TACC Basics

Information about TACC for bioinformatics is sparse on the web; the BioITeam Wiki (search for it) has some info. TACC has user guides, and a *very* useful consulting system for users. You can also email me or anyone else at the Bioinformatics Consulting Group.

TACC Website

`portal.tacc.utexas.edu`

- User Guides
- Consulting Ticket System. I've been impressed with their speed in answering questions (even very basic ones!), and their willingness to help me with odd problems.

Disk Sizes

- $HOME (`cdh` shortcut)
    - 5GB on Stampede, 1GB on Lonestar
    - Backed-up
- $WORK (`cdw` shortcut)
    - 400GB on Stampede, 250GB on Lonestar
    - Not backed-up
- $SCRATCH (`cds` shortcut)
    - 8.5PB (8,500,000GB) on Stampede, 1.4PB on Lonestar
    - Not backed-up, all files older than 10 days are deleted

Modules

- Search for a module: `module spider <search_term>`
- List current modules: `module list`
- Load a module: `module load <module_name>`
- Swap modules: `module swap <old_module> <new_module>`

Queues

- `normal` : best for most job submissions.
    - Stampede: 48 hour limit, 16 cores per node
    - Lonestar: 24 hour limit, 12 cores per node
- `largemem` : when you need *lots* of memory, these have 1TB.
    - Stampede: 48 hour limit, 32 cores per node

- Lonestar: 24 hour limit, 24 cores per node
- `development` : good for quick, small tests.
  - Stampede: 2 hour limit, 16 cores per node
  - Lonestar: 1 hour limit, 12 cores per node

Launcher Scripts

I recommend using `launcher_creator.py`. Information is available here: https://wikis.utexas.edu/display/bioiteam/launcher_creator.py (or you can search for "BioITeam wiki" and look under "Software")

To use `launcher_creator.py`, you should probably add a line to your `.profile` file (see last section).

Lonestar uses SGE as its job scheduling system, Stampede uses SLURM.

- Submit a job:
  - Stampede: `sbatch job.slurm`
  - Lonestar: `qsub job.sge`
- Check status:
  - Stampede: `qstat`
  - Lonestar: `qstat`
- Delete a job:
  - Stampede: `scancel job_id`
  - Lonestar: `qdel job_id`
  - (get `job_id` from `qstat`)

Pre-rolled BioITeam Scripts

- BWA-MEM: `map_BWAmem`
- BLAST+: `split_blast`
- Trinity: `assemble_trinity`

Add BioITeam To Your $PATH

One way to do it (but keep it on one line):

```
echo 'source /corral-repl/utexas/BioITeam/bin/profile_ngs_course.bash' >>
~/.profile_user
```

More Nodes Doesn't Make It Faster