



bw|HPC – C5

bwHPC course: File System, Software and Batch System

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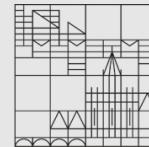


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bw|HPC – C5

- Most information given by this talk can be found at <http://bwhpc-c5.de/wiki>:

- Category:Hardware_and_Architecture
- Environment_Modules
- Batch_Jobs

The screenshot shows the main page of the bwHPC Wiki. The header features the bwHPC logo and navigation links for 'page', 'discussion', and 'view source'. The main content area is titled 'Main Page' and contains a large yellow box labeled 'Knowledge Base Wiki of Baden-Württemberg's HPC services'. Below this, there is a welcome message from the KIT, which states: 'Welcome to the Knowledge Base Wiki of services and projects for *high performance computing (HPC)* and *HPC data storage* in the state of Baden-Württemberg, Germany. Hosted as a Best Practices Repository, the knowledge base contains user guides and best practice guides (BPG) and is maintained by members of Baden-Württemberg's federated HPC competence centers for clusters of tier 3 as well as by members of the HPC competence center for the ForHLR (tier 2). Federated HPC competence centers of tier 3 are an integral part of the project **bwHPC-C5** which coordinates the *federated user and science support* for the *HPC Infrastructure* of tier 3 in the state of Baden-Württemberg.' To the left of the main content is a sidebar with a search bar and a vertical menu containing links to 'Home', 'Best Practices Repository', 'Wiki help', 'Best Practice Guides' (with sub-links for Compiler, Numerical Libraries, Parallel Programming, Software Modules, and Batch Jobs), 'bwHPC tier 3' (with sub-links for bwUniCluster and bwForCluster JUSTUS), 'bwHPC tier 2' (with sub-links for ForHLR Phase I), 'bwHPC Support Services' (with sub-links for Support/Ticket System and Cluster Information System), 'bwHPC Data Storage' (with sub-links for bwFileStorage), 'Tools' (with sub-links for What links here, Related changes, Special pages, Printable version, Permanent link), and 'Personal tools' (with sub-links for Log in).



Material: Slides & Scripts

bw|HPC – C5

- <https://indico.scc.kit.edu/indico/event/132/>
 - @bwUniCluster/ForHLR/IC2/HC3
/pfs/data1/software_uc1/bwhpc/kit/workshop/2015-09-22
- ## How to read the following slides

Abbreviation/Colour code	Full meaning
\$ command -option value	\$ = prompt of the interactive shell The full prompt may look like: user@machine : path\$ The command has been entered in the interactive shell session
<integer> <string>	<> = Placeholder for integer, string etc
foo, bar	Metasyntactic variables

Software System

File System

■ bwUniCluster (**U**) & ForHLR I (**F**) @ Karlsruhe, bwForCluster JUSTUS (**J**) @ Ulm

Property)	\$HOME	\$TMPDIR	workspaces	\$WORK	\$PROJECT
Where	U+F+J (all)	all	all	U + F	F
Visibility	global	nodelocal	global	global	global
Lifetime	permanent	batch job wallt.	240 d (U+F) 90 d (J)	28 d	permanent
Disk space:	469 TB (U+F) 200 TB (J)		938 TB (U+F) 200 TB (J)	938 (U+F)	469 TB
Disk @ thin n.		2 TB (U+F) 0/1 TB (J)			
Disk @ fat n.		7 TB (U), 8 TB (F) 2 TB (J)			
Quotas	yes: 1GB (F), 100 GB (J)	no	if required (U+F) no (J)	if required	yes (defined by proposal)
Backup	yes	no	no	no	yes

■ \$HOME, \$WORK and workspaces: on the parallel file system Lustre

→ **BUT:** only \$HOME under backup

\$HOME = Home directory

■ \$HOME:

@ bwUniCluster/ForHLR:

- Current quota: `$ lfs quota -u $(whoami) $HOME`
- Diskusage: `$ grep -E "\$(whoami)|Account" ~/.../.../diskusage`

@ KIT: \$HOME directories of bwUniCluster, ForHLR, IC2, HC3 are the same

- But: different operational systems, hardware, libraries, queueing etc.
→ bwUniCluster & ForHLR & (OS = REHL) vs. IC2 & HC3 (OS = SLES)
→ generalise your scripts to work on all systems using **\$CLUSTER**

```
if [ ${CLUSTER} == "uc1" ]; then
    <operations>
fi
```

@ JUSTUS:

- Diskusage: `$ less ~/.../.../diskusage/\$(whoami)`

\$PROJECT = Project directory of ForHLR

ONLY ForHLR:

- All features of \$HOME
- Access granted based on approved projects
 - assigned „name/acronym“
 - \$PROJECT_GROUP
- Access project home directory: `$ cd $PROJECT`
- Do not use: \$HOME → since it has very low quota for the project group
- Quota of Project: `$ lfs quota -g ${PROJECT_GROUP} ${PROJECT}`

\$WORK = Working directory

- bwUniCluster/ForHLR → additional parallel file system with limited lifetime, no redundancy, quotas
 - especially designed for parallel access and for a high throughput to large files
- 2 concepts of access via:
 - (A) → \$WORK
 - (B) → *workspaces*
- (A) \$WORK:
 - Change to it via: `$ cd $WORK`
 - Quota: `$ lfs quota -u $(whoami) $WORK`
 - But: files no longer needed should be removed
→ any file inside your \$WORK older than 28 days will be deleted

Workspaces = Working directory

■ (B) **Workspaces**: lifetime on allocated folder

■ HowTo:

→ http://www.bwhpc-c5.de/wiki/index.php/BwUniCluster_File_System#Workspaces

\$ ws_allocate foo 10 Allocate a workspace named *foo* for 10 days

\$ ws_list -a List all your workspaces

\$ ws_find foo Get absolute path of workspace *foo*

\$ ws_extend foo 5 Extend lifetime of your workspace *foo* by 5 days from now. You can extend 3 times
→ **max.** lifetime of *foo* =

240 days (U+F)
90 days (J)

\$ ws_release foo Manually erase your workspace *foo*

Example:

```
$ ws_allocate scratch
$ SDIR=$(ws_find scratch)
$ echo $SDIR
/work/workspace/scratch/ab1234-scratch-0
```

Software System

Environment modules

- Default → manual setup of
 - compilers, libraries and software packages etc.
→ complicated if multiple versions of same software installed
- Solution:
 - dynamic modification of the session environment by
→ instruction sets stored in *modulefiles*
- HowTo?
 - *load* and *unload* instruction sets (= modulefiles)
- How to use modulefiles in general?

\$ module help
- More information:
 - http://www.bwhpc-c5.de/wiki/index.php/Environment_Modules

modulefiles: available / search

Display all modulefiles

```
$ module avail
```

```
----- /opt/bwhpc/kit/modulefiles -----
cae/abaqus/6.13-5    cae/ansys/15.0    cae/comsol/4.4    system/d-default
cae/adina/9.0         cae/ansys/15.0.7   cae/starccm+/9.4

----- /opt/bwhpc/common/modulefiles -----
bio/bismark/0.10.1           lib/boost/1.55.0
bio/bowtie/1.0.1             lib/matplotlib/1.3.1
bio/bowtie2/2.1.0            lib/netcdf/3.6.3-gnu-4.8
bio/bowtie2/2.2.3            lib/netcdf/3.6.3-intel-13.1
bio/cufflinks/2.2.0          lib/pnetcdf/1.4.1
bio/qiime/1.8.0              math/R/3.0.2
bio/samtools/0.1.19          math/matlab/R2013a
bio/tophat/2.0.11            math/matlab/R2013b
bio/trimmomatic/0.32         math/matlab/R2014a
cae/ansys/15.0.7_bw          mpi/impi/4.1.0-gnu-4.4
cae/ansys/15.0_bw             mpi/impi/4.1.0-gnu-4.5
cae/openfoam/1.6-ext          mpi/impi/4.1.0-intel-12.1
```

Display all modulefiles with prefix „compiler“

```
$ module avail compiler
```

```
----- /opt/bwhpc/common/modulefiles -----
compiler/gnu/4.5           compiler/gnu/4.8           compiler/intel/12.1
compiler/gnu/4.7(default)    compiler/gnu/4.9           compiler/intel/13.1(default)
```

modulefiles: help / whatis

- Show help of modulefiles, e.g. `$ module help compiler/intel`

```
----- Module Specific Help for 'compiler/intel/13.1' -----  
  
This module provides the Intel(R) compiler suite version 13.1.3 via  
commands 'icc', 'icpc' and 'ifort', the debugger 'idb' as well as the Intel(R)  
Threading Building Blocks TBB and the Integrated Performance Primitives IPP  
libraries (for details see also 'http://software.intel.com/en-us/intel-compilers/').  
  
The related Math Kernel Library MKL module is 'numlib/mkl/11.0.5'.  
The related Intel MPI module is 'mpi/impi/4.1.1-intel-13.1'.  
The Intel icpc should work well with GNU compiler 4.7.  
  
Commands:  
 icc      # Intel(R) C compiler  
  icpc     # Intel(R) C++ compiler  
  ifort    # Intel(R) Fortran compiler  
  idb      # Intel(R) debugger in GUI mode  
  idbc     # Intel(R) debugger in console mode  
  
Local documentation:  
  Man pages: man icc; man icpc; man ifort  
  firefox $INTEL_DOC_DIR/documentation_c.htm  
  firefox $INTEL_DOC_DIR/documentation_f.htm
```

- Show short info modulefile

```
$ module whatis compiler/intel
```

```
compiler/intel      : Intel(R) compiler suite (icc, icpc, ifort), debugger (idb), IPP and TBB ver 13.1.3
```

modulefiles: show

- Show all instructions of modulefile

```
$ module show compiler/gnu/4.7
```

```
/opt/bwhpc/common/modulefiles/compiler/gnu/4.7:
```

```
module-whatis    GNU compiler suite version 4.7.3 (gcc, g++, gfortran)
setenv          GNU_VERSION 4.7.3
setenv          GNU_HOME /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64
setenv          GNU_BIN_DIR /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/bin
setenv          GNU_MAN_DIR /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/share/man
setenv          GNU_LIB_DIR /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/lib64
prepend-path    PATH /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/bin
prepend-path    MANPATH /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/share/man
prepend-path    LD_RUN_PATH /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/lib
prepend-path    LD_LIBRARY_PATH /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/lib
prepend-path    LD_RUN_PATH /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/lib64
prepend-path    LD_LIBRARY_PATH /opt/bwhpc/common/compiler/gnu/4.7.3/x86_64/lib64
setenv          CC gcc
setenv          CXX g++
setenv          F77 gfortran
setenv          FC gfortran
setenv          F90 gfortran
setenv          TEST_MODULE_SCRIPT /opt/bwhpc/common/compiler/gnu/4.7.3/install-doc/test-compiler-gnu.sh
setenv          TEST_MODULE_NAME compiler/gnu/4.7
conflict        compiler/gnu
-----
```

Load modulefiles (3)

- Modulefiles are sorted in categories, software name and versions:

```
$ module load <category>/<software_name>/<version>
```



- Load a default software:

```
$ module load <category>/<software_name>
```

- e.g. Intel compiler

```
$ module load compiler/intel mpi/impi
```

→ loads currently Intel compiler suite 14

→ loads currently Intel-MPI 4.1.3 for Intel compiler 14.0

```
$ module list
```

- Display all loaded modules

```
Currently Loaded Modulefiles:  
1) compiler/intel/14.0(default) 2) mpi/impi/4.1.3-intel-14.0(default)
```



modulefiles: categories & dependencies

- Module names already implicate dependencies:

→ **Category/softwarename/version_attributes-dependencies**

e.g. **numlib/fftw/3.3.3-impi-4.1.1-intel-13.1**

→ fftw package version 3.3.3, compiled with Intel 13.1 and Intel-MPI 4.1.1

- Categories:

compiler/	for compiler, e.g. intel, gnu, pgi, open64
devel/	for debugger, e.g. ddt, and development tools, e.g. cmake, itrac
mpi/	for MPI libraries, e.g. impi, openmpi, mvapich(2)
numlib/	for numerical libraries, e.g. Intel MKL, ACML, nag, gsl, fftw
lib/	for other libraries, e.g. netcdf, global array
bio/	for biology software, e.g. bowtie, abyss, mrbayes
cae/	for CAE software, e.g. ansys, abaqus, fluent
chem/	for chemistry software, e.g. gromacs, dacapo, turbomole
math/	for mathematics software, e.g. matlab, R
phys/	for physics software, e.g. geant4
vis/	for visualisation software, e.g. vmd, tigervnc

modulefiles: conflicts

■ Conflicts:

- a) load different software version in the same session, e.g. Intel:

```
$ module load compiler/intel/12.1  
$ module load compiler/intel/13.1
```

```
compiler/intel/13.1(394):ERROR:150: Module 'compiler/intel/13.1' conflicts  
with the currently loaded module(s) 'compiler/intel/12.1'
```

- b) load module with dependencies on other modules

```
$ module load mpi/openmpi/1.6.5-intel-13.1
```

```
Loading module dependency 'compiler/intel/13.1'.  
compiler/intel/13.1(394):ERROR:150: Module 'compiler/intel/13.1' conflicts  
with the currently loaded module(s) 'compiler/intel/12.1'
```

modulefiles: unload/swap

- To remove module *foo*:

```
$ module unload foo
```

```
$ module remove foo
```

be aware that you might create **inconsistencies**,

e.g. you can remove

compiler/intel/13.1 while *mpi/openmpi/1.6.5-intel-13.1* is still loaded

- Swap = remove + load

e.g.:

```
$ module swap compiler/intel/12.1 compiler/intel/13.1
```

Private modulefiles

- Each user can create own modulefiles:

e.g. modulefiles that adds path of own programs, \$HOME/special, to \$PATH

→ content of this modulefile „mybin“

```
#%Module1.0  
  
Append-path    PATH    "$env(HOME)/special"
```

→ place „mybin“ under \$HOME/privatemodules

→ to make all own modules visible to “module avail” command, enter:

```
$ module load use.own    or    $ module use $HOME/privatemodules
```

→ former: own modules have lower priority than system ones if equally named

→ latter: own module have higher priority

- Remove own modules:

```
$ module unload use.own    or    $ module unuse $HOME/privatemodules
```

Batch System

Resource management

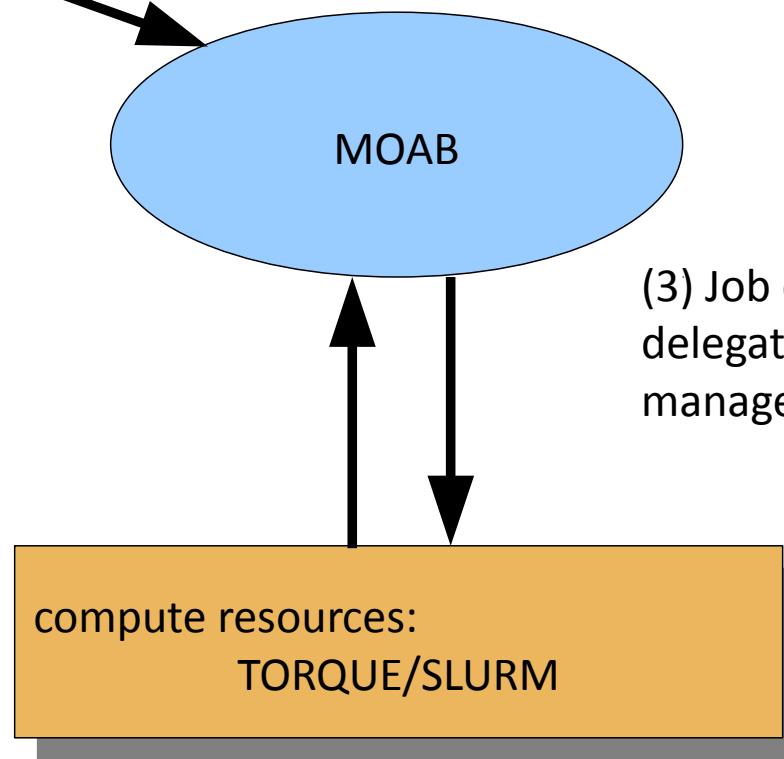
- Components of management system (Batch System)
 - **resource manager**
 - control over jobs and distributed compute nodes
 - SLURM (bwUniCluster, ForHLR)
 - TORQUE (bwForCluster JUSTUS)
 - **workload manager (scheduler)**
 - scheduling, managing, monitoring, reporting
 - MOAB

Resource and workload manager

```
#!/bin/bash  
#MSUB -l nodes=1:ppn=1  
#MSUB -l walltime=00:01:00  
#MSUB -l pmem=50mb  
  
echo "Hello from job"  
exit 0
```

(1) User creates a job script and submits it to MOAB via the “msub” command

(2) MOAB parses the job script:
→ where & when to run job



(3) Job execution:
delegated to resource manager on the node

(4) The resource manager (TORQUE/SLURM) executes the job and communicates status information to MOAB

Job's life circle

- Setup job script:

```
#!/bin/bash
#MSUB -l nodes=1:ppn=1
#MSUB -l walltime=00:01:00
#MSUB -l pmem=50mb

echo "Hello from job"
exit 0
```

- Submit job to workload manager **ONLY with “msub”**

```
$ msub <resource_options> <job_script>
<job_ID>
```

- Job waits for free resources in queue

```
$ showq
<job_ID> state "Idle" → "Running"
```

- Job is finished → check output (default job name)

```
bwUniCluster/ForHLR: job_<uc1,fh1>_<job_ID>.out
```

```
JUSTUS: STDIN.o<job_ID> or STDIN.e<job_ID>
```



msub options

- http://www.bwhpc-c5.de/wiki/index.php/Batch_Jobs#msub_Command
- msub options: command line or in your job script

Command line	Script	Purpose
<code>-l resources</code>	<code>#MSUB -l resources</code>	Defines the resources that are required by the job. See the description below for this important flag.
<code>-N name</code>	<code>#MSUB -N name</code>	Gives a user specified name to the job.
<code>-q queue</code>	<code>#MSUB -q queue</code>	Defines the queue class
<code>-m bea</code>	<code>#MSUB -m bea</code>	Send email when job begins (b), ends (e) or aborts (a).

→ command line option overwrites script option

msub -l *resource_list*

■ http://www.bwhpc-c5.de/wiki/index.php/Batch_Jobs#msub_-l_resource_list

Resource	Purpose
-l nodes=2:ppn=16	Number of nodes and number of processes per node
-l walltime=600	Wall-clock time (seconds)
-l walltime=01:30:00	HH:MM:SS format
-l pmem=1000mb	Max. amount of physical memory used by one process of the job (kb,mb,gb)
-l mem=1000mb	Max. total physical memory used by the job

→ for workshop: **-l advres=bwhpc-workshop.143**

→ resources can be combined, but must be separated by comma:

```
$ msub -l nodes=1:ppn=1,walltime=00:01:00,pmem=1gb <job_script>
```



msub -q queues (bwUniCluster)

- www.bwhpc-c5.de/wiki/index.php/Batch_Jobs_-_bwUniCluster_Features#msub_-q_queues

<i>queue</i>	<i>default resources</i>	<i>MIN resources</i>	<i>MAX resources</i>
automatic queue choosing			
develop	<i>procs=1, pmem=4000mb</i>	nodes=1	<i>walltime=00:30:00, nodes=1:ppn=16</i>
singlenode	<i>procs=1, pmem=4000mb</i>	<i>walltime=00:30:01, nodes=1</i>	<i>walltime=3:00:00:00, nodes=1:ppn=16</i>
multinode	<i>procs=1, pmem=4000mb</i>	<i>nodes=2</i>	<i>walltime=2:00:00:00, nodes=16:ppn=16</i>
explicit queue definition			
verylong	<i>procs=1, pmem=4000mb</i>	<i>walltime=3:00:00:01, nodes=1</i>	<i>walltime=6:00:00:00, nodes=1:ppn=16</i>
fat (fat nodes)	<i>procs=1, pmem=32000mb</i>	<i>nodes=1</i>	<i>walltime=3:00:00:00, nodes=1:ppn=32</i>

- **Automatic queue choosing** - walltime, nodes, processes

msub -q queues (ForHLR)

- http://www.bwhpc-c5.de/wiki/index.php/Batch_Jobs_-_ForHLR_Phase_I_Features

queue	default resources	MIN resources	MAX resources
explicit queue choosing			
develop	<i>procs=1, mem=3200mb, walltime=00:10:10</i>	nodes=1	<i>walltime=00:30:00, nodes=1:ppn=20</i>
singlenode	<i>procs=1, mem=3200mb, walltime=00:10:10</i>	nodes=1	<i>walltime=3:00:00:00, nodes=1:ppn=20</i>
multinode	<i>procs=1, mem=3200mb, walltime=00:10:10</i>	nodes=2	<i>walltime=3:00:00:00, nodes=128:ppn=20</i>
fat (fat nodes)	<i>procs=1, mem=160000mb, walltime=00:10:10</i>	nodes=1	<i>walltime=3:00:00:00, nodes=1:ppn=32</i>

msub -q *queues* (JUSTUS)

- www.bwhpc-c5.de/wiki/index.php/Batch_Jobs_-_bwForCluster_Chemistry_Features#Queues

Queue name	Walltime MIN	Walltime MAX	MAX nodes (total per user)	MAX run/idle jobs (total per user)
quick	00:00:01	00:05:00	2	1/1
short	00:05:01	2d. 48:00:00	64	
normal	48:00:01	7d. 168:00:00	16	
long	168:00:01	14d. 336:00:00	4	

- Automatic queue choosing
 - all queues
 - based on requested **walltime, nodes**
- DO NOT use “-q *queue*” or “#MSUB -q *queue*” by job-submitting

Environment variables

■ www.bwhpc-c5.de/wiki/index.php/Batch_Jobs#Environment_Variables_for_Batch_Jobs

■ bwUniCluster + ForHLR + JUSTUS

	Environment variables	Description
queue =	MOAB_CLASS	Class name
	MOAB_GROUP	Group name
	MOAB_JOBID	Job ID
	MOAB_JOBNAME	Job name
	MOAB_NODECOUNT	Number of nodes allocated to job
	MOAB_PARTITION	Partition name the job is running in
	MOAB_PROCCOUNT	Number of processors allocated to job
	MOAB_SUBMITDIR	Directory of job submission
	MOAB_USER	User name

\$ printenv | grep MOAB

■ Using in scripts:

```
## add suffix to job output file  
./program > $program_{$MOAB_JOBID}.log
```

Interactive jobs

■ Common

- Access to compute nodes
→ start your application direct there
- Specify resources what you need
- Auto logout when job is finished
- Submit job via “`msub -I -V`”
- **BwUniCluster/ForHLR only singlecore Jobs available**

```
$ msub -I -V -l nodes=1:ppn=1,walltime=02:00:00
```

- `-I` = interactive
- `-V` = all environment variables are exported to the compute node

■ bwUniCluster

- www.bwhpc-c5.de/wiki/index.php/Batch_Jobs_-_bwUniCluster_Features#Interactive_Jobs

■ JUSTUS

- www.bwhpc-c5.de/wiki/index.php/Batch_Jobs_-_bwForCluster_Chemistry_Features#Interactive_jobs

Check/change status of your jobs (1)

- after submission → msub returns <job-ID>

```
$ msub job.sh  
659562
```

- commands:

\$ showq -r \$ showq -i \$ showq -b \$ showq -c	All your active (running) jobs eligible(idle) jobs blocked jobs completed jobs
\$ showstart <job-ID>	Get information about start time of job with <job-ID>
\$ showstart 16@12:00:00	Get information about start time of 16 procs with run time of 12 hours
\$ checkjob <job-ID>	Get detailed information of your job → explains why your job is pending
\$ canceljob <job-ID>	Cancel the job with <job-ID>

Check status of your jobs (2)

■ Command “showq”:

```
$ showq
```

active jobs-----

JOBid	USERNAME	STATE	PROCS	REMAINING	STARTTIME
12345	///	Running	1	00:04:58	Thu Jan 22 19:21:56

1 active job

eligible jobs-----

JOBid	USERNAME	STATE	PROCS	REMAINING	STARTTIME
12346	///	Idle	1	00:04:58	Thu Jan 22 19:21:56

1 eligible job

blocked jobs-----

JOBid	USERNAME	STATE	PROCS	WCLIMIT	QUEUETIME
12347	///	Idle	1	00:05:00	Thu Jan 22 19:21:47

1 blocked job

Check status of your jobs (3)

■ STATE:

- Running OK, job is running
- Idle Job is waiting for free resources
- Deferred Buffer-state.
Job can not run (no free resources
or wrong resources)
- BatchHold Job is blocked by scheduler.
End-state.
Reasons: no resources,limits,failure

Idle → Running → Canceling == OK

Idle → Deferred → Idle → Deferred → ... → BatchHold → Canceling

Check status of your jobs (4)

- Check, why job can not start:

- `checkjob <job_ID>` get information of your job
- `checkjob -v -v -v <job_ID>` detailed information

Check status of your jobs (5)

example: MAXNODE limit

Submitted job (bwUniCluster)

```
$ msub -l nodes=1:ppn=8 -q fat <jobscript>  
12345
```

showq:

blocked jobs-----					
JOBID	USERNAME	STATE	PROCS	WCLIMIT	QUEUETIME
12345	///	Idle	5	00:05:00	Fri Jan 23 15:31:05

checkjob 12345:

```
State: Idle  
class:fat  
...  
NodeCount: 1  
...
```

```
BLOCK MSG: job 12345 violates active  
HARD MAXNODE limit of 2 for class fat user partition ALL  
(Req: 8 InUse: 64) (recorded at last scheduling iteration)
```



Check status of your jobs (6)

example: organisation limits

Submitted job (bwUniCluster)

```
$ msub -l nodes=1:ppn=1 <jobscript>  
55555
```

showq:

blocked jobs-----					
JOBID	USERNAME	STATE	PROCS	WCLIMIT	QUEUETIME
55555	///	Idle	1	00:10:00	Fri Jan 21 15:31:05

checkjob -v -v -v 55555:

```
State: Idle  
class:develop  
...
```

```
BLOCK MSG: job 55555 violates active SOFT MAXPROC limit of 1000  
for acct university X partition ALL (Req: 1 InUse: 1010) ...
```

* limits for **university_X**
* TODO: only wait!

Change status of your jobs

Change commands

- `canceljob <job_ID>` cancel the job with <job_ID>
- `mjobctl -c <job_ID>` cancel the job (new command)
- `mjobctl -c -w state=Idle` cancel ALL idle jobs
- `mjobctl -c -w state=Running` cancel ALL running jobs
- `mjobctl -c -w state=BatchHold` cancel ALL hold jobs
- `mjobctl -c -w user=$USER` **cancel ALL your jobs!**

```
$ showq

active jobs-----
JOBID      USERNAME   STATE PROCS  REMAINING      STARTTIME
31172      ///        Running  1      00:04:58  Thu Jan 22 19:21:56
...
blocked jobs-----
JOBID      USERNAME   STATE PROCS  WCLIMIT      QUEUETIME
31173      ///        Idle    1      00:05:00  Thu Jan 22 19:21:47
31174      ///        BatchHold 1      00:05:00  Thu Jan 22 19:21:48
```

Example

```
#!/bin/bash
#MSUB -l nodes=2:ppn=16
#MSUB -l walltime=01:00:00
#MSUB -l pmem=2gb
#MSUB -N serial-test

mpirun ./hello
```

→ Is equal to:

```
$ msub -l nodes=2:ppn=16,walltime=01:00:00,pmem=2gb -N serial-test
<job_script>
```

Common problems

- Wrong „ppn“ setting:

```
$ msub -l nodes=3:ppn=38,walltime=00:01:00,pmem=1gb <job_script>
```

- „mem“ instead of „pmem“:

```
$ msub -l nodes=4:ppn=16,walltime=00:01:00,mem=1gb <job_script>
```

- Wrong queue

- `# MSUB` instead of `#MSUB` (note the space...)