

Directions for installing R/Rstudio

1. Download R from <https://cran.rstudio.com/>
2. Download the free RStudio Desktop version from the following link:
<https://www.rstudio.com/products/rstudio/download/>

Directions for installing R packages from CRAN

Packages we will use in class will be installed on the school computers. However, you will need to install additional packages on your personal computer. Packages are installed in one or more locations that can be set by the user. It is easiest to use the default location for all packages. If you are unable to do so, see the next section and let me know if you have any questions.

1. Type the following from within *R* to install a package with the name “packageName”

```
install.packages("packageName")
```
2. You can then run the following command from within *R* to test whether this has worked correctly:

```
library(packageName)
```

3. If nothing happens, that means it works! If you get any error messages, the package did not install correctly and you should try again or see me if you need help.

Once a package has been installed, it can be loaded using the command from (2); you do *not* need to install the package again.

While installing a package, you may get the following prompt:

```
Update all/some/none? [a/s/n]:
```

If this happens, it is recommended to type ‘a’ (without quotes) and enter to update the packages.

The Course Information page (<http://gdancik.github.io/CSC-315/info/>) has a script that will install all required packages for this course, and a second script for testing whether several packages are installed correctly.

Directions for installing R packages from Bioconductor

Bioconductor is a repository of R packages for analyzing genomic data. Bioconductor packages are now installed through the *BioManager* package available on CRAN. See the *R* script for package installation for an example.

Directions for installing and loading *R* packages in specific locations (only if you are unable to use the default location)

You should use the default location for package installations, but if you are unable to do so (e.g., because of permission issues), then you may set the package location by following the directions below:

1. Type the following command into *R* to change the library path, which tells *R* where packages should be installed and loaded from. Note: do NOT put a slash at the end of the directory name.

```
.libPaths("/path/to/directory")
```

2. Install and load packages as in the previous section.

Before loading a package, you need to set the library path as in (1), by putting the appropriate statement at the top of each script, and executing it.