A Brief Introduction to Amarel

See https://sites.google.com/view/cluster-user-guide for details

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Cluster Access

Connecting via SSH Command Line Tool

- On Mac OS:
 - ssh <netid>@amarel.rutgers.edu
- On Linux/Unix
 - ssh <netid>@amarel.rutgers.edu
- Windows
 - Download an SSH Client (PuTTY)
 - Set Host Name: <u>amarel.rutergs.edu</u>
 - Log In: <netid>

Setting up an SSH Key

- Currently works with Mac OS
- ssh-keygen -t rsa
 - Asks for a passphrase (leave empty) and location where to save the new key (select default)
 - ssh-copy-id -i ~/.ssh/id_rsa.pub <netid>@amarel.rutgers.edu
- Setup an alias
 - vi ~/.bashrc
 - alias="ssh <netid>@amarel.rutgers.edu"

• https://superuser.com/questions/8077/how-do-i-set-up-ssh-so-i-dont-have-to-type-my-password

Navigating Amarel

- /home/<netid>
 - 100 GB storage allocated
- /scratch/<netid>
 - 20 TB temporary storage
 - 90 day purge policy

Login Node

- Starting shell after sign on to Amarel
- Not meant for running commands
- provide a shared environment where users can transfer data, build software, and prepare their calculations.

Interactive Shells

- Gives you an active connection to a compute node (or collection of compute nodes) where you will have a login shell and you can run commands directly on the command line.
- Example:
 - srun --partition=main --mem=2000 —time=30:00 --pty bash

SLURM Job Scheduler

• SLURM job script for a serial job

```
#!/bin/bash
#SBATCH --partition=main
                              # Partition (job queue)
#SBATCH --requeue
                             # Return job to the queue if preempted
#SBATCH --job-name=test
                             # Assign a short name to your job
#SBATCH --nodes=1
                             # Number of nodes you require
                             # Total # of tasks across all nodes
#SBATCH --ntasks=1
                               # Cores per task (>1 if multithread tasks)
#SBATCH --cpus-per-task=1
#SBATCH --mem=2000
                               # Real memory (RAM) required (MB)
                               # Total run time limit (HH:MM:SS)
#SBATCH --time=02:00:00
#SBATCH --output=slurm.%N.%j.out # STDOUT output file
#SBATCH --error=slurm.%N.%j.err # STDERR output file (optional)
cd scratch/$USER
conda activate < conda environment>
python <script>.py <CLI inputs>
```

Transferring Files To/From Amarel

- On your local machine open a terminal window
- Run sftp <netdi>@amarel.rutgers.edu:/home/<netid>
- This will open a connection between your machine and amarel
- Use get/put to retrieve/upload files from/to amarel
- Use lpwd to view the local working directory
- Use lcd to navigate folders locally
- Use pwd to view the remote (amarel) working directory

Transfer from amarel directly to google drive/box

- Setup:
 - ssh -Y <netid>@amarel.rutgers.edu
 - Connects to Amarel with X11 tunneling
 - module use /projects/community/modulefiles
 - module load rclone
 - rclone config
 - Enter 'n' for new and name your connection 'amarel-box'
 - For box storage: Storage> 7
 - Leave client_id> through access_token> blank
 - box_sub_type>1
 - Choose No for edit advanced config
 - Choose Yes for auto config
 - Wait for a Firefox window to open (it can take a while to load)
 - Enter box login credentials
 - Use single sign on
- Navigation:
 - rclone lsd amarel-box: lists all top level directories in your box drive
 - rclone copy <amarel directory> amarel-box:<box-directory>

Install Miniconda on Amarel

- Download the proper command line installer
 - https://docs.conda.io/projects/miniconda/en/latest/
 - Miniconda3 Linux 64-bit
- Save this file to your /home/<netid>/Downloads path
- Run: bash Miniconda3-latest-Linux-x86_64.sh in the CLI
- Follow prompts

Running a Jupyter Lab Session

- First install Jupyter lab in your conda environment
 - conda activate <your-env>
 - pip install jupyterlab
 - jupyter server password
 - Enter password you will remember
- On amarel run the command
 - srun jupyter lab --no-browser —ip=o.o.o.o —port=9999
 - Next run squeue -u <netid> to find the node your session is running on
 - This can start with hal or slepner
- Open a local terminal window
 - Run ssh -L 8888:<node>: 9999 <netid>@amarel.rutgers.edu
- Navigate to your internet browser and enter the url
 - Localhost:9999
 - You may need to enter the password from earlier
 - You should see a jupyter lab session now

Other material

- SLURM commands:
- https://slurm.schedmd.com/pdfs/summary.pdf