



MAX PLANCK INSTITUTE FOR **BIOLOGY OF AGEING**



Help yourself on a remote server

bioinformatics@age.mpg.de

<https://mpg-age-bioinformatics.github.io>

Outline

- Connecting to a remote server
- Copying files to/from a remote server
- The modules system
- Installing software without `su` access
- Installing R packages
- Installing python packages
- Installing perl packages
- SLURM

Connecting to a remote server

Connecting to a remote server over a Secure Shell (ssh) — ssh [username@remote.adress](#) :

```
ssh JBoucas@amalia.age.mpg.de
```

With X forwarding:

```
ssh -X JBoucas@amalia.age.mpg.de
```

Copying files to/from a remote server

Copying files over ssh to your home folder on a remote server:

```
scp file.txt UName@ServerAddress:~/
```

Copying files over ssh from your home folder on a remote server:

```
scp UName@ServerAddress:~/file.txt .
```

Both `scp` will only allow you to copy files (not directories) unless you use the `-r` argument for `recursively`. For speed use `-o Cipher=arcfour`.

rsync to a remote server

```
rsync -rtvh -e "ssh -c arcfour" source_folder \  
UName@ServerAddress:destination
```

Not all servers will have the less costly cipher arcfour encryption algorithm and therefore you can remove the whole `-e "ssh -c arcfour"` block.

The modules system

A centralized software system.


The modules system **loads software** (version of choice) and changes **environment variables** (eg. LD_LIBRARY_PATH)

```
module avail          # shows available modules
module whatis SAMtools # shows a description of the SAMtools module
module show SAMtools  # shows environment changes for SAMtools
module load SAMtools   # loads SAMtools
module list           # lists all loaded modules
module unload SAMtools # unloads the SAMtools module
module purge          # unloads all loaded modules
```

more on <http://modules.sourceforge.net>

module avail

Example `module avail` output.



```
----- /beegfs/common/software/2017/modules/modulefiles/general -----
gcc/4.9.2
gcc/6.3.0(default)
java/8.0.111(default)
jdk/8u121(default)
jup/0.1(default)
jupyterhub/0.7.2(default)
perl/5.24.1(default)
pigz/2.3.4(default)
python/2.7.12(default)
python/3.6.0
rlang/3.3.2(default)
ruby/2.4.0(default)
ruby-install/0.6.1(default)
tmux/2.3(default)
tools/0.1(default)

----- /beegfs/common/software/2017/modules/modulefiles/bioinformatics -----
allpathsng/52488(default)
bamutil/1.0.13(default)
bcl2fastq/2.17.1.14(default)
bedtools/2.24.0
bedtools/2.26.0(default)
bowtie/1.2.0
bowtie/2.2.9(default)
bwa/0.7.15(default)
bwtool/git170623(default)
cufflinks/2.2.1(default)
cutadapt/1.13.0(default)
epiteome/1.0.0(default)
expat/2.2.0(default)
fastqc/0.11.5(default)
gatk/3.4.46(default)
graphviz/2.40.1(default)
hisat/2.0.4(default)
igvtools/2.3.89(default)
imtornado/2.0.3.3(default)
lofreq/2.1.2(default)
meme/4.11.3
meme/4.12.0(default)
methpipe/3.4.2(default)
ngsutils/0.5.9(default)
picard/2.8.1(default)
qiime/1.9.1(default)
rsem/1.3.0(default)
samtools/1.3.1(default)
segemehl/0.2.0(default)
seqtk/1.2.r94(default)
skewer/0.2.2(default)
snpeff/4.3.i(default)
spades/3.10.0(default)
sratoolkit/2.8.1
sratoolkit/2.8.1-3(default)
star/2.5.2b(default)
stringtie/1.3.0(default)
tophat/2.1.1(default)
vcftools/0.1.14(default)
walt/1.0.0(default)
```

Notice the 2 arrows and the two distinct blocks of software being shown.

The distinct blocks are generated by the different paths kept on the `MODULEPATH` variable set like this:

```
export MODULEPATH=/beegfs/common/software/2017/modules/modulefiles\
/general:/beegfs/common/software/2017/modules/modulefiles/bioinformatics
```

The modules system

``module avail`` simply lists the contents of the ``MODULEPATH`` variable.

```
amaliax:~$ tree -L 2 /beegfs/common/software/2017/modules/modulefiles/general
/beegfs/common/software/2017/modules/modulefiles/general
├── gcc
│   ├── 4.9.2
│   └── 6.3.0
├── java
│   └── 8.0.111
├── jdk
│   └── 8u121
├── jup
│   └── 0.1
├── jupyterhub
│   └── 0.7.2
├── perl
│   └── 5.24.1
├── pigz
│   └── 2.3.4
├── python
│   ├── 2.7.12
│   └── 3.6.0
├── rlang
│   └── 3.3.2
├── ruby
│   └── 2.4.0
├── ruby-install
│   └── 0.6.1
├── tmux
│   └── 2.3
├── tools
│   └── 0.1
└── 13 directories, 15 files

amaliax:~$ ls -la /beegfs/common/software/2017/modules/modulefiles/general/python
total 8
drwxrwsr-x  2 DRosskopp group_beesw   3 Jun 24 05:15 .
drwxrwsr-x 15 DRosskopp group_beesw  13 Jun 24 05:15 ..
-rw-rw-r--  1 DRosskopp group_beesw 3078 Jun 24 05:15 2.7.12
-rw-rw-r--  1 DRosskopp group_beesw 3058 Jun 24 05:15 3.6.0
-rw-rw-r--  1 DRosskopp group_beesw  137 Jun 24 05:15 .version
```

Example content of a folder in the ``MODULEPATH``.

Example content for Python.

The modules system

```
amali@~$ ls -la /beegfs/common/software/2017/modules/modulefiles/general/python
total 8
drwxrwsr-x  2 DRosskopp group_beew  3 Jun 24 05:15 .
drwxrwsr-x 15 DRosskopp group_beew 13 Jun 24 05:15 ..
-rw-rw-r--  1 DRosskopp group_beew 3078 Jun 24 05:15 2.7.12
-rw-rw-r--  1 DRosskopp group_beew 3058 Jun 24 05:15 3.6.0
-rw-rw-r--  1 DRosskopp group_beew 137 Jun 24 05:15 .version
```

`2.7.12` module file for python 2.7.12

`3.6.0` module file for python 3.6.0

`.version` file defining the default version:

```
##%Module1.0#####
##
## version file for python
##
set ModulesVersion "2.7.12"
```


module file

```
##Module3.2.10#####
proc ModulesHelp { } {
    global version
    puts stderr "\n\tVersion 2.7.12 of python\n"
}

module-whatis    "Version 2.7.12 of python"

# for Tcl script use only
set      version    "3.2.10"

conflict python
prepend-path PATH /beegfs/common/software/2017/modules/software/python/2.7.12/bin
prepend-path LD_LIBRARY_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/lib
prepend-path CPATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path C_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path CPLUS_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path OBJC_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path MANPATH /beegfs/common/software/2017/modules/software/python/2.7.12/share/man
prepend-path INFODIR /beegfs/common/software/2017/modules/software/python/2.7.12/share/man
set home $::env(HOME)
set pythonuser $home/.python/2.7.12/bin
exec /bin/mkdir -p $pythonuser
prepend-path PATH $home/.python/2.7.12/bin
set jupyter_runtime_dir $home/.python/2.7.12/jupyter/run
exec /bin/mkdir -p $jupyter_runtime_dir
setenv JUPYTER_RUNTIME_DIR $home/.python/2.7.12/jupyter/run
set jupyter_data_dir $home/.python/2.7.12/jupyter/data
exec /bin/mkdir -p $jupyter_data_dir
setenv JUPYTER_DATA_DIR $home/.python/2.7.12/jupyter/data
setenv PYTHONHOME /beegfs/common/software/2017/modules/software/python/2.7.12/
setenv PYTHONPATH /beegfs/common/software/2017/modules/software/python/2.7.12/lib/python2.7
setenv PYTHONUSERBASE $home/.python/2.7.12/
exec /bin/mkdir -p $home/.python/2.7.12/pythonpath/site-packages
module load gcc/6.3.0 bzip2/1.0.6 xz/5.2.2 ncurses/6.0 libevent/2.0.22 pcre/8.39 curl/7.51.0 freetype/2.7 openblas/0.2.19
setenv CFLAGS "-I/beegfs/common/software/2017/modules/software/openblas/0.2.19/include -I/beegfs/common/software/2017/modules/software/ncurses/6.0/include/ncurses -I/beegfs/common/software/2017/modules/software/libevent/2.0.22/include -I/beegfs/common/software/2017/modules/software/bzip2/1.0.6/include -I/beegfs/common/software/2017/modules/software/xz/5.2.2/include -I/beegfs/common/software/2017/modules/software/pcre/8.39/include -I/beegfs/common/software/2017/modules/software/curl/7.51.0/include -I/beegfs/common/software/2017/modules/software/openblas/0.2.19/include -I/beegfs/common/software/2017/modules/software/rlang/3.3.2/lib64/R/include"
setenv LDFLAGS "-L/beegfs/common/software/2017/modules/software/openblas/0.2.19/lib -L/beegfs/common/software/2017/modules/software/ncurses/6.0/lib -L/beegfs/common/software/2017/modules/software/libevent/2.0.22/lib -L/beegfs/common/software/2017/modules/software/bzip2/1.0.6/lib -L/beegfs/common/software/2017/modules/software/xz/5.2.2/lib -L/beegfs/common/software/2017/modules/software/pcre/8.39/lib -L/beegfs/common/software/2017/modules/software/curl/7.51.0/lib -L/beegfs/common/software/2017/modules/software/rlang/3.3.2/lib64/R/lib"
```

15,1

All

```

# for Tcl script use only
set version "3.2.10"

conflict python
prepend-path PATH /beegfs/common/software/2017/modules/software/python/2.7.12/bin
prepend-path LD_LIBRARY_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/lib
prepend-path CPATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path C_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path CPLUS_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path OBJC_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include
prepend-path MANPATH /beegfs/common/software/2017/modules/software/python/2.7.12/share/man
prepend-path INFODIR /beegfs/common/software/2017/modules/software/python/2.7.12/share/man
set home $::env(HOME)
set pythonuser $home/.python/2.7.12/bin
exec /bin/mkdir -p $pythonuser
prepend-path PATH $home/.python/2.7.12/bin
set jupyter_runtime_dir $home/.python/2.7.12/jupyter/run
exec /bin/mkdir -p $jupyter_runtime_dir
setenv JUPYTER_RUNTIME_DIR $home/.python/2.7.12/jupyter/run
set jupyter_data_dir $home/.python/2.7.12/jupyter/data
exec /bin/mkdir -p $jupyter_data_dir
setenv JUPYTER_DATA_DIR $home/.python/2.7.12/jupyter/data
setenv PYTHONHOME /beegfs/common/software/2017/modules/software/python/2.7.12/
setenv PYTHONPATH /beegfs/common/software/2017/modules/software/python/2.7.12/lib/python2.7
setenv PYTHONUSERBASE $home/.python/2.7.12/
exec /bin/mkdir -p $home/.python/2.7.12/pythonpath/site-packages
module load gcc/6.3.0 bzip2/1.0.6 xz/5.2.2 ncurses/6.0 libevent/2.0.22 pcre/8.39 curl/7.51.0 freetype
setenv CFLAGS "-I/beegfs/common/software/2017/modules/software/openblas/0.2.19/include -I/beegfs/common/software/2017/modules/software/ncurses/6.0/include/ncurses -I/beegfs/common/software/2017/modules/software/libevent/2.0.22/include -I/beegfs/common/software/bzip2/1.0.6/include -I/beegfs/common/software/2017/modules/software/xz/5.2.2/include -I/beegfs/common/software/pcre/8.39/include -I/beegfs/common/software/2017/modules/software/curl/7.51.0/include -I/beegfs/common/software/openblas/0.2.19/include -I/beegfs/common/software/2017/modules/software/rlang/3.3.2/lib64/R/include"
setenv LDFLAGS "-L/beegfs/common/software/2017/modules/software/openblas/0.2.19/lib -L/beegfs/common/software/2017/modules/software/ncurses/6.0/lib -L/beegfs/common/software/2017/modules/software/libevent/2.0.22/lib -L/beegfs/common/software/2017/modules/software/bzip2/1.0.6/lib -L/beegfs/common/software/2017/modules/software/xz/5.2.2/lib -L/beegfs/common/software/2017/modules/software/pcre/8.39/lib -L/beegfs/common/software/2017/modules/software/curl/7.51.0/lib -L/beegfs/common/software/2017/modules/software"

```

module file

```
##Module3.2.10#####  
proc ModulesHelp { } {  
    global version  
    puts stderr "\n\tVersion 2.7.12 of python\n"  
}
```

Help message shown for this modules with ``module help python/2.7.12``

```
module-whatism "Version 2.7.12 of python"
```

Message to be shown by ``module whatism python/2.7.12``.

```
# for Tcl script use only  
set version "3.2.10"
```

Modules system version.

```
conflict python
```

Conflicts. ie. Do not load if a different python version is already loaded.

```
prepend-path PATH /beegfs/common/software/2017/modules/software/python/2.7.12/bin  
prepend-path LD_LIBRARY_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/lib  
prepend-path CPATH /beegfs/common/software/2017/modules/software/python/2.7.12/include  
prepend-path C_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include  
prepend-path CPLUS_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include  
prepend-path OBJC_INCLUDE_PATH /beegfs/common/software/2017/modules/software/python/2.7.12/include  
prepend-path MANPATH /beegfs/common/software/2017/modules/software/python/2.7.12/share/man  
prepend-path INFODIR /beegfs/common/software/2017/modules/software/python/2.7.12/share/man
```

Paths prepended when the module is loaded and removed when the module is unloaded.

module file

```
set home $::env(HOME)
```

``$::env(HOME)`` captures the variable HOME from the environment of the user loading the module.

``set home $::env(HOME)`` sets a variable ``home`` to be used within the module with the result of ``$::env(HOME)``.

```
set pythonuser $home/.python/2.7.12/bin
```

Sets the python user variable to be used within the module.

```
exec /bin/mkdir -p $pythonuser
```

Executes the command ``/bin/mkdir -p $pythonuser`` every time the module is loaded.

```
prepend-path PATH $home/.python/2.7.12/bin
```

Prepends ``$home/.python/2.7.12/bin`` to the user environment PATH variable.

module file

```
setenv PYTHONUSERBASE $home/.python/2.7.12/  
exec /bin/mkdir -p $home/.python/2.7.12/pythonpath/site-packages
```

Please notice `PYTHONUSERBASE`

```
module load gcc/6.3.0 bzip2/1.0.6 xz/5.2.2 ncurses/6.0 libevent/2.0.22 pcre/8.39 curl/7.51.0 freetype
```

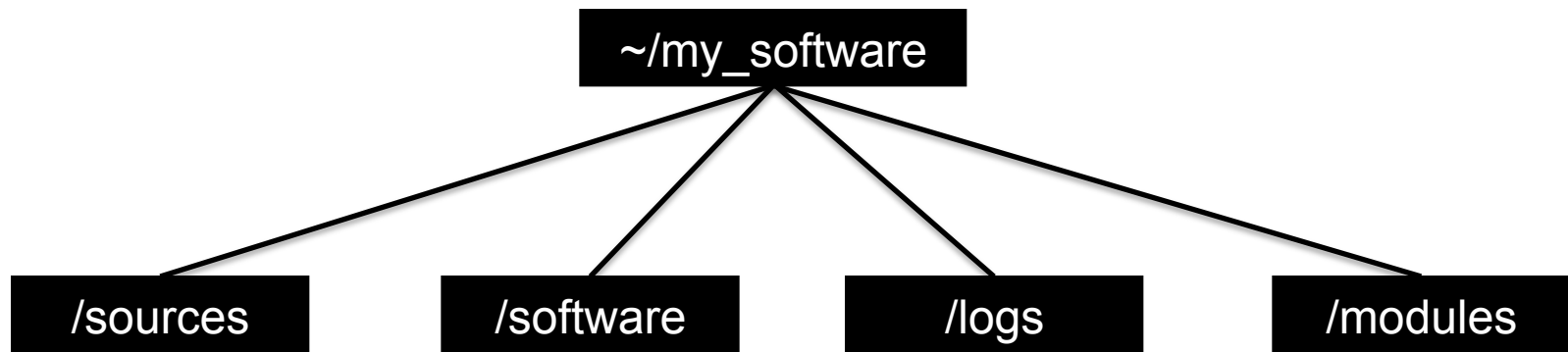
Loads other modules as dependencies when loading the python module.

Installing software without `su` access

Several examples can be obtained from:

https://github.com/mpg-age-bioinformatics/draco_pipelines/blob/master/software/software.sh

Structure:



```
mkdir -p ~/my_software/sources ~/my_software/software \
~/my_software/logs ~/my_software/modules
```

Installing software without `su` access

Download and edit the script for automatic generation of module files:

```
cd ~/
wget https://raw.githubusercontent.com/mpg-age-bioinformatics/
draco_pipelines/master/software/newmod.sh

sed -i 's/\u/jboucas/modules/~\my_software/g newmod.sh
chmod +x newmod.sh
```

Add the `~/my_software/modules` to the MODULEPATH:

```
export MODULEPATH=$MODULEPATH:~/my_software/modules
```

You might want to add this line to your `~/.bashrc`

Installing software without `su` access

```
cd ~/my_software/sources
wget http://zlib.net/pigz/pigz-2.3.4.tar.gz
tar -zxvf pigz-2.3.4.tar.gz
cd pigz-2.3.4
make
mkdir -p ~/my_software/software/pigz/2.3.4/bin
cp pigz unpigz ~/my_software/software/pigz/2.3.4/bin
~/newmod.sh -s pigz -p ~/my_software/modules -v 2.3.4 -d 2.3.4

# TEST #
module avail
module show pigz/2.3.4
module load pigz/2.3.4
which pigz
```


Installing software without `su` access

```
cd ~/my_software/sources
wget http://zlib.net/zlib-1.2.11.tar.gz
tar -zxvf zlib-1.2.11.tar.gz
cd zlib-1.2.11
make
mkdir -p ~/my_software/software/libz/1.2.11
./configure --prefix=~/my_software/software/libz/1.2.11
make
make install
~/newmod.sh -s libz -p ~/my_software/modules -v 1.2.11 -d 1.2.11
```

Installing software without `su` access

```
echo "#!/bin/bash
cd ~/my_software/sources
wget http://zlib.net/zlib-1.2.11.tar.gz
tar -zxvf zlib-1.2.11.tar.gz
cd zlib-1.2.11
make
mkdir -p ~/my_software/software/libz/1.2.11
./configure --prefix=~/my_software/software/libz/1.2.11
make
make install
~/newmod.sh -s libz -p ~/my_software/modules -v 1.2.11 -d 1.2.11
" > ~/my_software/logs/libz-1.2.11.sh
chmod +x ~/my_software/logs/libz-1.2.11.sh
~/my_software/logs/libz-1.2.11.sh 2>&1 | tee \
~/my_software/logs/libz-1.2.11.log
```

Installing software without `su` access

```
if [ ! -f $MODF/general/tmux/2.3 ]; then
    echo 'tmux-2.3'
    echo '#!/bin/bash'
    module list
    cd $SOUR && \
    wget -O t.tar.gz https://github.com/tmux/tmux/releases/download/2.3/tmux-2.3.ta
r.gz && \
    mv t.tar.gz tmux-2.3.tar.gz && \
    tar -zxvf tmux-2.3.tar.gz && \
    cd tmux-2.3 && \
    mkdir -p $SOFT/tmux/2.3/ && \
    ./configure --prefix=$SOFT/tmux/2.3/ CFLAGS="-I$SOFT/libevent/2.0.22/include -I
$SOFT/ncurses/6.0/include/ncurses" LDFLAGS="-L$SOFT/libevent/2.0.22/lib -L$SOFT/ncu
rses/6.0/lib" && \
    make && make install
    newmod.sh \
    -s tmux \
    -p $MODF/general/ \
    -v 2.3 \
    -d 2.3
    echo "set home $::env(HOME)" >> $MODF/general/tmux/2.3
    echo "exec /bin/mkdir -p \${home}/.tmux.socket" >> $MODF/general/tmux/2.3
    echo "module load ncurses/6.0" >> $MODF/general/tmux/2.3
    echo "module load libevent/2.0.22" >> $MODF/general/tmux/2.3
    echo "setenv TMUX_TMPDIR \${home}/.tmux.socket" >> $MODF/general/tmux/2.3
    ' > $LOGS/tmux-2.3.sh
    chmod 755 $LOGS/tmux-2.3.sh
    srun -o $LOGS/tmux-2.3.out $LOGS/tmux-2.3.sh
fi
```

Installing R packages

R standard packages:

```
base  datasets  graphics  grDevices  methods  parallel  stats  stats4  
tcltk  tools  utils
```

This are the only packages that should be inside ``lib64/R/library``. The ``library`` folder should have permissions ``chmod -R 555 library``. This will enforce the use of the ``R_LIBS_USER`` variable for installation of new packages.

Alternative (eg. install biomaRt):

```
source("https://bioconductor.org/biocLite.R")  
biocLite("biomaRt", lib=Sys.getenv("R_LIBS_USER"))
```

The ``lib`` argument can also be used in (eg. install packrat):

```
install.packages("packrat", lib=Sys.getenv("R_LIBS_USER"))
```

Installing python packages

Installing the AGEpy package:

```
module load python  
pip install AGEpy --user
```

Alternative 1:

```
module load python  
git clone https://github.com/mpg-age-bioinformatics/AGEpy  
cd AGEpy  
pip install ../AGEpy --user
```

Alternative 1b (no package control):

```
cd AGEpy  
python setup.py install --user
```

The `--user` argument will make use of the `PYTHONUSERBASE` variable.

Installing perl packages

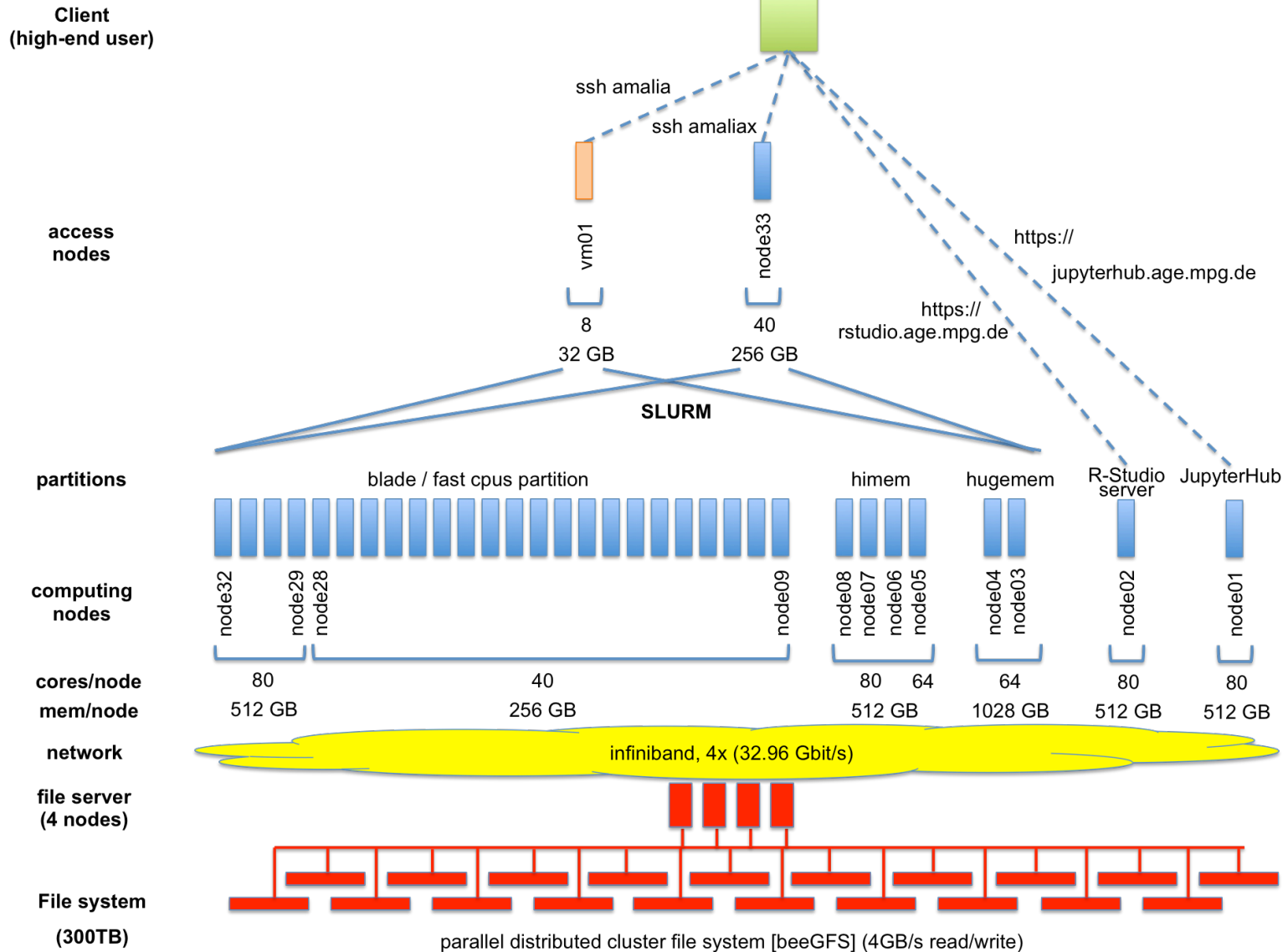
Perl libraries are loaded from the value of ``PERL5LIB``. We have added a variable to module perl to ease local installations - ``PERLUSER`` - check out the content of these two variables.

Example instalation of `Log::Log4perl`:

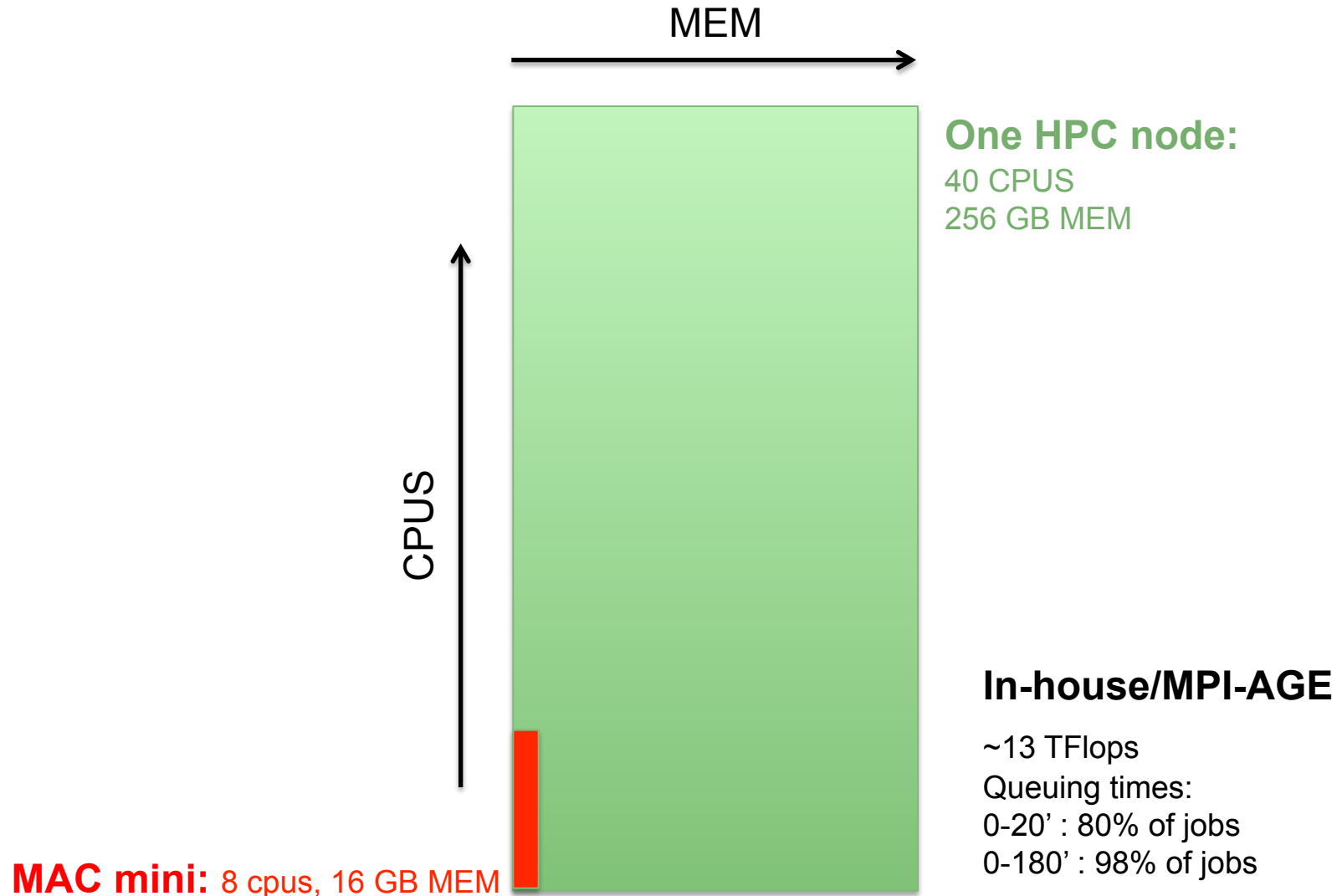
```
module load perl/5.24.1
cpanm Log::Log4perl -l $PERLUSER

# check where it got installed
perldoc -l Log::Log4perl
```

SLURM (Simple Linux Utility for Resource Management)



SLURM: Why an HPC cluster?



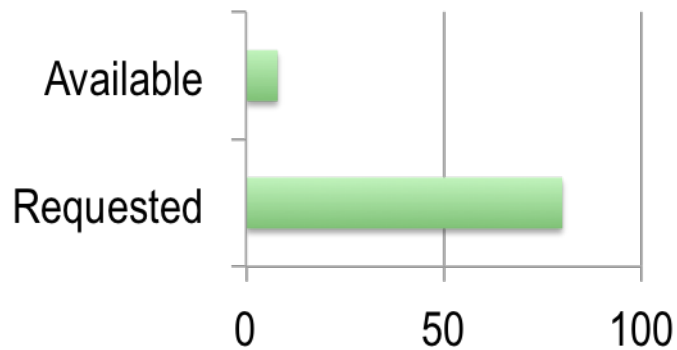
SLURM: Why an HPC cluster?

MAC mini

1 user

4 raw data files

20 cpus / raw file

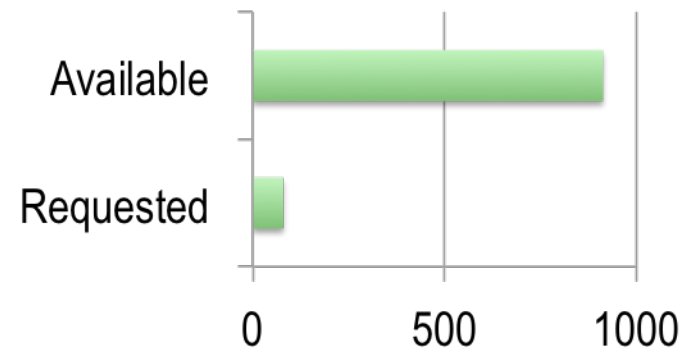
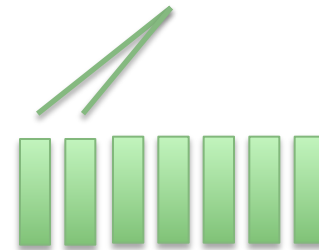


HPC CLUSTER

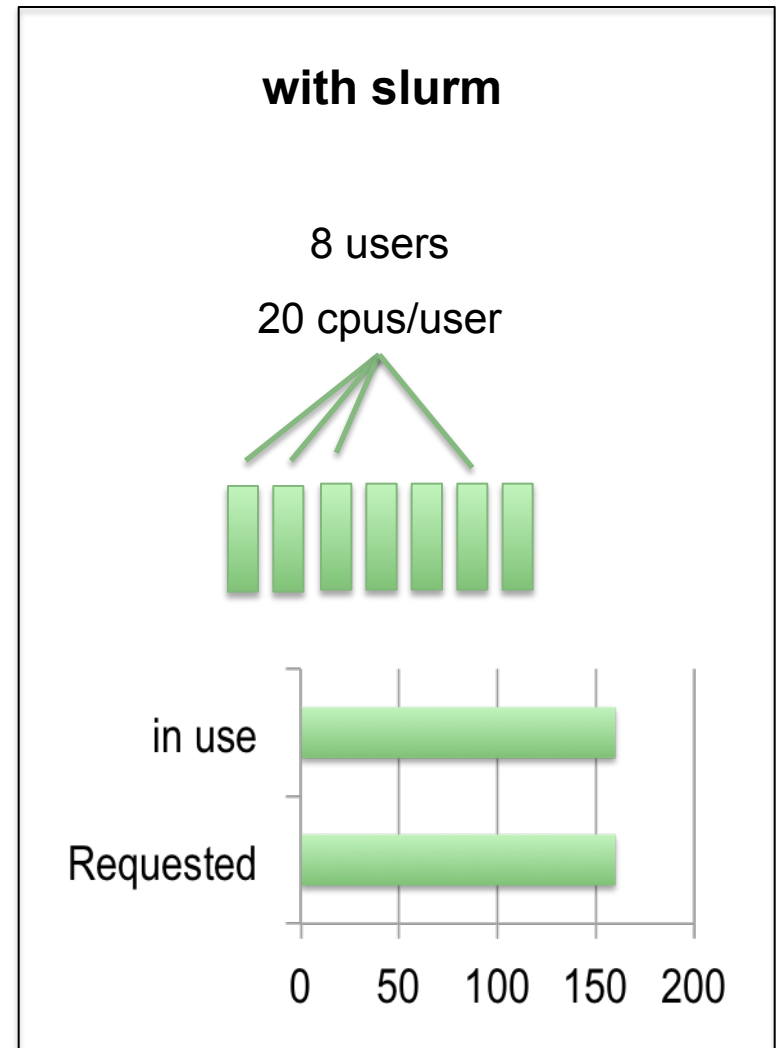
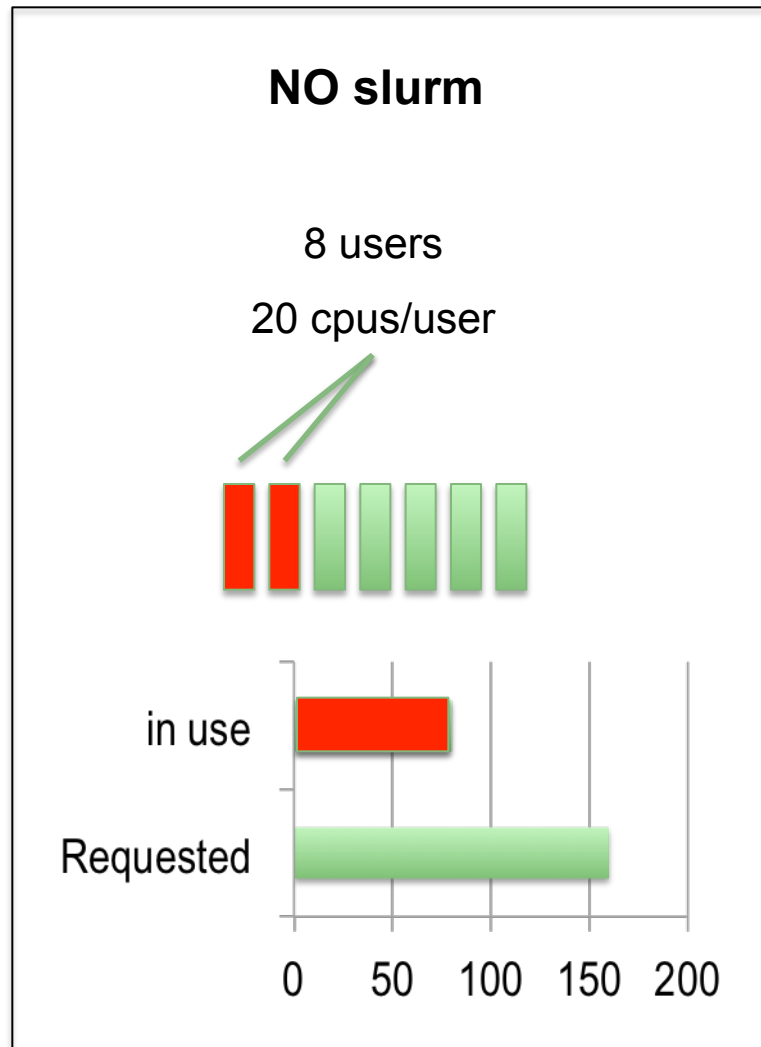
1 user

4 raw data files

20 cpus / raw file



SLURM: Why SLURM?



SLURM: Why SLURM?

NO slurm

```
bwa mem sample1.fastq
```

with slurm

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

SLURM: How to?

NO slurm

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

with slurm

```
srun --cpus-per-task=18 \  
bwa mem -T 18 sample1.fastq
```

SLURM: How to?

NO slurm

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

with slurm

```
srun --cpus-per-task=18 \  
--mem=64gb \  
bwa mem -T 18 sample1.fastq
```

SLURM: How to?

NO slurm

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

with slurm

```
srun --cpus-per-task=18 \  
--mem=15gb \  
--time=5-24 \  
bwa mem -T 18 sample1.fastq
```

(5 days and 24 hours = 6 days
alternative: 144:00:00;
maximum = 14 days)

SLURM: How to?

NO slurm

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

with slurm

```
srun --cpus-per-task=18 \  
--mem=15gb \  
--time=5-24 \  
-p blade \  
bwa mem -T 18 sample1.fastq
```

SLURM: How to?

NO slurm

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

with slurm

```
srun --cpus-per-task=18 \  
--mem=15gb \  
--time=5-24 \  
-p blade \  
-o slurm_logs/bwa_1.out \  
bwa mem -T 18 sample1.fastq
```


SLURM: How to?

NO slurm

```
./align_1.sh
```

```
#!/bin/bash  
bwa mem -T 18 sample1.fastq  
exit
```

with slurm

```
sbatch --cpus-per-task=18 \  
--mem=15gb \  
--time=5-24 \  
-p blade \  
-o slurm_logs/bwa_1.out \  
align_1.sh
```

SLURM: scripting

NO slurm

```
#!/bin/bash
cd ~/project/raw_data
bwa mem -T 18 sample1.fastq
exit

./align_1.sh
```

with slurm

```
#!/bin/bash
#SBATCH --cpus-per-task=18
#SBATCH --mem=15gb
#SBATCH --time=5-24
#SBATCH -p blade
#SBATCH -o slurm_logs/bwa_1.out
cd ~/project/raw_data
bwa mem -T 18 sample1.fastq
exit

sbatch align_1.sh
```

SLURM: iterating jobs over files

```
#!/bin/bash
cd ~/project/raw_data # go to folder containing files

for f in $(ls *.fastq); do echo "#!/bin/bash
cd ~/project/raw_data
bwa mem -T 18 ${f}
rm ~/project/tmp/${f}.sh
" > ~/project/tmp/${f}.sh # for each file, echo a script
# that goes to folder
# executes job on file and
# once completed removes
# temporary script

chmod 755 ~/project/tmp/${f}.sh
rm ~/project/slurm_logs/${f}.*.out # removes pre-existing logs

sbatch --cpus-per-task=18 --mem=15gb \ # start batch job
--time=5-24 -p blade \
-o ~/project/slurm_logs/${f}.*j.out \ # keeps log with job number
~/project/tmp/${f}.sh

done; exit
```

SLURM: iterating jobs over files

```
#!/bin/bash
cd ~/project/raw_data

for f in $(ls *.fastq);
do rm ~/project/slurm_logs/${f}.*.out

    sbatch --cpus-per-task=18 --mem=15gb --time=5-24 \
    -p blade -o ~/project/slurm_logs/${f}.*j.out << EOF

#!/bin/bash
cd ~/project/raw_data
bwa mem -T 18 ${f}
EOF

done
exit
```

SLURM: iterating without crashing

```
#!/bin/bash
cd ~/project/raw_data
for f in $(ls *.fastq);
do rm ~/project/slurm_logs/${f}.*.out

while [ `squeue -u Jboucas | wc -l` -gt "500" ];
do echo "sleeping"; sleep 300
done

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

done
exit
```

SLURM: other options

```
--mail-type=BEGIN, END, FAIL, REQUEUE, ALL
```

```
# Specifies when email is sent to the job owner. The option argument may consist of a  
combination of the allowed mail types
```

```
--mail-user=username@age.mpg.de
```

SLURM: sview

The screenshot shows the SLURM sview application window. The title bar includes standard macOS window controls and system status icons. The menu bar contains 'Grab', 'File', 'Edit', 'Capture', 'Window', and 'Help'. Below the menu bar is a toolbar with icons for 'Jobs', 'Partitions', 'Reservations', 'Nodes', and 'Visible Tabs'. The main area displays a table of running jobs. A context menu is open over the last row of the table, showing options: 'Full Info', 'Signal', 'Requeue', 'Cancel', 'Suspend/Resume', 'Edit Job', 'Partition', 'Nodes', and 'Reservation'.

JobID	Partition	UserID	Name	State	Time Running	Node Count	NodeList
▶ 165733	blade	WBradshaw	interactive_shell_WBradshaw	RUNNING	7-20:41:54	1	bioinf-node05
▶ 166640	blade	WBradshaw	interactive_shell_WBradshaw	RUNNING	6-06:17:45	1	bioinf-node15
▶ 166970	blade	MPiechotta	interactive_shell_MPiechotta	RUNNING	5-00:24:27	1	bioinf-node15
▶ 167097	blade	MPiechotta	interactive_shell_MPiechotta	RUNNING	4-03:34:43	1	bioinf-node15
▶ 167648	blade	RSehlke	rsem-calculate-expression	RUNNING	3-01:49:49	1	bioinf-node09
▶ 168275	blade	MPiechotta	interactive_shell_MPiechotta	RUNNING	1-05:59:20	1	bioinf-node09
▶ 168353	blade	STempler	interactive_shell_STempler	RUNNING	09:05:15	1	bioinf-node10
▶ 168504	himem	JBoucas	go.sh	RUNNING	00:01:14	1	bioinf-node03

- Full Info
- Signal
- Requeue
- Cancel
- Suspend/Resume
- Edit Job
- Partition
- Nodes
- Reservation

SLURM: other useful commands

show the partitions

`sinfo`

show information on nodes

`sinfo -N -O partitionname,nodehost,cpus,cpusload,freemem,memory`

requires X forwarding and allows viewing and manipulation of submitted jobs

`sview`

lists running jobs

`squeue`

show the queue for a user

`squeue -u <user name>`

SLURM: other useful commands

```
# cancels job 65673
```

```
scancel 65673
```

```
# cancels all jobs of user JBoucas
```

```
scancel -u JBoucas
```

```
# shows detailed resource information on job 43433
```

```
scontrol show job 43433
```

```
# show information on a partition
```

```
scontrol show partition <partition name>
```

```
# show information on a node
```

```
scontrol show node <node name>
```

SLURM: other useful commands

```
# starts an interactive terminal window on node15
```

```
srun -w node15 --pty bash
```

```
# submit a job3 after job1 and job2 are successfully ready
```

```
job1=$(sbatch --parsable <script1>)
```

```
job2=$(sbatch --parsable <script2>)
```

```
sbatch -d afterok:${job1}:${job2} <script3>
```

```
# attach to a running job and run a command
```

```
srun --jobid <JOBID> --pty <command>
```

```
# change the partitions of a pending job
```

```
scontrol update job <job id> partition=<partition1>,<partition2>,<partition3>
```

Notes:

For current information on RStudio server and JupyterHub please check our cluster first steps page:

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

SLURM manual:

http://slurm.schedmd.com/man_index.html

Coming soon:

docker on HPC

END

bioinformatics@age.mpg.de

<https://mpg-age-bioinformatics.github.io>