

## Step 1. Download and install R

Note current R versions: R version 3.3.1 and Rstudio version .99.903.

### Windows:

1. Download R: <https://cran.r-project.org/bin/windows/base/R-3.3.1-win.exe>
2. Install R by double clicking the .exe file
3. Download Rstudio: <https://download1.rstudio.org/RStudio-0.99.903.exe>
4. Install Rstudio by clicking the .exe file
5. Open Rstudio to ensure correct installation

### Mac:

1. Download R: <https://cran.r-project.org/bin/macosx/R-3.3.1.pkg>
2. Install R by double clicking the .pkg file
3. Download Rstudio: <https://download1.rstudio.org/RStudio-0.99.903.dmg>
4. Install Rstudio by clicking the .dmg file
5. Open Rstudio to ensure correct installation

### Linux Ubuntu LTS 16:

In terminal, run the following:

```
sudo echo "deb http://cran.rstudio.com/bin/linux/ubuntu xenial/"
| sudo tee -a /etc/apt/sources.list

gpg --keyserver keyserver.ubuntu.com --recv-key E084DAB9

gpg -a --export E084DAB9 | sudo apt-key add -

sudo apt-get update

sudo apt-get install r-base r-base-dev

sudo apt-get install gdebi-core

wget https://download1.rstudio.org/rstudio-0.99.896-amd64.deb

sudo gdebi -n rstudio-0.99.896-amd64.deb

rm rstudio-0.99.896-amd64.deb
```

## Step 2. Install R packages

In Rstudio, in the console, type the following:

```
install.packages(c('ggplot2', 'heatmap3', 'plotly', 'readr'))
```

May be asked

Do you want to install from sources the package which needs compilation -- respond with y

### Step 3. Install Bioconductor

In Rstudio, in the console, type the following:

```
source("https://bioconductor.org/biocLite.R")
```

```
biocLite()
```

May be asked

Update all/some/none? [a/s/n] -- respond with a

Would you like to use a personal library instead? (y/n) -- respond with y

```
biocLite(c('Biostrings'))
```

May be asked

Update all/some/none? [a/s/n] -- respond with a

Would you like to use a personal library instead? (y/n) -- respond with y