





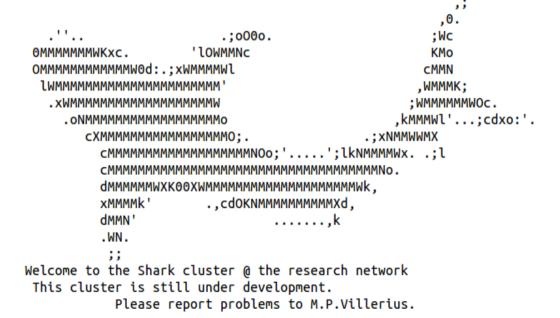


Shark Cluster Overview

- 36 Execution Nodes
- 1 Head Node (shark)
- Graphical login node (rivershark)

596 Cores = slots

437 TB Storage













Introduction

What is a cluster?

- A cluster is a group of computers connected with a tcp/ip-network.
 - The group can work as one large computer or as singe computers called nodes.
 - The cluster is controlled by a resource manager Open Grid Scheduler

There are different type of nodes

- Head node
 - Uses a resource manager to manage all the resources
- Compute node
 - A single blade server
- Login node
 - Shark.researchlumc.nl / rivershark.researchlumc.nl
- Storage node
 - Isilon storage







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Key Terms

Cluster = are a groups of PC's coupled together

Blade server = a compact like workstation (PC)

Chassis = where we store max. 16 blade servers together

Node = is a blade server attached to a cluster

Head node = is the controller/master node of a cluster

Execute node = is the blade that calculate your jobs

Worker node = same as execution node

Storage node = is a special server that will store your data on hard disks

CPU = Central Processing Unit

Core = is another name for the CPU

Slot = in a cluster one CPU is also called a SLOT

Job = your job that needs to be calculated

Queue = a waiting line for all jobs (jobs that cannot be processed)

Fair share = everyone gets CPU power according to what the paid for.

SSH = Secure Shell, a protocol to connect to a server

OGS = Open Grid Scheduler/Grid Engine batch-queuing system for distributed resource management.







Open Grid Scheduler

- OGS is a scheduler which divides the available resources(CPU,mem,etc) into queues
- OGS places the compute tasks (jobs) in a large list.
- OGS searches the right queue for the requested resources in a job and starts that job.
- When the resources are full, the jobs are placed in a waiting list
- Jobs with a higher priority are placed higher in the list
- The priority is based on the priority resource and the fair-share policy







Where can I place my data?

Directory	Description	Size
/exports/	Mount point for Isilon evey department has his own bought isilon export mounted here	715TB
/home/	Home dir, can hold: scripts, R library, compiled code	2TB
/bam-export	Everyone can save BAM files here that can be reached from the UCSC genome browser. External address: https://barmsijs.lumc.nl/	1TB

Location of important directories

- •/usr/local Where programs are located
- •/usr/local/Genomes Where the reference genomes are located







What is your responsibility

- Describe what resources are necessary to ensure success for your jobs (memory, run time, disk space, number of cores, CPU usage, network)
- Not to overload the systems resources, CPU, mem, disk space, network, run time
- Kill the job if the system is getting overloaded
- Keep track of jobs when you are not sure what resources the job uses

Important Note:
qdel "JOB_ID" to kill a job
qdel -u "your username" to kill all your jobs

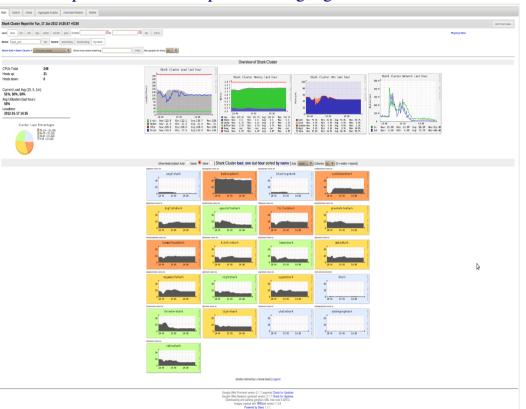




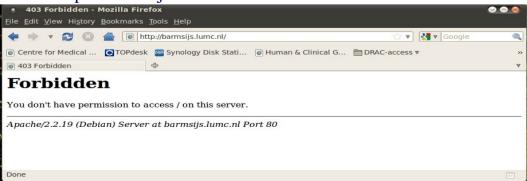


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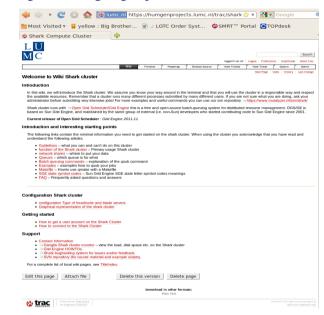
http://shark.lumcnet.prod.intern/ganglia/



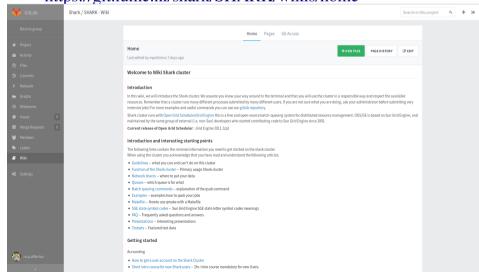
https://barmsijs.lumc.nl/



https://humgenprojects.lumc.nl/trac/shark/



https://git.lumc.nl/shark/SHARK/wikis/home









How to connect to Shark from LUMC

- You need to use your RESEARCHLUMC username and password to connect to the Shark cluster
- Linux / MAC use SSH protocol
 - Command in terminal: ssh researchlumcusername@145.88.65.151
- Windows
 - use putty, cygwin or mobaxterm

host: shark.researchlumc.nl

port : 22

- Login from outside the LUMC
 - Use the SSH jump server : ip = 145.88.35.10





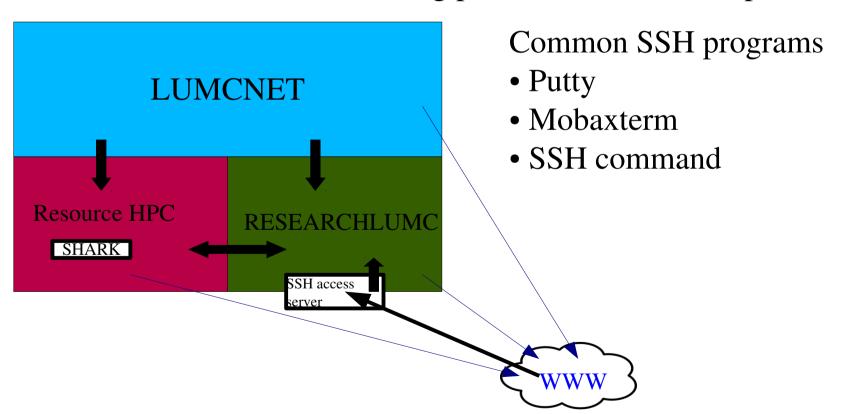


SSH schema

- SSH Default SSH port : 22
- SFTP
- SCP
- SSHFS

SSH server properties

- 3 times wrong user name / session : ip banned
- 3 times wrong password / session : ip banned









Getting started

Important Note: default memory of every job is set to 3GB / slot

qlogin.q and notebook.q maximum run time 12 hrs.

QUEUES

username@shark:~\$ qstat -g c

CLUSTER QUEUE	CQLOAD	USED	RES	AVAIL	TOTAL	aoACDS	cdsuE
all.q	0.26	195	0	368	563	0	0
notebook.q	0.63	1	0	8	9	0	0
qlogin.q	0.20	12	0	8	20	0	0

Parallel environments

username@shark:~\$ qconf -spl

Name allocation rule

BWA pe_slots make pe_slots mpich2 round robin







Interactive use of SGE

username@shark:~\$ qlogin

Your job 822125 ("QLOGIN") has been submitted

waiting for interactive job to be scheduled ...

Your interactive job 822125 has been successfully scheduled.

Establishing /usr/local/Scripts/qlogin_wrapper session to host angelshark.researchlumc.nl ...

username@angelshark:~\$ qstat

prior name user state submit/start at queue Job-ID slots ja-task-ID

822125 0.50075 QLOGIN username r 06/04/2014 13:17:25 qlogin.q@angelshark.researchlumc.nl

username@shark:~\$ qlogin -pe BWA 4 -q all.q

Your job 110997 ("QLOGIN") has been submitted

waiting for interactive job to be scheduled ...

Your interactive job 110997 has been successfully scheduled.

Establishing built in session to host angelshark.researchlumc.nl ...

vill@angelshark:~\$

username@angelshark:~\$ qstat

job-ID prior name user state submit/start at queue slots ja-task-ID 110997 0.53227 QLOGIN vill r 08/03/2011 03:13:59 all.q@angelshark.researchlumc.nl 4

Important Note: default memory of every job is set to

3GB / slot







Qsub your job

Only a script can be submitted with qsub !!!!!!!!

Syntax qsub command:

qsub [options] [scriptfile | -- [script args]]

Binary files can not be submitted directly to SGE.

Example submit "date" command to SGE (with script):

#!/bin/bash

/bin/date

-cwd

Submit this script with:

\$ qsub sge-date

SGE will then run the program, and place two files in your home directory:

sge-date.e sge-date.o

The most common options:

T		771	C .1	
-N	[name]	The name o	t the	10b

-l h_rt=hr:min:sec -- Maximum walltime for this job

-l h_vmem -- Maximum memory your job can use

-r [y,n] -- Should this job be re-runnable (default y)

-pe [type] [num] -- Request [num] amount of [type] nodes.

-- Place the output files (.e,.o) in the current working directory.

The default is to place them in the users home directory.

-S [shell path] -- Specify the shell to use when running the job script

Important Note: default memory of every job is set to 3GB / slot
-l h vmem=3G



echo End time: `date`





Qsub your job

```
Qsub options can be placed inside your script.

vill@shark:/home/vill/shark/trunk# cat run_my_first_job.sh

#!/bin/bash

#$ -S /bin/bash

#$ -q all.q <= use with care

#$ -N my_first_job

#$ -pe BWA 4 <==== the number 4 is only if you need 4 CPU's

#$ -1 h_vmem=4g <== maximum memory that can be used.

#$ -cwd

#$ -j Y

#$ -W

#$ -m be

#$ -m be

#$ -M email@address.lumc

echo Start time: `date`

/bin/hostname
```

username@shark:~/shark/trunk\$ qsub run_my_first_job.sh

Your job 220282 ("my_first_job") has been submitted

```
vill@shark:~/shark/trunk$ qstat
job-ID prior name user state submit/start at queue slots ja-task-ID
220282 0.60500 my_first_j vill r 09/07/2011 09:26:55 all.q@kitefinshark.cluster.loc 4
```

Important Note: default memory of every job is set to 3GB







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vill@shark:~/shark/trunk\$ qacct -j 220282

```
all.q
qname
hostname kitefinshark.cluster.loc
        NexGenSeq
group
owner
        vill
        NONE
project
department defaultdepartment
jobname my_first_job
jobnumber 220282
taskid
       undefined
        sge
account
priority 20
qsub_time Wed Sep 7 09:26:53 2011
start_time Wed Sep 7 09:26:54 2011
end_time Wed Sep 7 09:27:15 2011
granted_pe BWA
slots
      4
failed 0
exit_status 0
ru wallclock 21
ru_utime 0.040
ru stime 0.010
ru_maxrss 1500
ru_ixrss 0
ru ismrss 0
ru_idrss 0
ru_isrss 0
ru_minflt 2332
ru_majflt 0
ru_nswap 0
ru_inblock 16
ru_oublock 192
ru_msgsnd 0
ru_msgrcv 0
ru_nsignals 0
ru_nvcsw 148
ru_nivcsw 5
       0.050
cpu
mem
         0.000
       0.000
io
       0.000
iow
maxvmem 30.523M <= note the maximum memory that has been used
       undefined
arid
                                                         Important Note: default memory of every job is set to 3GB
                                            Job has been submitted with 4GB times 4 slots = 16GB can be submitted with 15MB
```

-1 h vmem = 15 m







Configure a task dependency

#qsub test1.sh
#qsub -hold_jid (jobID for test1.sh) test2.sh

test2.sh will wait for test1.sh to complete

Run 3rd job that depends on test2.sh

#qsub -hold_jid (jobID for test2.sh) test3.sh







What can I run where?

- HEAD Node
 - Small non memory/cpu intensive jobs
 - vi, vim, nano
 - scp, sftp
 - Compile small programs
- Graphical Login Node
 - Firefox, fslview, gedit, etc
- Execution Nodes
 - Large jobs
 - R(run only on here!)
 - Pipelines
 - Matlab
 Do not run Qlogin and go to lunch while this slot is doing nothing.







Evironment Modules

• The Environment Modules package provides for the dynamic modification of a user's environment via modulefiles.

```
# module list
Currently Loaded Modulefiles:
 1) OpenGridScheduler 2) History
                               3) R/3.0.2
#module avail
          -----/usr/local/Modules/versions ------
3.2.10
   ------/usr/local/Modules/3.2.10/modulefiles------/usr/local/Modules/3.2.10/modulefiles--------------
dot java/Oracle-JRE-1.7 module-info OpenGridScheduler R/2.15.3 smrtanalysis
            java/Oracle-JRE-1.8 modules python/python-3.4.1 R/3.0.2
History
                                                                          use.own
               module-git
                             null
                                         giime
                                                     R/3.1.1
java/openjdk-7
#module load R/3.0.2
#module unload R/3.0.2
#module switch R/3.1.1
```







Summary

- qsub submit a job to the batch scheduler
- qlogin submit an interactive login session to Grid Engine
- qstat examine the job queue
- qdel delete a job from the queue
- qacct report and account for Grid Engine usage
- unique-user-slots
- /home Home dir do not store DATA here
- /data/... for storage of your data
- /usr/local/Genomes/ dir where ref. Files are located
- /bam-export dir for temp. bam files and share files.
- Do not abuse QLOGIN use qsub or qmake
- http://barmsijs.lumc.nl/