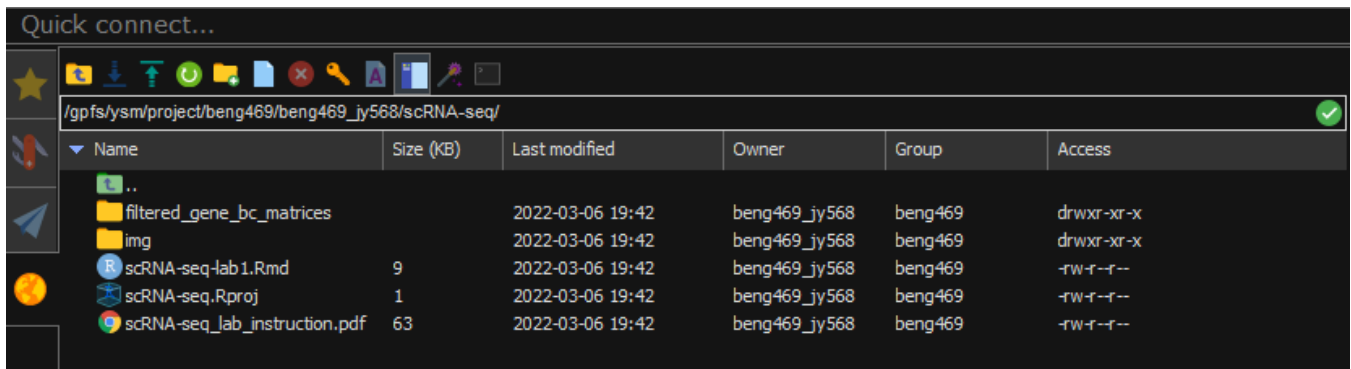


BENG 469 Lab (scRNA-seq) instructions

• Pre-lab tasks:

1. Download the “scRNA-seq” folder from HPC (/gpfs/ysm/project/beng469/beng469_jy568/scRNA-seq/) to local. Files in the folder should be the same as below:



Name	Size (KB)	Last modified	Owner	Group	Access
..					
filtered_gene_bc_matrices		2022-03-06 19:42	beng469_jy568	beng469	drwxr-xr-x
img		2022-03-06 19:42	beng469_jy568	beng469	drwxr-xr-x
scRNA-seq-lab1.Rmd	9	2022-03-06 19:42	beng469_jy568	beng469	-rw-r--r--
scRNA-seq.Rproj	1	2022-03-06 19:42	beng469_jy568	beng469	-rw-r--r--
scRNA-seq_lab_instruction.pdf	63	2022-03-06 19:42	beng469_jy568	beng469	-rw-r--r--

3. Open “scRNA-seq.Rproj” then “scRNA-seq-lab1.Rmd” file using RStudio.

4. Run the code shown below in the “scRNA-seq-lab1.Rmd” to install required packages (Note: Most of the packages should already have been installed in the scATAC-seq lab session, here we run this installation step just as a sanity check).

```
# Install the packages

```{r}
if (!require("dplyr")) install.packages("dplyr")
if (!require("ggplot2")) install.packages("ggplot2")
if (!require("Seurat")) install.packages("Seurat")
if (!require("patchwork")) install.packages("patchwork")
```
```

5. Verify the packages are properly installed by running the code below in the “scRNA-seq-lab1.Rmd” (make sure there is no error message).

```
# Load the packages
```

```
``{r}  
library(dplyr)  
library(ggplot2)  
library(Seurat)  
library(patchwork)  
``
```

- **In the lab:**

In this lab we will use R to walk through some basic steps of scRNA-seq analysis.

The R codes are in the “scRNA-seq-lab1.Rmd” file.