Hands-on Short Course from the Genomics Research Core

Installation Guide

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In this hands-on course, we will use several R packages to play with RNA-Seq data. We all have different computers, operation systems and environment settings. You can directly use the R console from the command line or choose RStudio – a user-friendly integrated development environment (IDE). Although the latest version of R is recommended, you do not need to install from scratch if your computer already has R/RStudio. Just simply check the packages to make sure your version supports them. And feel free to opt out the packages you only want to see how it works on my screen. If it is your first time installing R, very likely you will need all following steps. Let's get started, or scroll down to where interests you!
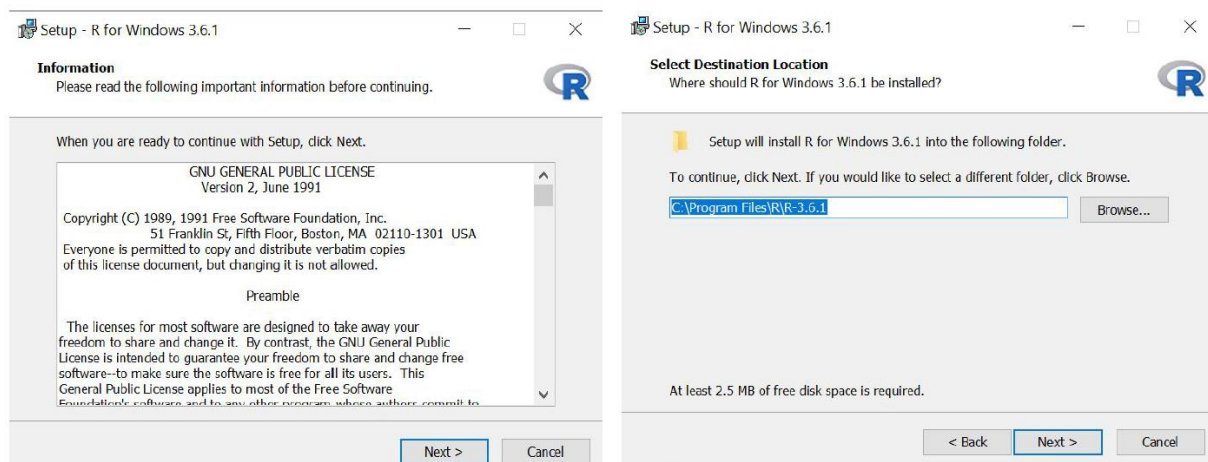
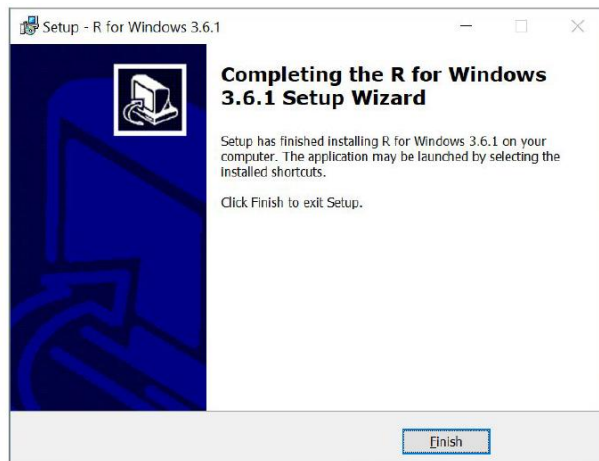## Step 1: Install R

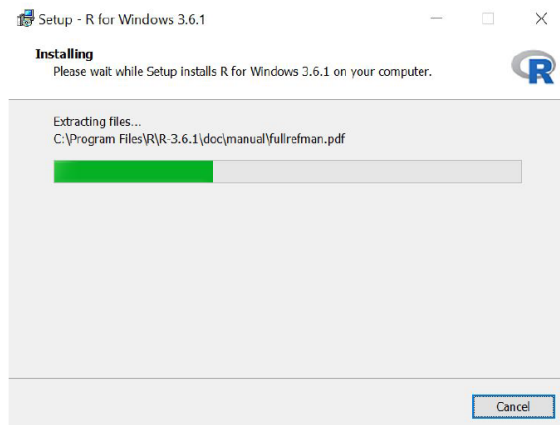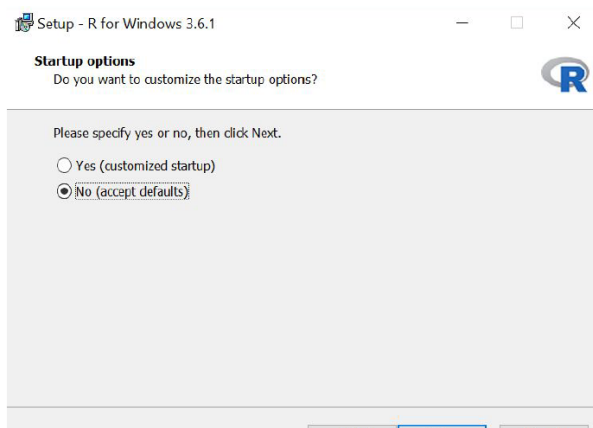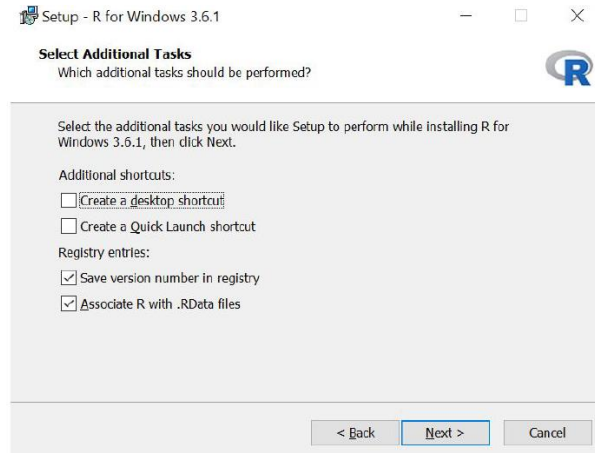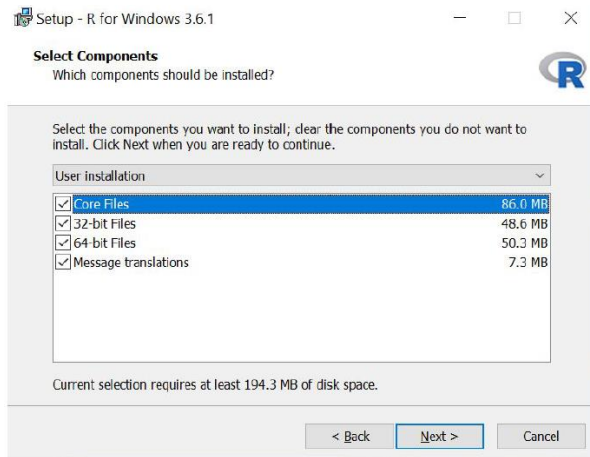**1.1** The latest version is R-3.6.3 (https://cran.rstudio.com/).

Download precompiled binary distributions for your operation system:

Windows (32/64 bit)	https://cran.rstudio.com/bin/windows/base/R-3.6.3-win.exe
Mac (OS X 10)	https://cran.rstudio.com/bin/macosx/R-3.6.3.pkg
Linux	https://cran.rstudio.com/bin/linux/

Note: you OS might ask for additional tools to build R. The Rtools download link is near the base link you just used.

1.2 Here is an example of installation on Windows.

Setup - R for Windows 3.6.1

Select Components
Which components should be installed?

Select the components you want to install; clear the components you do not want to install. Click Next when you are ready to continue.

User installation ▼

☑ Core Files	86.0 MB
☑ 32-bit Files	48.6 MB
☑ 64-bit Files	50.3 MB
☑ Message translations	7.3 MB

Current selection requires at least 194.3 MB of disk space.

< Back   Next >   Cancel

Setup - R for Windows 3.6.1

Select Additional Tasks
Which additional tasks should be performed?

Select the additional tasks you would like Setup to perform while installing R for Windows 3.6.1, then click Next.

Additional shortcuts:
☐ Create a desktop shortcut
☐ Create a Quick Launch shortcut

Registry entries:
☑ Save version number in registry
☑ Associate R with .RData files

< Back   Next >   Cancel

Setup - R for Windows 3.6.1

Startup options
Do you want to customize the startup options?

Please specify yes or no, then click Next.

○ Yes (customized startup)
● No (accept defaults)

Setup - R for Windows 3.6.1

Installing
Please wait while Setup installs R for Windows 3.6.1 on your computer.

Extracting files...
C:\Program Files\R\R-3.6.1\doc\manual\fullrefman.pdf

Cancel

Setup - R for Windows 3.6.1

Completing the R for Windows 3.6.1 Setup Wizard

Setup has finished installing R for Windows 3.6.1 on your computer. The application may be launched by selecting the installed shortcuts.

Click Finish to exit Setup.

Finish

Note: you can choose to only install 64-bit files by unclicking 32-bit files on 64-bit windows 10/8/7.

Step 2: Install RStudio

**2.1** Download free RStudio Desktop 1.2.5042 from
https://rstudio.com/products/rstudio/download/#download

Windows	https://download1.rstudio.org/desktop/windows/RStudio-1.2.5042.exe
Mac (OS X 10)	https://download1.rstudio.org/desktop/macos/RStudio-1.2.5042.dmg
Linux (red hat)	https://download1.rstudio.org/desktop/fedora28/x86_64/rstudio-1.2.5042-x86_64.rpm

Note: other linux installers and tarballs are on the same page.

2.2 Here is an example of installation on Windows.
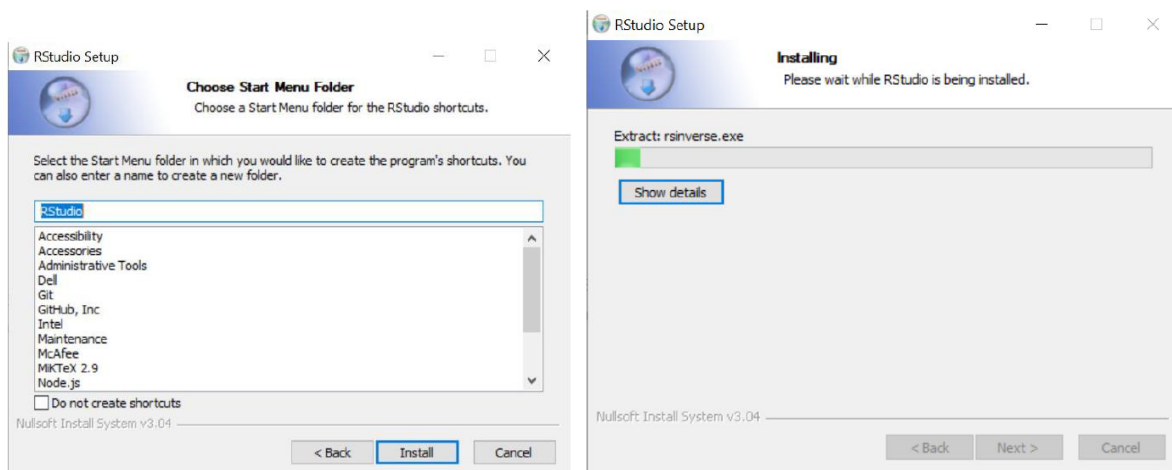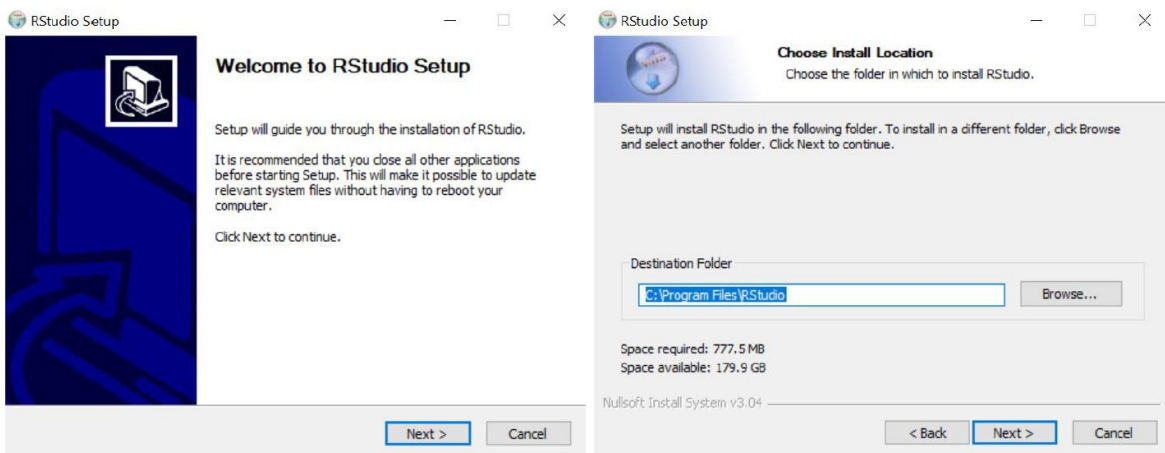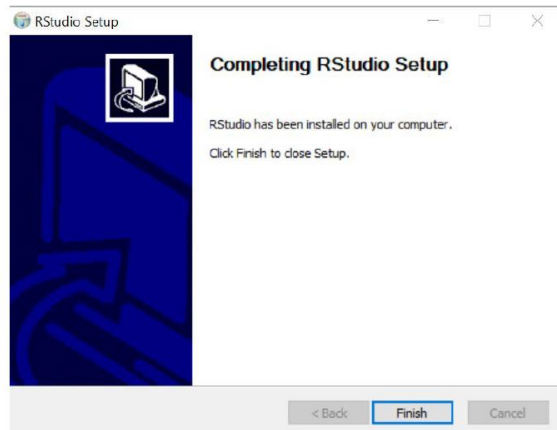
Step 3: Install R packages (Bioconductor packages and other R packages)

3.1 Install Bioconductor https://www.bioconductor.org/install/

3.1.1 Open a R console and enter the command to install BiocManager (an installation tool).

```
if (!requireNamespace("BiocManager", quietly = TRUE))

    install.packages("BiocManager")
```
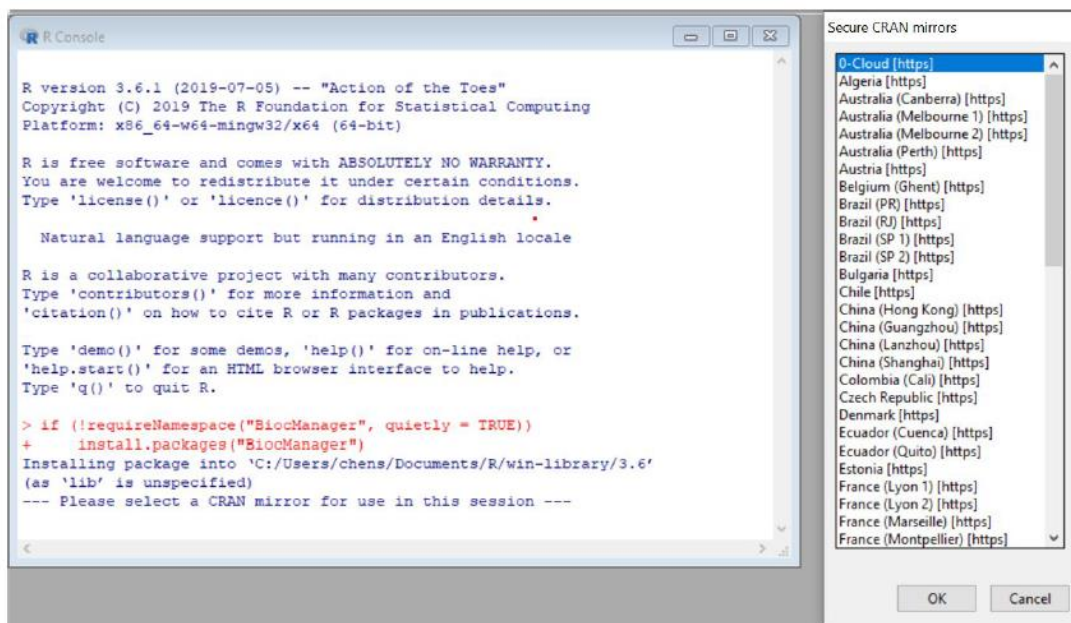

3.1.2 Once you have Biocmanager, you can install any available packages you want.

The whole latest version 3.10:
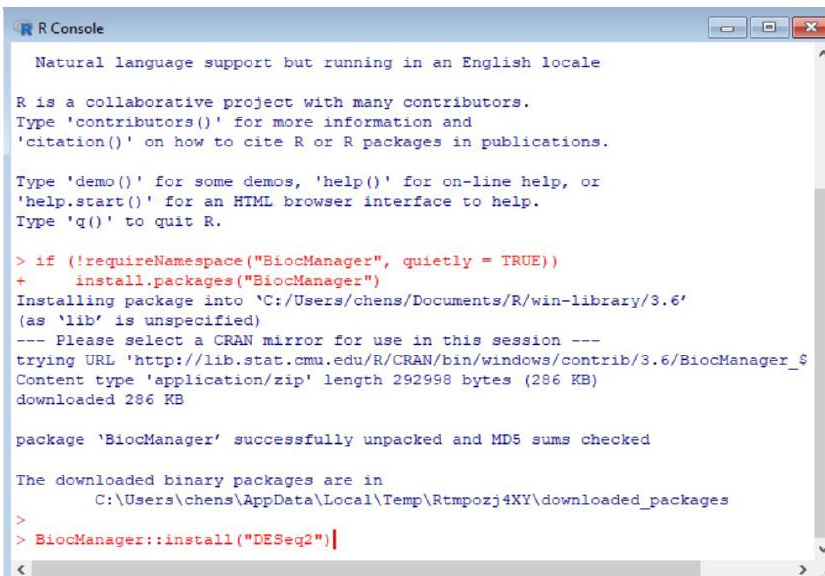
```
BiocManager::install(version = "3.10")
```

The core packages or update installed packages:

```
BiocManager::install()
```

Specific package by name:

```
BiocManager::install("DESeq2")
```


3.1.3 Install Bioconductor packages we need for the course:

```
BiocManager::install("clusterProfiler")

BiocManager::install("edgeR")

BiocManager::install("org.Hs.eg.db")
```

org.Hs.eg.db is Bioconductor's human genome wide annotation package. The full list of annotation packages can be found in this link.

https://www.bioconductor.org/packages/release/BiocViews.html#___Organism

3.2 Install other R packages we need for the course in R prompt.

install.packages("dplyr")

install.packages("tidyr")

install.packages("ggplot2")

Can't wait to start playing in R? Go ahead!

Here are a few cheat sheets I keep at hand.

Base R:

http://github.com/rstudio/cheatsheets/raw/master/base-r.pdf

dplyr:

https://github.com/rstudio/cheatsheets/raw/master/data-transformation.pdf

ggplot2:

https://github.com/rstudio/cheatsheets/raw/master/data-visualization-2.1.pdf

RStudio IDE:

https://github.com/rstudio/cheatsheets/raw/master/rstudio-ide.pdf