

RUNNING JOBS ON BRIAREE

1. Test on interactive node
2. Decide how much memory & time you need
3. Choose a queue
4. Write a submission script
5. Submit your job
6. Check on your job

https://wiki.calculquebec.ca/w/Running_jobs

RUNNING JOBS ON BRIAREE

Pre-req's (just google it):

- ssh
- scp or rsync
- text editor (emacs, vi, pico...)

RUNNING JOBS ON BRIAREE

1. Test on interactive node

```
$ qsub -I -l nodes=1:ppn=7 -l mem=40gb -l walltime=1:00:00
```

RUNNING JOBS ON BRIAREE

- Decide how much memory & time you need

...based on your interactive job

may need to 'guess and test'

RUNNING JOBS ON BRIAREE

- Choose a queue

```
$ qstat -q
```

```
server: egeon2
```

Queue	Memory	CPU	Time	Walltime	Node	Run	Que	Lm	State
-----	-----	-----	-----	-----	----	---	---	--	-----
urgence	--	--	48:00:00		4	0	0	--	E R
hp	--	--	168:00:0		171	33	22	--	E R
soumet	--	--	--		--	36	-130	--	E R
courte	--	--	48:00:00		4	145	386	--	E R
longue	--	--	336:00:0		4	0	0	--	E R
hpcourte	--	--	48:00:00		171	6	55	--	E R
ssd	--	--	--		2	0	0	--	E R
test	--	--	01:00:00		--	2	1	--	E R
normale	--	--	168:00:0		4	131	995	--	E R
speciale	--	--	--		630	0	0	--	E R
						-----	-----		
						353	1329		

RUNNING JOBS ON BRIAREE

- Write a submission script

```
$ cat PAMLtest.sh
```

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

```
#PBS -l walltime=167:00:00
```

```
#PBS -l nodes=1:ppn=7
```

```
#PBS -l mem=32gb
```

```
#PBS -q normale
```

```
#PBS -r n
```

specify your needs



go to your desired directory



```
cd /RQusagers/shapiro/analysis/141113_PAML/test
```

```
./codeml > gpc.paml.aa.guide.screenout
```

execute your command



RUNNING JOBS ON BRIAREE

- Submit your job

```
$ qsub PAMLtest.sh
```

RUNNING JOBS ON BRIAREE

- Check on your job

```
$ qstat -a -u shapiro
```

egeon2:

Job ID	Username	Queue	Jobname	Req'd SessID	Req'd NDS	Elap TSK	Memory	Time	S	Time
2976514.egeon2	shapiro	normale	PAMLtest.sh	--	1	7	--	150:0	Q	--



```
$ qstat -q normale
```

server: egeon2

Queue	Memory	CPU	Time	Walltime	Node	Run	Que	Lm	State
normale	--	--	168:00:0	4	96 850	--	E	R	

96 850



There are 96 jobs running and 850 jobs in the queue.

RUNNING JOBS ON BRIAREE

- Check on your job

```
$ qstat -a -u shapiro
```

egeon2:

Job ID	Username	Queue	Jobname	Req'd SessID	Req'd NDS	Elap TSK	Memory	Time	S Time
2976514.egeon2	shapiro	normale	PAMLtest.sh	--	1	7	--	150:0 Q	--

Later....

```
$ qstat -a -u shapiro
```

egeon2:

Job ID	Username	Queue	Jobname	Req'd SessID	Req'd NDS	Elap TSK	Memory	Time	S Time
2976514.egeon2	shapiro	normale	PAMLtest.sh	25765	1	7	--	150:0 R	16:30



RUNNING JOBS ON BRIAREE

- Check on your job

When job is done, check for successful completion or errors

```
$ ls
```

```
2NG.dN    aa_gpc.tree.paml.tree  gpc.paml.aa.guide.screenout  PAMLtest.sh      rst
2NG.dS    codeml                 lnf                          PAMLtest.sh~     rst1
2NG.t     codemlctl             nt_gpc.pruned.noStop.paml.phy PAMLtest.sh.e2976514 rub
4fold.nuc codemlctl~            nt_gpc.pruned.paml.aa.guide.tree.out PAMLtest.sh.o2976514
```

```
$ cat PAMLtest.sh.e2976514
```

```
$ cat PAMLtest.sh.o2976514
```

```
-----
Begin PBS Prologue Thu Nov 13 21:22:55 EST 2014 1415931775
Job ID: 2976514.egeon2
Username: shapiro
Group: cpq-000-01
Nodes: node-c1-80
End PBS Prologue Thu Nov 13 21:22:57 EST 2014 1415931777
-----
```

```
-----
Begin PBS Epilogue Mon Nov 17 19:02:24 EST 2014 1416268944
Job ID: 2976514.egeon2
Username: shapiro
Group: cpq-000-01
Job Name: PAMLtest.sh
Session: 25765
Limits: neednodes=1:ppn=7,nodes=1:ppn=7,walltime=150:00:00
Resources: cput=93:23:52,mem=148272kb,vmem=221892kb,walltime=93:39:27
Queue: normale
Account: cpq-000-aa
Nodes: node-c1-80
Killing leftovers...
-----
```

```
End PBS Epilogue Mon Nov 17 19:02:24 EST 2014 1416268944
-----
```

ARCHIVE STORAGE ON BRIAREE

```
$ ssh shapiro@tf-briaree.calculquebec.ca  
$ cd $ARCHIVE  
$ pwd
```

/CQarch/your_username  **ok to put stuff in here**

**but make sure that ALL RAW SEQUENCING DATA
goes here**



/CQarch/GROUP/shapiro/COMMUN/RAW

ARCHIVE STORAGE ON BRIAREE

tar or zip folders before archiving:

```
$ tar -cvzf output.tgz input_folder/
```

always use the original file names, e.g.:

```
121026_M00266_0111_A000000000-A23FU/
```

rsync or scp to transfer files, e.g.

```
[shapiro@briaree3 RAW]$ rsync -avzh jshapiro@cu.broadinstitute.org:/idi/sabeti-data/jesse/sequencing_storage/121026_M00266_0111_A000000000-A23FU.tgz .
```

LAB THINKSTATIONS

nohup is your friend

```
$ nohup perl some_script.pl input.txt > output.txt &
```

```
[1] 413
```



your job ID, which you can check on using top

```
$ top -u shapiro
```

```
top - 16:47:28 up 75 days, 3:23, 141 users, load average: 3.40, 3.56, 3.35
Tasks: 973 total, 3 running, 948 sleeping, 22 stopped, 0 zombie
Cpu(s): 12.6%us, 4.7%sy, 0.0%ni, 82.6%id, 0.1%wa, 0.0%hi, 0.0%si, 0.0%st
Mem: 37004548k total, 21426872k used, 15577676k free, 82028k buffers
Swap: 25165816k total, 831048k used, 24334768k free, 314872k cached
```

PID	USER	PR	NI	VIRT	RES	SHR	S	%CPU	%MEM	TIME+	COMMAND
17491	shapiro	20	0	13800	2088	1080	R	0.7	0.0	0:00.09	top