

Class 2
Installation of R/RStudio
and
Basic Syntax

R package sources –
Downloading and install



Installing R

Downloading R

Link to download R - <https://cloud.r-project.org/>

The Comprehensive R Archive Network

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Download R for Linux](#)
- [Download R for \(Mac\) OS X](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Click the Download link based on your operating systems



File extensions

Linux –

- Debian/Ubuntu → `sudo apt install r-base`
- Fedora/Redhat → `sudo yum install r-base`

Mac –

- Download .pkg file and double click

Windows –

- Download .exe file and open executable file












Installing RStudio

Downloading RStudio

<https://rstudio.com/products/rstudio/download/>

	RStudio Desktop Open Source License	RStudio Desktop Commercial License	RStudio Server Open Source License	RStudio Server Pro Commercial License
	Free	\$995 /year	Free	\$4,975 /year (5 Named Users)
	DOWNLOAD Learn more	BUY Learn more	DOWNLOAD Learn more	BUY Evaluation Learn more
Integrated Tools for R	✓	✓	✓	✓
Priority Support		✓		✓
Access via Web Browser			✓	✓
Enterprise Security				✓
Project Sharing				✓
Manage Multiple R Sessions & Versions				✓

RStudio Installers

OS	Download	Size	SHA-256
Windows 10/8/7	 RStudio-1.3.959.exe	171.41 MB	3d493ae5
macOS 10.13+	 RStudio-1.3.959.dmg	148.57 MB	7c5b695d
Ubuntu 16	 rstudio-1.3.959-amd64.deb	124.57 MB	c2931495
Ubuntu 18/Debian 10	 rstudio-1.3.959-amd64.deb	126.11 MB	411ab500
Fedora 19/Red Hat 7	 rstudio-1.3.959-x86_64.rpm	146.24 MB	a144e4e6
Fedora 28/Red Hat 8	 rstudio-1.3.959-x86_64.rpm	150.32 MB	57169bee
Debian 9	 rstudio-1.3.959-amd64.deb	126.42 MB	b2d9366f
SLES/OpenSUSE 12	 rstudio-1.3.959-x86_64.rpm	119.02 MB	bbc9387e
OpenSUSE 15	 rstudio-1.3.959-x86_64.rpm	127.59 MB	a4f404f0



R vs RStudio

R	RStudio
User can execute code independently	Only RStudio is not enough to execute code
R may be used without R	RStudio may not be used without R
Provides command line interface	It provides IDE

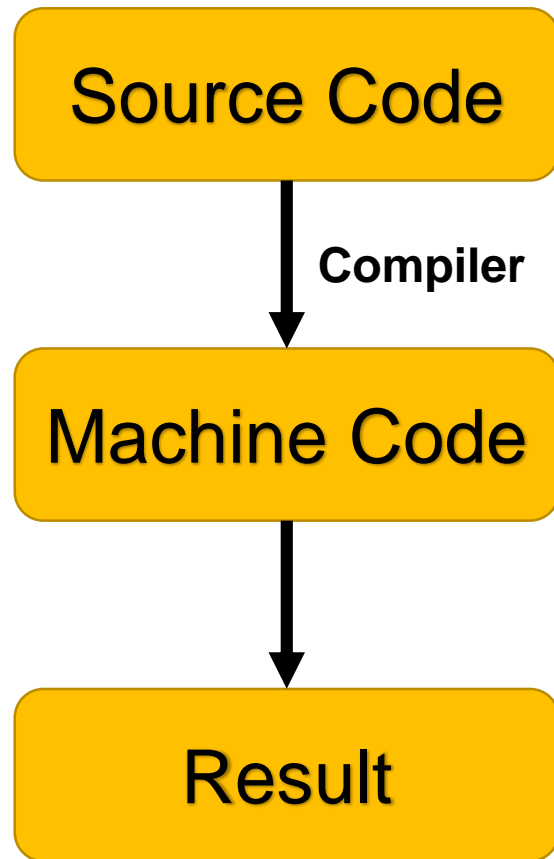
R Features

Interpreted
Programming
Language

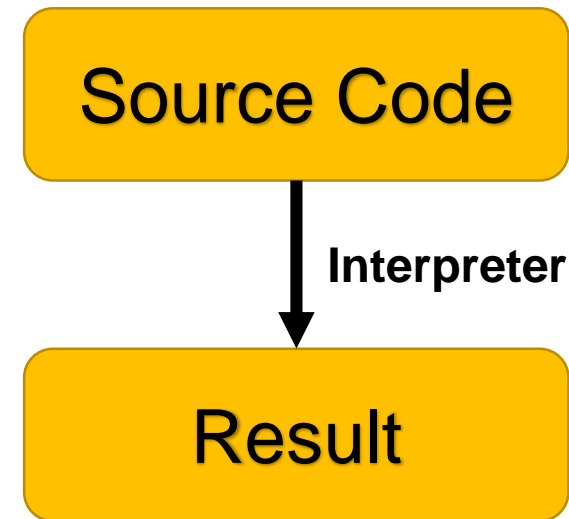
Case sensitive

R index starts
from 1

Interpreted Programming Language



Example. C



Example. Python

Case sensitive

- Uppercase and lower case letter as treated as distinct.
- Ex.

var = 10

Var = 5

Indexing from 1

- R index start from 1
- Many languages are starts with 0

Index 0	0	1	2	3	4
	H	E	L	L	O

Index 1	1	2	3	4	5
	H	E	L	L	O

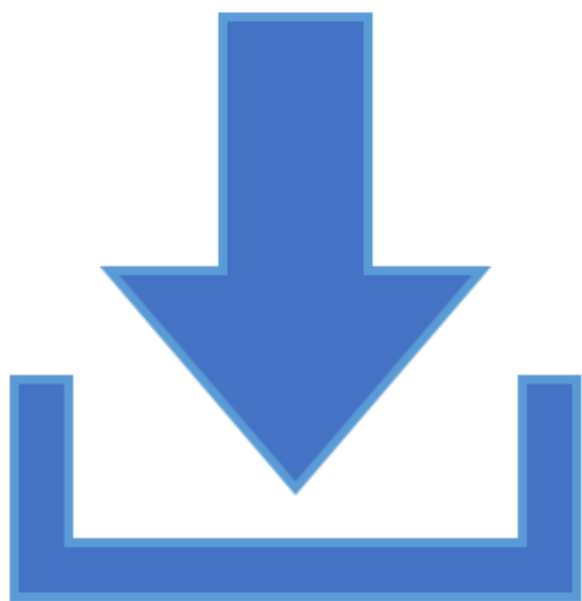
Example: Sequence

Index 0

0	1	2	3	4
A	T	G	C	T
A	T	G	G	T

Index 1

1	2	3	4	5
A	T	G	C	T
A	T	G	G	T



R Package Sources
(Downloading and Install)



gplots googleVis
ggplot2
RSQL
stats
DNA

Packages

- It is a collection of
Data (Sample data)
R Functions and
Compiled code
- Well defined format
- R having standard set of packages

- While starting R console (Rstudio), the default packages will be available in the environment.
- Further, you can install more packages based on your analysis.
- Newly installed packages should be loaded explicitly.
- With the help of **search()** command, user can find packages from the R package sources.

Library

- The “directory which packages are stored”
- Command to get/identify library locations

`.libPaths()`

```
> .libPaths()  
[1] "C:/Users/BioBros/Documents/R/win-library/4.0"  
[2] "C:/Program Files/R/R-4.0.2/library"
```

R packages

- List installed packages:-
`>installed.packages()`
- Types of Installation
 - Install from repositories
 - Manual installation





Repositories of R Packages

- CRAN (Comprehensive R Archive Network)
- Bioconductor
- GitHub and others



CRAN - Packages

- Available packages in R – **more than 16000**
- These all packages can able to install in Windows, Unix, Mac, and Solaris (tested in multiple operating systems)
- **`help(install.pacakges)`** in R provides information on how to install packages





CRAN

[Mirrors](#)

[What's new?](#)

[Task Views](#)

[Search](#)

About R

[R Homepage](#)

[The R Journal](#)

Software

[R Sources](#)

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Documentation

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Contributed Packages

Available Packages

Currently, the CRAN package repository features 16024 available packages.

[Table of available packages, sorted by date of publication](#)

[Table of available packages, sorted by name](#)

Installation of Packages

Please type `help("INSTALL")` or `help("install.packages")` in R for information on how to install packages from this repository. The manual [R Installation and Administration](#) (also contained in the R base sources) explains the process in detail.

[CRAN Task Views](#) allow you to browse packages by topic and provide tools to automatically install all packages for special areas of interest. Currently, 41 views are available.

Package Check Results

All packages are tested regularly on machines running [Debian GNU/Linux](#), [Fedora](#), macOS (formerly OS X), Solaris and Windows.

The results are summarized in the [check summary](#) (some [timings](#) are also available). Additional details for Windows checking and building can be found in the [Windows check summary](#).

Writing Your Own Packages

The manual [Writing R Extensions](#) (also contained in the R base sources) explains how to write new packages and how to contribute them to CRAN.

Repository Policies

The manual [CRAN Repository Policy \[PDF\]](#) describes the policies in place for the CRAN package repository.

Bioconductor

- Open source software for Bioinformatics
- Provides tools for high throughput genome data analysis
- 1903 packages are available in Bioconductor
- Also available as an AML (Amazon Machine Image) and Docker images.
- Current release of biocondutor version – 3.11 (supports R 4.0.0)





GitHub

- US based global company
- Provides hosting for software development and version control using Git
- More than 1000 of packages are hosted in GitHub

Installing R Package using Terminal / Command Prompt

- Open Terminal or Command Prompt
- Change the location into package directory
- Type Command

```
>R CMD INSTALL findlnc_0.1.tar.gz
```


Installing R Package using inbuilt function

- `install_packages()` utils function used to install R package

Example:

Single Package:

```
install.packages("gplots")
```

Multiple Package:

```
install.packages("gplots","ggplot2")
```

Install packages through devtools

Load devtools package in your environment

```
library(devtools)
```

`install_*` functions to install R Packages

- From GitHub `install_github()`

```
install_github("rstudio/shiny")
```

- From GitLab `install_gitlab()`

```
install_gitlab("jimhester/covr")
```

Contd...

From Bitbucket `install_bitbucket()`

```
install_bitbucket("djnavarro/lsr")
```

From URL `install_url()`

```
install_url("https://github.com/hadley/  
stringr/archive/master.zip")
```

Contd...

From Git `install_git()`

```
install_git("git://github.com/hadley/st  
ringr.git")
```

From CRAN `install_cran()`

```
install_cran("gplots")
```

Contd...

From Dev `install_dev()`

```
install_dev("dplyr")
```

From SVN `install_svn()`

```
install_svn("https://github.com/hadley/  
stringr/trunk")
```

Contd...

From Bioconductor Github `install_bioc()`

```
install_bioc("SummarizedExperiment")
```

From Local files `install_local()`

```
install_local("C:/Users/BioBros/Downloads/ace2fastq_0.6.0.tar.gz")
```

Using R packages

- Load Library

```
library(gplots)
```

- Unload Library

```
detach(package:gplots)
```

Other package related commands

- Update package

```
update_packages()
```

- List available packages in the repositories

```
available.packages()
```

- List installed packages

```
installed.packages()
```


Building R Packages

`build()`

Builds a package file from the package sources

- **Open Command Prompt/Terminal Window**
- **Change the location to package directory**
- **Type:** `R CMD build findlnc`

Building R Packages

```
> R CMD build findlnc
```

```
* checking for file 'findlnc/DESCRIPTION' ... OK
```

```
* preparing 'findlnc':
```

```
* checking DESCRIPTION meta-information ... OK
```

```
* checking for LF line-endings in source and make files
```

```
* checking for empty or unneeded directories
```

```
* creating default NAMESPACE file
```

```
* building 'findlnc_0.1.tar.gz'
```