­**R and RSTUDIO**

OPTION 1 - Download R and RStudio from online repositories:

Downloading R:

<https://cran.rstudio.com/>

Downloading RStudio:

<https://www.rstudio.com/products/rstudio/download/#download>

OPTION 2 – Download R and RStudio using conda/anaconda

From your command line – install r and rstudio into your base environment

“”” Conda install r rstudio “””

OR create a new environment with R installed if you don’t want it in your base environment

“”” conda create -n renvironment r rstudio

Where [renvironment] is the name of the environment

“”” conda activate renvironment “””

Launch rstudio by simply entering in “”” rstudio “”” into the command line

OPTION 3 – Running R off of the cluster

<https://wikis.nyu.edu/display/NYUHPC/Running+RStudio+on+the+HPC+Prince+Cluster>

this wiki explains it well

NOTE - <https://www.xquartz.org/>

MAC users will need this for port forwarding to use RSTUDIO with the cluster, you will need to RESTART COMPUTER after installation

PC users – just need to follow the wiki and make sure that port forwarding is turned on

ssh -Y [mgc439@bigpurple.nyumc.org](mailto:mgc439@bigpurple.nyumc.org)

srun --x11 --pty --time=05:00:00 /bin/bash

then either load rstudio using “”” module load””” (like in the wiki)

or if you are using conda on the cluster as well – you can download and run in the same way you would locally

**DOWNLOADING R PACKAGES**

OPTION 1 – standard download and install using R

To install the ggplot2 package, use the following:

> install.packages("ggplot2")

And then to load it, use the following:

> library("ggplot2")

OPTION 2 – use conda. If you have set your channels to conda-forge and bioconda, most packages are available via conda very easily

“”” conda config --add channels bioconda “””

“”” conda config --add channels conda-forge “””

“”” Conda install r-…. “””

“”” Conda install bioconductor-…. “””