examining the cluster

```
pc_cluster_2 <-kmeans(rescale_df, 7)
```

As mention before, you can access the remaining interesting information in the list returned by kmean().

```
pc_cluster_2$cluster
pc_cluster_2$centers
pc_cluster_2$size
```

The evaluation part is subjective and relies on the use of the algorithm. Our goal here is to gather computer with similar features. A computer guy can do the job by hand and group computer based on his expertise. However, the process will take lots of time and will be error prone. K-mean algorithm can prepare the field for him/her by suggesting clusters.

As a prior evaluation, you can examine the size of the clusters.

```
pc_cluster_2$size
```

Output:

```
## [1] 608 1596 1231  580 1003  699  542
```

The first cluster is composed of 608 observations, while the smallest cluster, number 4, has only 580 computers. It might be good to have homogeneity between clusters, if not, a thinner data preparation might be required.

You get a deeper look at the data with the center component. The rows refer to the numeration of the cluster and the columns the variables used by the algorithm. The values are the average score by each cluster for the interested column. Standardization makes the interpretation easier. Positive values indicate the z-score for a given cluster is above the overall mean. For instance, cluster 2 has the highest price average among all the clusters.

```
center <-pc_cluster_2$centers
center
```

Output:

```
##   price_scal    hd_scal     ram_scal screen_scal   ads_scal
trend_scal
## 1 -0.6372457 -0.7097995 -0.691520682  -0.4401632  0.6780366
-0.3379751
## 2 -0.1323863  0.6299541  0.004786730   2.6419582
-0.8894946  1.2673184
## 3  0.8745816  0.2574164  0.513105797  -0.2003237  0.6734261
-0.3300536
## 4  1.0912296 -0.2401936  0.006526723   2.6419582  0.4704301
-0.4132057
## 5 -0.8155183  0.2814882 -0.307621003  -0.3205176
-0.9052979  1.2177279
## 6  0.8830191  2.1019454  2.168706085   0.4492922
-0.9035248  1.2069855
## 7  0.2215678 -0.7132577 -0.318050275  -0.3878782 -1.3206229
-1.5490909
```

You can create a heat map with ggplot to help us highlight the difference between categories.

The default colors of ggplot need to be changed with the RColorBrewer library. You can use the conda library and the code to launch in the terminal:

conda install -c r r-rcolorbrewer

To create a heat map, you proceed in three steps:

- Build a data frame with the values of the center and create a

variable with the number of the cluster
- Reshape the data with the gather() function of the tidyr library. You want to transform data from wide to long.
- Create the palette of colors with colorRampPalette() function

Step 1) Build a data frame

Let's create the reshape dataset

```
library(tidyr)

# create dataset with the cluster number

cluster <- c(1: 7)
center_df <- data.frame(cluster, center)

# Reshape the data

center_reshape <- gather(center_df, features, values,
price_scal: trend_scal)
head(center_reshape)
```

Output:

```
##   cluster   features     values
## 1       1 price_scal -0.6372457
## 2       2 price_scal -0.1323863
## 3       3 price_scal  0.8745816
## 4       4 price_scal  1.0912296
## 5       5 price_scal -0.8155183
## 6       6 price_scal  0.8830191
```

Step 2) Reshape the data

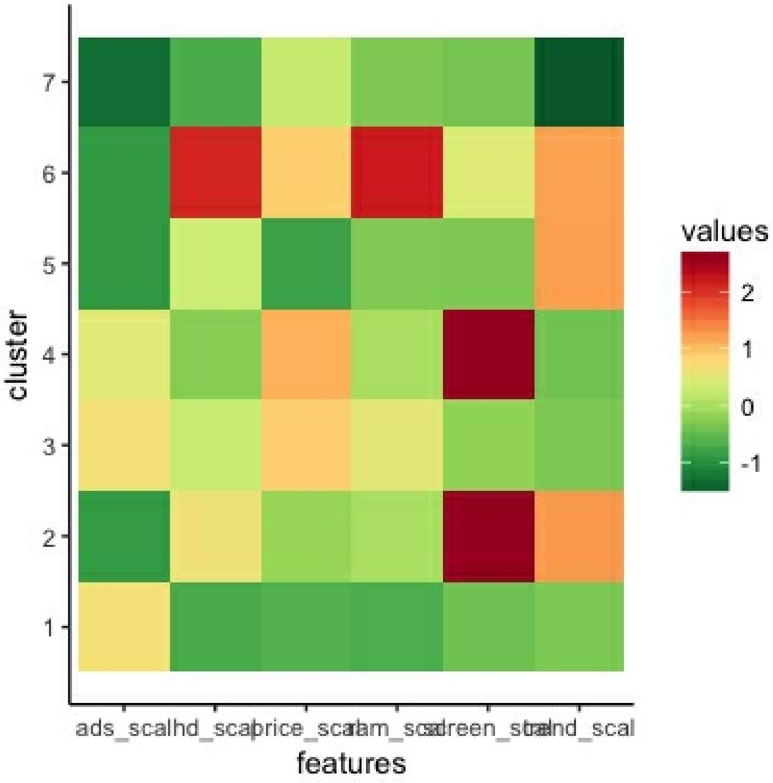
The code below create the palette of colors you will use to plot the heat map.

```
library(RColorBrewer)
# Create the palette
hm.palette <-colorRampPalette(rev(brewer.pal(10,
'RdYlGn')),space='Lab')
```

Step 3) Visualize

You can plot the graph and see what the clusters look like.

```
# Plot the heat map
ggplot(data = center_reshape, aes(x = features, y = cluster,
fill = values)) +
    scale_y_continuous(breaks = seq(1, 7, by = 1)) +
    geom_tile() +
    coord_equal() +
    scale_fill_gradientn(colours = hm.palette(90)) +
    theme_classic()
```



Summary

We can summarize the k-mean algorithm in the table below

Package	**Objective**	**function**	**argument**

base	Train k-mean	kmeans()	df, k
	Access cluster	kmeans()$cluster	
	Cluster centers	kmeans()$centers	
	Size cluster	kmeans()$size	

Chapter 32: R Vs Python: What's the Difference?

R and Python are both open-source programming languages with a large community. New libraries or tools are added continuously to their respective catalog. R is mainly used for statistical analysis while Python provides a more general approach to data science.

R and Python are state of the art in terms of programming language oriented towards data science. Learning both of them is, of course, the ideal solution. R and Python requires a time-investment, and such luxury is not available for everyone. Python is a general-purpose language with a readable syntax. R, however, is built by statisticians and encompasses their specific language.

R

Academics and statisticians have developed R over two decades. R has now one of the richest ecosystems to perform data analysis. There are around 12000 packages available in CRAN (open-source repository). It is possible to find a library for whatever the analysis you want to perform. The rich variety of library makes R the first choice for statistical analysis, especially for specialized analytical work.

The cutting-edge difference between R and the other statistical products is the output. R has fantastic tools to communicate the results. Rstudio comes with the library knitr. Xie Yihui wrote this package. He made reporting trivial and elegant. Communicating the findings with a presentation or a document is easy.

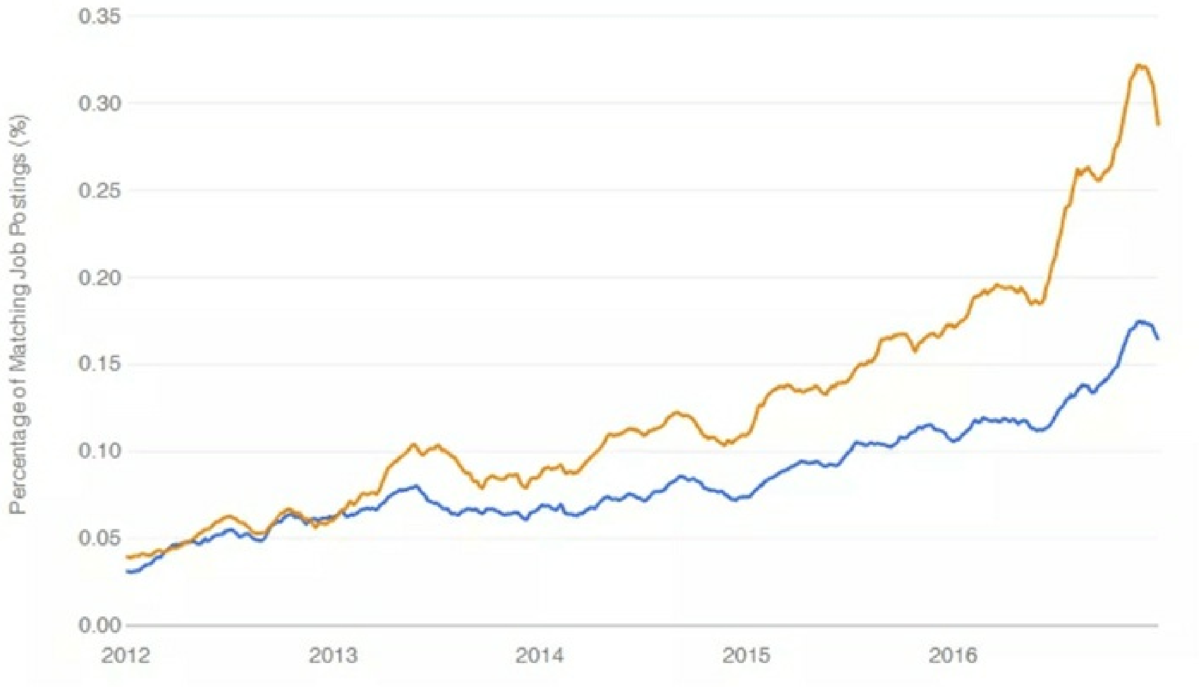
Python

Python can pretty much do the same tasks as R: data wrangling, engineering, feature selection web scrapping, app and so on. Python is a tool to deploy and implement machine learning at a large-scale. Python codes are easier to maintain and more robust than R. Years ago; Python didn't have many data analysis and machine learning libraries. Recently, Python is catching up and provides cutting-edge API for machine learning or Artificial Intelligence. Most of the data science job can be done with five Python libraries: Numpy, Pandas, Scipy, Scikit-learn and Seaborn.

Python, on the other hand, makes replicability and accessibility easier than R. In fact, if you need to use the results of your analysis in an application or website, Python is the best choice.

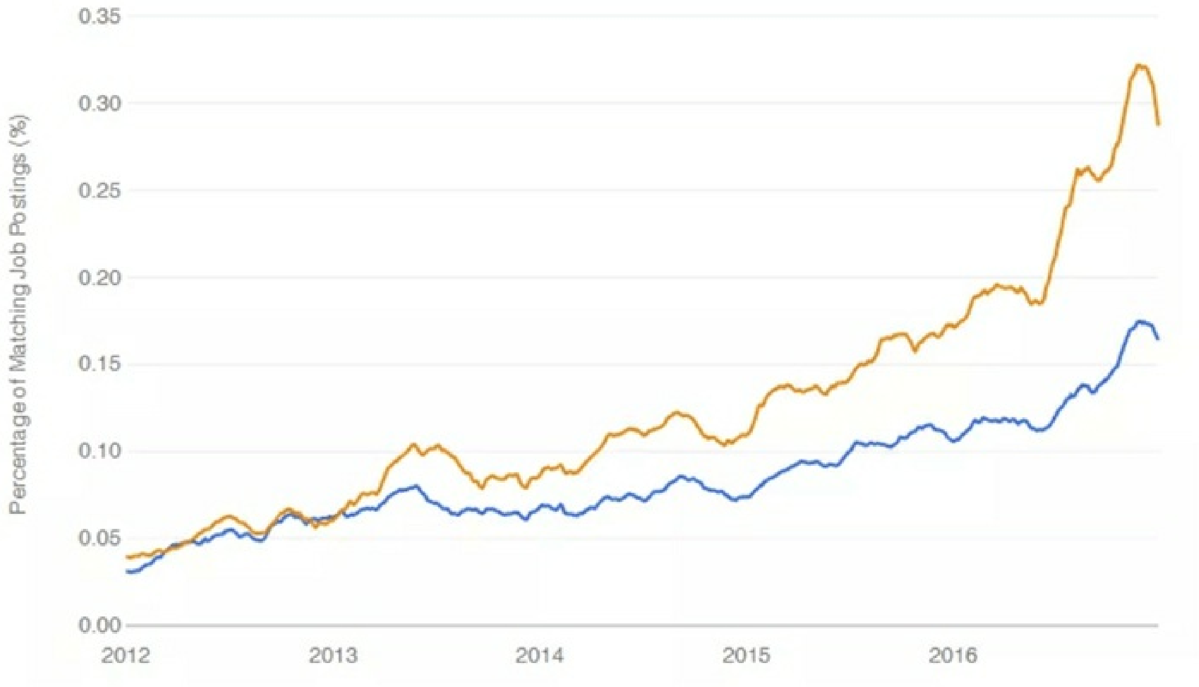
Popularity index

The IEEE Spectrum ranking is a metrics that quantify the popularity of a programming language. The left column shows the ranking in 2017 and the right column in 2016. In 2017, Python made it at the first place compared to a third rank a year before. R is in 6th place.



Job Opportunity

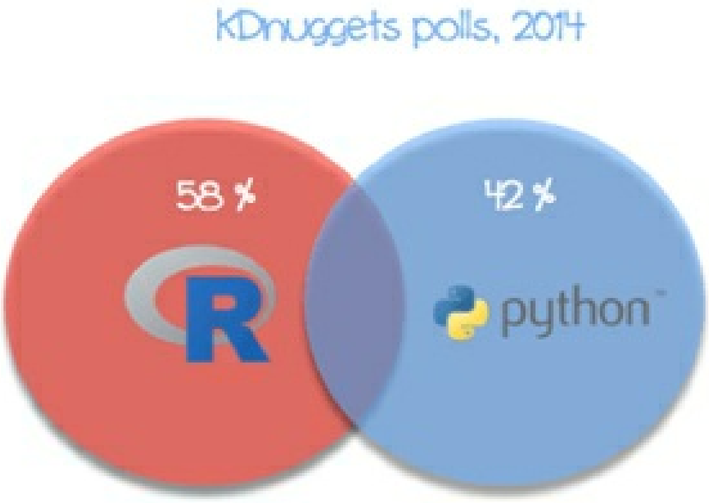
The picture below shows the number of jobs related to data science by programming languages. SQL is far ahead, followed by Python and Java. R ranks 5th.



If we focus on the long-term trend between Python (in yellow) and R (blue), we can see that Python is more often quoted in job description than R.

Analysis done by R and Python

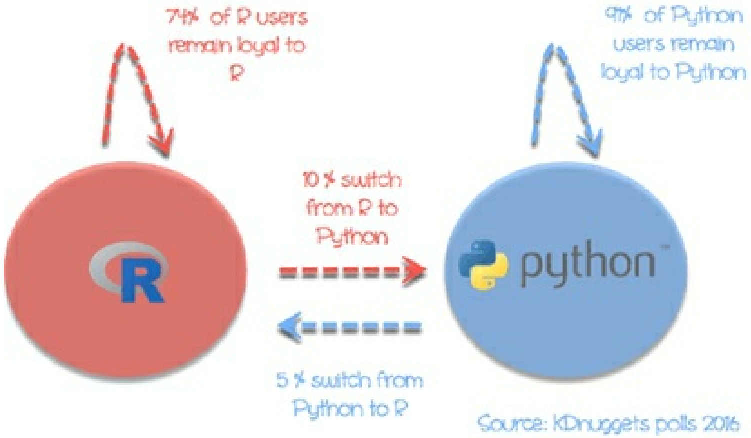
However, if we look at the data analysis jobs, R is by far, the best tool.



Percentage of people switching

There are two keys points in the picture below.

- Python users are more loyal than R users
- The percentage of R users switching to Python is twice as large as Python to R.


74% of R users remain loyal to R
91% of Python users remain loyal to Python
10 % switch from R to Python
5 % switch from Python to R
R
python

Source: KDnuggets polls 2016

Difference between R and Python

Parameter	R	Python

Objective	Data analysis and statistics	Deployment and production
Primary Users	Scholar and R&D	Programmers and developers
Flexibility	Easy to use available library	Easy to construct new models from scratch. I.e., matrix computation and optimization
Learning curve	Difficult at the beginning	Linear and smooth
Popularity of Programming Language. Percentage change	4.23% in 2018	21.69% in 2018
Average Salary	$99.000	$100.000
Integration	Run locally	Well-integrated with app
Task	Easy to get primary results	Good to deploy algorithm
Database size	Handle huge size	Handle huge size
IDE	Rstudio	Spyder, Ipthon Notebook
Important Packages and library	tydiverse, ggplot2, caret, zoo	pandas, scipy, scikit-learn, TensorFlow, caret
Disadvantages	Slow High Learning curve Dependencies between library	Not as many libraries as R
Advantages	• Graphs are made to talk. R makes it beautiful • Large catalog for data analysis • GitHub interface • RMarkdown • Shiny	• Jupyter notebook: Notebooks help to share data with colleagues • Mathematical computation • Deployment • Code Readability • Speed • Function in Python

R or Python Usage

Python has been developed by Guido van Rossum, a computer guy, circa 1991. Python has influential libraries for math, statistic and Artificial Intelligence. You can think Python as a pure player in Machine Learning. However, Python is not entirely mature (yet) for econometrics and communication. Python is the best tool for Machine Learning integration and deployment but not for business analytics.

The good news is R is developed by academics and scientist. It is designed to answer statistical problems, machine learning, and data science. R is the right tool for data science because of its powerful communication libraries. Besides, R is equipped with many packages to perform time series analysis, panel data and data mining. On the top of that, there are not better tools compared to R.

In our opinion, if you are a beginner in data science with necessary statistical foundation, you need to ask yourself following two questions:

- Do I want to learn how the algorithm work?
- Do I want to deploy the model?

If your answer to both questions is yes, you'd probably begin to learn Python first. On the one hand, Python includes great libraries to manipulate matrix or to code the algorithms. As a beginner, it might be easier to learn how to build a model from scratch and then switch to the functions from the machine learning libraries. On the other hand, you already know the algorithm or want to go into the data analysis right away, then both R and Python are okay to begin with. One advantage for R if you're going to focus on statistical methods.

Secondly, if you want to do more than statistics, let's say deployment and reproducibility, Python is a better choice. R is more suitable for your work if you need to write a report and create a dashboard.

In a nutshell, the statistical gap between R and Python are getting closer. Most of the job can be done by both languages. You'd better choose the one that suits your needs but also the tool your colleagues are using. It is better when all of you speak the same language. After you know your first programming language, learning the second one is simpler.

Conclusion

In the end, the choice between R or Python depends on:

- The objectives of your mission: Statistical analysis or deployment
- The amount of time you can invest
- Your company/industry most-used tool

Chapter 33: SAS vs R: What's the Difference?

What is SAS?

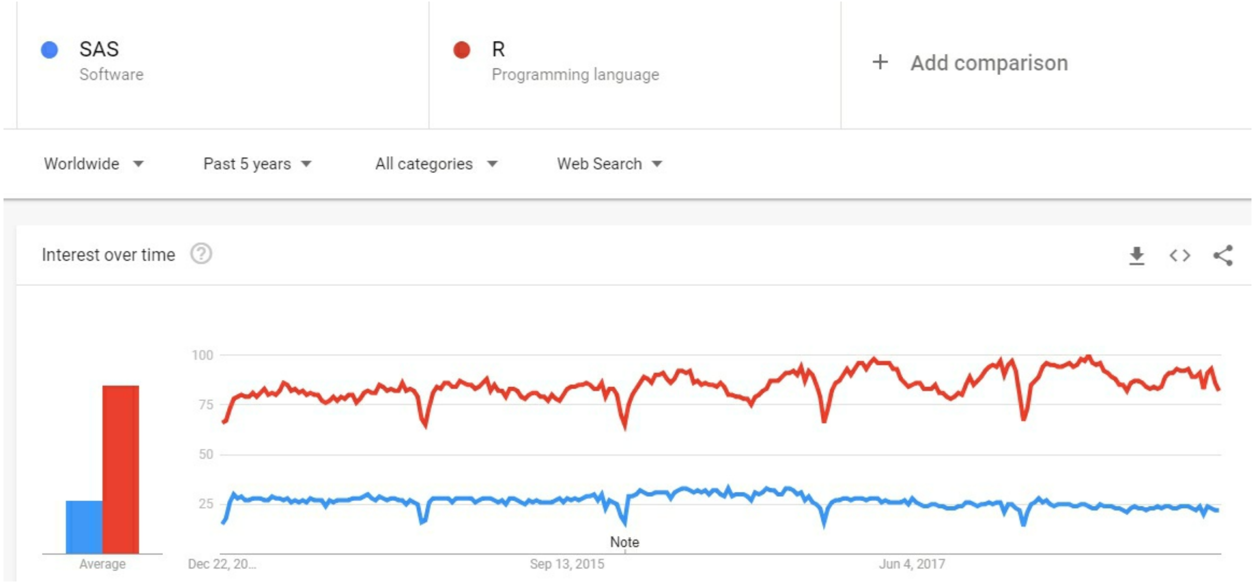
SAS stands for **S**tatistical **A**nalysis **S**oftware which is used for Data Analytics. It helps you to use qualitative techniques and processes which allows you to enhance employee productivity and business profits. SAS is pronounced as SaaS.

In SAS, data is extracted & categorized which helps you to identify and analyze data patterns. It is a software suite which allows you to perform advanced analysis, Business Intelligence, Predictive Analysis, data management to operate effectively in the competitive & changing business conditions. Moreover, SAS is platform independent which means you can run SAS on any operating system either Linux or Windows.

What is mean by R?

R is a programming language is widely used by data scientists and major corporations like Google, Airbnb, Facebook etc. for data analysis.

R language offers a wide range of functions for every data manipulation, statistical model, or chart which is needed by the data analyst. R offers inbuilt mechanisms for organizing data, running calculations on the given information and creating graphical representations of that data sets.



Google Trend SAS vs R

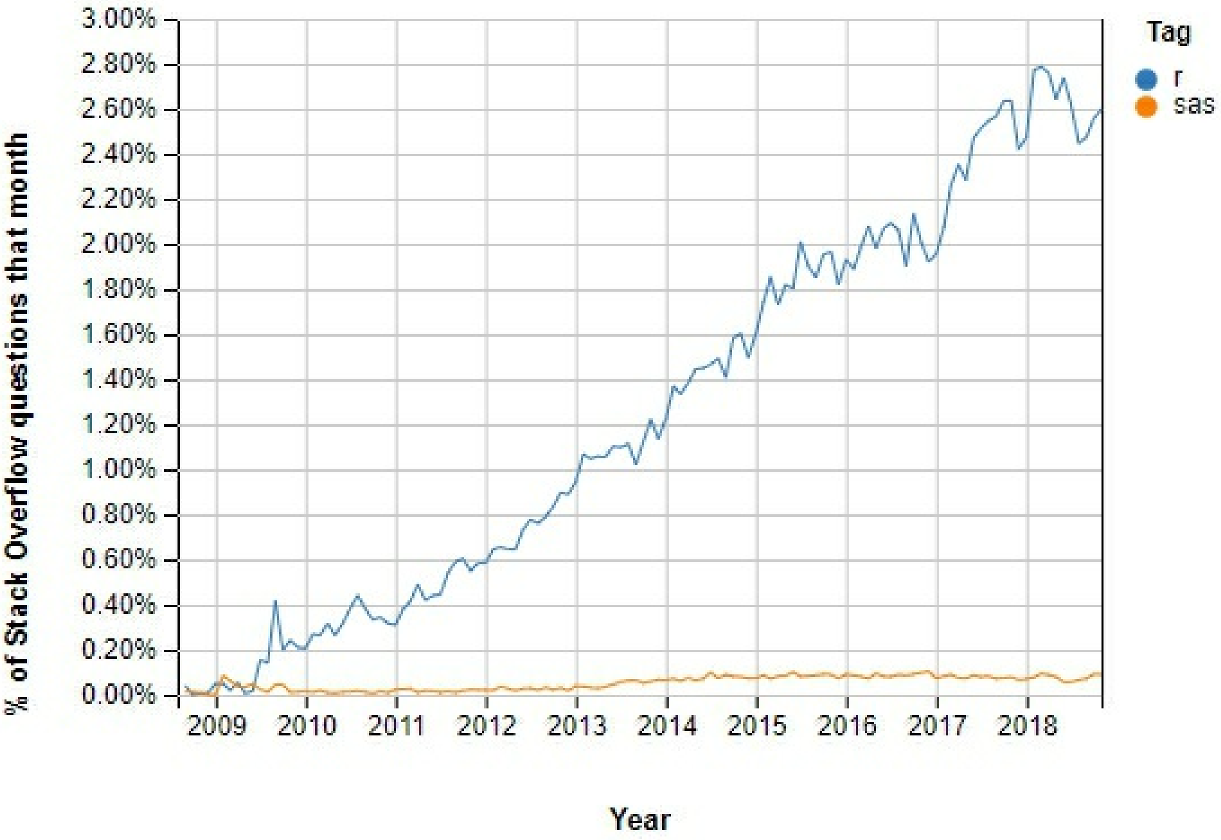
Why use SAS?

- Access raw data files and data in external database
- Analyze data using statics, descriptive, multivariate techniques, forecasting, modeling, and linear programming
- Helps you to manage data entry, formatting, conversion, editing & retrieval
- Advanced analytics feature allows you to make changes and improvements in business practices
- Helps businesses to know about their historical data

Why use R?

- R offers a useful programming constructs for data analytics like conditionals, loops, input and output facilities, user-defined recursive functions, etc.
- R has a rich and expanding ecosystem and plenty of documentation available over the internet
- You can run this tool on a variety of platforms including Windows, Unix, and MacOS

- Good graphics capabilities Supported by an extensive user network



R Vs Sas Stackoverflow Questions

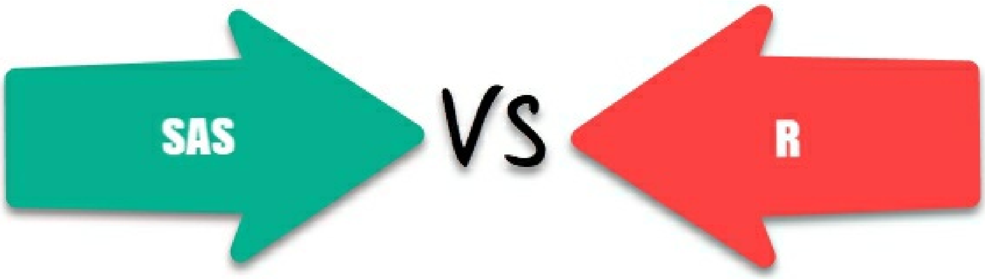
History of SAS

- SAS was developed by Jim Goodnight and John Shall in 1970 at N.C. University
- Initially, it was developed for Agricultural Research.
- Later, it expanded to a gamut of tools to include Predictive Analytics, Data Management, BI among others.
- Today 98 of world's top companies in fortune 400 uses SAS data analytical tool for Data analysis.

History of R

- 1993- R is a programming language developed by Ross Ihaka and Robert Gentleman
- 1995: R first distributed as an open-source tool under GPL2 license
- 1997: R core group and CRAN founded
- 1999: The R website, r-project.org, launched
- 2000: R 1.0.0 released
- 2004: R 2.0.0 released
- 2009: First edition of the R Journal
- 2013: R 3.0.0 released
- 2016: New R logo adopted

SAS Vs. R



Parameters	SAS	R
Availability / Cost	SAS is commercial software, so it needs a financial investment.	R is open source software, So, anyone can use it.
Ease of Learning	SAS is the easiest tools to learn. So, people with limited knowledge of SQL can learn it easily.	R programmers need to write tedious and lengthy codes.
Statistical Abilities	SAS offers a powerful package which offers all types of statistical analysis and techniques.	R is an open source tool which allows users to submit their own packages/libraries. The latest technologies are often released in R first.
File Sharing	You can't share SAS generated files with another user who does not use SAS.	Since anyone uses r, it is much easier to share files with another user.

Updates	SAS relatively less frequently updated.	R is an open source tool, so it is continuously updated.
Market Share	Currently, SAS is facing stiff competition from R, and other Data analytical tool as a result market share of SAS is gradually declining.	R has seen exponential growth in the last past five years with its increasing popularity. That is why its market share is increasing rapidly.
Graphical Capabilities	SAS has good graphical support. However, it does not offer any customization.	Graphical support of R tool is poor.
Customer Support	SAS provides dedicated customer support.	R has the biggest online communities but no customer service support.
Support for Deep learning	Deep Learning in SAS is still in its early stages, and there's a lot to work for before it matures.	R offers advanced deep learning integrations.
Job Scenario	SAS analytic tool is still the market leader as far as corporate jobs are concerned. Many big companies still work on SAS.	Jobs on R have been reported to increase over the last few years.
Salary Range	The average salary for any SAS programmer is $81,560 per year in the U.S.A.	The average salary for "R" programmer" ranges from approximately $127,937 per year for Data Scientist to $147,189 per year.
Best features	• Variables • Mixins • Nested rules • Maintainable • Functions	• Data analysis • Graphics and data Flexible statistical analysis • Highly interactive
Famous companies using	Airbnb, StacShare, Asana, Hubspot	Instacart, Adroll, Opbandit, Custora
TIOBE Rating	22	16

Feature of R

- R helps you to connect to many databases and data types
- A large number of algorithms and packages for statistics flexible
- Offers effective data handling and storage facility
- Collect and analyze social media data
- Train machines to make predictions

- Scrape data from websites
- A comprehensive and integrated collection of intermediate tools for data analysis
- Interface with other languages and scripting capabilities
- Flexible, extensible and comprehensive for productivity
- Ideal platform for data visualization

Features of SAS

- Operations Research and project Management
- Report formation with standard graphics
- Data updating and modification
- Powerful Data handling language
- Read and write almost any data format
- Best data cleansing functions
- Allows you to Interact with multiple host systems

The Final Verdict

After comparing some main differences between both these tools, we can say that both have their own set of users. There are many companies, who prefer SAS because of data security issues, which show despite a drop in a recent year, there is still a huge demand for SAS certified professionals.

On the other hand, R is an ideal tool for those professionals who want to do deep cost-effective Data analytics job. Numbers of startup companies are increasing all over the world. Therefore, the demand for R certified developers are also increasing. Currently, both have the equal potential for growth in the market, and both are equally popular tools.

One Last Thing....

DID YOU ENJOY THE BOOK?

IF SO, THEN LET ME KNOW LEAVING A REVIEW! Reviews are lifeblood of independent authors. I would appreciate even a few words and rating if that's all you have time for

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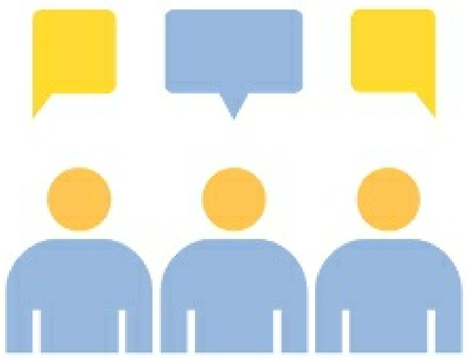
IF YOU DID NOT LIKE THIS BOOK, THEN PLEASE TELL ME! EMAIL me and Let me know what you didn't like! Perhaps I can change it. In today's world a book doesn't have to be stagnant, it can improve with time and feedback from readers like you. You can impact this book, and I welcome your feedback. Help make this book better for everyone!

Community



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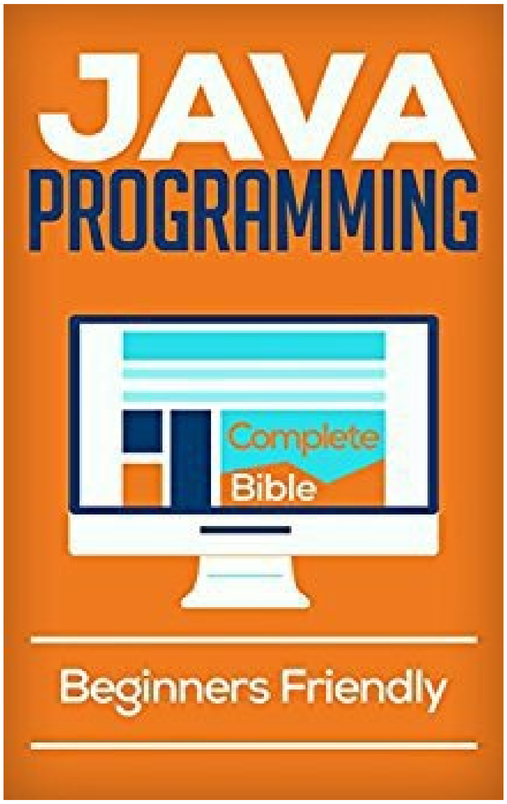

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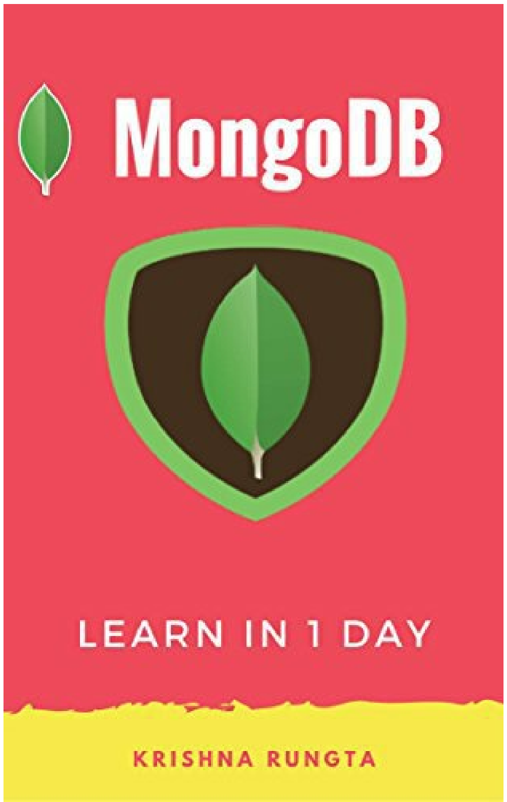
MongoDB
LEARN IN 1 DAY
KRISHNA RUNGTA