HiPerGator

The University of Florida supercomputer is a cluster that includes the latest generation of processors and offers nodes for memory-intensive computation. Official website

There's a lot of resources to learn about using hipergator provided by UF research. You can find these here.

Important instructions

1. Make sure you're on the UF network to be able to access all resources of hipergator. If not on campus use VPN.

Ways to access

While there are multiple ways to access hipergator, just to get started here are some basic ways to access it:

1. Open OnDemand: Using a web interface to access many resources provided by hipergator. You can use tools like VS code, Spyder or a linux UI through this.
2. **Ssh** through terminal/ command prompt/ powershell: Use `ssh <gatorlink>@hpg.rc.ufl.edu`
    a. After logging in using 2-factor authentication, change directory to your account which would be:

```
cd /blue/eel5840/<gatorlink>
```

    b. You can use all the linux terminal commands here and create a directory for your project.
3. Jupyter lab: A jupyter lab server where you can create a custom spec machine.

Running a python script

To run a script, you need to copy all the required data files on the hipergator and your python script. A best practice to make sure you have all the required libraries is to create a conda virtual environment. Here are the steps to do that:

1. Use this to create a virtual environment: `conda create --name myenv`
   Replace myenv with the environment name. This environment will be empty, meaning that you need to install the required packages.
2. First activate this environment by using `conda activate myenv` you'll see myenv in your terminal. For example check below, this is how an activate environment testenv looks like

```
(test_env) [riteshchowdhry@c0900a-s11 ~]$ conda install anaconda
Collecting package metadata (current_repodata.json): done
Solving environment: done
```

3. You can install all required libraries here using conda install commands. The major ones being Pytorch, numpy, scikit-learn, pandas, matplotlib. Just google “conda install <library name>, and there should be a command in anaconda docs.
4. If you want to use this virtual environment as a jupyter notebook kernel use this command:
   `python -m ipykernel install --user --name=myenv` to see this environment in your jupyter notebook kernels.

Finally, in order to run any script you need to write a bash script. Here's a format for that:

```
#!/bin/bash

# Command line args for dict
sbatch <<EOT
#!/bin/bash
#SBATCH --job-name=<enter any name here>   # Job name
#SBATCH --mail-type=END               # Mail events
#SBATCH --mail-user=<your email address>  # Where to send mail
#SBATCH --account=eel5840 #the group name through which you've access to
HPG
#SBATCH --nodes=1                 # Number of MPI ran
#SBATCH --cpus-per-task=20
#SBATCH --mem=2GB
#SBATCH --time=24:00:00       #Time limit hrs:min:sec
#SBATCH --output=/home/<gatorlink>/logs/<file_name>%j.out   # Standard
output and error log
#SBATCH --error=/home/<gatorlink>/logs/<file_name>%j.err
#SBATCH --partition=gpu
#SBATCH --gpus=1

ulimit -c 0

cd /blue/eel5840/  #change directory to where your python script is
located.
python <scriptname>.py
EOT
```

This doc is just a brief overview, for more details and tutorials please refer to the [HPG help page.]