

# Installing R

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Why R? R is a programming environment for data analysis and graphics that is easily extensible. The user may add new functions to perform statistical calculations. The user can add new classes to accommodate new data types. One function of statisticians is to develop methods and software to aid in the interpretation of data. Use of R enables ones to implement new methodologies and post them for others to use. R facilitates new developments.

R is a freely available programming environment structured after S, now commercially available from Insightful (Seattle, WA) as S-Plus. Download R by going to <http://cran.r-project.org/>. To download a version that will run on Windows 95 or a later version, click on the ‘**Download R for Windows**’ link located under **Download and install R**. Then click on the **base** subdirectory and subsequently click on the **Download R-2.15.1 for Windows** link to save the R-2.15.1-win32.exe file to your hard drive.

To install R, simply go to <Start> <Run> and then browse for the R-2.15.1-win32.exe file and follow the prompts.

## Installing user contributed packages

Once R has been installed, open R by double clicking on the icon or accessing it through the Start menu. To install user contributed R packages, select ‘**Packages**’ from the Toolbar, then select ‘**Select repositories**’ and choose the appropriate repository (**CRAN** or **CRAN extras**). The command

```
> setRepositories()
```

can also be issued at the command line to accomplish the same thing. Thereafter, select ‘**Packages**’ from the Toolbar, then ‘**Install package(s)**.’ A list of packages available for download will appear.

## Installing Bioconductor

Once R has been installed, open R by double clicking on the icon or accessing it through the Start menu. Install the *biocLite* script which will install a subset of the most frequently used Bioconductor packages. From the R prompt,

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

then

```
> biocLite()
```

To install additional Bioconductor R add-on packages, select ‘**Packages**’ from the Toolbar, then select ‘**Select repositories**’ and choose ‘**BioC software**’. Thereafter, select ‘**Packages**’ from the Toolbar, then ‘**Install package(s)**.’ A list of packages will appear. Install the additional packages needed by highlight them (multiple packages may be installed by highlighting the desired packages while holding the <Ctrl> key). For further instructions see <http://www.bioconductor.org/download>.