

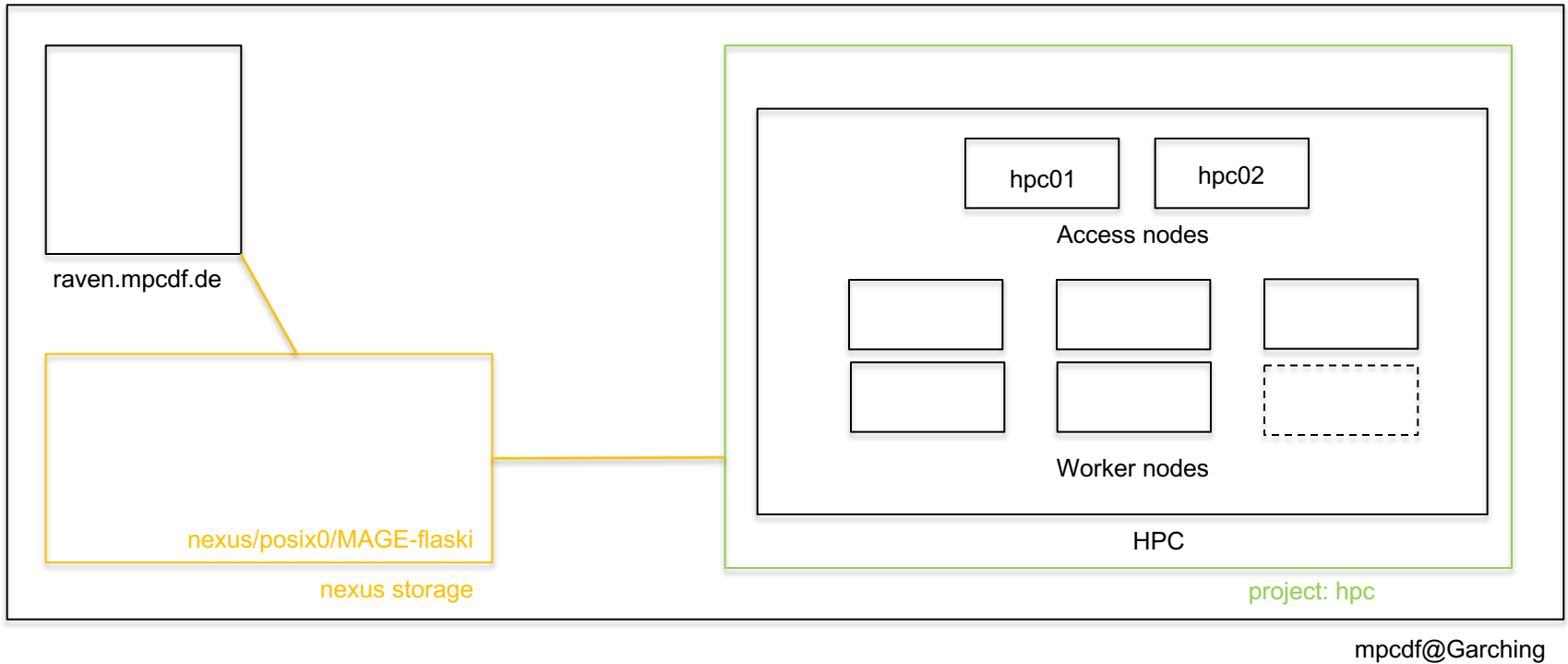


MAX PLANCK INSTITUTE FOR **BIOLOGY OF AGEING**

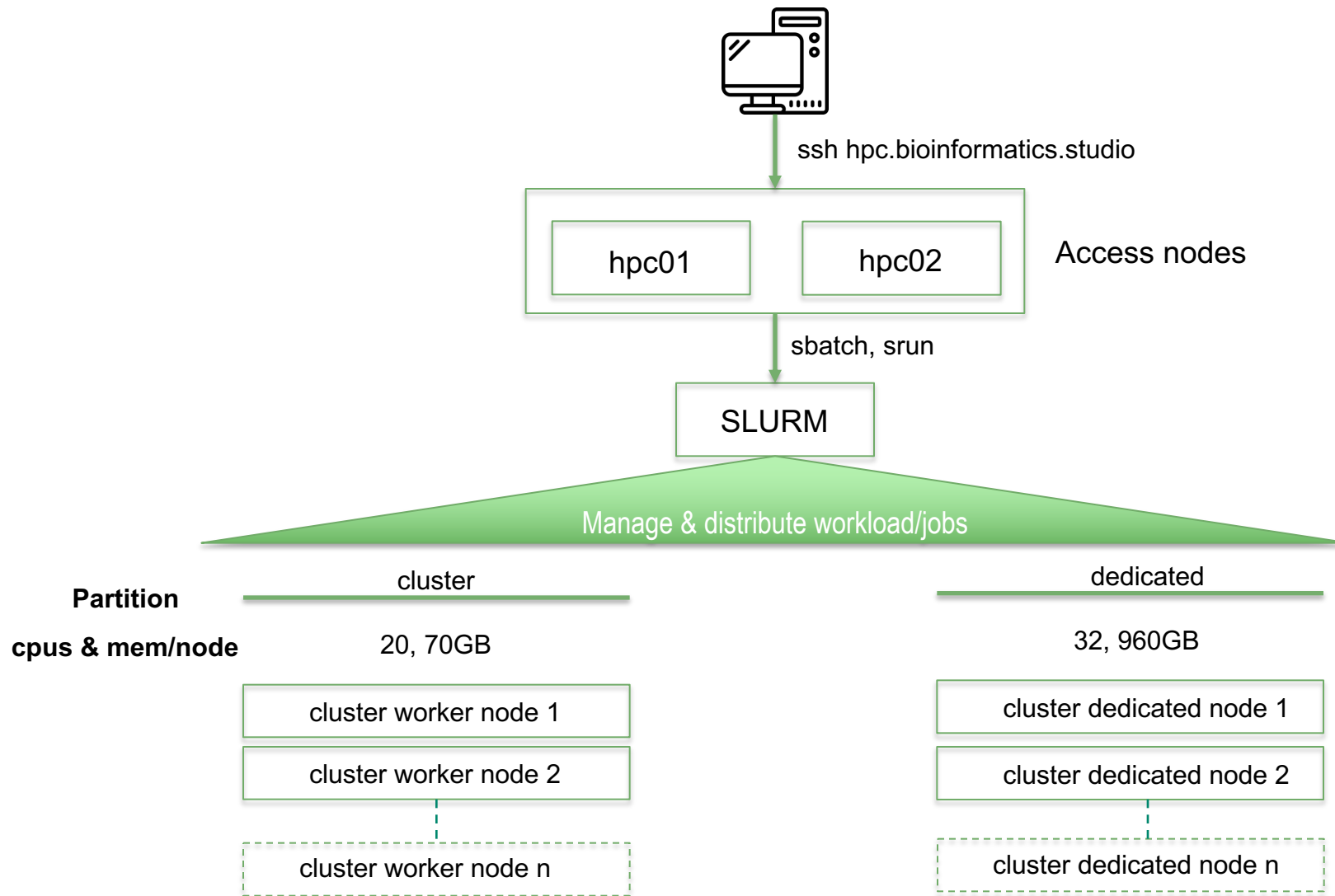


Introduction to `hpc.bioinformatics.studio`

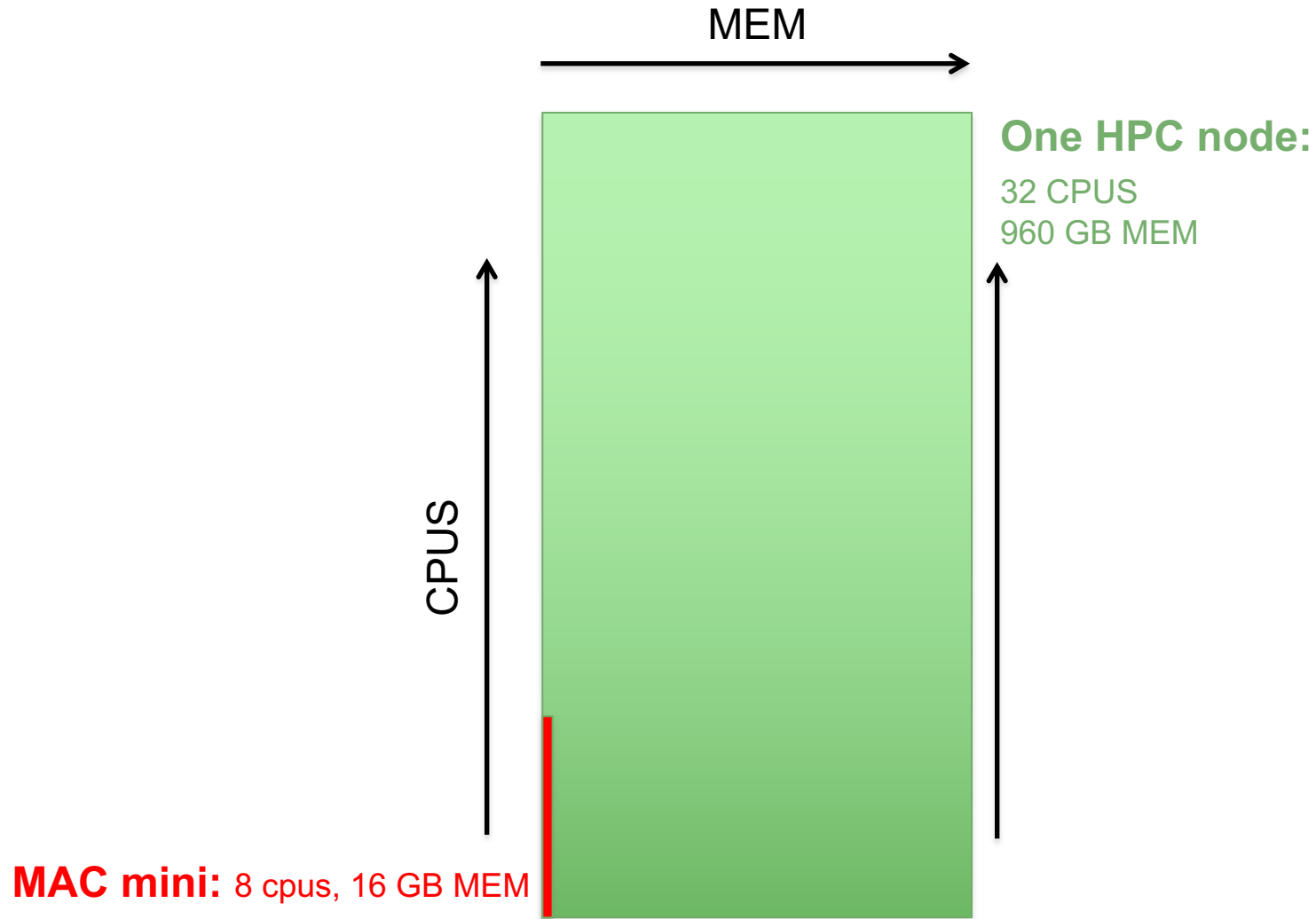
Cloud Infrastructure



Workflow Architecture



Why a HPC cluster?



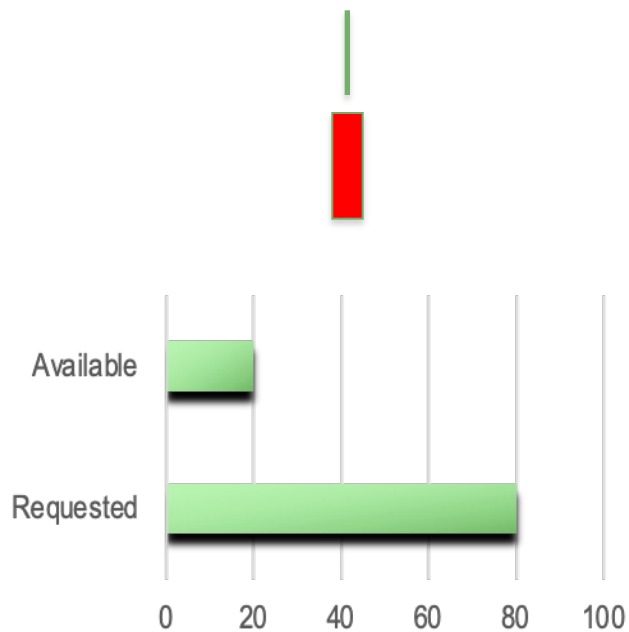
Why a HPC cluster?

MAC mini

1 user

4 raw data files

20 cpus / raw file

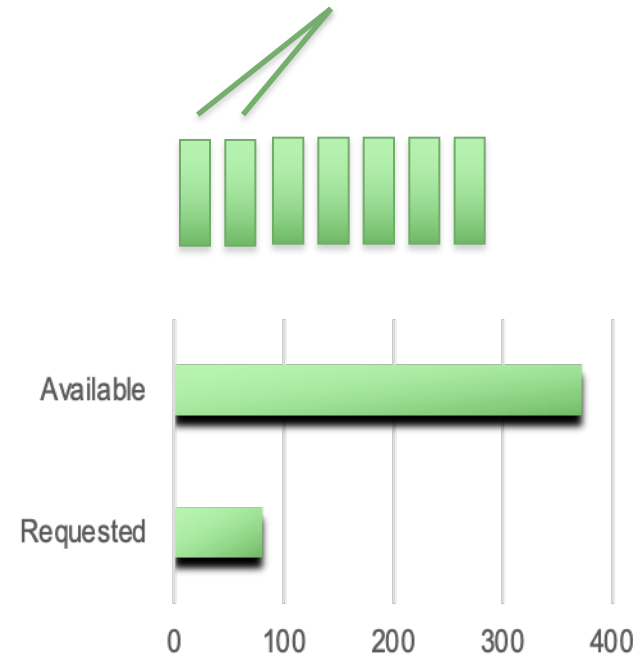


HPC CLUSTER

1 user

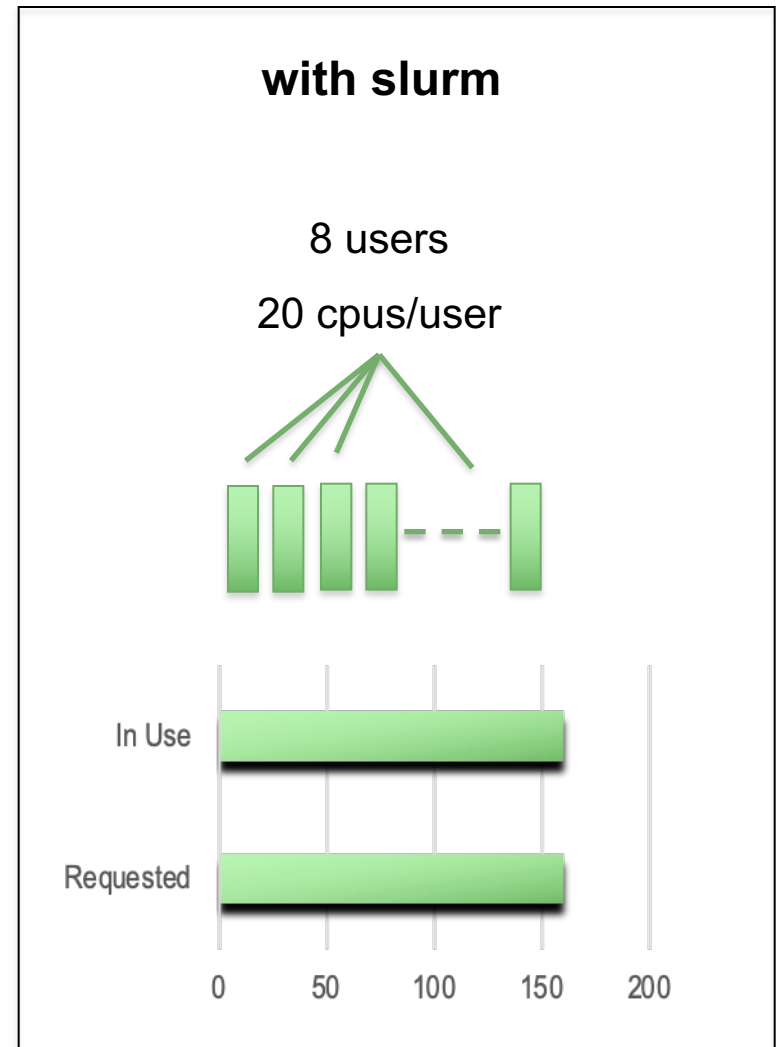
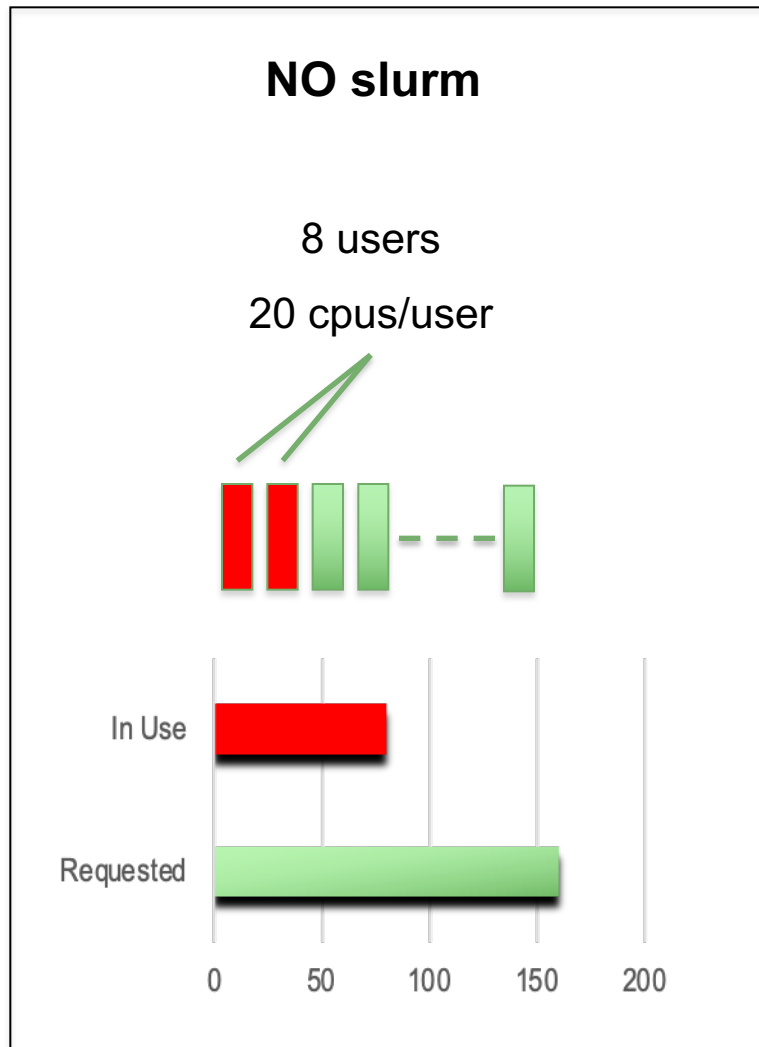
4 raw data files

20 cpus / raw file



*** The resources shown here are to provide an overview, the numbers are not exact as the hpc.bioinformatics.studio

Why SLURM?



How SLURM?

NO slurm

```
> bwa mem sample1.fastq
```

with slurm

```
> srun bwa mem sample1.fastq
```

How SLURM?

NO slurm

```
> bwa mem -T 18 sample1.fastq
```

with slurm

```
> srun --cpus-per-task=18 \
```

```
--mem=15gb \
```

```
--time=5-24 \
```

```
--partition=cluster
```

```
bwa mem -T 18 sample1.fastq
```

(5 days and 24 hours = 6 days

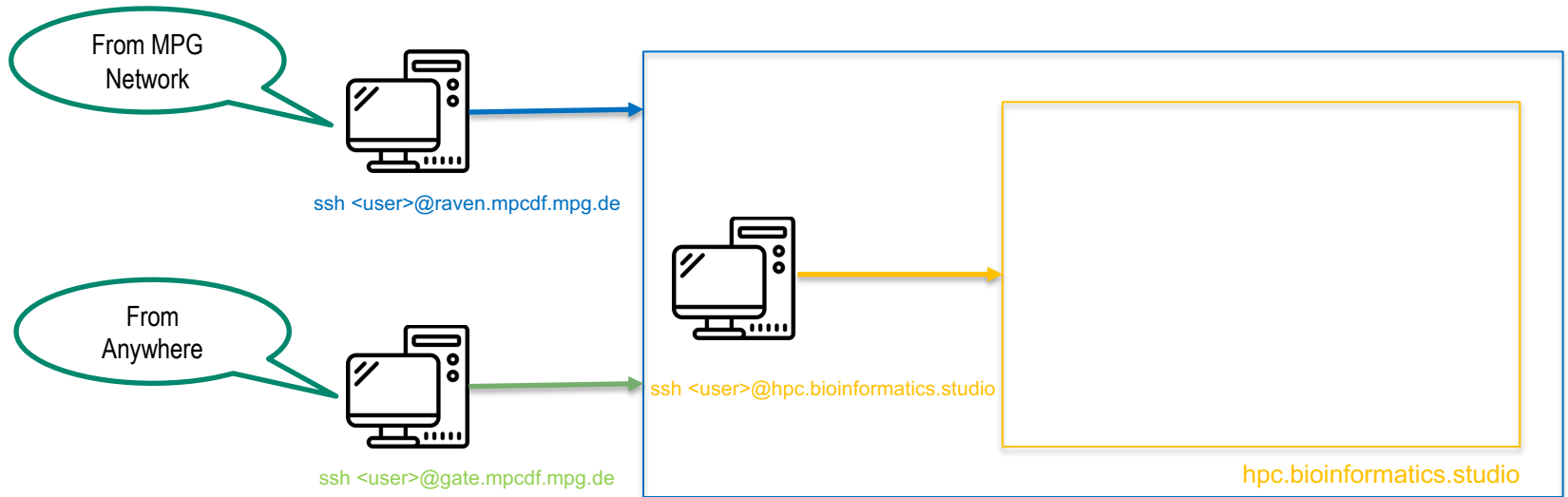
alternative: 144:00:00;

maximum = 14 days)

Getting Started

Prerequisite

- A user account at MPCDF ([MPCDF Registration](#))
- A hpc.bioinformatics.studio account (contact: bioinformatics@age.mpg.de)



SLURM Commands: cluster info

```
hpc02:~$ # View partition information
hpc02:~$ sinfo ←
```

PARTITION	AVAIL	TIMELIMIT	NODES	STATE	NODELIST
cluster*	up	14-00:00:0	9	idle	slurm-worker-cluster-[0-8]
dedicated	up	14-00:00:0	2	mix	slurm-worker-dedicated-[2-3]
dedicated	up	14-00:00:0	2	alloc	slurm-worker-dedicated-[0-1]
dedicated	up	14-00:00:0	2	idle	slurm-worker-dedicated-[4-5]

```
hpc02:~$ # Show information of nodes
hpc02:~$ sinfo -N ←
```

NODELIST	NODES	PARTITION	STATE
slurm-worker-cluster-0	1	cluster*	idle
slurm-worker-cluster-1	1	cluster*	idle
slurm-worker-cluster-2	1	cluster*	idle
slurm-worker-cluster-3	1	cluster*	idle
slurm-worker-cluster-4	1	cluster*	idle
slurm-worker-cluster-5	1	cluster*	idle
slurm-worker-cluster-6	1	cluster*	idle
slurm-worker-cluster-7	1	cluster*	idle
slurm-worker-cluster-8	1	cluster*	idle
slurm-worker-dedicated-0	1	dedicated	mix
slurm-worker-dedicated-1	1	dedicated	alloc
slurm-worker-dedicated-2	1	dedicated	mix
slurm-worker-dedicated-3	1	dedicated	mix
slurm-worker-dedicated-4	1	dedicated	idle
slurm-worker-dedicated-5	1	dedicated	idle

SLURM Commands: cluster info

```
hpc02:~$ # Show information of nodes
```

```
hpc02:~$ sinfo -N -o partitionname,nodehost,cpus,cpusload,freemem,memory
```

PARTITION	HOSTNAMES	CPUS	CPU_LOAD	FREE_MEM	MEMORY
cluster	slurm-worker-cluster20		0.00	69565	70365
cluster	slurm-worker-cluster20		0.00	69609	70365
cluster	slurm-worker-cluster20		0.00	67129	70365
cluster	slurm-worker-cluster20		0.00	66891	70365
cluster	slurm-worker-cluster20		0.00	66889	70365
cluster	slurm-worker-cluster20		0.00	66894	70365
cluster	slurm-worker-cluster20		0.00	66905	70365
cluster	slurm-worker-cluster20		0.00	66933	70365
cluster	slurm-worker-cluster20		0.00	66911	70365
dedicated	slurm-worker-dedicat32		15.88	769817	967194
dedicated	slurm-worker-dedicat32		15.20	679470	967194
dedicated	slurm-worker-dedicat32		14.98	738568	967194
dedicated	slurm-worker-dedicat32		3.79	929163	967194
dedicated	slurm-worker-dedicat32		0.00	964917	967194
dedicated	slurm-worker-dedicat32		0.01	964890	967194

```
hpc02:~$ # Show information about nodes with a specific state (e.g., idle, alloc, mix, etc.)
```

```
hpc02:~$ sinfo -t alloc
```

PARTITION	AVAIL	TIMELIMIT	NODES	STATE	NODELIST
cluster*	up	14-00:00:0	0	n/a	
dedicated	up	14-00:00:0	2	mix	slurm-worker-dedicated-[2-3]
dedicated	up	14-00:00:0	2	alloc	slurm-worker-dedicated-[0-1]

SLURM Commands: submitting jobs

```
hpc02:~$ # Submit jobs to SLURM
hpc02:~$ # sbatch [options] script.sh
hpc02:~$ # Where script.sh is the shell script containing the commands you want to execute
hpc02:~$ sbatch script.sh
Submitted batch job 7540
hpc02:~$ # Common options:
hpc02:~$ # -p <partition>: Specify the partition/queue for the job.
hpc02:~$ # -n <tasks>: Number of tasks in the job.
hpc02:~$ # --cpus-per-task=<cores>: Specify the number of CPU cores per task.
hpc02:~$ # --mem=<memory>: Request memory for the job
hpc02:~$ sbatch -p cluster --cpus-per-task=1 --mem=1gb -t 00:10:00 test.sh
Submitted batch job 7541
hpc02:~$ # Check running jobs
hpc02:~$ squeue
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
7540	cluster	test_job	hamin	R	1:22	1	slurm-worker-cluster-0
7541	cluster	test_job	hamin	R	0:34	1	slurm-worker-cluster-0

SLURM Commands: submitting jobs

```
hpc02:~$ # Submissions without arguments specifications will result in -p "cluster" and a time limit of "2 weeks"
hpc02:~$ # You can also include SLURM parameters inside the script ie.
hpc02:~$ cat script.sh ←
#!/bin/bash
#SBATCH --job-name=test_job      # Job name
#SBATCH -p cluster              # Assign to a cluster
#SBATCH --cpus-per-task=1       # Number of CPUs for task
#SBATCH --mem=1gb               # Job memory request
#SBATCH --time=00:05:00         # Time limit hrs:min:sec
#SBATCH -o test_output.log       # Define the output path
pwd; hostname; date; sleep 300
hpc02:~$ sbatch script.sh ←
Submitted batch job 7542
hpc02:~$ # Check the running jobs
hpc02:~$ squeue ←
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
7542	cluster	test_job	hamin	R	0:19	1	slurm-worker-cluster-0

SLURM Commands: checking queue status

```
hpc02:~$ # Show the queue information
```

```
hpc02:~$ squeue
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
7548	cluster	script.s	hamin	R	5:05	1	slurm-worker-cluster-0
7549	cluster	script.s	hamin	R	5:02	1	slurm-worker-cluster-0
7550	cluster	script.s	hamin	R	5:02	1	slurm-worker-cluster-0
7551	cluster	script.s	hamin	R	2:51	1	slurm-worker-cluster-0
7552	dedicated	script.s	hamin	R	0:27	1	slurm-worker-dedicated-0
7553	dedicated	script.s	hamin	R	0:24	1	slurm-worker-dedicated-0
7554	dedicated	script.s	hamin	R	0:21	1	slurm-worker-dedicated-0

```
hpc02:~$ # Queue information with option
```

```
hpc02:~$ # -u <username>: Show jobs for a specific user
```

```
hpc02:~$ # -p <partition>: Show jobs in a specific partition
```

```
hpc02:~$ squeue -p dedicated
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
7552	dedicated	script.s	hamin	R	1:39	1	slurm-worker-dedicated-0
7553	dedicated	script.s	hamin	R	1:36	1	slurm-worker-dedicated-0
7554	dedicated	script.s	hamin	R	1:33	1	slurm-worker-dedicated-0

SLURM Commands: controlling jobs

```
hpc02:~$ # Show detailed information about a job
hpc02:~$ # scontrol show job <job_id>
hpc02:~$ scontrol show job 7552 ←
JobId=7552 JobName=script.sh
  UserId=hamin(60571) GroupId=mage(17600) MCS_label=N/A
  Priority=4294894274 Nice=0 Account=bioinformatics QOS=normal
  JobState=COMPLETED Reason=None Dependency=(null)
  Requeue=1 Restarts=0 BatchFlag=1 Reboot=0 ExitCode=0:0
  RunTime=00:10:01 TimeLimit=00:15:00 TimeMin=N/A
  SubmitTime=2023-09-28T12:12:04 EligibleTime=2023-09-28T12:12:04
  AccrueTime=2023-09-28T12:12:04
  StartTime=2023-09-28T12:12:05 EndTime=2023-09-28T12:22:06 Deadline=N/A
  SuspendTime=None SecsPreSuspend=0 LastSchedEval=2023-09-28T12:12:05
  Partition=dedicated AllocNode:Sid=hpc-login:1634788
  ReqNodeList=(null) ExcNodeList=(null)
  NodeList=slurm-worker-dedicated-0
  BatchHost=slurm-worker-dedicated-0
  NumNodes=1 NumCPUs=2 NumTasks=0 CPUs/Task=2 ReqB:S:C:T=0:0:*:*
  TRES=cpu=2,node=1,billing=2
  Socks/Node=* NtasksPerN:B:S:C=0:0:*:* CoreSpec=*
  MinCPUsNode=2 MinMemoryNode=2G MinTmpDiskNode=0
  Features=(null) DelayBoot=00:00:00
  OverSubscribe=OK Contiguous=0 Licenses=(null) Network=(null)
  Command=/nexus/posix0/MAGE-flaski/service/hpc/home/hamin/script.sh
  WorkDir=/nexus/posix0/MAGE-flaski/service/hpc/home/hamin
  StdErr=/nexus/posix0/MAGE-flaski/service/hpc/home/hamin/slurm-7552.out
  StdIn=/dev/null
  StdOut=/nexus/posix0/MAGE-flaski/service/hpc/home/hamin/slurm-7552.out
  Power=
```

SLURM Commands: controlling jobs

```
hpc02:~$ # Show information about a partition
hpc02:~$ # scontrol show partition <partition_name>
hpc02:~$ scontrol show partition dedicated ←
PartitionName=dedicated
  AllowGroups=ALL AllowAccounts=ALL AllowQos=ALL
  AllocNodes=ALL Default=NO QoS=N/A
  DefaultTime=NONE DisableRootJobs=NO ExclusiveUser=NO GraceTime=0 Hidden=NO
  MaxNodes=UNLIMITED MaxTime=14-00:00:00 MinNodes=0 LLN=NO MaxCPUsPerNode=UNLIMITED
  Nodes=slurm-worker-dedicated-1,slurm-worker-dedicated-2,slurm-worker-dedicated-0,slurm-worker-dedicated-3,slurm-worker-dedicated-5,slurm-worker-dedicated-4
  PriorityJobFactor=1 PriorityTier=1 RootOnly=NO ReqResv=NO OverSubscribe=NO
  OverTimeLimit=NONE PreemptMode=OFF
  State=UP TotalCPUs=192 TotalNodes=6 SelectTypeParameters=NONE
  JobDefaults=(null)
  DefMemPerNode=UNLIMITED MaxMemPerNode=UNLIMITED
```


SLURM Commands: controlling jobs

```
hpc02:~$ # Show information about a node
hpc02:~$ # scontrol show node <node_name>
hpc02:~$ scontrol show node slurm-worker-dedicated-2 ←
NodeName=slurm-worker-dedicated-2 Arch=x86_64 CoresPerSocket=32
CPUAlloc=32 CPUTot=32 CPULoad=8.49
AvailableFeatures=(null)
ActiveFeatures=(null)
Gres=(null)
NodeAddr=192.168.42.6 NodeHostName=slurm-worker-dedicated-2 Version=19.05.5
OS=Linux 5.4.0-117-generic #132-Ubuntu SMP Thu Jun 2 00:39:06 UTC 2022
RealMemory=967194 AllocMem=0 FreeMem=176841 Sockets=1 Boards=1
State=ALLOCATED ThreadsPerCore=1 TmpDisk=0 Weight=1 Owner=N/A MCS_label=N/A
Partitions=dedicated
BootTime=2023-08-04T14:12:48 SlurmdStartTime=2023-08-24T10:29:46
CfgTRES=cpu=32,mem=967194M,billing=32
AllocTRES=cpu=32
CapWatts=n/a
CurrentWatts=0 AveWatts=0
ExtSensorsJoules=n/s ExtSensorsWatts=0 ExtSensorsTemp=n/s
```

SLURM Commands: cancel a job

```
hpc02:~$ squeue -u hamin ←
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
7710	cluster	script.s	hamin	R	8:34	1	slurm-worker-cluster-0
7709	cluster	script.s	hamin	R	8:37	1	slurm-worker-cluster-0

```
hpc02:~$ # Cancel a job
```

```
hpc02:~$ # scancel <job_id>
```

```
hpc02:~$ scancel 7709 ←
```

```
hpc02:~$ squeue -u hamin ←
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
7710	cluster	script.s	hamin	R	8:59	1	slurm-worker-cluster-0

Procedures: prevent overloading the cluster

```
#!/bin/bash
# Limit the number of simultaneously running jobs
cd ~/project/raw_data
for f in $(ls *.fastq);
do rm ~/project/slurm_logs/${f}.*.out

# wait if the running jobs exceed the limit
while [ `squeue -u username | wc -l` -gt "500" ];
do echo "sleeping"; sleep 300
done

sbatch --cpus-per-task=18 --mem=15gb --time=5-24 \
-p cluster -o ~/project/slurm_logs/${f}.*.out ~/project/tmp/${f}.sh << EOF
#!/bin/bash
# necessary operations
EOF

done
exit
```

SLURM Concepts: at a glance

An open-source workload manager and job scheduler

Manages and schedules tasks across a cluster of computers

Job: Unit of work submitted to SLURM for execution

Partitions: Groups of nodes with similar characteristics

Nodes: Individual computers in the cluster that execute jobs

Resources: Includes CPU cores, memory, and other hardware resources

Singularity/Apptainer

Why Singularity?

- Container engine for HPC
- No root privilege required
- Reproducible, portable, distributable container
- Easy conversion from docker to singularity container

Singularity: example

```
hpc02:~$ # Build a singularity container from Docker image
hpc02:~$ singularity pull my_container.sif docker://ubuntu:latest
INFO:   Converting OCI blobs to SIF format
INFO:   Starting build...
Getting image source signatures
Copying blob 445a6a12be2b done
Copying config c6b84b685f done
Writing manifest to image destination
```


```
hpc02:~$ # Execute the built container
hpc02:~$ singularity exec my_container.sif /bin/bash
Apptainer> ls /
bin  dev      etc  lib    lib64  media  nexus  proc  run  singularity  sys  usr
boot environment home lib32 libx32 mnt    opt   root  sbin  srv         tmp  var
Apptainer> 
```

```
hpc02:~$ # Execute bioinformatics_software container
hpc02:~$ singularity exec /nexus/posix0/MAGE-flaski/service/images/bioinformatics_software.v4.0.3.sif /bin/bash
container:..laski/service/hpc/home/hamin$
```

The Modules System

- Our `mpggebioinformatics/bioinformatics_software` make use of the modules system to load and unload required software
- The modules system loads software (version of choice) and changes environment variables (eg. `LD_LIBRARY_PATH`)

```
container:..laski/service/hpc/home/hamin$ # Shows available modules
container:..laski/service/hpc/home/hamin$ module avail
```



```
----- /modules/modulefiles/general -----
jdk/18.0.2(default)  jupyterhub/2.3.1(default)  perl/5.32.1(default)  python/3.9.13(default)  rlang/4.2.1(default)

----- /modules/modulefiles/libs -----
bzip2/1.0.8(default)  gsl/2.7.1(default)  htlib/1.16(default)  imagemagick/7.1.0-47(default)  openblas/0.3.21(default)  xz/5.2.5(default)

----- /modules/modulefiles/bioinformatics -----
abismal/3.0.0(default)  emboss/6.6.0(default)  kallisto/0.48.0(default)  rsem/1.3.3(default)  subread/2.0.3(default)
bamutil/1.0.15(default)  epiteome/1.0.0(default)  kenttools/435(default)  samtools/1.15.1(default)  tophat/2.1.1(default)
bedtools/2.30.0(default)  expat/2.4.8(default)  lofreq/2.1.5(default)  segemehl/0.3.4(default)  trimalore/0.6.7(default)
bismark/0.24.0(default)  fastqc/0.11.9(default)  meme/5.4.0(default)  seqtk/1.3.0(default)  trimmomatic/0.39(default)
blast/2.13.0(default)  flexbar/3.5.0(default)  mitools/1.5.0(default)  skewer/0.2.2(default)  vcftools/0.1.16(default)
bowtie/1.3.1  gatk/4.2.6.1(default)  near/1.0.0(default)  snpeff/4.3.t(default)  vjtools/1.2.1(default)
bowtie/2.4.5(default)  gsea/4.3.2(default)  ngsutils/0.5.9(default)  spades/3.15.4(default)  walt/1.1.0(default)
```


The Modules System

```
container:..laski/service/hpc/home/hamin$ # Shows a description of the SAMtools module
container:..laski/service/hpc/home/hamin$ module whatis samtools ←
----- /modules/modulefiles/bioinformatics -----
      samtools/1.15.1: Version 1.15.1 of samtools
container:..laski/service/hpc/home/hamin$ # Show environment changes for SAMtools
container:..laski/service/hpc/home/hamin$ module show samtools ←
-----
/modules/modulefiles/bioinformatics/samtools/1.15.1:

module-whatis  {Version 1.15.1 of samtools}
conflict       samtools
prepend-path   PATH /modules/software/samtools/1.15.1/bin
prepend-path   MANPATH /modules/software/samtools/1.15.1/share/man
prepend-path   INFODIR /modules/software/samtools/1.15.1/share/man
-----
container:..laski/service/hpc/home/hamin$ # Load SAMtools
container:..laski/service/hpc/home/hamin$ module load samtools ←
container:..laski/service/hpc/home/hamin$ # List all loaded modules
container:..laski/service/hpc/home/hamin$ module list ←
Currently Loaded Modulefiles:
  1) samtools/1.15.1(default)
container:..laski/service/hpc/home/hamin$ # Unload the SAMtools module
container:..laski/service/hpc/home/hamin$ module unload samtools ←
container:..laski/service/hpc/home/hamin$ # Unload all loaded modules
container:..laski/service/hpc/home/hamin$ module purge ←
container:..laski/service/hpc/home/hamin$ # Check again the module list
container:..laski/service/hpc/home/hamin$ module list ←
No Modulefiles Currently Loaded.
```

RAVEN & hpc.bioinformatics.studio

Where to Run Your Jobs?

You can run your slurm jobs in both Raven & `hpc.bioinformatics.studio`

RAVEN	<code>hpc.bioinformatics.studio</code>
<ul style="list-style-type: none">• For all MPI institutes• More resources• More users• Less time-limit	<ul style="list-style-type: none">• For MPG users only• Less resources• Less users• Higher time-limit (14 days)

Use Bioinformatics Containers

Useful Bioinformatics software containers are available to use in:
</nexus/posix0/MAGE-flaski/service/images/>

Raven

```
hamin@raven02:~> # Load singularity module  
hamin@raven02:~> module load singularity
```

In 2021 the Singularity open source project split into two projects called Apptainer and SingularityCE. On this cluster, this Singularity module will just load the Apptainer module. Please, consider adjusting your scripts accordingly.

```
Loading singularity/link2apptainer  
Loading requirement: apptainer/1.1.7
```

```
hamin@raven02:~> # Use Bioinformatics Software image to launch container  
hamin@raven02:~> singularity exec /nexus/posix0/MAGE-flaski/service/images/bioinformatics_software.v4.0.3.sif /bin/bash  
INFO: fuse2fs not found, will not be able to mount EXT3 filesystems  
container:~$
```

Use Bioinformatics Containers

Useful Bioinformatics software containers are available to use in:
</nexus/posix0/MAGE-flaski/service/images/>

hpc.bioinformatics.studio

```
hpc01:~$ # Singularity module is loaded by default
hpc01:~$ # Use Bioinformatics Software image to launch container
hpc01:~$ singularity exec /nexus/posix0/MAGE-flaski/service/images/bioinformatics_software.v4.0.3.sif /bin/bash
container:..laski/service/hpc/home/hamin$ # Check the available modules in Bioinformatics Software container
container:..laski/service/hpc/home/hamin$ module avail
```

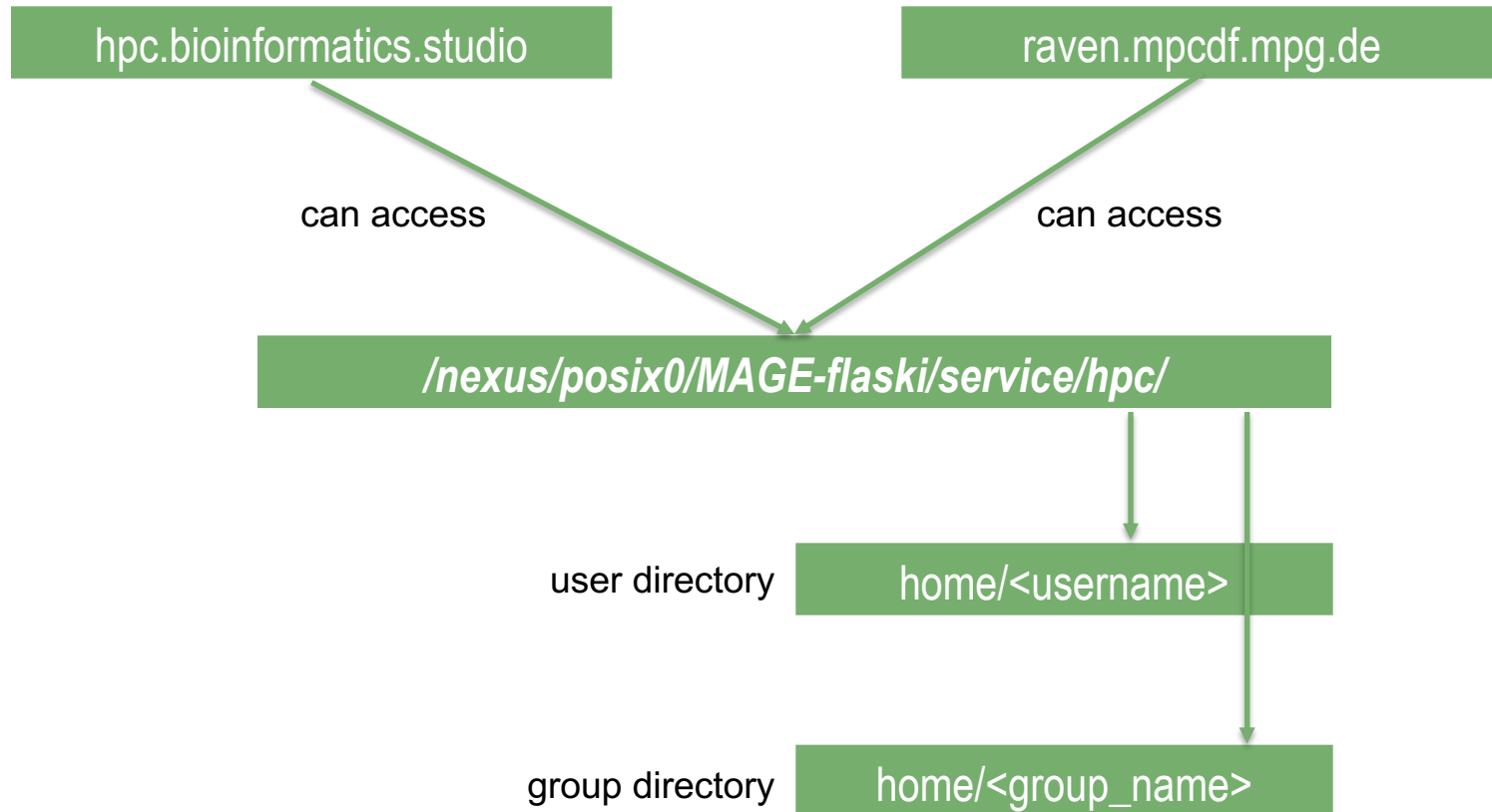
/modules/modulefiles/general					
jdk/18.0.2(default)	jupyterhub/2.3.1(default)	perl/5.32.1(default)	python/3.9.13(default)	rlang/4.2.1(default)	

/modules/modulefiles/libs					
bzip2/1.0.8(default)	gsl/2.7.1(default)	htslib/1.16(default)	imagemagick/7.1.0-47(default)	openblas/0.3.21(default)	xz/5.2.5(default)

/modules/modulefiles/bioinformatics					
abismal/3.0.0(default)	cufflinks/2.2.1(default)	hisat2/2.1.0(default)	near/1.0.0(default)	seqtk/1.3.0(default)	tophat/2.1.1(default)
bamutil/1.0.15(default)	cytoscape/3.9.1(default)	homer/4.11.0(default)	ngsutils/0.5.9(default)	skewer/0.2.2(default)	trimalore/0.6.7(default)
bedtools/2.30.0(default)	emboss/6.6.0(default)	igrec/3.1.1(default)	nlopt/2.7.1(default)	snpeff/4.3.t(default)	trimmomatic/0.39(default)
bismark/0.24.0(default)	epiteome/1.0.0(default)	iseerna/1.2.2(default)	picard/2.27.4(default)	spades/3.15.4(default)	vcftools/0.1.16(default)
blast/2.13.0(default)	expat/2.4.8(default)	kallisto/0.48.0(default)	primer3/2.6.1(default)	sratoolkit/2.11.3(default)	vdjtools/1.2.1(default)
bowtie/1.3.1	fastqc/0.11.9(default)	kenttools/435(default)	quast/5.2.0(default)	star/2.7.10a(default)	walt/1.1.0(default)
bowtie/2.4.5(default)	flexbar/3.5.0(default)	lofreq/2.1.5(default)	rsem/1.3.3(default)	star/2.7.10b	
bwa/0.7.17(default)	gatk/4.2.6.1(default)	meme/5.4.0(default)	samtools/1.15.1(default)	stringtie/2.2.1(default)	
bwtool/face601(default)	gsea/4.3.2(default)	mitools/1.5.0(default)	segemehl/0.3.4(default)	subread/2.0.3(default)	

Data Handling

Data Access



Data Limit

user directory

home/<username>

Data limit: *100 GB per user*
Close to threshold (80 GB+): *warning email*
Cross limit (100 GB+): *notify to limit size*
Failed to limit: *data cleaned up*

User not logged in for 3 months: *tar data & deactivate user*

group directory

home/<group_name>

File not accessed in 6 weeks: *delete file*

Backup Data

From raven.mpcdf.mpg.de transfer data to /raven/ptmp

```
rsync -rtvh /nexus/posix0/MAGE-flaski/service/hpc/group/<group>/<folder> /raven/ptmp/<user>/
```

```
hamin@raven01:~> rsync -rtvh /nexus/posix0/MAGE-flaski/service/hpc/group/Bioinformatics/fol1 /raven/ptmp/hamin/
sending incremental file list
fol1/
fol1/f1
fol1/f2

sent 176 bytes  received 58 bytes  468.00 bytes/sec
total size is 0  speedup is 0.00
hamin@raven01:~> ls /raven/ptmp/hamin/fol1
f1 f2
```

Or to archive file system /r

```
rsync -rtvh /nexus/posix0/MAGE-flaski/service/hpc/group/<group>/<folder> /r/<username first letter>/<user>/
```

```
hamin@raven01:~> rsync -rtvh /nexus/posix0/MAGE-flaski/service/hpc/group/Bioinformatics/fol1 /r/h/hamin/
sending incremental file list
fol1/
fol1/f1
fol1/f2

sent 176 bytes  received 58 bytes  468.00 bytes/sec
total size is 0  speedup is 0.00
hamin@raven01:~> ls /r/h/hamin/fol1
f1 f2
```

Thank You!

Documentation: https://github.com/mpg-age-bioinformatics/cluster_first_steps

Support: bioinformatics@age.mpg.de

Website: <https://bioinformatics.age.mpg.de/>