**Using the SCC at CAMH with MobaXterm**

**Change the working directory to**: cd /imaging/scratch/Imhpr/kpuka/nhis

**Use the GUI (graphical user interface) to add the files into that folder.**

**Use the GUI to create a new file with its name ending with “.sh”. and paste the following script**:

#!/bin/bash -l

#SBATCH --job-name=serial\_job\_test              # Job name

#SBATCH --mail-type=END,FAIL                         # Mail events (NONE, BEGIN, END, FAIL, ALL)

#SBATCH --mail-user=klajdi.puka@camh.ca   # Where to send mail

#SBATCH --ntasks=24                                             # Run on a single CPU

#SBATCH --mem=200gb                                        # Job memory request

#SBATCH --time=45-00:00:00                            # Time limit days-hrs:min:sec

#SBATCH --output=serial\_test\_%j.log              # Standard output and error log

pwd; hostname; date

module load lang/R/4.0.3-Python-3.8.5-Anaconda3-2020.11

echo "Running  R script on a single CPU core"

R --vanilla < 5\_CausalMediation\_f.R > results\_f.txt

Note 1: The first part of the script is for the HPC scheduler to indicate what resources you want; the second part is what you want to run.

Note 2: In the example above, the R syntax is called “CausMed\_f.R” and the results are called “results\_f.txt”; also, the script above is saved to a file called “CausalMed\_f.sh”

**Commands to interact with the scheduler:**

**To Submit the job**: sbatch CausalMed\_f.sh

**Check job status**: squeue

**Cancel a job:** scancel *job\_id*

**See job stats after completion**: seff *job\_id*

**After job finished:**

**Use GUI to copy the output files into your PC and view on R**

**Alternatively, can directly open the contents by using the GUI or by using:** cat results\_f.txt

Other Commands

**To create a new folder**: mkdir folder\_name

**To create R file**: echo ‘sessionInfo()’ > file\_name.R

**To check folder contents**: ls