HPC Starter's Microguide

July 2025

Welcome to the Amarel cluster! This guide provides a quick start for new users, focusing on terminal and command-line usage. For a more comprehensive guide, please see the Amarel Cluster User Guide.

1. Logging In

You can log in to the Amarel cluster using your Rutgers NetID and password. Your username is your NetID.

```
ssh <NetID>@amarel.rutgers.edu
```

For more details on getting started, please refer to the Welcome Guide.

2. Navigating Module Usage

Environment modules are used to manage software packages on the cluster. You can load and unload different software versions as needed for your work.

Searching for Modules

To find available software, you can use the `module spider` or `module avail` commands:

```
# Search for a specific package
module spider <package_name>

# List all available modules
module avail
```

Loading a Module

To load a specific module into your environment, use the `module load` command. For example, to load a version of Apptainer:

```
module load apptainer/1.3.6
```

Some software is contributed by the community and requires an extra step to see the modules:

```
module use /projects/community/modulefiles
module avail
```

For more detailed information on available applications, see the Applications Guide and the Community Contributed Software Guide.

3. Submitting a Simple Job

Jobs on the cluster are submitted using the SLURM scheduler. You submit jobs by creating a submission script and using the `sbatch` command.

Here is a simple example of a SLURM script that runs a basic command:

```
#!/bin/bash
#SBATCH --job-name=simple_job      # Job name
#SBATCH --nodes=1                  # Number of nodes
#SBATCH --ntasks=1                 # Total number of tasks
#SBATCH --cpus-per-task=1          # Cores per task
#SBATCH --mem=1G                   # Memory per node
#SBATCH --time=00:10:00            # Walltime
#SBATCH --output=simple_job_%j.out   # Standard output and error log

# Your commands go here
echo "Hello, HPC World!"
hostname
date
```

Key `#SBATCH` Directives:

- `--job-name`: A name for your job.
- `--nodes`: The number of compute nodes to request.
- `--ntasks`: The total number of tasks your job will run.
- `--cpus-per-task`: The number of CPU cores per task.
- `--mem`: The amount of memory your job needs.
- `--time`: The maximum time your job is allowed to run.
- `--output`: The file where standard output and errors will be written.

To submit this job, save it as a file (e.g., `submit.sh`) and run: `sbatch submit.sh`

You can find more complex examples in the Applications Guide.

4. Basic HPC Do's and Don'ts

To ensure the cluster runs smoothly for everyone, please follow these best practices:

- **Storage:**
  - Use your `/home/<NetID>` directory (100 GB, backed up) for important files, source code, and small datasets.
  - Use your `/scratch/<NetID>` directory (1 TB, not backed up) for temporary files and large data needed for actively running jobs. Files in `/scratch` older than 90 days are automatically deleted.
- **Login Nodes:** Login nodes should be used for file transfers, installing software, editing/compiling code, and submitting jobs. Do **not** run computationally intensive or long-running processes on them.

  - **File Transfers:** Always use login nodes for transferring files (e.g., with `rclone`, `scp`). They have higher bandwidth for better performance.
  - **Compute Jobs:** All intensive work must be submitted to the compute nodes via SLURM jobs.
- **Acceptable Use:** Be sure to read and understand the Acceptable Use Policies. Misuse of resources can lead to account suspension.

For more details, refer to the Welcome Guide, Owner Guide, and the main Cluster User Guide.