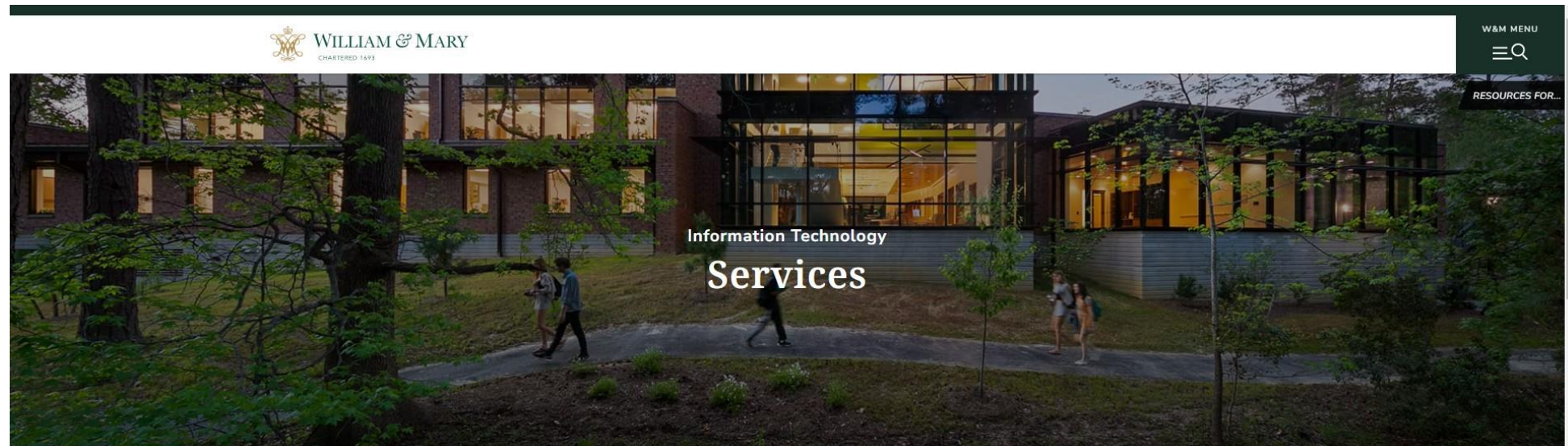


Updated Guide for Using FEKO on the W&M High Performance Computing Cluster

Russell Kamback (September 2024)

Step 1: Create a W&M HPC Account

Visit <https://www.wm.edu/offices/it/services/researchcomputing/acctreq/>



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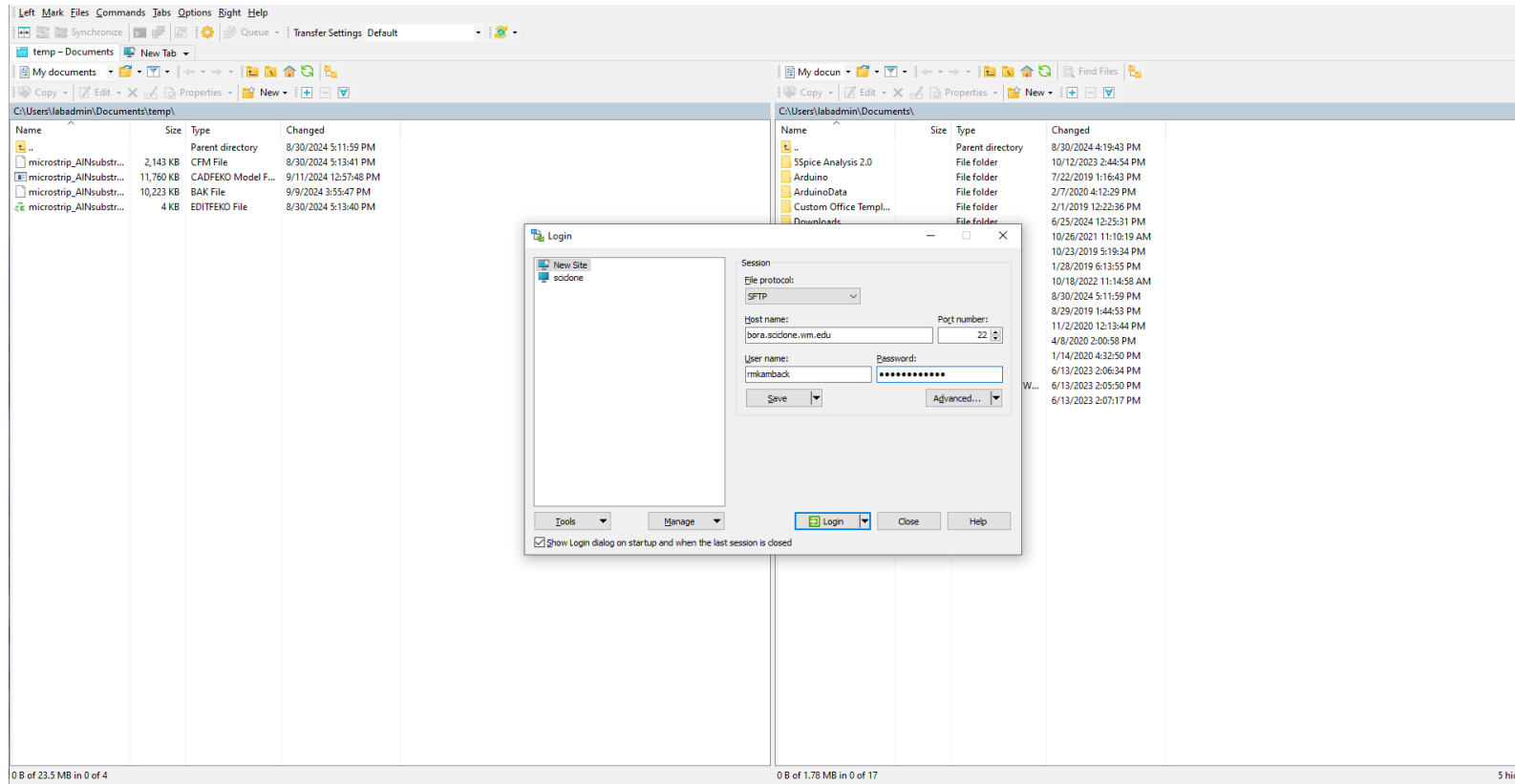
Request an Account

You must have a W&M Username to **request or renew an HPC account.** External collaborators must first be sponsored for and obtain an affiliate W&M Username.

William & Mary (including VIMS) faculty, staff, and students with computation- or data-intensive applications from any discipline are welcome to apply for accounts on the university's centrally-administered HPC clusters (SciClone and Chesapeake), which are both available at no cost to any member of the William & Mary community with a legitimate need for their services. A single account provides access to both clusters.

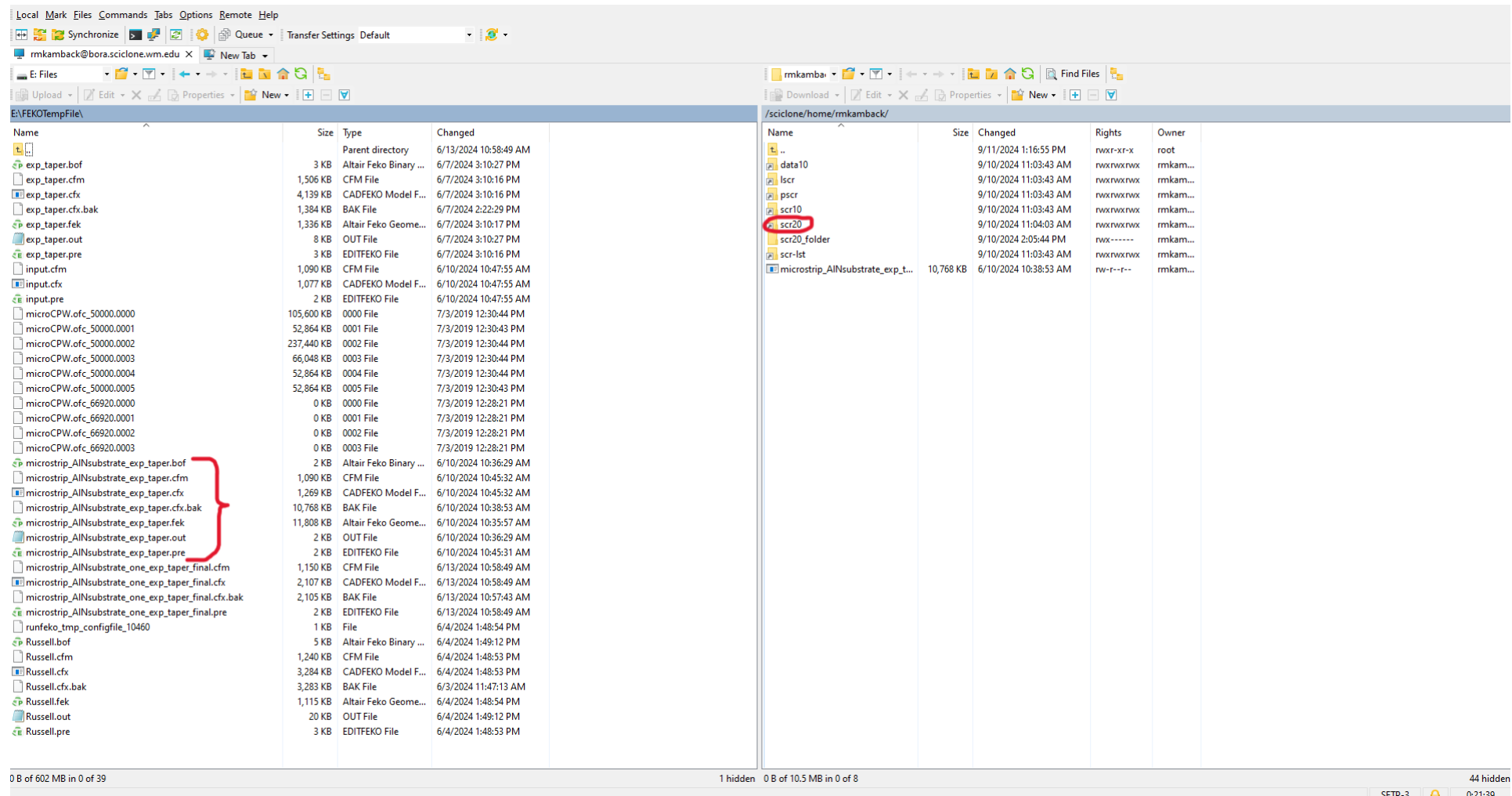
These clusters may also be made available on a case-by-case basis to external collaborators of W&M faculty, staff, and students, or to other academic users who are developing software tools or conducting research of direct interest to the W&M HPC community. For more information, please contact the Research Computing team at rc@wm.edu.

Step 2: Open the SSH Secure File Transfer (called WinSCP on Magnolia) and log into bora.sciclone.wm.edu

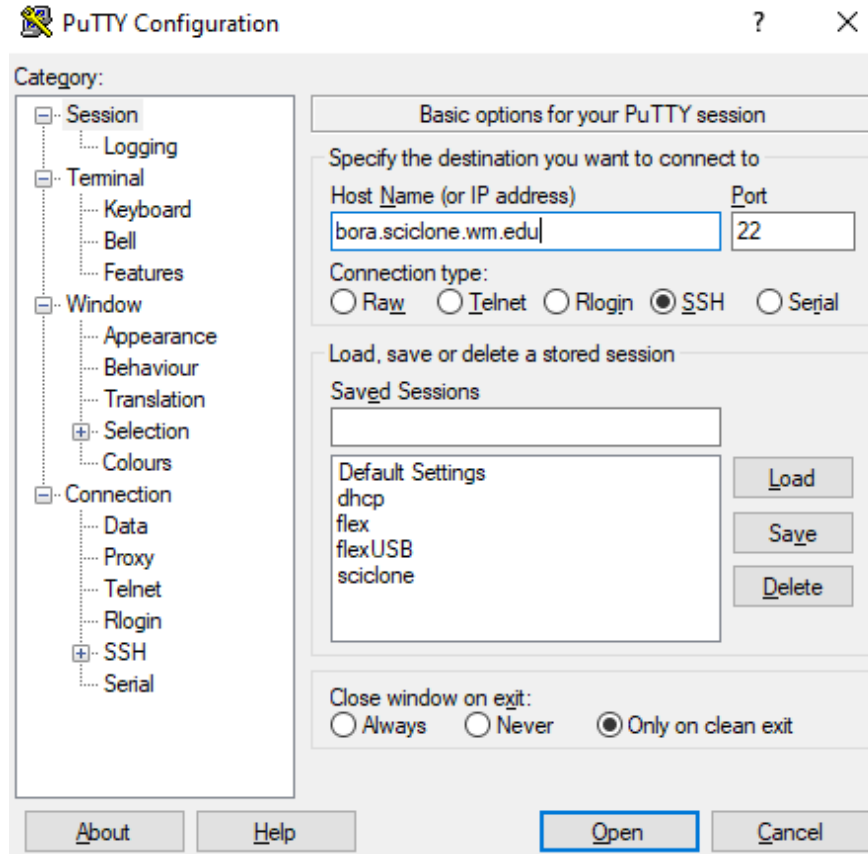


Note: the above image is taken from WinSCP, but most computers in this lab as of now have SSH Secure File Transfer. Both serve the same purpose of transferring local files to and from the HPC cluster, and the way to do that is basically the same between the two applications.

Step 3: Find the model you want to process on the left side, then drag over the .cfx and the .bak files to the 'scr20' folder on the right side

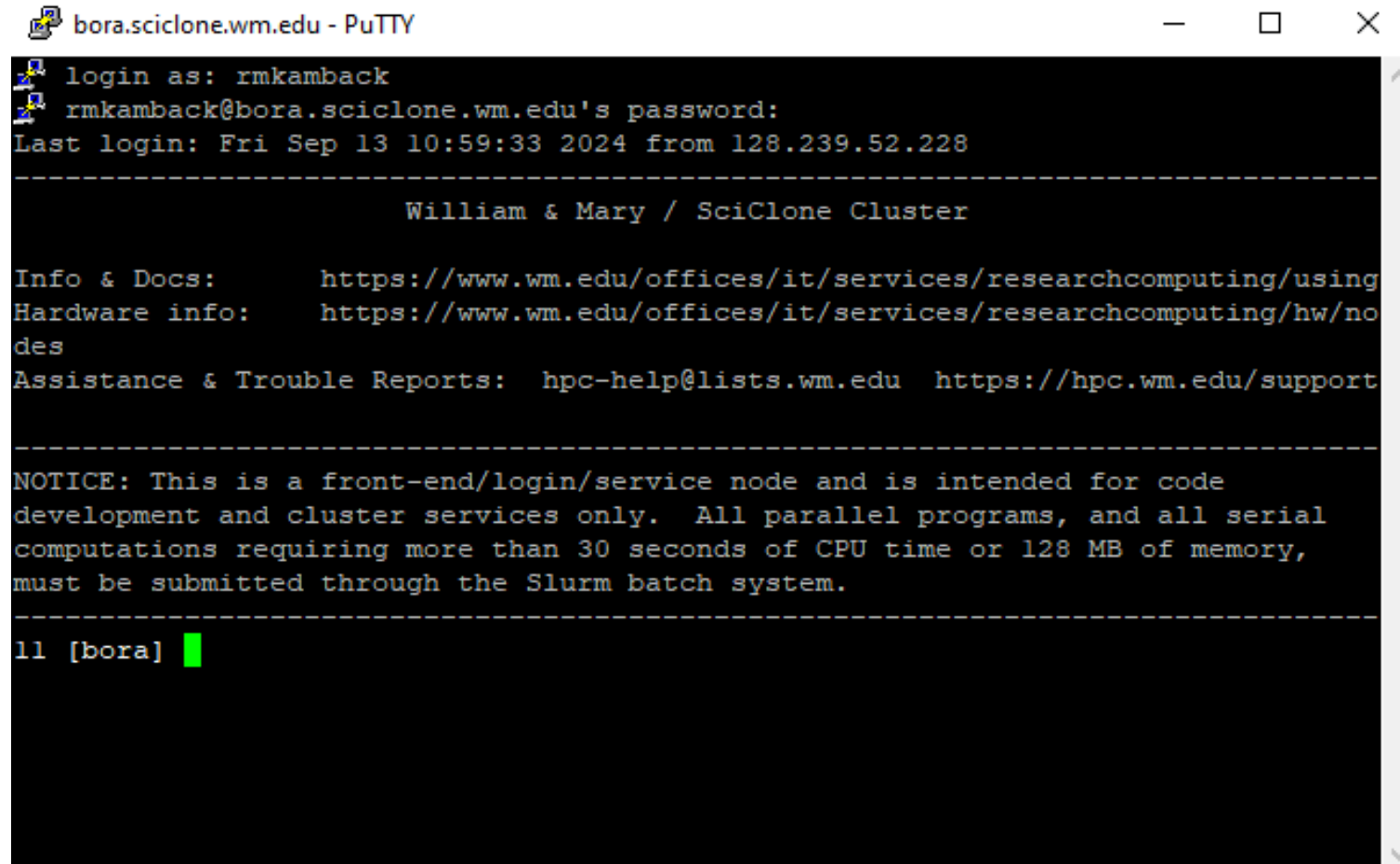


Step 4: Open PuTTY, type 'bora.sciclone.wm.edu' in the Host Name, and click Open



Note: do not worry about the "Saved Sessions" box below the host name entry, there is no need to select any of those options

Step 5: Log in with your HPC account



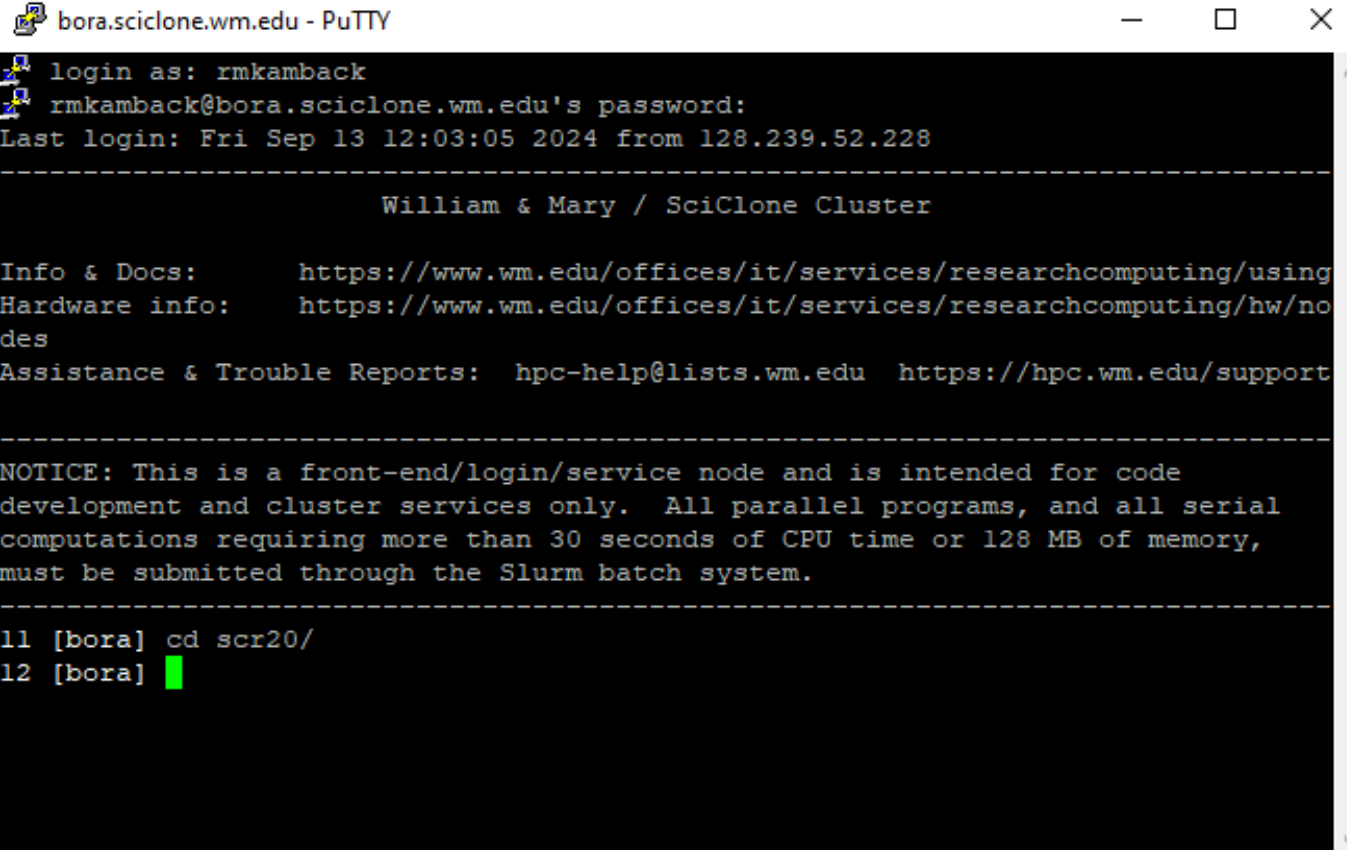
```
bora.sciclone.wm.edu - PuTTY
login as: rmkamback
rmkamback@bora.sciclone.wm.edu's password:
Last login: Fri Sep 13 10:59:33 2024 from 128.239.52.228
-----
                        William & Mary / SciClone Cluster

Info & Docs:           https://www.wm.edu/offices/it/services/researchcomputing/using
Hardware info:        https://www.wm.edu/offices/it/services/researchcomputing/hw/nodes
Assistance & Trouble Reports: hpc-help@lists.wm.edu https://hpc.wm.edu/support
-----

NOTICE: This is a front-end/login/service node and is intended for code
development and cluster services only. All parallel programs, and all serial
computations requiring more than 30 seconds of CPU time or 128 MB of memory,
must be submitted through the Slurm batch system.
-----

ll [bora] █
```

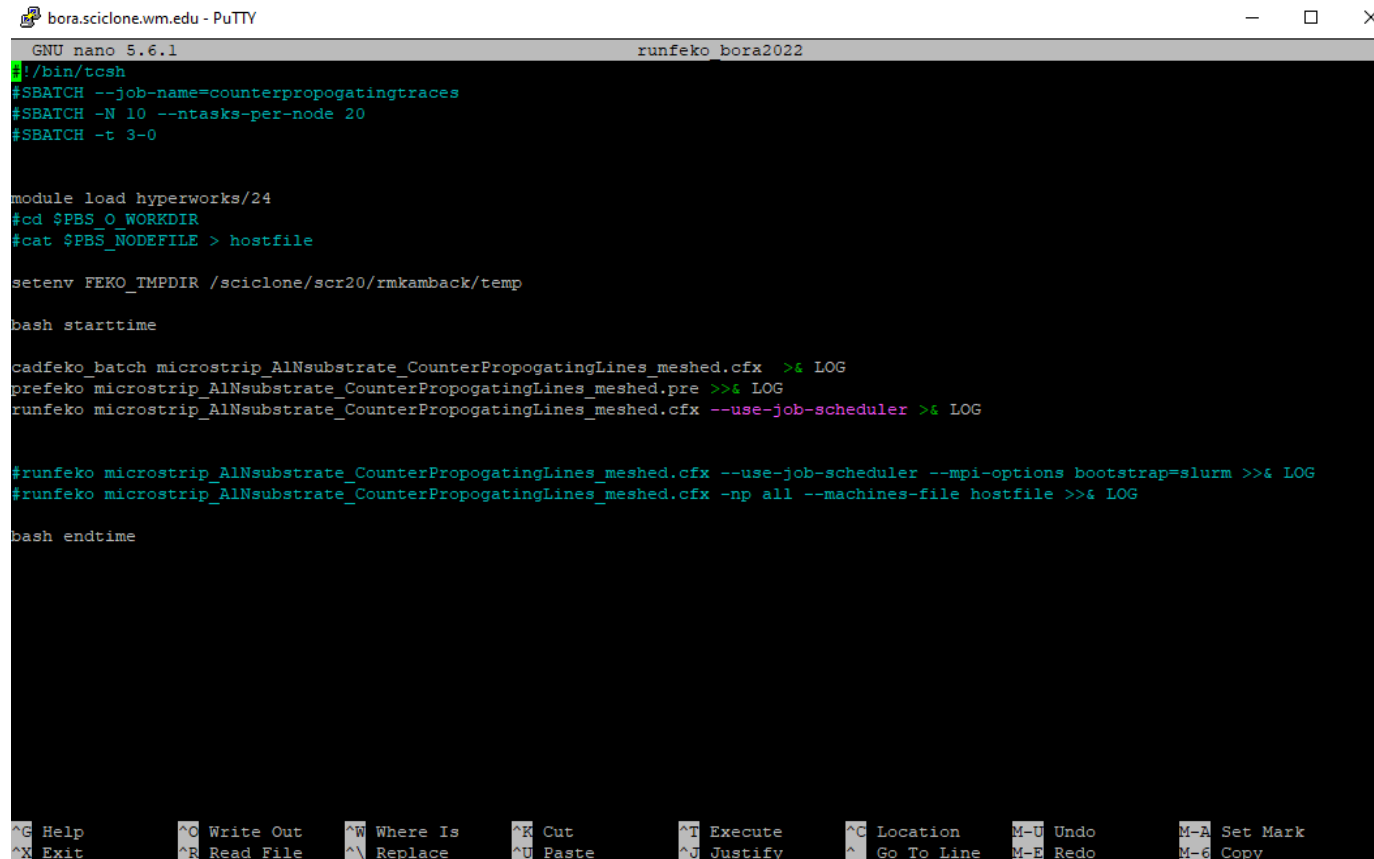
Step 6: Change your directory to your scr20 folder



```
bora.sciclone.wm.edu - PuTTY
login as: rmkamback
rmkamback@bora.sciclone.wm.edu's password:
Last login: Fri Sep 13 12:03:05 2024 from 128.239.52.228
-----
                William & Mary / SciClone Cluster
-----
Info & Docs:      https://www.wm.edu/offices/it/services/researchcomputing/using
Hardware info:   https://www.wm.edu/offices/it/services/researchcomputing/hw/nodes
Assistance & Trouble Reports: hpc-help@lists.wm.edu https://hpc.wm.edu/support
-----
NOTICE: This is a front-end/login/service node and is intended for code
development and cluster services only. All parallel programs, and all serial
computations requiring more than 30 seconds of CPU time or 128 MB of memory,
must be submitted through the Slurm batch system.
-----
11 [bora] cd scr20/
12 [bora] █
```

Note: The 'cd' command changes your directory to whatever you type immediately after it (in this case, scr20). If you type the 'ls' command, it will list items in your directory.

Step 7: Open a nano-window for runfeko by typing "nano runfeko_bora2022"; something like this should pop up:



```
GNU nano 5.6.1 runfeko_bora2022
#!/bin/tcsh
#SBATCH --job-name=counterpropogatingtraces
#SBATCH -N 10 --ntasks-per-node 20
#SBATCH -t 3-0

module load hyperworks/24
#cd $PBS_O_WORKDIR
#cat $PBS_NODEFILE > hostfile

setenv FEKO_TMPDIR /sciclone/scr20/rmkamback/temp

bash starttime

cadfeko_batch microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx >& LOG
prefeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.pre >>& LOG
runfeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx --use-job-scheduler >& LOG

#runfeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx --use-job-scheduler --mpi-options bootstrap=slurm >>& LOG
#runfeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx -np all --machines-file hostfile >>& LOG

bash endtime

^G Help      ^O Write Out  ^W Where Is   ^X Cut        ^T Execute    ^C Location   M-U Undo     M-A Set Mark
^X Exit      ^R Read File  ^\ Replace    ^U Paste      ^J Justify    ^_ Go To Line  M-B Redo     M-G Copy
```

Note: you will likely need to change some things as explained on the following slide

Step 8: Adjust project parameters

Firstly, if necessary, change your nano window so that it is identical to the picture on the right, with exception to things circled in red detailed below:

- 1) Type "--job-name=<YOUR JOB NAME>"
- 2) Insert the number of nodes to run your projects on. The bigger the project, the more nodes. Usually, 10-15 is good enough.
- 3) Here goes your folder, so type "/sciclone/scr20/<YOUR FOLDER>"
- 4) This should look exactly like the picture except with the name of *your file* instead of mine
- 5) You don't need to type any of this (the # means it's commented out)

```
GNU nano 5.6.1 runfeko bora2022
#!/bin/tcsh
#SBATCH --job-name=counterpropogatingtraces 1
#SBATCH -N 10 --ntasks-per-node 20
#SBATCH -t 3-0 2

module load hyperworks/24
#cd $PBS_O_WORKDIR
#cat $PBS_NODEFILE > hostfile

setenv FEKO_TMPDIR /sciclone/scr20/rmkamback/temp 3

bash starttime

cadfeko_batch microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx >& LOG
prefeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.pre >>& LOG
runfeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx --use-job-scheduler >& LOG 4

#runfeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx --use-job-scheduler --mpi-options bootstrap=slurm >>& LOG
#runfeko microstrip_AlNsubstrate_CounterPropogatingLines_meshed.cfx -np all --machines-file hostfile >>& LOG 5

bash endtime

^G Help      ^O Write Out  ^W Where Is   ^K Cut        ^T Execute    ^C Location   M-U Undo     M-A Set Mark
^X Exit      ^R Read File  ^\ Replace    ^U Paste      ^J Justify    ^_ Go To Line  M-E Redo     M-6 Copy
```

Step 9: Type Ctrl+O then Enter to write out your code, then type Ctrl+X to exit the window

Step 10: Submit your job for processing using the 'sbatch' command as seen below in line 13



```
borasciclone.wm.edu - PuTTY
login as: rmkamback
rmkamback@borasciclone.wm.edu's password:
Last login: Fri Sep 13 13:11:51 2024 from 128.239.52.228
-----
                William & Mary / SciClone Cluster
-----
Info & Docs:      https://www.wm.edu/offices/it/services/researchcomputing/using
Hardware info:   https://www.wm.edu/offices/it/services/researchcomputing/hw/nodes
Assistance & Trouble Reports: hpc-help@lists.wm.edu https://hpc.wm.edu/support
-----
NOTICE: This is a front-end/login/service node and is intended for code
development and cluster services only. All parallel programs, and all serial
computations requiring more than 30 seconds of CPU time or 128 MB of memory,
must be submitted through the Slurm batch system.
-----
11 [bora] cd scr20/feko
12 [bora] nano runfeko_bora2022
13 [bora] sbatch runfeko_bora2022
Submitted batch job 2793
14 [bora] █
```

Additional notes

- To check the status of your job, type 'squeue' in the PuTTY command window.
- To cancel your job, type 'scancel'
- When your job is finished, you can go into your scr20 folder in the SSH Secure File Transfer (or WinSCP) program and check the LOG file. If there was an error in running your job, it will also appear there. The output files will appear in the scr20 folder as well. You'll likely care about the PostFEKO file (.fek file).