

Laptop Programs to Install:

1) Install the most recent version of R for your operating system by following the links from <http://www.r-project.org/> For help installing R, see last bullet.

1.1) Download and install the most recent version of R Studio desktop from <http://www.rstudio.com/>

1.2) Install R Markdown within R Studio

File -> New File -> R Markdown. If prompted to install packages, click yes.

Select Document on the left menu within the window which pops up.

Enter title "R Markdown". Leave as default HTML. Click Ok.

Within one of the screens in your R Studio, there is a knitting needle icon. Press the "Knit HTML" button (found near top) to make sure it works.

After a few moments a window entitled R Markdown will appear = it is working. Close this window.

1.3) Install Shiny within R Studio

File -> New File -> R Markdown.

Select Shiny on the left menu.

Enter title "Shiny". Leave as default Shiny Document. Click Ok.

If prompted to install packages, click yes.

Within one of the screens in your R Studio, there is now a Run Document icon. Press the "Run Document" (found near top) to make sure it works.

After a few moments a window entitled Shiny will appear = it is working. Close this window.

2) Install the BioConductor core packages. To do this, open R and type at the > prompt, then wait for the prompt to reappear and type second command:

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

3) Install some workshop specific packages. Again, type at the > prompt, then wait for the prompt to reappear before typing the

next command.

```
install.packages("ggplot2");
install.packages("gplots");
install.packages("dplyr");
install.packages("plyr");
install.packages("data.table");
install.packages("reshape2");
install.packages("stringr");

source("http://bioconductor.org/biocLite.R");
biocLite("ggbio");
biocLite("GenomicRanges");
biocLite("GenomicAlignments");
biocLite("biovizBase");
biocLite("Gviz");
biocLite("Homo.sapiens");
biocLite("VariantAnnotation");
biocLite("grid");
biocLite("biomaRt");
```

To check if the packages have been installed properly, you can check under the 'Packages&Data' tab in the header (I am on a MAC so wording and location may be different on a PC). Within the 'Package Manager' section, all of the above packages should be listed. During class to use these packages, you will have to load them.

Alternatively to check which packages have been installed you can use the following command:

```
installed.packages();
```

4) A robust text editor. For Windows/PC - notepad++ (<http://notepad-plus-plus.org/>). For Linux - gEdit (<http://projects.gnome.org/gedit/>). For Mac – TextWrangler (<http://www.barebones.com/products/textwrangler/download.html>)

5) A file decompression tool. For Windows/PC – 7zip (<http://www.7-zip.org/>). For Linux – gzip (<http://www.gzip.org>). For Mac – already there.

6) A robust internet browser such as Firefox or Safari (Internet Explorer and Chrome are not recommended because of Java issues).

7) Java -The visualization program that we will be using (IGV) requires Java. Check if you have Java installed: <https://www.java.com/verify/> and download Java if you do not have it installed.

8) Integrative Genomics Viewer (IGV) - Once java is installed, go to <http://www.broadinstitute.org/igv/> and register in order to get access to the downloads page. Once you have gained access to the downloads page, click on the appropriate launch button that matches the amount of memory available on your laptop (if you have space, 1.2GB is good, more is better). Chrome: Chrome does not launch "java webstart" files by default. Instead, the launch buttons below will download a "jnlp" file. This should appear in the lower left corner of the browser. Double-click the downloaded file to run. Windows users: To run with more than 1.2 GB you must install 64-bit Java. This is often not installed by default even with the latest Windows 7 machines with many GB of memory. In general trying to launch with more memory than your OS/Java combination supports will result in the obscure error "could not create virtual machine".

9) SSH client - Mac and Linux users already have a command line ssh program that can be run from the terminal. For Windows users, please download PuTTY: <http://www.chiark.greenend.org.uk/~sgtatham/putty/download.html>

10) SCP/SFTP client - We will be moving data from the servers to the student laptops for visualization. Mac and Linux users already have a command line scp and sftp program. For Windows users, please install WinSCP: <http://winscp.net/eng/download.php>

11) Install Cytoscape 3.2.1: <http://www.cytoscape.org>

12) Within the Cytoscape program, install the following Cytoscape plugins.

From the menu bar, Apps > Manage Apps

Within all apps, Search for the following and install:

- jActiveModules (should already be installed. Install if not)
- GeneMania (should already be installed. Install if not).
- EnrichmentMap
- BiNGO
- Reactome FI Plugin

Select GeneMania from Apps Manager → Choose Another Data Set.

From the list of available data sets, select the most recent (2014-08-12/1 June 2014) and under Include only these networks: select All → Download.

An Install Window will pop-up. Select H.Sapiens Human (2384 MB) → Install

This requires time and a good network connection to download completely, so be patient.

13) A PDF viewer (Adobe Acrobat or equivalent).

15) fastqc which is available for Windows/Mac/Linux

here: <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>

16) Sign up for a GenePattern account at Broad

<http://www.broadinstitute.org/cancer/software/genepattern/>

When you go to this homepage, there is under the "Getting Started" section an icon for "Run analyses on the Broad public server". Click here and sign up for an account so that in class we can use the tool on the web.

17) For help installing R, you may find the following directions helpful resources:

Tutorial on how to install R on windows only look at the "getting started"

section: <http://www.biostat.wisc.edu/~kbroman/Rintro/Rwin.html>
!

and MACS only look at the "getting started"
section: [http://www.biostat.wisc.edu/~kbroman/Rintro/Rmac.ht
ml](http://www.biostat.wisc.edu/~kbroman/Rintro/Rmac.html)