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

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### Step 1: Create a W&M HPC Account

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



	Departments & Offices / / Research Computing / Request an Account
RESEARCH COMPUTING	
Research Computing at W&M	Request an Account
Using HPC	You must have a W&M Username to request or renew an HPC account. External collaborators must first be sponsored for
Get Help with HPC	and obtain an affiliate W&M Username.
Request an Account	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
External Collaborators	Chesapeake), which are both available at no cost to any member of the William & Mary community with a legitimate need
Publications & Projects	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

#### 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

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microstrip_AlNsubstrate_one_exp_taper_final.cfm	1,150 KB	CFM File	6/13/2024 10:58:49 AM							
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runfeko_tmp_configfile_10460	1 KB	File	6/4/2024 1:48:54 PM							
nussell.bof	5 KB	Altair Feko Binary	6/4/2024 1:49:12 PM							
Russell.cfm	1,240 KB	CFM File	6/4/2024 1:48:53 PM							
Russell.cfx	3,284 KB	CADFEKO Model F	6/4/2024 1:48:53 PM							
Russell.cfx.bak	3,283 KB	BAK File	6/3/2024 11:47:13 AM							
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Russell.out	20 KB	OUT File	6/4/2024 1:49:12 PM							
<€ Russell.pre	3 KB	EDITFEKO File	6/4/2024 1:48:53 PM							

### 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



### 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/researcho Hardware info: https://www.wm.edu/offices/it/services/researcho des Assistance & Trouble Reports: hpc-help@lists.wm.edu https://hpc.	omput: omput: wm.ed	ing/us ing/hw u/supp	ing /no ort
NOTICE: This is a front-end/login/service node and is intended for development and cluster services only. All parallel programs, and computations requiring more than 30 seconds of CPU time or 128 MB must be submitted through the Slurm batch system.	code all s of men	serial mory,	
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:



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)



### 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

🧬 bora.sciclone.wm.edu - PuTTY	—	×
2 login as: rmkamback 7 rmkamback@bora.sciclone.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/no des 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.		
<pre>11 [bora] cd scr20/feko 12 [bora] nano runfeko_bora2022 13 [bora] sbatch runfeko_bora2022 Submitted batch job 2793 14 [bora]</pre>		

### 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).