WORKING IN THE SERVER WITH R

First, connect to the server by:

$ ssh maider@ciilogin.c2b2.columbia.edu

Then log into qlogin by:

$ qlogin -l mem=30G

To install packages in your own folder do the following:

Since the packages will use temporary folder and our temp/ server doesnt have much space we will need to send our packages to another path of choice:

$ export TMPDIR=$HOME

Then we go into R.
$R

The first time you will try installing a package you will prompt to this:
>install.packages("package")

```
> install.packages("RSpectra")
Installing package into '/usr/lib64/R/library'
(as 'lib' is unspecified)
Warning in install.packages("RSpectra") :
  'lib = "/usr/lib64/R/library"' is not writable
Would you like to use a personal library instead? (yes/No/cancel) yes
Would you like to create a personal library
'~/R/x86_64-redhat-linux-gnu-library/4.1'
to install packages into? (yes/No/cancel) yes
--- Please select a CRAN mirror for use in this session ---
Secure CRAN mirrors

 1: 0-Cloud [https]
 2: Australia (Canberra) [https]
 3: Australia (Melbourne 1) [https]
 4: Australia (Melbourne 2) [https]
 5: Australia (Perth) [https]
 6: Austria [https]
 7: Belgium (Brussels) [https]
 8: Brazil (PR) [https]
 9: Brazil (RJ) [https]
```

Once you select one region the package will be installed. These packages will be installed in the location that is suggested in the picture. In this case:
"~/R/x86_64-redhat-linux-gnu-library/4.1"

If you continue installing other packages they will be installed there. However if you quit the session:
$ q

And log in again next time, your library path by default will be:

```
.libPaths()[1]"/usr/lib64/R/library" "/usr/share/R/library"
```

So in order to specify the location where you want to install your packages you will do:

```
> .libPaths("/share/home/komalj/R/x86_64-redhat-linux-gnu-library/4.1")
```

The packages needed for Seurat script are the following:

```
>install.packages("dplyr")
>install.packages("RSpectra")
>install.packages("Seurat")
>install.packages("patchwork")
>install.packages("stringr")
>install.packages("plyr")
>install.packages("data.table")
>install.packages("ggplot2")
>install.packages("Matrix")
>install.packages("SeuratDisk")
>install.packages("SeuratData")
>install.packages("config")
>install.packages("knitr")
>install.packages("markdown")
```

Documentation for this problem and solutions:

https://researchcomputing.princeton.edu/support/knowledge-base/rrstudio

Then in order to run the Rscript create a Shell script to launch it:

```
#!/bin/bash
#
#$
#$ -cwd
#$ -j y
#$ -N single_cell
#$ -S /bin/bash
#$ -l h_vmem=10g


Rscript ~/pipelines/scRNAseq/scRNASeq_Integration.R

#done
Integration_R.sh (END)
```

Same for downstream analysis:

```
[maider@hdx2-d scRNAseq_test]$ vim Downstream_Seurat.sh

#!/bin/bash
#
#$
#$ -cwd
#$ -j y
#$ -N single_cell_DE
#$ -S /bin/bash
#$ -l h_vmem=10g


Rscript ~/pipelines/scRNAseq/scRNAseq_downstream_analysis.R

#done
~


```

Finally, to summit the job:

$ qsub Integration_R.sh