Workflow for using HiPerGator

- Create application using a text editor on your local machine
- Transfer code to hpg.rc.ufl.edu
  - Use your favorite SFTP program: e.g., MobaXterm, WinSCP (use port 22)
- Log onto hpg.rc.ufl.edu
  - Use your favorite ssh client: (e.g., MobaXterm, putty) to connect to hpg.rc.ufl.edu
  - Log in using gatorlink credentials
- Load necessary modules (best to put these lines in /home/yourusername/.bashrc)
  - module load intel openmpi
- Compile code, fix any errors on login node
  - mpicc -o ***hello_world hello_world.c*** will compile and generate the executable name hello_world file (or any name you want)
- Run code as a batch job using a script (see below for sample job script):

sbatch job-hw.sh to execute the Slurm script in batch mode (i.e., put into queue)

squeue -u hlam to view job info of all jobs submitted by hlam
squeue -j <jobID> to view job info for job number <jobID>.

scancel <jobID> to cancel job number <jobID>.
Ex: **scancel 40103005**

For additional useful SLURM commands - https://help.rc.ufl.edu/doc/SLURM_Commands

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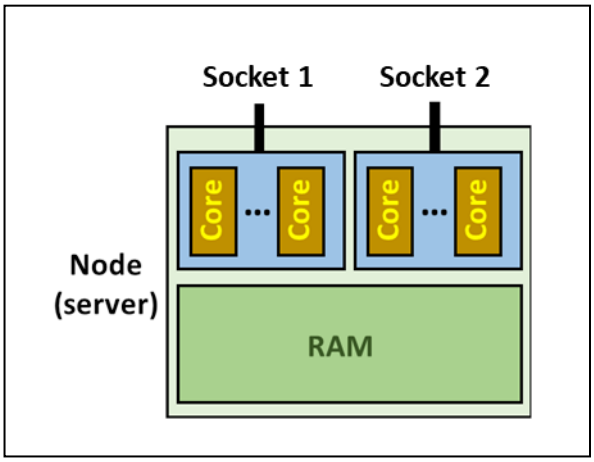
Sample job script

```
#!/bin/bash
#SBATCH --job-name=helloWorld_MPI
#SBATCH --mail-type=FAIL
#SBATCH --mail-user=youremailaddress
#SBATCH --account=eel6763
#SBATCH --qos=eel6763
#SBATCH --nodes=1
#SBATCH --ntasks=4
#SBATCH --ntasks-per-node=4
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1000mb
#SBATCH -t 00:05:00
#SBATCH -o myoutput
#SBATCH -e myerr
srun --mpi=pmix_v3 ./hello_world
```

ntasks = "number of MPI ranks" (<=32)
ntasks, nodes, and ntasks-per-node should be consistent
cpus-per-task = "number of cores per rank"



Each **hpg2**-compute **node** has 2 **sockets**, with 16 cores each **(32 cores total)**
Each **hpg3**-compute **node** has 2 **sockets**, with 64 cores each **(128 cores total)**