

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, 5GB on Lonestar5
 - Backed-up
- \$WORK (`cdw` shortcut)
 - 1 TB across all TACC systems
 - Not backed-up
- \$SCRATCH (`cds` shortcut)
 - 8.5PB (8,500,000GB) on Stampede, 5.5PB on Lonestar5
 - Not backed-up, files older than 10 days deleted with no warning

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
 - Lonestar5: 48 hour limit, 24 cores per node
- `largemem` : when you need *lots* of memory, these have 1TB.
 - Stampede: 48 hour limit, 32 cores per node

- Lonestar5: ? (Not clear from user guide)
- `development`: good for quick, small tests.
 - Stampede: 2 hour limit, 16 cores per node
 - Lonestar5: 2 hour limit, 24 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).

Stampede and Lonestar5 both use SLURM as their job scheduling systems.

- Submit a job: `sbatch job.slurm`
- Check status: `squeue -u <username>` or `qstat`
- Delete a job:
 - Specific job: `scancel job_id` (get `job_id` from `qstat`)
 - All your jobs: `scancel -u <username>`

Pre-rolled BioITeam Scripts

Not working on Stampede yet, but soon!

- 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