

If you are in Bioinformatics II, you might want to download and install R and Bioconductor on your computer. These packages are available for Windows, Mac, Unix and Linux. Installation requires administrative permission on the computer - so if you are using a departmental or lab computer, you will likely need to ask your computer administrator to do the installation.

Install R first.

Go to [www.r-project.org](http://www.r-project.org) and follow the instructions for your platform.

You might also want to download the following documents:  
from [www.r-project.org](http://www.r-project.org) > manuals "An Introduction to R"

This goes through the R language in detail and covers just about everything that is covered about R in Stat 597C.

<http://cran.r-project.org/doc/contrib/Verzani-SimpleR.pdf#search='verzani%20statistics'>

This is a manual showing how R is used to do elementary statistics.

Bioconductor can be downloaded as an R package from [www.bioconductor.org](http://www.bioconductor.org) . We will be using the 2 packages, affy and limma.

Linux and Unix users can go to the website and install from there.  
Windows users can more readily install from the R menu system.

Windows: double-click on the R icon to start the program. On the menu system, select packages>select repository>Bioconductor

packages>install packages>limma

packages>install packages>affy

We will also need some "metadata" for Affymetrix analysis. Go back to [www.bioconductor.org](http://www.bioconductor.org).  
click on metadata> ath1121501cdf

This will download a zip folder to your computer. On Unix/linux, this is installed in the same way as limma and affy.

On Windows, go back to the menu system and select packages> install packages from local zip files