

## 2.1 Installing R and Bioconductor packages

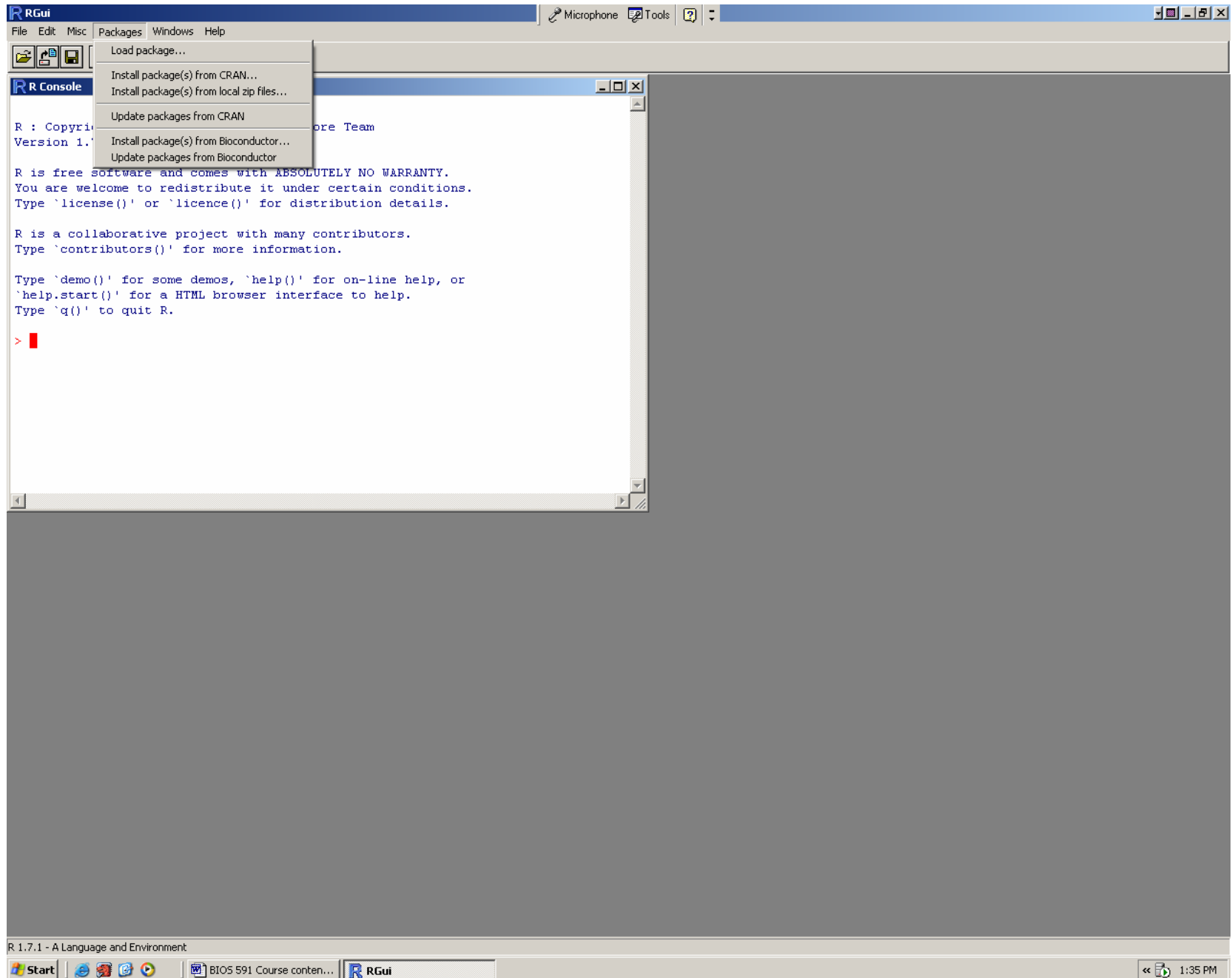
R is a programming environment for data analysis and graphics.

R is a freely available software package structure after S, now commercially available from Insightful (Seattle, WA) as S-Plus. Download R by going to <http://lib.stat.cmu.edu/R/CRAN/>. To download a version that will run on Windows 95 or a later version, click on the '**Windows (95 and later)**' link located under precompiled binary distributions. Then click on **base**, and save **rw1081.exe** to your hard drive. To install R, simply go to <Start> <Run> and then browse for the rw1081.exe file and follow the prompts.

### 2.1.1 Installing Bioconductor

Once R has been installed, open R by double clicking on the icon or accessing it through the Start menu. To install the Bioconductor R add-on packages, select '**Packages**' from the Toolbar, then select '**Install package(s) from Bioconductor**'. A list of packages will appear; because there are dependencies across the Bioconductor packages, it is best to install all of them. To do so, highlight all packages by clicking on the first listed package then press <Shift> and scroll to select the last package list (thereby all packages should be highlighted). This should take <10 minutes using the VCU network but is not recommended if you are using a dial-up connection from home. For a home installation you may want to copy the rw1081.exe from <http://lib.stat.cmu.edu/R/CRAN/> and the Bioconductor packages \*.zip files from <http://www.bioconductor.org/> to a CD-R. There are two methods that can be used to download the \*.zip packages directly from the Bioconductor website. First, from <http://www.bioconductor.org/> go to the left side under **Software**, click on '**Release 1.3 Packages**' and download the packages by clicking on the name of the desired package, then Win32 Package Download, and save the \*.zip file to the R\library directory. These packages may then be installed by opening R, then using the toolbar menu item '**Packages**,' '**Install package(s) from local zip file**' and install each downloaded package. The second (not preferred) method that can be used is to click on the **Bioconductor Install Script**, then click Edit, Select All, Edit, Copy and then paste the text into R. Pasting the text creates the function that will install the packages, but you also need to run `getBioc()` from the R command line to install Bioconductor. When using the install script you must be sure the version number is accurate.

BIOS 691 Statistical Methods for Microarray Data



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