

Triton Cheatsheet^{v2.0}

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/

Accounts *docs: Triton accounts, see scicomp.aalto.fi/triton/accounts/*

- Accounts are same as Aalto accounts, but need activation: request from link above.
- Login: ssh to `triton.aalto.fi` with Aalto username/password or ssh keys.
- ood.triton.aalto.fi and jupyter.triton.aalto.fi provide alternative interfaces.

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=backded up, S=shared

	B	S	
\$HOME	+	+	Home dir, 10GB. Codes and configuration, not calculation files.
<code>/m/\$dept/scratch/\$project/</code>		+	Shared Lustre FS. Large and fast. Per-project. NO BACKUPS.
<code>/m/\$dept/work/\$username/</code>		+	Same as above, per-user. NO BACKUPS
<code>/tmp/</code>			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`” prints these.
- Admins can install common software for you: just ask.
- The “module” function makes software available. Example: `module load matlab` or `module load matlab/r2019a` (better, as you know which version you get).
- 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.

<code>module avail PATTERN</code>	Search for modules matching pattern.
<code>module spider PATTERN</code>	Search (full) for modules matching pattern.
<code>Module show NAME</code>	Show module details, exactly what it does.
<code>module load NAME</code>	Load a module. Specify version with <code>\$name/\$version</code> .
<code>module unload NAME</code>	Unload a module.
<code>module list</code>	List currently loaded modules.
<code>module purge</code>	Remove all loaded modules from the current session.
<code>module save ALIAS</code>	Save/restore currently loaded modules to a collection. Loading a collection is much faster.
<code>module restore ALIAS</code>	
<code>module savelist</code>	List saved collections.

Common software

- Python: we recommend the Anaconda modules for general-purpose Python. “`module load anaconda`” for Python 3. For custom packages, see “conda” below.
- R: `module load r`
- 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*

- Conda is the recommended way to install Python software
- Module `miniconda` provides `conda` command
- 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 miniconda` and `source activate NAME`
- More information can be found at scicomp.aalto.fi/triton/apps/python-conda/
- `mamba` is a much faster drop-in replacement for `conda`.

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

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*

- Once you run interactively, you can make batch jobs which run in the background - submit and return for results later.
- Example script at left. 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.

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

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

Parallel jobs *docs: Tutorials/Parallel computing*

- Easy: Array jobs. Use `--array=M-N` with `sbatch` and you can easily scan parameters using `$SLURM_ARRAY_TASK_ID`. The command is run once with each parameter. Good for parameter sweeps.
 - Example at left: Run with `sbatch script.sh`
- MPI, OpenMP, etc instructions in docs.
- OpenMP: Usually with `-c. export OMP_NUM_THREADS=$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 $job_id` to verify efficiency.

```
#!/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}
```

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 comment -p` after job completion.
- GPUs can be hard to use efficiently (especially data loading)! 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:

<code>slurm queue (slurm qq)</code>	Your currently queued jobs, or <code>slurm watch queue</code> for updating view
<code>slurm history 1day 2hour ...</code>	Your recently completed jobs, with detailed time/memory info.
<code>slurm job \$jobid</code>	Info on a certain job.
<code>seff \$jobid</code>	Check effectiveness of requested resources.
<code>squeue / sacct / scontrol</code>	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.

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

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

<code>--time XXX</code>	Total job run time (HH:MM[:SS] or DD-HH)
<code>-c N</code>	Number of cores (per task)
<code>--mem nnG</code>	Total memory per node, only for single node jobs.
<code>--mem-per-cpu nnG</code>	Total memory per CPU
<code>-p \$partition</code>	Partition to use (usually leave off) <code>slurm p</code>
<code>-N \$N</code>	Number of nodes
<code>-n \$n</code>	Number of tasks to start (number of individual <code>srun</code> processes to start)
<code>-J \$job-name</code>	Specify memorable job name
<code>-o \$file, -e \$file</code>	Job stdout/stderr is saved to this file name. Default to same dir+jobid.
<code>--array=N-M</code>	Array job, easy parallelization (<i>only</i> with <code>sbatch</code>). <code>\$SLURM_ARRAY_TASK_ID</code>
<code>--constraint XXX</code>	Request hardware type (hsw,ivb,wsm,opt,)
<code>--gres=gpu:n</code> (request n GPUs, for gpu partition), <code>--exclusive</code> (whole-node), <code>--constraint=</code> (limit hardware, e.g. <code>avx</code> , <code>hsw</code> , ..., or GPU generations: <code>kepler</code> , <code>pascal</code> , <code>volta</code>),	