Triton Cheatsheet v2.3 / 2025-05-30

Full documentation: scicomp.aalto.fi/triton/ Quick reference: scicomp.aalto.fi/triton/ref/

About Triton

- Over 10000 CPUs, 200 GPUs available, up to 256GB or 2TB memory/node.
- Available for all Aalto staff for any research.
- Good integration with department workstations: most filesystems are cross-mounted and you can easily open and process files as if they were local.
- Rather than expect your workstation to do everything, develop to Triton and you can scale up to whatever resources you need.
- Example Triton workflows: Test code on frontend node. Submit interactive test jobs with "`srun -p debug ./your-command`" for *fast* testing. For production runs, do the same but to bigger partitions using more CPUs, or use batch submissions. Examine output on your own workstation via `/m/DEPT/scratch/`.

Getting help *docs: Getting Triton help, see also scicomp.aalto.fi/help/*

- All information on scicomp.aalto.fi/triton/. Includes quickstart tutorials.
- SciComp garage (help session): daily at 13:00: scicomp.aalto.fi/help/garage/
- Issue tracker: scicomp.aalto.fi/triton/issues (please no personal mail)
- Chat: scicomp.zulip.cs.aalto.fi - good for quick questions
- CS, NBE, and PHYS IT overlap with Triton support and can provide advice as well.
- Many courses in practical computing topics: scicomp.aalto.fi/training/
- Aalto RSE service gives advanced support: scicomp.aalto.fi/rse/

Connecting *docs: Tutorials/Connecting, see scicomp.aalto.fi/triton/tut/connecting/*

- Accounts are same as Aalto accounts, but need activation: request from link above.
- Login: ssh to `triton.aalto.fi` with Aalto user/pass or ssh keys. Use Aalto VPN.
- ondemand.triton.aalto.fi provides a web interface (including Jupyter).

Data Storage *docs: Tutorials/Data storage*

- /scratch is a Lustre filesystem: 5PB, networked and highly parallel. Also available on (CS,NBE) workstations. All calculation data goes here.
- Using local disks can be more efficient for high I/O processes.
- Other department filesystems (CS,NBE) are on login node and group servers.

B=backed up, S=shared

	B	S	
$HOME	+	+	Home dir, 10GB. Codes and configuration, not calculation files.
/m/DEPT/scratch/PROJ/		+	Shared Lustre FS. Large and fast. Per-project. **NO BACKUPS.**
/m/DEPT/work/USER/		+	Same as above, per-user. **NO BACKUPS**
/tmp/			Local disk storage. Not backed up.
version.aalto.fi			Aalto git repository.
$XDG_RUNTIME_DIR			Ramfs (in-memory filesystem): very temporary but fast space

Software availability *docs: Tutorials/Applications*

- Most software and libraries are in the "module" system. This allows you to select what you need, including exact versions. It just changes environment variables like `$PATH`, `$LD_LIBRARY_PATH`, etc. Use "`env`" to print these.
- Admins can install common software for you: just ask.
- The "`module`" function makes software available. Example: `module load matlab` or `module load matlab/r2023b` (better, as you know which version you get).
- Since 2025 May, we have "software stacks": for example `triton/2025.1-gcc` may need to be loaded before some other modules.
- Modules also contain dependencies: if you load E, it will automatically load A, B, C, D if needed. So just request what you need.
- "`which`" shows exactly what a command name will run.

`module spider PATTERN`	Search (full) for modules matching pattern.
`module spider PATTERN/VER`	Show how to load this module, **including possible software stack modules you need to load first.**
`Module show NAME`	Show module details, exactly what it does.
`module load NAME`	Load a module. Specify version with `NAME/VERSION`.
`module unload NAME`	Unload a module.
`module list`	List currently loaded modules.
`module purge`	Remove all loaded modules from the current session.
`module save ALIAS`	Save/restore currently loaded modules to a collection named `ALAIS`. Loading a collection is much faster.
`module restore ALIAS`	
`module savelist`	List saved collections.

Common software

- Python: we recommend the Anaconda modules for general-purpose Python. "`module load scicomp-python-env`" for Python 3. For custom packages, see "conda" below.
- R: `module load scicomp-r-env`
- Matlab: `module load matlab`
- Mathematica: `module load mathematica`
- And so on… see user guide and/or discuss your needs with us.

Conda *docs: Apps / Python environments with Conda*

```
name: example-env
channels:
    - conda-forge
dependencies:
    - numpy
```

- Conda is the recommended way to install Python software.
- Module `mamba` provides `mamba` and `conda` commands.
- `mamba` is a much faster drop-in replacement for `conda` .
- We recommend *not* running `conda init`, and instead use `source activate` instead of `conda activate`.
- `environment.yml` makes environments reproducible, example at right.
- Make own environment: `conda env create --file environment.yml`
- In batch scripts: `module load mamba` and `source activate NAME`
- More information can be found at scicomp.aalto.fi/triton/apps/python-conda/

Interactive jobs *docs: Tutorials/Interactive jobs*

- Easiest way to use triton: "**Just add srun!**" to your working command, and specify how much power you need. (details described on next page)
- Example: `srun --mem=50G --time=5:00 --cpus-per-task 6 ./your_command`
  - (50GB Memory, 5 hours max runtime, 6 CPUs)
- `sinteractive` gets you a shell which is also usable for graphical applications.
- `slurm history` shows detailed CPU/memory usage of the process.

Batch jobs *docs: Tutorials/Serial jobs*

```
#!/bin/bash -l
#SBATCH --mem=50G
#SBATCH --cpus-per-task 4
#SBATCH --gres=gpu

module purge
module load NAME

srun ./step_1 1 5
srun ./step_2 1 5
```

- Once you run interactively, you can make batch jobs which run in the background - submit and return for results later.
- Example script at right. Options can be inside the script. Output goes to files in the same directory.
- Submit job with `sbatch script-name.sh`
- Monitor with `slurm queue`.
- `slurm history` shows resource usage, including details on CPU/time/memory for *each srun step*.
- Slurm will run the batch script only once.
- Slurm will allocate as many CPUs as you request (`-c N`). It is up to you to make sure your job can use them.

Parallel jobs *docs: Tutorials/Parallel computing*

```
#!/bin/sh
#SBATCH --time=5:00
#SBATCH -n 4
#SBATCH --array=1-10

srun ./my-command  \
    input_$SLURM_ARRAY_TASK_ID  \
    -o OUTPUT_$SLURM_ARRAY_TASK_ID
```

- Easy: Array jobs. Use `--array=M-N` with sbatch and you can easily scan parameters using `$SLURM_ARRAY_TASK_ID`. The command is run once with each parameter. Good for parameter sweeps.
  - Example at right: Run with `sbatch script.sh`
- MPI, OpenMP, etc instructions in docs.
- OpenMP: Usually with `-c`. Use `export OMP_NUM_THREADS=$SLURM_CPUS_PER_TASK`
- MPI: See docs. Usually with `-n`.
- Python/R/other languages: Usually with `-c`, but depends on the code. Must be checked individually.
- Use `seff JOBID` to verify efficiency.

GPUs *docs: Tutorials/GPU computing*

- request with `--gres=gpu` . Can select type with `--constraint=NAME` . Recent names include `ampere`, `volta` , `pascal`, and `kepler`.
- Check efficiency with `sacct -j JOBID -o TRESUsageInAve -p` after job completion.
- GPUs can be hard to use efficiently (especially data loading)! Usage statistics only show the active time but do not the real occupancy levels. Ask for help early.

Slurm details *docs: User guide/Reference, Running programs on Triton*

- *Slurm* is the system which allocates CPU, GPUs, etc. to people doing computation.
- The core is a queuing system which fairly prioritizes users. The less you run, the higher your priority.
- Work is submitted as jobs. CPUs, memory, and time must be declared for jobs. Jobs killed if these limits are exceeded too much.
- In general, just declare what you need and Slurm will do the right thing.

The following commands give history about jobs:

`slurm queue  (slurm qq)`	Your currently queued jobs, or `slurm watch queue` for updating view
`slurm history 1day|2hour|...`	Your recently completed jobs, with detailed time/memory info.
`slurm job JOBID`	Info on a certain job.
`seff JOBID`	Check effectiveness of requested resources.
`squeue / sacct / scontrol`	Advanced info on waiting jobs / finished jobs / running jobs.

Slurm commands **Further reference:** scicomp.aalto.fi/triton/ref/#job-submission

The following commands submit jobs. All require some of the slurm options.

`srun`	Run a single command on nodes, I/O connected to terminal.
`srun (in batch script)`	Run a job step so that time/memory can be separately tracked
`srun --pty [bash]`	Run a command (or shell) with full terminal support.
`sinteractive`	Start a shell on a node, usable for graphical applications.
`sbatch`	Run a batch script. Submits and returns immediately.
`scancel JOBID`	Cancel a running job

Slurm options for `srun`, `sbatch`, or `#SBATCH` in batch scripts:

`--time XXX`	Total job run time (`HH:MM[:SS]` or `DD-HH`)
`-c N`	Number of cores (per task)
`--mem nnG`	Total memory per node, only for single node jobs.
`--mem-per-cpu nnG`	Total memory per CPU
`-p PARTITION`	Partition to use (usually leave off) `slurm p`
`-N N`	Number of nodes
`-n n`	Number of tasks to start (number of individual srun processes to start)
`-J JOBNAME`	Specify memorable job name
`-o FILE, -e FILE`	Job stdout/stderr is saved to this file name. Default to same dir+jobid.
`--array=N-M`	Array job, easy parallelization (*only* with `sbatch`). `$SLURM_ARRAY_TASK_ID`
`--constraint XXX`	Request hardware type (`hsw`, `bdw`, `skl`, `csl`, `milan`, `avx`, `avx2`, `avx512`,)
`--gpus=n` (request n GPUs, for gpu partition), `--constraint=` (GPU generations: `kepler`, `pascal`, `volta`, `ampere`). AMD GPUs: `-p gpu-amd` and no `--gres` . `--exclusive` (whole-node)	