

Help yourself on a remoter server

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

Outline

- Connecting to a remote server
- Copying files to/from a remoter 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 <u>username@remote.adress</u>:

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 remoter 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
                             jupyterhub/0.7.2(default)
                                                          rlang/3.3.2(default)
gcc/6.3.0(default)
                             perl/5.24.1(default)
                                                          ruby/2.4.0(default)
java/8.0.111(default)
                             pigz/2.3.4(default)
                                                          ruby-install/0.6.1(default)
jdk/8u121(default)
                             python/2.7.12(default)
                                                          tmux/2.3(default)
jup/0.1(default)
                                                          tools/0.1(default)
                             python/3.6.0
                 -- /beegfs/common/software/2017/modules/modulefiles/bioinformatics
allpathslg/52488(default)
                              gatk/3.4.46(default)
                                                            segemehl/0.2.0(default)
                                                            seqtk/1.2.r94(default)
bamutil/1.0.13(default)
                              graphviz/2.40.1(default)
bcl2fastg/2.17.1.14(default) hisat/2.0.4(default)
                                                            skewer/0.2.2(default)
bedtools/2.24.0
                              igvtools/2.3.89(default)
                                                            snpeff/4.3.i(default)
bedtools/2.26.0(default)
                              imtornado/2.0.3.3(default)
                                                            spades/3.10.0(default)
bowtie/1.2.0
                              lofreg/2.1.2(default)
                                                            sratoolkit/2.8.1
bowtie/2.2.9(default)
                              meme/4.11.3
                                                            sratoolkit/2.8.1-3(default)
bwa/0.7.15(default)
                              meme/4.12.0(default)
                                                            star/2.5.2b(default)
bwtool/git170623(default)
                              methpipe/3.4.2(default)
                                                            stringtie/1.3.0(default)
cufflinks/2.2.1(default)
                              ngsutils/0.5.9(default)
                                                            tophat/2.1.1(default)
cutadapt/1.13.0(default)
                              picard/2.8.1(default)
                                                            vcftools/0.1.14(default)
epiteome/1.0.0(default)
                              qiime/1.9.1(default)
                                                            walt/1.0.0(default)
expat/2.2.0(default)
                              rsem/1.3.0(default)
fastgc/0.11.5(default)
                              samtools/1.3.1(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
     -4.9.2
     -6.3.0
     -8.0.111
     — 8u121
     - 0.1
   jupyterhub
    perl
    └─ 5.24.1
    L- 2.3.4
   python
     -2.7.12
     — 3.6.0
    └─ 3.3.2
    └─ 2.4.0
   ruby-install
    └─ 0.6.1
   tools
    └─ 0.1
13 directories, 15 files
amaliax:~$ ls -la /beegfs/common/software/2017/modules/modulefiles/general/python
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  137 Jun 24 05:15 .version
```

Example content of a folder in the `MODULEPATH`.

Example content for Python.

The modules system

```
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
```

- `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:

```
proc ModulesHelp { } {
             global version
             puts stderr "\n\tVersion 2.7.12 of python\n"
module-whatis "Version 2.7.12 of python"
             version
                                    "3.2.10"
conflict python
prepend-path PATH /beeqfs/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/.pvthon/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/ncu
rses/6.0/include/ncurses -I/beegfs/common/software/2017/modules/software/libevent/2.0.22/include -I/beegfs/common/software/libevent/2.0.22/include -I/beegfs/common/software/libevent/
e/pcre/8.39/include -I/beegfs/common/software/2017/modules/software/curl/7.51.0/include -I/beegfs/common/software/2017/modules/software/or
s/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/
 mmon/software/2017/modules/software/curl/7.51.0/lib -L/beegfs/common/software/2017/modules/software/rlang/3.3.2/lib64/R/lib"
```

```
# for Tcl script use only
          version
                                     "3.2.10"
set
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/pvthon/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 freetyp
setenv CFLAGS "-I/beegfs/common/software/2017/modules/software/openblas/0.2.19/include -I/beegfs/com
rses/6.0/include/ncurses -I/beegfs/common/software/2017/modules/software/libevent/2.0.22/include -I/
ftware/bzip2/1.0.6/include -I/beegfs/common/software/2017/modules/software/xz/5.2.2/include -I/beeg
e/pcre/8.39/include -I/beegfs/common/software/2017/modules/software/curl/7.51.0/include -I/beegfs/co
enblas/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
s/6.0/lib -L/beegfs/common/software/2017/modules/software/libevent/2.0.22/lib -L/beegfs/common/softw
lib -L/beegfs/common/software/2017/modules/software/xz/5.2.2/lib -L/beegfs/common/software/xz/5.2.2/lib -L/beegfs/common/softwa
ommon/software/2017/modules/software/curl/7.51.0/lib -L/beegfs/common/software/2017/modules/software
```

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

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

Message to be shown by `module whatis 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.

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.

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

Please notice `PYTHONUSERBASE`

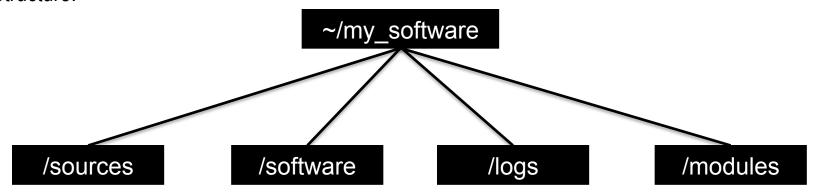
```
module load gcc/6.3.0 bzip2/1.0.6 xz/5.2.2 ncurses/6.0 libevent/2.0.22 pcre/8.39 curl/7.51.0 freetyp
```

Loads other modules as dependencies when loading the python module.

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

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`

```
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
```

```
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
```

```
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
\sim/my_software/logs/libz-1.2.11.sh 2>&1 | tee \
~/my_software/logs/libz-1.2.11.log
```

```
if [ ! -f $MODF/general/tmux/2.3 ]; then
    echo 'tmux-2.3'
    echo '#!/bin/bash
    module list
    cd $SOUR && \
    wget -0 t.tar.gz https://github.com/tmux/tmux/releases/download/2.3/tmux-2.3.ta
r.qz && \
    mv t.tar.gz tmux-2.3.tar.gz && \
    tar -zxvf tmux-2.3.tar.gz && \
    cd tmux-2.3 && \
    mkdir -p $S0FT/tmux/2.3/ && \
    ./configure --prefix=$S0FT/tmux/2.3/ CFLAGS="-I$S0FT/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 \
    -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

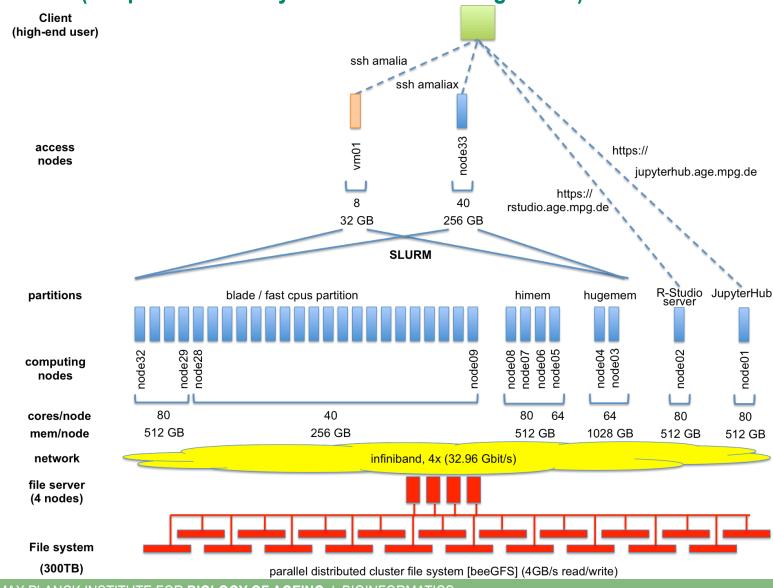
Perl libraries are loaded from the value of `PERL5LIB`. We have added a variable to module perl to ease local installations - `PERLUSER` - check out the content of these two variables.

Example instalation of Log::Log4perl:

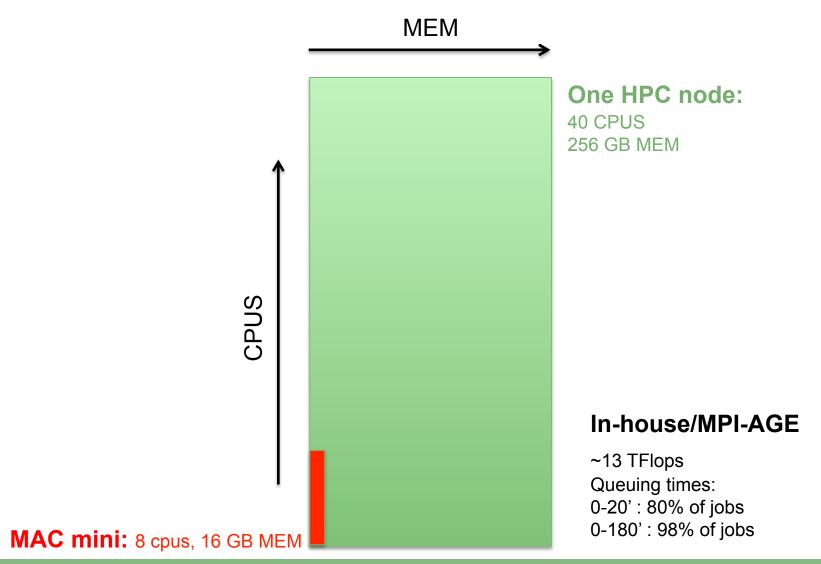
```
module load perl/5.24.1
cpanm Log::Log4perl -l $PERLUSER

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

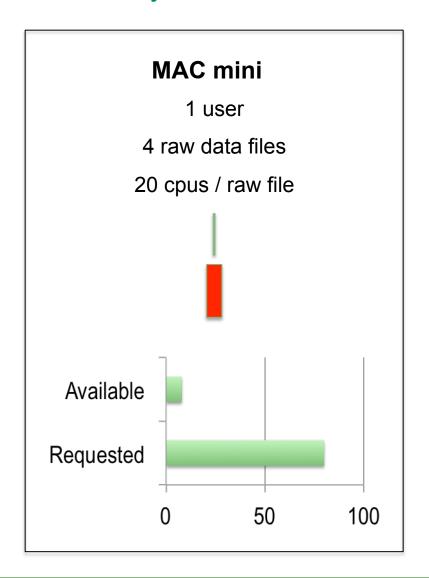
SLURM (Simple Linux Utility for Resource Management)

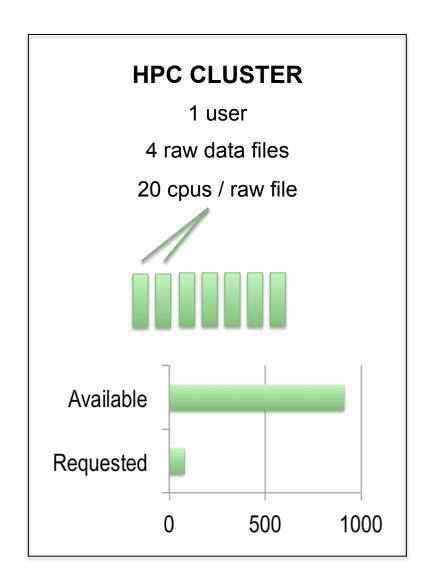


SLURM: Why an HPC cluster?

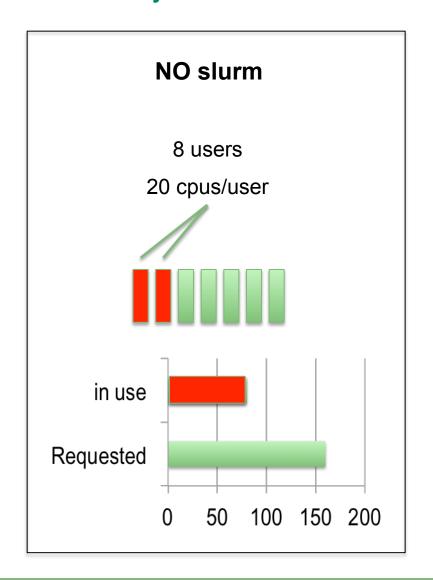


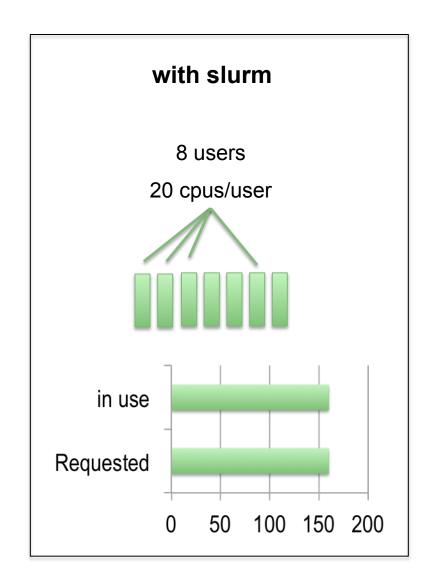
SLURM: Why an HPC cluster?





SLURM: Why SLURM?





SLURM: Why SLURM?



with slurm srun bwa mem sample1.fastq

NO slurm

bwa mem -T 18 sample1.fastq

with slurm

srun --cpus-per-task=18 \

bwa mem —T 18 sample1.fastq

NO slurm

bwa mem —T 18 sample1.fastq

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

NO slurm

bwa mem -T 18 sample1.fastq

```
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 )
```

NO slurm

bwa mem -T 18 sample1.fastq

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

NO slurm

bwa mem -T 18 sample1.fastq

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

NO slurm

```
./align_1.sh
```

```
#!/bin/bash
```

bwa mem -T 18 sample1.fastq
exit

```
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

```
#!/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 $(ls *.fastq); do echo "#!/bin/bash # for each file, echo a script
                                          # that goes to folder
cd ~/project/raw_data
bwa mem -T 18 \{f\}
                                          # executes job on file and
                                          # once completed removes
" > ~/project/tmp/${f}.sh
                                          # temporary script
chmod 755 ~/project/tmp/${f}.sh
                               # removes pre-existing logs
rm ~/project/slurm logs/${f}.*.out
--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</pre>
E<sub>0</sub>F
done
exit
```

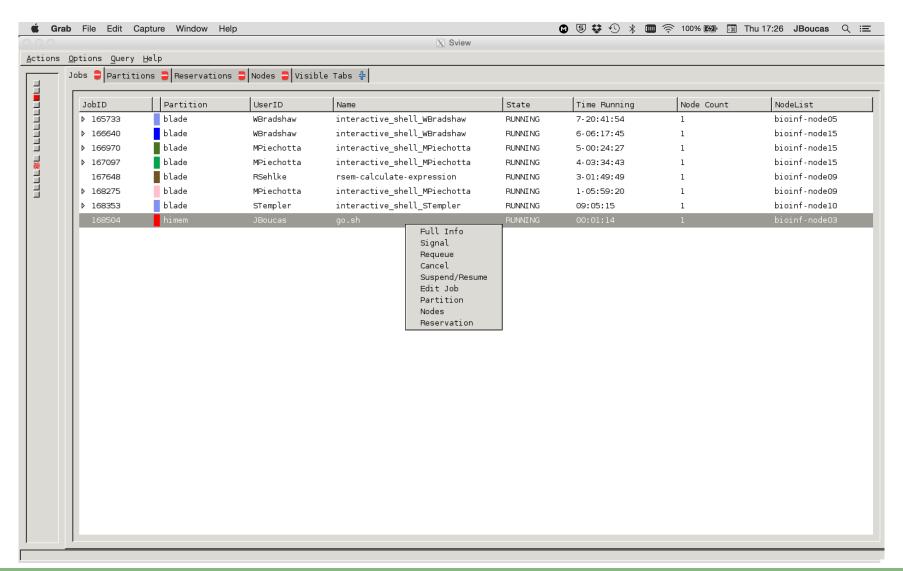
SLURM: iterating without crashing

```
#!/bin/bash
cd ~/project/raw_data
for f in $(ls *.fastq);
   do rm ~/project/slurm_logs/${f}.*.out
   while [ `squeue -u Jboucas | wc -l` -qt "500" ];
      do echo "sleeping"; sleep 300
   done
   sbatch --cpus-per-task=18 --mem=15gb --time=5-24 \
   -p blade -o ~/project/slurm_logs/${f}.%j.out ~/project/tmp/${f}.sh <<EOF</pre>
#!/bin/bash
E0F
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



SLURM: other useful commands

```
# show the partitions
sinfo
# show information on nodes
sinfo −N −0 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 <parition 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 --jodib <JOBID> --pty <command>
# change the partitions of a pending job
scontrol update job <job id> partition=<partition1>,<partition2>,<partition3>
```

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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