

FLASH GORDON

A

DINO DE LAURENTIIS
Presents

FLASH GORDON

SAM J. JONES • ORNELLA MUTI • MELODY ANDERSON
as Flash Gordon as Princess Aura as Dale Arden

MAX VON SYDOW • TOPOL • TIMOTHY DALTON • BRIAN BLESSED
as The Emperor Ming as Dr. Hans Zarkov as Prince Barin as Prince Vultan

PETER WYNGARDE • MARIANGELA MELATO • Music Composed, Performed and Produced by
as Klytus as Kala QUEEN

Screenplay by Producer Director
LORENZO SEMPLE, JR. • DINO DE LAURENTIIS • MIKE HODGES

Music by QUEEN on EMI Records and Tapes. EMC 3351

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EMI

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Gordon

- 1024 compute nodes
 - 2 x 8 core (2.6 GHz EM64T Xeon E5)
 - 64 GB RAM (DDR3-1333)
- 64 I/O nodes
 - 2 x 6 core
 - 48 GB (DDR3-1333)
 - 4.8 TB flash storage (16 x 300 GB Intel 710 SSDs)
- 40 Gbps interconnects
- 341 TFlops
- 87 TB/s memory bandwidth
- 1.5 PB storage



Connect to Gordon using your XSEDE username / pass

```
[14:36 dskola@kerner ~] > ssh phage@gordon.sdsc.edu
```

The authenticity of host 'gordon.sdsc.xsede.org (198.202.104.118)' can't be established.

RSA key fingerprint is 5e:47:dc:37:3e:2e:62:2a:31:57:41:a3:35:d1:82:22.

Are you sure you want to continue connecting (yes/no)? yes

Warning: Permanently added 'gordon.sdsc.xsede.org,198.202.104.118' (RSA) to the list of known hosts.

Password:



Modules

- Modules are predefined sets of environment variables to configure the system for a particular application.

\$ module avail

list the available modules

\$ module load <module name>

load the specified module

\$ module display <module name>

see what that module does

\$ module purge

unload all modules

- Go ahead and load the biotools module . . .

\$ module load biotools

My account

```
$ show_accounts
```

ID name	project	used	available	used_by_proj
---------	---------	------	-----------	--------------

phage	csd399	0	40000	0
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To charge your job to one of these projects replace << project >> with one from the list and put this PBS directive in your job script:

```
#PBS -A << project >>
```

Account “billing”

- 1 SU = 1 CPU-hour
- Each node has 16 CPUs and can't share jobs
- So even if you only use 1 CPU on a node that's 16 SU / hour
- $4 \times 10^5 / 18 \text{ students} / 16 \text{ cores} = 139 \text{ node-hours.}$
- Hopefully enough for your group project ;-)

Running jobs

- Controlled by TORQUE Resource Manager
- qsub executes batch scripts that define the jobs

```
$ qsub my_batch_script
```

- Sample-template batch script:

```
#!/bin/bash
#PBS -q normal
#PBS -l nodes=<2>:ppn=<16>:native
#PBS -l walltime=<1:00:00>
#PBS -N <jobname>
#PBS -o <my.out>
#PBS -e <my.err>
#PBS -A <abc100>
#PBS -M <email_address>
#PBS -m abe
#PBS -V
# Start of user commands - comments start with a hash sign (#)
cd /oasis/scratch/$USER/temp_project
<usercommands>
```

Header parameters: queue

```
#!/bin/bash
#PBS -q normal
#PBS -l nodes=<2>:ppn=<16>:native
#PBS -l walltime=<1:00:00>
#PBS -N <jobname>
#PBS -o <my.out>
#PBS -e <my.err>
#PBS -A <abc100>
#PBS -M <email_address>
#PBS -m abe
#PBS -V
# Start of user commands - comments start with a hash sign (#)
cd /oasis/scratch/$USER/temp_project
<usercommands>
```

- '-q' specifies which queue to use.
- In our case we want 'normal'

Header parameters: resources

```
#!/bin/bash
#PBS -q normal
#PBS -l nodes=<2>:ppn=<16>:native
#PBS -l walltime=<1:00:00>
#PBS -N <jobname>
#PBS -o <my.out>
#PBS -e <my.err>
#PBS -A <abc100>
#PBS -M <email_address>
#PBS -m abe
#PBS -V
# Start of user commands - comments start with a hash sign (#)
cd /oasis/scratch/$USER/temp_project
<usercommands>
```

- '-l nodes' specifies how many nodes and CPUs to request
 - here it is 2 nodes with 16 processors per node
- '-l walltime' specifies the max running time (wall time as in clock-on-the wall)
 - Try to be realistic - too long will delay your job

Header parameters: personalization

```
#!/bin/bash
#PBS -q normal
#PBS -l nodes=<2>:ppn=<16>:native
#PBS -l walltime=<1:00:00>
#PBS -N <jobname>
#PBS -o <my.out>
#PBS -e <my.err>
#PBS -A <abc100>
#PBS -M <email_address>
#PBS -m abe
#PBS -V
# Start of user commands - comments start with a hash sign (#)
cd /oasis/scratch/$USER/temp_project
<usercommands>
```

- '-N' naming your job makes it easier to keep track of (obviously)
- '-o', '-e' redirect stdout and stderr (respectively) to these files.
- '-M' send email notifications to this address
- '-m' which notifications?
 - 'a' when the job **a**borts
 - 'b' when the job **b**egins
 - 'e' when the job **e**nds
- '-V' export your current environment variables to the job environment

Header parameters: personalization

```
#!/bin/bash
#PBS -q normal
#PBS -l nodes=<2>:ppn=<16>:native
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```

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Checking on jobs

- What's running?
 - qstat
- Whoa, too much. What am I running?
 - qstat -u \$USER

Job ID	Username	Queue	Jobname	SessID	NDS	TSK	Req'd Memory	Req'd Time	Elap S	Time
934931.gordon-fe	phage	normal	alignA549	--	2	32	--	00:10:00	Q	--

Checking on jobs

- Kill it
 - `qdel jobid`
 - *jobid* can be found with `qstat`

We're doing it live!



- Log in to Gordon
- Use wget to download the following data set:
 - wget
<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeSydhTfbs/wgEncodeSydhTfbsA549Bhlhe40lggrabRawDataRep2.fastq.tgz>

We're doing it live!



- Create a directory called “data” in /oasis/projects/nsf/csd399/\$USER.
- Use tar to extract the sequence data
 - tar xvfz
wgEncodeSydhTfbsA549Bhlhe40lggrabRawData
Rep2.fastq.tgz
- Move the extracted files to your data directory

We're doing it live!



- Bowtie2 needs an index to align against (a reference genome)
 - wget
`ftp://ftp.ccb.jhu.edu/pub/data/bowtie2_indexes/hg19.zip`
- Unzip it (`unzip file`) into a directory called “bt2” off of `/oasis/projects/nsf/csd399/$USER`

We're doing it live!



- We have the raw reads, we have the reference genome.
- Let's map them using bowtie2
- In the github repository is a script called “align_test.pbs”
- Download and edit to put your email address on the -M line

We're doing it live!



- The moment of truth (or consequences):
 - `qsub align_test.pbs`
- Is it running?
 - `qstat -u user`
- What appears in your home folder?