

## Installing R

To use R, you first need to install the R program on your computer.

### Installing R on a Windows PC

To install R on your Windows computer, follow these steps:

1. Go to <http://cran.r-project.org>.
2. Under “Download and Install R”, click on the “Download R for Windows” link.
3. Under “Subdirectories”, click on the “base” link.
4. On the next page, you should see a link saying something like “Download R 2.15.2 for Windows” (or R X.X.X, where X.X.X gives the version of R, eg. R 2.15.2). Click on this link.
5. You may be asked if you want to save or run a file “R-2.15.2-win.exe”. Choose “Save” and save the file on the Desktop. Then double-click on the icon for the file to run it.
6. You will be asked what language to install it in - choose English.
7. The R Setup Wizard will appear in a window. Click “Next” at the bottom of the R Setup wizard window.
8. The next page says “Information” at the top. Click “Next” again.
9. The next page says “Information” at the top. Click “Next” again.
10. The next page says “Select Destination Location” at the top. By default, it will suggest to install R in “C:\Program Files” on your computer.
11. Click “Next” at the bottom of the R Setup wizard window.
12. The next page says “Select components” at the top. Click “Next” again.
13. The next page says “Startup options” at the top. Click “Next” again.
14. The next page says “Select start menu folder” at the top. Click “Next” again.
15. The next page says “Select additional tasks” at the top. Click “Next” again.
16. R should now be installed. This will take about a minute. When R has finished, you will see “Completing the R for Windows Setup Wizard” appear. Click “Finish”.
17. To start R, you can either follow step 18, or 19:
18. Check if there is an “R” icon on the desktop of the computer that you are using. If so, double-click on the “R” icon to start R. If you cannot find an “R” icon, try step 19 instead.
19. Click on the “Start” button at the bottom left of your computer screen, and then choose “All programs”, and start R by selecting “R” (or R X.X.X, where X.X.X gives the version of R, eg. R 2.15.2) from the menu of programs.
20. The R console (a rectangle) should pop up:

## How to install R on non-Windows

The instructions above are for installing R on a Windows PC. If you want to install R on a computer that has a non-Windows operating system (for example, a Macintosh or computer running Linux, you should download the appropriate R installer for that operating system at <http://cran.r-project.org> and follow the R installation instructions for the appropriate operating system at [http://cran.r-project.org/doc/FAQ/R-FAQ.html#How-can-R-be-installed\\_003f](http://cran.r-project.org/doc/FAQ/R-FAQ.html#How-can-R-be-installed_003f)).

## Installing R packages

R comes with some standard packages that are installed when you install R. However, in this booklet I will also tell you how to use some additional R packages that are useful, for example, the “rmeta” package. These additional packages do not come with the standard installation of R, so you need to install them yourself.

## How to Install an R Package

Once you have installed R on a Windows computer (following the steps above), you can install an additional package by following the steps below:

1. To start R, follow either step 2 or 3:
2. Check if there is an “R” icon on the desktop of the computer that you are using. If so, double-click on the “R” icon to start R. If you cannot find an “R” icon, try step 3 instead.
3. Click on the “Start” button at the bottom left of your computer screen, and then choose “All programs”, and start R by selecting “R” (or R X.X.X, where X.X.X gives the version of R, eg. R 2.15.2) from the menu of programs.
4. The R console (a rectangle) should pop up.
5. Once you have started R, you can now install an R package (eg. the “rmeta” package) by choosing “Install package(s)” from the “Packages” menu at the top of the R console. This will ask you what website you want to download the package from, you should choose “India” (or another country, if you prefer). It will also bring up a list of available packages that you can install, and you should choose the package that you want to install from that list (eg. “rmeta”).
6. This will install the “rmeta” package.
7. The “rmeta” package is now installed. Whenever you want to use the “rmeta” package after this, after starting R, you first have to load the package by typing into the R console:

```
> library("rmeta")
```

Note that there are some additional R packages for bioinformatics that are part of a special set of R packages called **Bioconductor** ([www.bioconductor.org](http://www.bioconductor.org)) such as the “yeastExpData” R package, the “Biostrings” R package, etc.). These Bioconductor packages need to be installed using a different, Bioconductor-specific procedure.

## How to install a Bioconductor R package

The procedure above can be used to install the majority of R packages. However, the Bioconductor set of bioinformatics R packages need to be installed by a special procedure. Bioconductor ([www.bioconductor.org](http://www.bioconductor.org)) is a group of R packages that have been developed for bioinformatics. This includes R packages such as “yeastExpData”, “Biostrings”, etc.

To install the Bioconductor packages, follow these steps:

1. To start R, follow either step 2 or 3:
2. Check if there is an “R” icon on the desktop of the computer that you are using. If so, double-click on the “R” icon to start R. If you cannot find an “R” icon, try step 3 instead.
3. Click on the “Start” button at the bottom left of your computer screen, and then choose “All programs”, and start R by selecting “R” (or R X.X.X, where X.X.X gives the version of R, eg. R 2.15.2) from the menu of programs.
4. The R console (a rectangle) should pop up.
5. Once you have started R, now type in the R console:

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

6. This will install a core set of Bioconductor packages (“affy”, “affydata”, “affyPLM”, “annaffy”, “annotate”, “Biobase”, “Biostrings”, “DynDoc”, “gcrma”, “genefilter”, “geneplotter”, “hgu95av2.db”, “limma”, “marray”, “matchprobes”, “multtest”, “ROC”, “vsn”, “xtable”, “affyQCReport”). This takes a few minutes (eg. 10 minutes).
7. At a later date, you may wish to install some extra Bioconductor packages that do not belong to the core set of Bioconductor packages. For example, to install the Bioconductor package called “yeastExpData”, start R and type in the R console:

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("yeastExpData")
```

8. Whenever you want to use a package after installing it, you need to load it into R by typing:

```
> library("yeastExpData")
```