NHR FAU

Friedrich-Alexander-Universität Erlangen-Nürnberg

High Performance Computing in a Nutshell

HPC Services, NHR@FAU

hpc-support@fau.de

https://doc.nhr.fau.de

HPC High Performance Computing

Survey

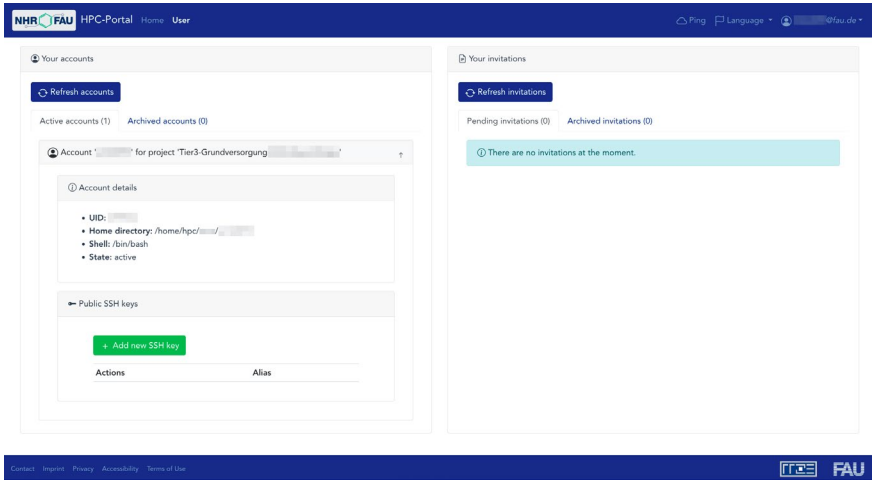
Which application area do you come from?

Getting an HPC account

https://doc.nhr.fau.de/account/

HPC account – HPC-portal

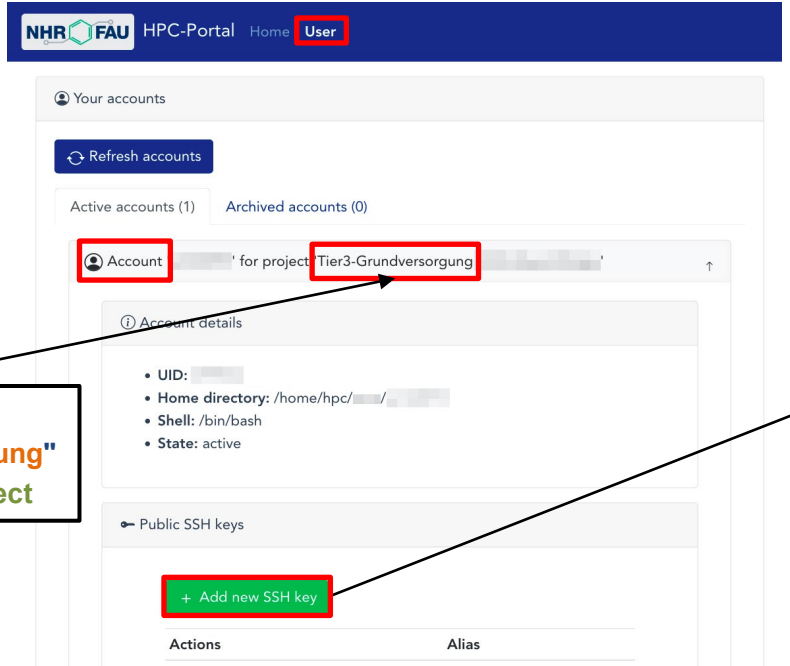
- Account via portal.hpc.fau.de
- Login to HPC portal with credentials of home institution via SSO
- Invitation has to be sent by project PI/technical contact/contact person at chair
- If you change your affiliation or project, you need a new HPC account. Data migration may be required



https://doc.nhr.fau.de/hpc-portal/

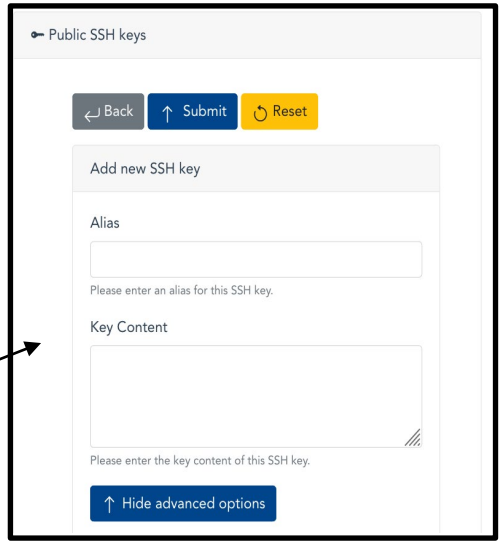
HPC account – HPC-portal

- No account passwords, cluster login only via SSH keys!
- SSH keys can be managed over HPC portal



project is either:

- **"Tier3-Grundversorgung"**
- **name of an NHR project**



How to create SSH keys:
https://doc.nhr.fau.de/access/ssh-command-line/

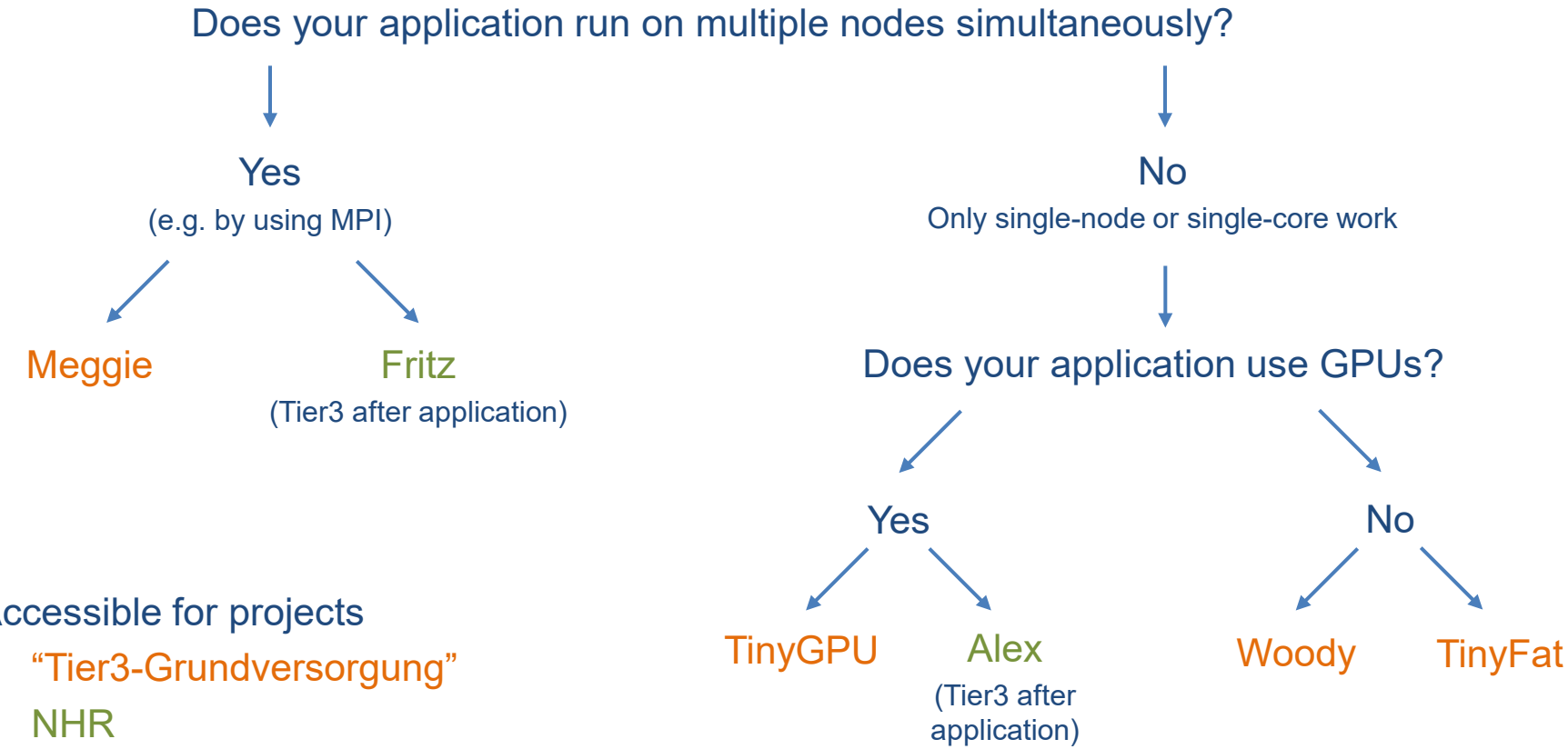
NHR FAU

FAU Friedrich-Alexander-Universität Erlangen-Nürnberg

HPC systems at NHR@FAU

https://doc.nhr.fau.de/clusters/overview/

Which cluster should I use?



Accessible for projects

- “Tier3-Grundversorgung”
- NHR

“Fritz” cluster

NHR parallel cluster, open for Tier3 users after application

- 992 compute nodes (71.424 cores)
  - 2 Intel Xeon Platinum 8360Y “Ice Lake” 2.4 GHz (36 cores)
  - 256 GB main memory per node
- 64 huge-memory nodes
  - 2 Intel Xeon Platinum 8470 “Sapphire Rapids” 2.0 GHz (52 cores)
  - 1 or 2 TB of main memory per node
- Blocking (1:4) HDR100 Infiniband network, up to 100 GBit/s
- Parallel file system with 3,5 PB capacity

“Meggie” cluster

cluster for parallel jobs, intended for highly parallel jobs (Tier3)

- 728 Compute nodes (14.560 cores)
  - 2 Intel Xeon E5-2630 v4 (Broadwell) 2.2 GHz (10 cores)
  - 20 cores/node
  - 64 GB main memory
- No local disks
- Intel OmniPath network: Up to 100 Gbit/s

- To be decommissioned “soon”

“Alex” cluster

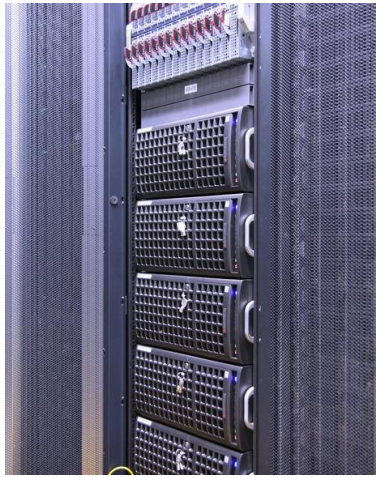
NHR GPGPU cluster, open for Tier3 users after application

- 44 nodes with
  - 8x NVIDIA A100 (each 40 GB / 80GB HBM2)
  - 2x AMD EPYC 7713 “Milan” 2.0 GHz, 1024 GB / 2048 GB of main memory
  - 14TB local NVMe SSD
  - HDR200 Infiniband network
- 38 nodes with
  - 8x NVIDIA A40 (each with 48 GB DDR6)
  - 2x AMD EPYC 7713 “Milan” 2.0 GHz, 512 GB of main memory
  - 7 TB local NVMe SSD

“TinyGPU” cluster

for GPU workloads – not all nodes always generally available (Tier3)

- 12 nodes with 2x “Skylake” @ 3.2 GHz, 96 GB RAM, 1.8 TB SSD, 4x RTX 2080Ti
- 4 nodes with 2x “Skylake” @3.2 GHz, 96 GB RAM, 2.9 TB SSD, 4x Tesla V100
- 7 nodes with 2x “Cascade Lake” @2.9 GHz, 384 GB RAM, 3.8 TB SSD, 8x RTX3080
- 8 nodes with 2x AMD Rome 7662 @2.0 GHz, 512 GB RAM, 5.8 TB SSD, 4x Volta A100



“Woody” cluster

Main workhorse for throughput and single-node jobs (Tier3)

- 176 nodes with 4 cores and high clock frequency (3.5/3.7 GHz) Intel Xeon E3-1240 v? processors
  - 64x Intel Skylake, 32 GB RAM
  - 112x Intel Kaby Lake, 32 GB RAM
- 70 nodes with 2x Intel Xeon Gold 6326 (32 cores total @2.9 GHz, 256 GB RAM)
- at least 960 GB local HDD/SSD
- Gbit network only

Survey

Which cluster(s) are you planning to use?

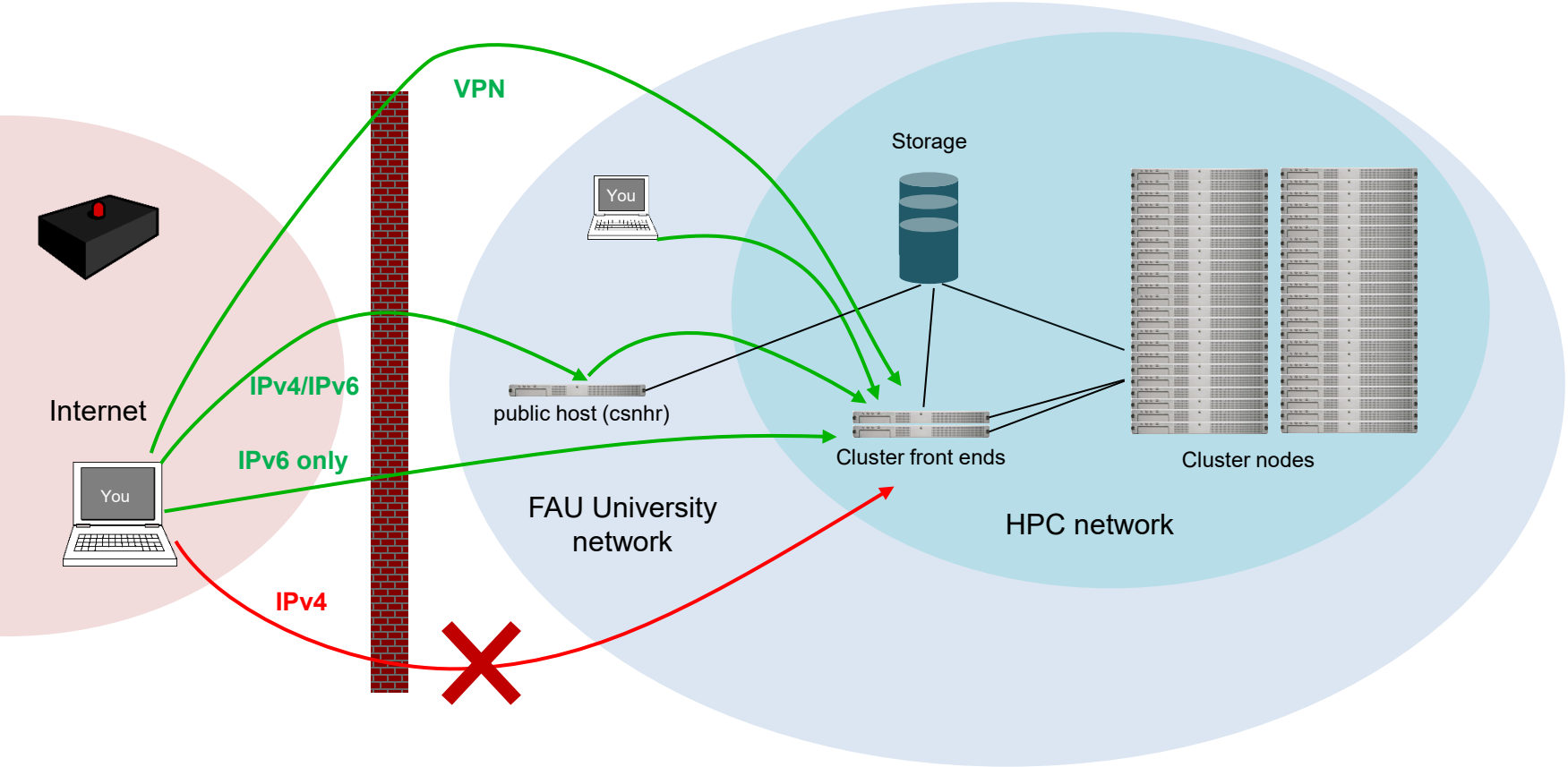
NHR FAU

Friedrich-Alexander-Universität
Erlangen-Nürnberg

Accessing HPC systems

https://doc.nhr.fau.de/access/overview/

Cluster access



Cluster access

- Cluster frontends: only directly available from within FAU network or via IPv6

  meggie.rrze.fau.de

  tinyx.nhr.fau.de (for TinyGPU/TinyFat)

  woody.nhr.fau.de

  alex.nhr.fau.de

  fritz.nhr.fau.de

- Access from outside FAU network via ProxyJump over dialog server

  csnhr.nhr.fau.de

SSH – Secure Shell

- No GUI is available on the HPC systems. Basic knowledge of file handling, scripting, editing, etc. under Linux is required.

- SSH usage:

```
ssh hpcaccount@csnhr.nhr.fau.de
```

- Authentication only with SSH keys uploaded to HPC Portal, no passwords!
- General documentation on SSH, how to generate an SSH key and example ssh-config including ProxyJump: https://doc.nhr.fau.de/access/ssh-command-line

Secure Shell client programs

- Linux: OpenSSH available
- Mac: OpenSSH available
- Windows
  - MobaXterm (https://doc.nhr.fau.de/access/ssh-mobaxterm/)
  - OpenSSH via Command/PowerShell (since Windows 10 v1803)
  - Linux Subsystem for Windows

SSH – Troubleshooting

- Troubleshooting guide: https://doc.nhr.fau.de/access/ssh-command-line/#troubleshooting
- FAQs for most frequent SSH problems: https://doc.nhr.fau.de/faq/#ssh

- In case of problems with login, send output of the following command to hpc-support@fau.de: `ssh -vv hpcaccount@csnhr.nhr.fau.de`

NHR FAU

FAU Friedrich-Alexander-Universität Erlangen-Nürnberg

Working with data

https://doc.nhr.fau.de/data/filesystems/

File systems overview

Available file systems differ in size, redundancy and how they should be used

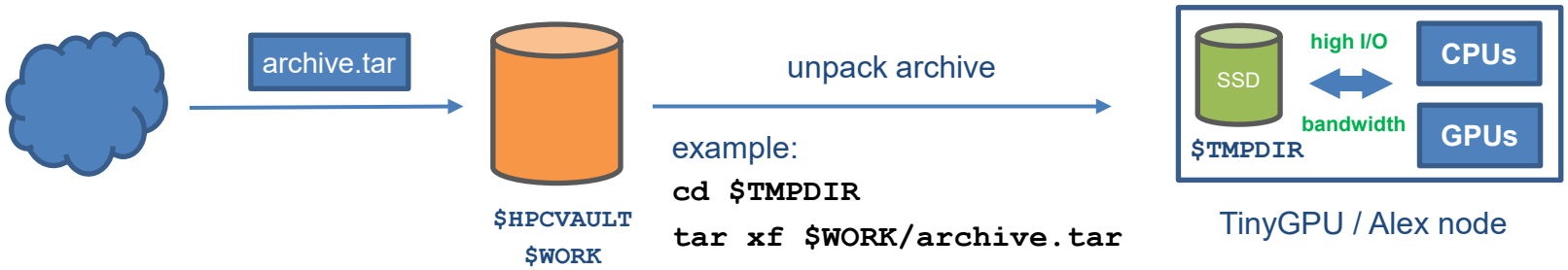
Mount point	Access	Purpose	Technology	Backup	Snap-shots	Data lifetime	Quota
/home/hpc	$HOME	Source, input, important results	NFS	YES	YES	Account lifetime	50 GB
/home/vault	$HPCVAULT	Mid-/long-term storage	NFS	YES	YES	Account lifetime	500 GB
/home/{woody, saturn, titan, janus, atuin}	$WORK	General-purpose, log files	NFS	NO	NO	Account lifetime	500 GB NHR project
/lxfs /lustre	$FASTTMP (fritz)	High performance parallel I/O	Lustre via InfiniBand	NO	NO	High watermark	Only inodes
/???	$TMPDIR	Node-local job-specific dir	SSD/ ramdisk	NO	NO	Job runtime	NO

Working with large datasets containing small files

Best case: use a container file format (HDF5, Parquet, …)

Alternative: pack small files into archive. Do not unpack archive to `$HOME/$HPCVAULT/$WORK`

Unpack files to node-local SSDs only and use them from there



More details: https://doc.nhr.fau.de/data/staging/

File system quotas

- File system may impose quotas on data volume and/or number of files
- Quotas may be set per user or per group (or both)
- Soft quota
  - Can be exceeded temporarily (7 days)
  - Turns into hard quota at end of grace period
- Hard quota:
  - absolute upper limit, cannot be exceeded

```
$ quota -s            # generic command

$ shownicerquota.pl   # only on RRZE systems
   Path               Used     SoftQ    HardQ    Gracetime  Filec    FileQ    FiHaQ    FileGrace

   /home/hpc             5.7G    52.5G    104.9G       N/A      72K     500K   1,000K         N/A
   /home/woody           112G   333.0G    499.5G       N/A     188K                           N/A
```

https://doc.nhr.fau.de/data/filesystems/#quotas

Data transfer

- **`$HOME`**, **`$HPCVAULT`**, **`$WORK`** are mounted on all HPC systems
- **`scp`** / **`rsync`** is used to transfer files from and to the outside
  https://doc.nhr.fau.de/data/copying/

```
scp [options] source destination
source/destination:  local-path | username@host:remote-path
```

```
# local file to remote
# -r  recurse into directories
scp -r code unrz55@csnhr.nhr.fau.de:/home/woody/unrz/unrz55
# remote file to local
scp unrz55@csnhr.nhr.fau.de:results/output.dat .
```

- Additionally on Windows: WinSCP, MobaXTerm
- Mount filesystems locally via **`sshfs`** or your Linux desktop
  https://doc.nhr.fau.de/data/mounting/

NHR FAU

Friedrich-Alexander-Universität
Erlangen-Nürnberg

Software

Environment modules: https://doc.nhr.fau.de/environment/modules/
Development and Tools: https://doc.nhr.fau.de/sdt/overview/
Applications: https://doc.nhr.fau.de/apps/overview/

Survey

What type of software are you using?

One thing up front…

- The clusters at the computing center are not like your own PC
  - You are not root, even if the “How-To” in the github repo you found assumes that
  - Do not blindly copy&paste commands you do not understand
  - Your home directory is not a local hard disk but a shared volume that is mounted over the network

- Things that do not work:
  - `sudo apt install python-3.9`
  - `make && sudo make install`
  - `sudo <anything>`
  - `pip install pandas`

Environment modules

- Linux standard distro packages are available on frontends and to some extend on compute nodes, but they might be outdated.

- Additional software is provided via environment modules
  - Compilers, libraries, commercial and open software
  - Installed on central server and available on all cluster nodes

- Environment modules are managed through the `module` command

- All `module` commands affect the current shell only!

The `module` command

Show all available modules: `module avail`

```
$ module avail
--------------------- /apps/modules/data/applications ----------------------------------------
amber/20p12-at21p11-impi-gnu                    gromacs/2021.5-gcc11.2.0-impi-mkl
amber/20p12-at21p11-impi-intel                  gromacs/2022.1-gcc11.2.0-ompi-mkl
amber/20p12-at21p11-openmpi-gnu-cuda11.5        gromacs/2022.1-gcc11.2.0-mkl-cuda
--------------------- /apps/modules/data/compiler --------------------------------------------
gcc/10.3.0  gcc/11.2.0  gcc/12.1.0  intel/2021.4.0  intel/2022.1.0   nvhpc/22.1  nvhpc/22.2
--------------------- /apps/modules/data/development -----------------------------------------
cuda/11.3.1             intelmpi/2021.4.0               openmpi/4.1.2-gcc11.2.0-cuda
cuda/11.4.2             intelmpi/2021.6.0               openmpi/4.1.2-intel2021.4.0-cuda
cuda/11.5.0             openmpi/4.1.2-gcc10.3.0-cuda    openmpi/4.1.2-oneapi2021.4.0-cuda
```

The `module` command

Load a module: `module load <modulename>`

```
$ module load intel/2021.4.0
$ icc -V
Intel(R) C Intel(R) 64 Compiler Classic for applications running on Intel(R) 64, Version 2021.4.0 Build 20210910_000000
Copyright (C) 1985-2021 Intel Corporation.  All rights reserved.
```

Display loaded modules: `module list`

```
$ module load openmpi/4.1.2-intel2021.4.0
$ module list
Currently Loaded Modulefiles:
1) intel/2021.4.0 <aL>   2) openmpi/4.1.2-intel2021.4.0
```

Module command summary

Command	What it does
`module avail`	List available modules
`module whatis`	Shows verbose listing of all modules
`module list`	Shows which modules are currently loaded
`module load <pkg>/<version>`	Loads specific version of module package, i.e. adjusts environment
`module unload <pkg>`	Undoes what the load command did
`module help <pkg>`	Shows a detailed description of package
`module show <pkg>`	Shows which environment variables are modified and how

https://doc.nhr.fau.de/environment/modules/

Using Python

- Use anaconda modules instead of system installation

```
$ module avail python
------------ /apps/modules/modulefiles/tools ------------
python/3.6-anaconda   python/3.7-anaconda(default) python/3.8-anaconda
```

- Install packages via conda/pip with **`--user`** option
- Change default package installation path from **`$HOME`** to **`$WORK`**
- It might be necessary to configure a proxy to access external repositories
- Build packages in an interactive job on the target cluster (especially for GPUs)

- More details:
  - https://doc.nhr.fau.de/sdt/python/
  - https://doc.nhr.fau.de/environment/python-env/

NHR FAU

FAU Friedrich-Alexander-Universität Erlangen-Nürnberg

Running jobs

https://doc.nhr.fau.de/batch-processing/batch_system_slurm/

Interactive work on the front-ends

- The cluster frontends are for interactive work
  - Editing, compiling, preparing input,…
  - Front-ends are shared among all users, so be considerate!
  - Amount of compute time per binary is limited by system limits
    - E.g., after 1 hour of CPU time your process will be killed
  - MPI jobs are not allowed on front ends
- Submit computational intensive work to the batch system to be run on the compute nodes!
- Use interactive batch jobs for debugging and testing.

Batch System

- Users can interact with the resources of the cluster via the “Batch system”
- “Batch jobs” encapsulate:
  - Resource requirements (number of nodes, number of GPUs, …)
  - Job runtime (usually max. 24 hours)
  - Setup of runtime environment
  - Commands for application run

- Batch system will handle queuing of jobs, resource distribution and allocation
- Job will run when resources become available

Example: Batch script for Fritz

```
#!/bin/bash -l
#SBATCH --nodes=4
#SBATCH --ntasks-per-node=72
#SBATCH --time=06:00:00
#SBATCH --job-name=testjob_cpu
#SBATCH --export=NONE

unset SLURM_EXPORT_ENV

module load openmpi

srun ${HOME}/bin/a.out -i inputfile -o outputfile
```

Resource requirements

Max. runtime

Other job options (name, notifications,…)

Prevent export of environment to job

Set up job environment

Actual run of your binary

Example: Batch script for Alex

```
#!/bin/bash -l
#SBATCH --gres=gpu:a40:1
#SBATCH --time=06:00:00
#SBATCH --job-name=testjob_gpu
#SBATCH --export=NONE

unset SLURM_EXPORT_ENV

module load python
conda activate test-environment

python train.py
```

Resource requirements

Max. runtime

Other job options (name, notifications,…)

Prevent export of environment to job

Set up job environment

Actual run of your binary

Example: Batch script for Alex

```
#!/bin/bash -l
#SBATCH --gres=gpu:a40:1
#SBATCH --time=06:00:00
#SBATCH --job-name=testjob_gpu
#SBATCH --export=NONE

unset SLURM_EXPORT_ENV

module load python
conda activate test-environment

cd $TMPDIR
tar xzf $WORK/large-archive-with-small-files.tar.gz

python train.py
```

Resource requirements

Max. runtime

Other job options (name, notifications,…)

Prevent export of environment to job

Set up job environment

Actual run of your binary

Slurm batch job submission

```
hpcuser@fritz1$ sbatch script.sh
Submitted batch job 675329

hpcuser@fritz1:~ $ squeue -l
JOBID   PARTITION  NAME         USER     STATE     TIME     TIME_LIMI  NODES   NODELIST(REASON)
675329  multinode  testjob_cpu  hpcuser  RUNNING   0:06     06:00:00   4       f[0116,0120,0159,0264]
```

Job stdout/stderr will be stored in files in the submit directory

- Use `--output=<outfile>` and `--error=<errfile>` options to change that

Specific for TinyFat/TinyGPU:

- All jobs are submitted from the frontend **`tinyx.nhr.fau.de`**
- Wrapper scripts have to be used for all Slurm commands (e.g. **`sbatch.tinygpu`**, **`sbatch.tinyfat`**, **`squeue.tinygpu`**, ...)

GPU Jobs on TinyGPU / Alex

- Nodes are shared, GPUs are always exclusive
- Granularity is one GPU with a corresponding portion of CPU and main memory
- Request GPUs with **`sbatch`** option e.g.
  - **`--gres=gpu:rtx3080:1`** (to request a specific type)
  - **`--gres=gpu:a100:1 --partition=a100`** (necessary for V100 and A100 GPUs on TinyGPU)

- More details and examples:
  https://doc.nhr.fau.de/clusters/alex/
  https://doc.nhr.fau.de/clusters/tinygpu/

Interactive batch job with Slurm

- TinyGPU / Alex

```
iww042@tinyx$ salloc.tinygpu --gres=gpu:1 --time=01:00:00
```

```
iww042@alex1$ salloc --gres=gpu:a40:1 --time=01:00:00
```

- Meggie / Fritz:

```
iww042@meggie1$ salloc --nodes=1 --time=01:00:00
```

- Woody / TinyFat

```
iww042@woody$ salloc --ntasks=1 --time=01:00:00
```

```
iww042@tinyx$ salloc.tinyfat --cpus-per-task=10 --time=01:00:00
```

Slurm documentation

- NHR@FAU
  - General: https://doc.nhr.fau.de/batch-processing/batch_system_slurm/
  - Cluster-specific: https://doc.nhr.fau.de/clusters/overview/
  - HPC Café on “Slurm - basics, best practices and advanced usage”: https://hpc.fau.de/files/2022/04/2022-04-12-hpc-cafe-slurm.pdf, https://www.fau.tv/clip/id/41306

- Official Slurm documentation
  - Separate documentation for every command and the available options: https://slurm.schedmd.com/man_index.html
  - Slurm commands and their counterparts in different batch systems: https://slurm.schedmd.com/rosetta.pdf
  - Slurm tutorials: https://slurm.schedmd.com/tutorials.html

NHR FAU

FAU Friedrich-Alexander-Universität Erlangen-Nürnberg

Some Dos and don’ts

Good practices

- Be considerate. Clusters are valuable shared resources that have been paid by the taxpayer.

- Use the appropriate amount of parallelism
  - Most workloads are not highly scalable
  - Best to run scaling experiments to figure out “sweet spot”

- Use the appropriate file system(s)
  - #1 mistake: Overload file servers by doing tiny-size, high-frequency I/O to FS
  - Delete obsolete data

Good practices

- Check your jobs regularly
  - Are the results OK?
  - Does the job actually use the allocated nodes in the intended way? Does it run with the expected performance?
  - Check if your job makes use of the GPUs
    - Attach to a running job (https://doc.nhr.fau.de/batch-processing/batch_system_slurm/#attach-to-a-running-job)
    - Use e.g. nvidia-smi to check GPU utilization

- Job Monitoring
  - How to use it and what to look out for: https://doc.nhr.fau.de/job-monitoring-with-clustercockpit/

Good practices

- Talk to co-workers who are more experienced cluster users; let them educate you
- Do not re-use other people's job scripts if you don't understand them completely

- Look at tips and tricks for various applications (e.g. example batch scripts): https://doc.nhr.fau.de/apps/overview/

- Have a look at HPC Café talks from past events:

  https://hpc.fau.de/systems-services/support/hpc-cafe/

Good practices

When reporting a problem to NHR@FAU:

- Mail to hpc-support@fau.de – this will immediately open a helpdesk ticket
- Provide as much detail as possible so we know where to look
  - “My jobs always crash” will not do
  - Cluster, JobID, file system, time of event, …
  - Batch script, output files, …
  - SSH problems: ssh -vv

NHR FAU

FAU Friedrich-Alexander-Universität Erlangen-Nürnberg

THANK YOU.

NHR@FAU

https://doc.nhr.fau.de

hpc-support@fau.de

HPC High Performance Computing