Running Applications on the Hoffman2 Cluster: Case Studies

Doing research on the Hoffman2 cluster

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Learning outcomes:

- run a batch job
  - Serial, multi-threaded, distributed jobs
- create matlab stand-alone executables
- running matlab in batch
- running abaqus python scripts
- array jobs
- array jobs w/ abaqus
- array jobs w/ R
- can my workflow be run via an array job
- jupiter notebooks

Applications already available on Hoffman2: Python

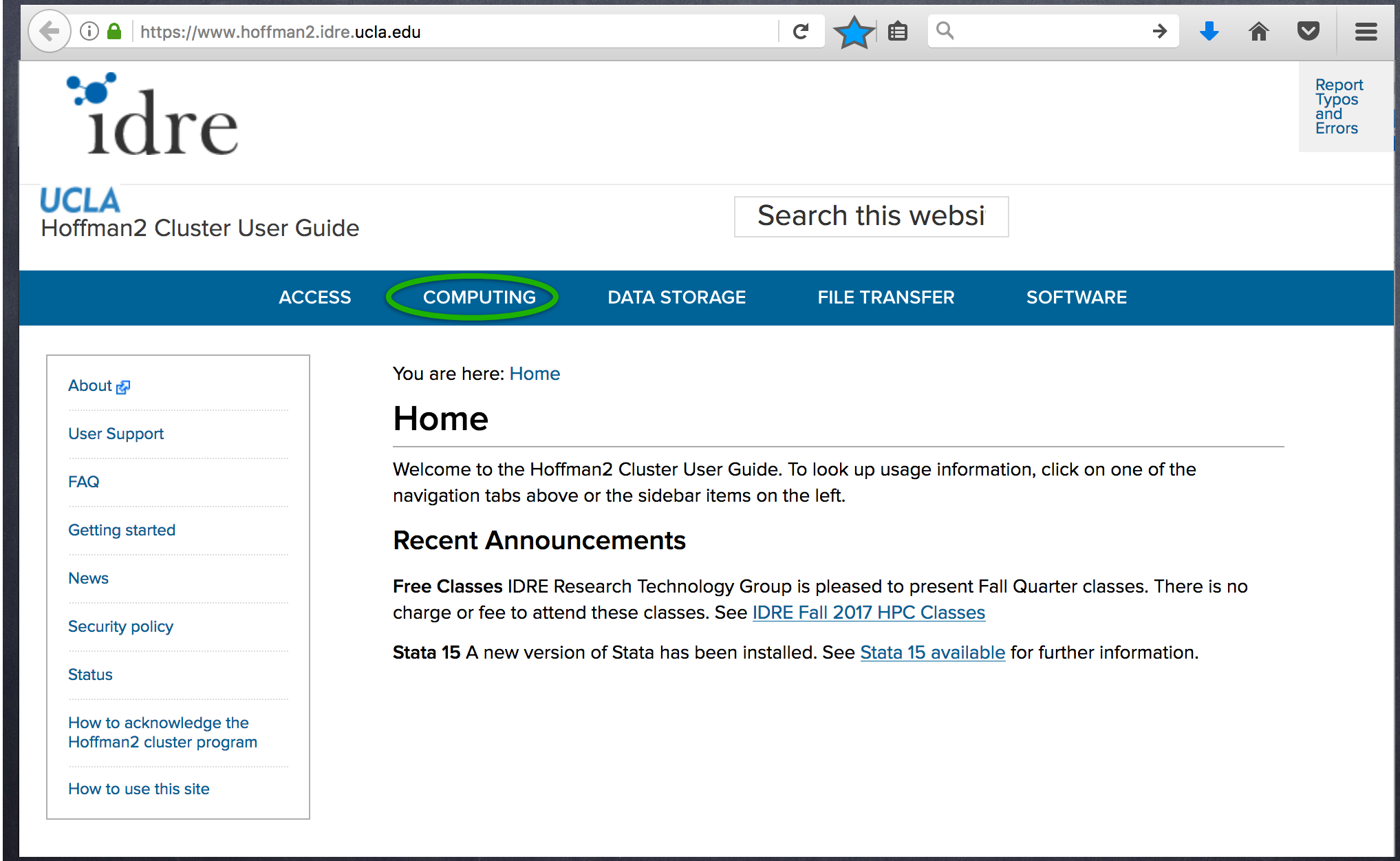
Correction to Intro slide no. 54!

```
[rdtest@n9860 ~]$ ls -t $HOME/.local/bin
run_miso.py    compare_miso     summarize_miso  exon_utils  sam_to_bam      miso
filter_events  miso_zip         plot.py         pe_utils    index_gff       f2py
test_miso      run_events_analysis.py  sashimi_plot  miso_pack  module_availability
[rdtest@n9860 ~]$ which miso
miso: Command not found.
[rdtest@login3 ~]$ echo "export PATH=$HOME/.local/bin:$PATH" >> $HOME/.bash_profile
[rdtest@login3 ~]$ tail -n1 $HOME/.bash_profile
export PATH=/u/home/r/rdtest/.local/bin
[rdtest@login3 ~]$ . /u/home/r/rdtest/.bash_profile
[rdtest@login3 ~]$ which miso
~/.local/bin/miso
```

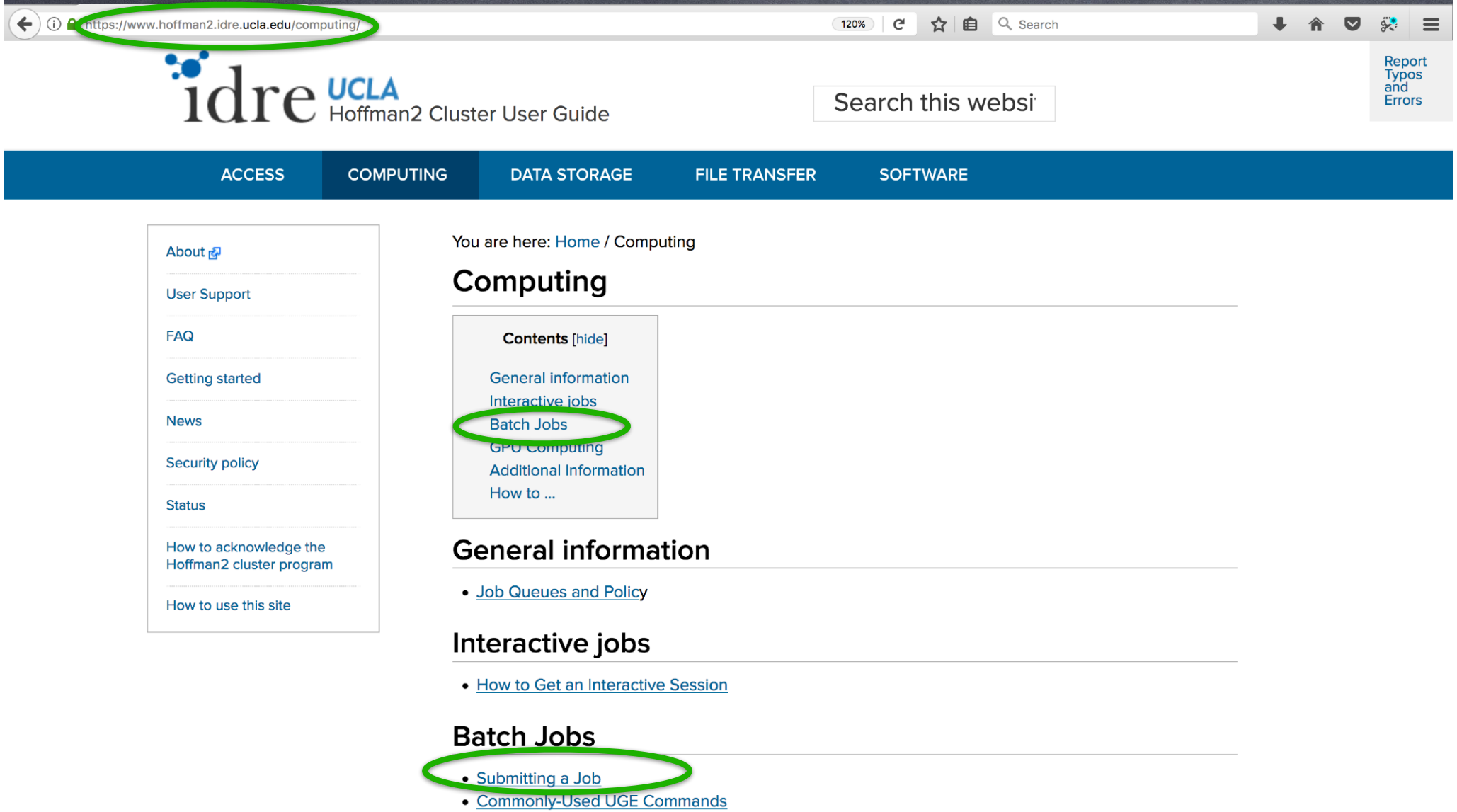
Running a batch job

Why?

Running a batch job



Running a batch job



Running a batch job

```
[rdtest@login3 ~]$ cp /u/local/apps/submit_scripts/submit_job.sh ./
[rdtest@login3 ~]$ ls -lat submit_job.sh
-rwxr--r-- 1 rdtest systems 575 Oct 11 14:05 submit_job.sh
[rdtest@login3 ~]$
```

If submit_job.sh had not been executable we should have issued:

```
[rdtest@login3 ~]$ chmod u+x submit_job.sh
```

To submit the job:

```
[rdtest@login3 ~]$ qsub submit_job.sh
Your job 865688 ("submit_job.sh") has been submitted
[rdtest@login3 ~]$
```

Checking the status of a job in the queue

```
[rdtest@login3 ~]$ myjob
job-ID  prior   name       user    state submit/start at     queue                  slots ja-ta
-----------------------------------------------------------------------------------------
865688 10.00000 submit_job rdtest   r  10/11/2017 14:24:34 c2_smp.q@n9860     1
[rdtest@login3 ~]$
```

If submit_job.sh had been pending its "state" would have been "qw"

```
[rdtest@login3 ~]$ qstat -s p | head -n 6
job-ID  prior   name       user         state   submit/start at     queue                  slots ja-task-ID
-----------------------------------------------------------------------------------------
 861033 5.75286 mayo_cruce caroartc     qw    10/10/2017 22:59:11                    4
 862844 2.87643 QRLOGIN    caroartc     qw    10/11/2017 07:20:43                    4
 121156 1.91801 roms_TEST_ hfrenzel     qw    07/14/2017 11:24:01                   96
 740935 1.91771 in.ThreeD_ tjones19     qw    09/27/2017 12:37:24                   24
```

Anatomy of a batch job script

Shell that will be used

Submission script preamble

#$ scheduler commands

comments

```
#!/bin/bash
#$ -cwd
# error = Merged with joblog
#$ -o joblog.$JOB_ID
#$ -j y
#$ -l h_rt=1:00:00,h_data=1G
# Email address to notify
#$ -M $USER@mail
# Notify when
#$ -m bea

# echo job info on joblog:
echo "Job $JOB_ID started on:   " `hostname -s`
echo "Job $JOB_ID started on:   " `date `
echo " "

# load the job environment:
. /u/local/Modules/default/init/modules.sh
module load <APP>
module li
echo " "

# run <APP>
echo '<execution command>'
<execution command>


# echo job info on joblog:
echo "Job $JOB_ID ended on:   " `hostname -s`
echo "Job $JOB_ID ended on:   " `date `
echo " "
```

Anatomy of a batch job script

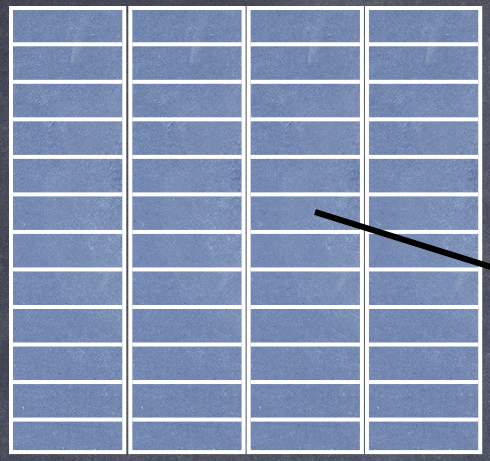
```
[rdtest@login3 ~]$ myjob

You do not have any active SGE jobs currently.


[rdtest@login3 ~]$ cat joblog.865688
Job 865688 started on:    n9860
Job 865688 started on:    Wed Oct 11 14:24:35 PDT 2017


The 'gcc/4.9.3' module is being loaded

pwd; sleep 500
/u/home/r/rdtest
Job 865688 ended on:    n9860
Job 865688 ended on:    Wed Oct 11 14:32:55 PDT 2017

[rdtest@login3 ~]$
```

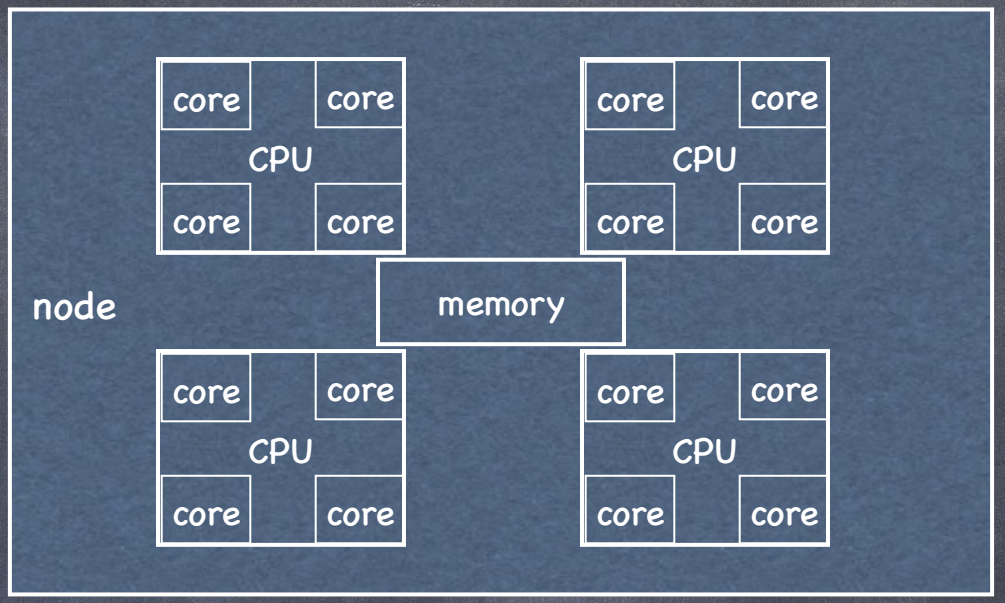
Running a batch job

You can also use our own queue scripts, such as:

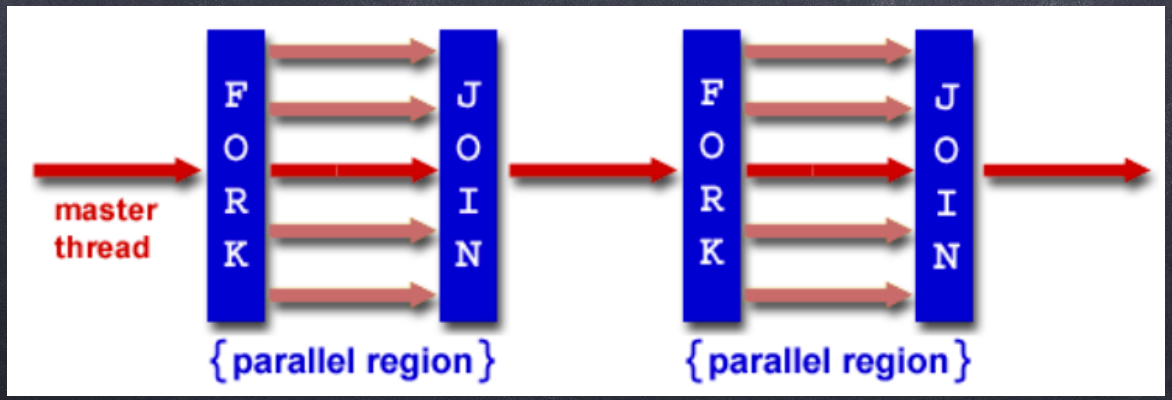
- job.q (serial jobs)
- openmp.q (multiple threads/shared memory jobs)
- intelmpi.q (distributed memory jobs w/ intelmpi)
- openmpi.q (distributed memory jobs w/ openmpi)
- parallel.q (distributed memory jobs DIY)
- <APP>.q:
  - stata.q. (allows serial/multiple threads)
  - R.q (serial only version of R set)
  - etc.
- jobarray.q. (embarrassingly parallel jobs)

Shared Memory jobs





- Use more than one core (slot in queue jargon)
- All cores are from the same node (server/computer)
- The program spawns threads each of which runs on a separate core



Shared Memory jobs

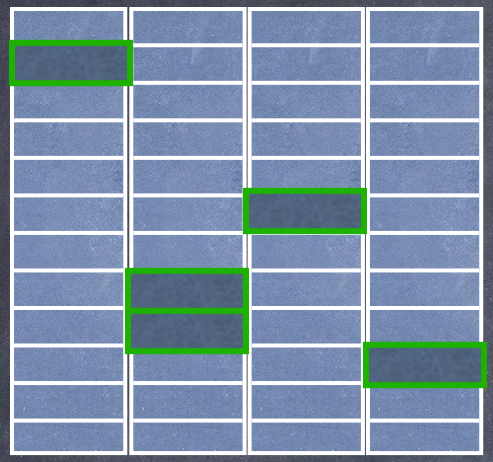
You may be running in shared memory jobs b/c:

- You link to multi-threaded libraries (MKL, blas, lapak, etc.)
- You have explicitly included threads/openmp chunks of code
- You are running an app, developed by a third party, which spawns threads
  - ➡ You should accordingly request multiple cores
    - Either with openmp.q
    - Or generalize your submission script preamble:

```
#!/bin/bash
#$ -cwd
# error = Merged with joblog
#$ -o joblog.$JOB_ID
#$ -j y
#$ -l h_rt=1:00:00,h_data=1G
#$ -pe shared 6
# Email address to notify
#$ -M $USER@mail
# Notify when
#$ -m bea
```

```
#!/bin/bash
#$ -cwd
# error = Merged with joblog
#$ -o joblog.$JOB_ID
#$ -j y
#$ -l h_rt=1:00:00,h_data=1G,exclusive
# Email address to notify
#$ -M $USER@mail
# Notify when
#$ -m bea
```

Distributed memory jobs



racked nodes

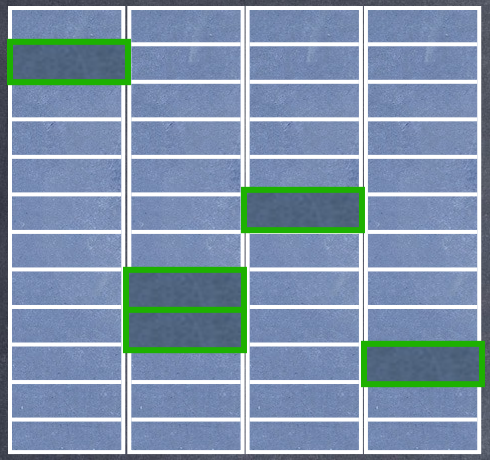
- Each parallel worker has its own private memory space
- All communications is done with message passing (MPI)
- Your code contains parallel instructions

As you need multiple cores possibly coming from multiple nodes

- ➡ Either use intelmpi.q/openmpi.q/parallel.q
- ➡ Or generalize your job script preamble

```
#!/bin/bash
#$ -cwd
# error = Merged with joblog
#$ -o joblog.$JOB_ID
#$ -j y
#$ -l h_rt=1:00:00,h_data=1G
#$ -pe dc* 24
# Email address to notify
#$ -M $USER@mail
# Notify when
#$ -m bea
```

Hybrid distributed memory/shared memory jobs



racked nodes

- Message passing between the nodes
- Shared memory within each node
- Used by:
  - comsol.q (sorry no public licenses)
  - gaussian.q

As you need multiple cores possibly coming from multiple nodes

➡ generalize your job script preamble

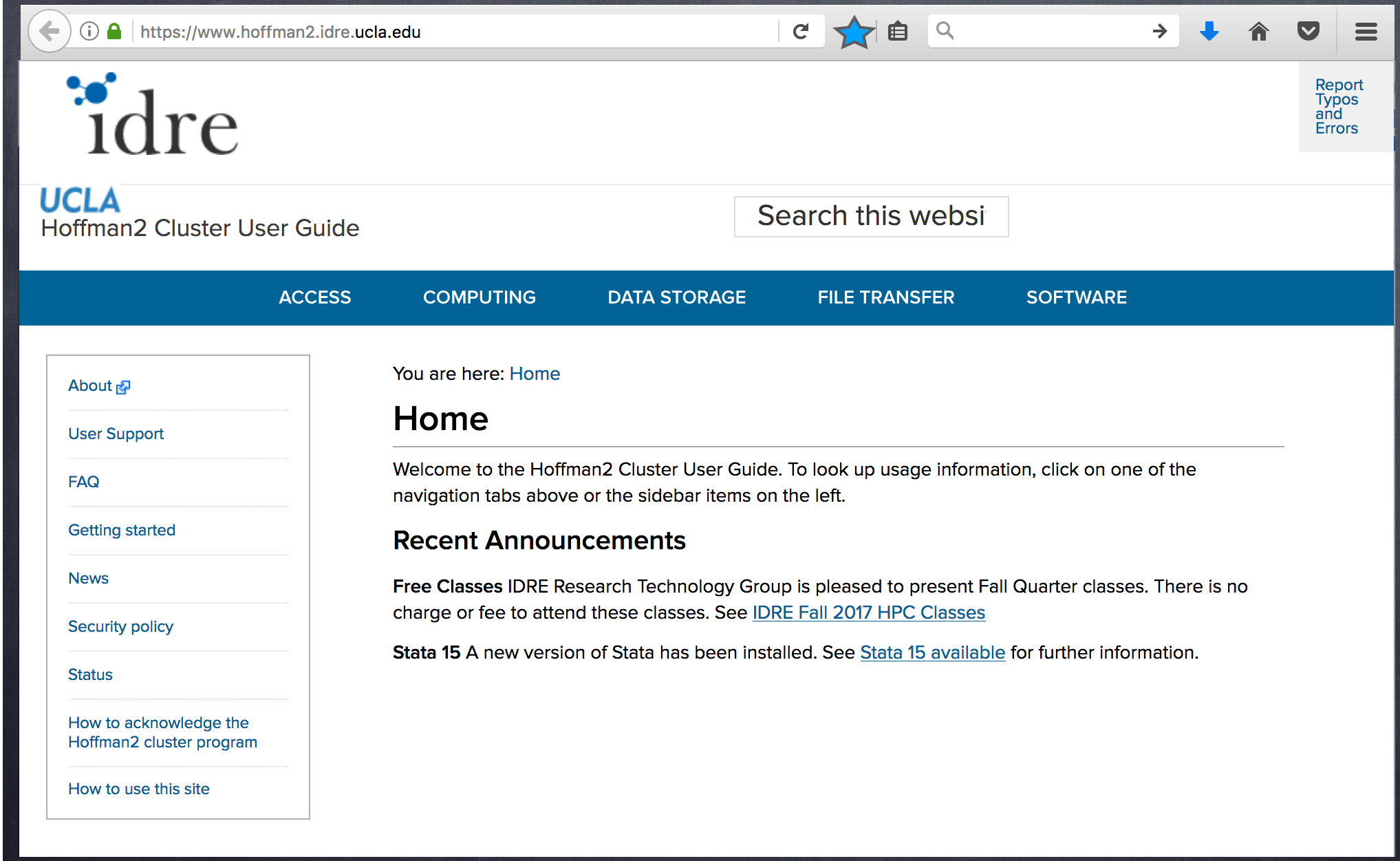
```
#!/bin/bash
#$ -cwd
# error = Merged with joblog
#$ -o joblog.$JOB_ID
#$ -j y
#$ -l h_rt=1:00:00,h_data=1G,exclusive
#$ -pe node 3
# Email address to notify
#$ -M $USER@mail
# Notify when
#$ -m bea
```

Matlab stand-alone executables

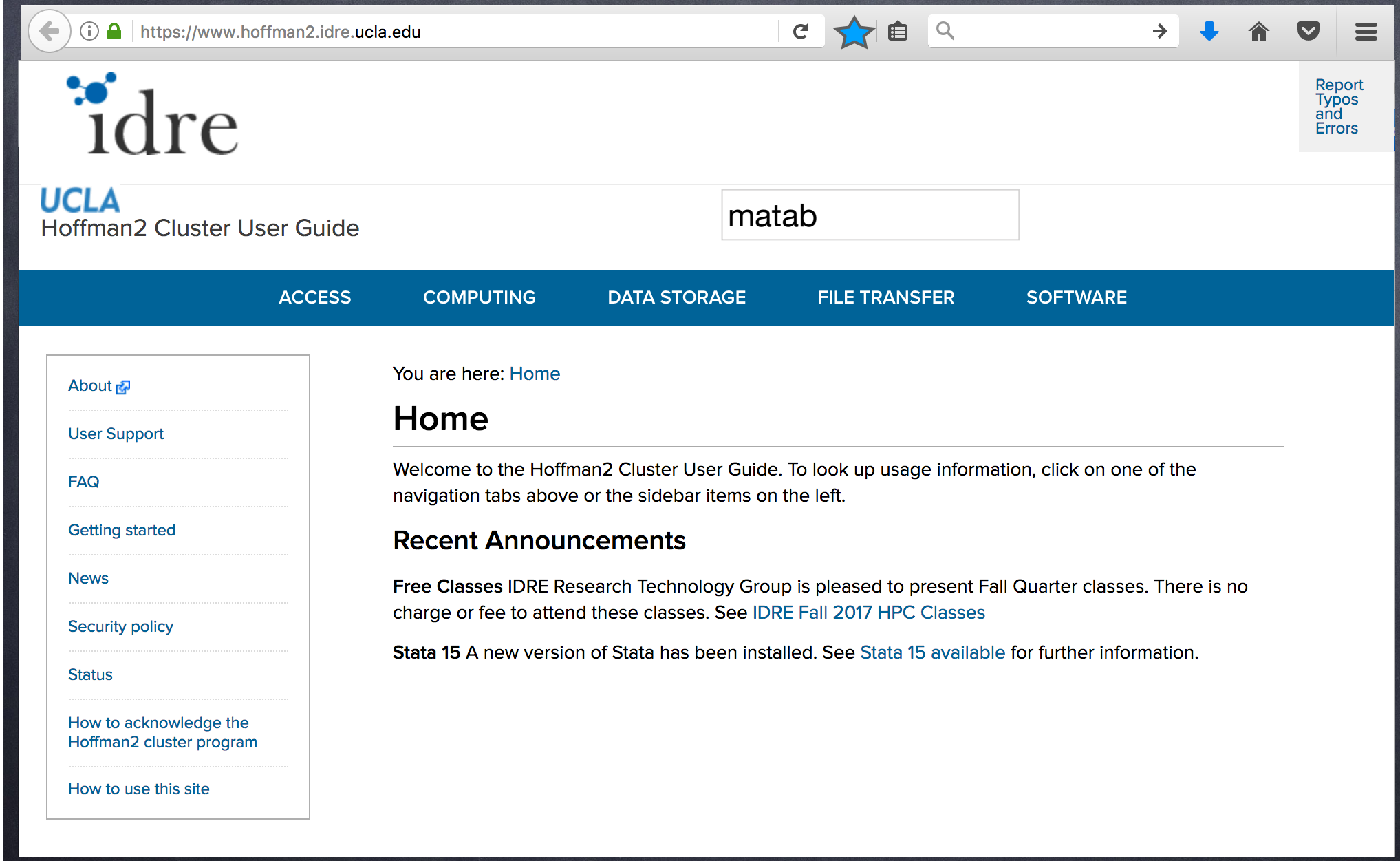
Matlab is a very hot commodity (limited licenses/highly coveted):

- Interactive work checks out a license for the entire time of the session
  - ✳ Please never forget a matlab desktop open
- Batch matlab jobs that run a matlab script also check out a license for the entire duration of the job
- Matlab scripts can be compiled with the matlab compiler!
  - ➡ Matlab stand-alone executables
  - ✳ Licenses are checked out only during compilation!
  - ✳ You can run as many copies of your stand-alone as you will: no license limit!

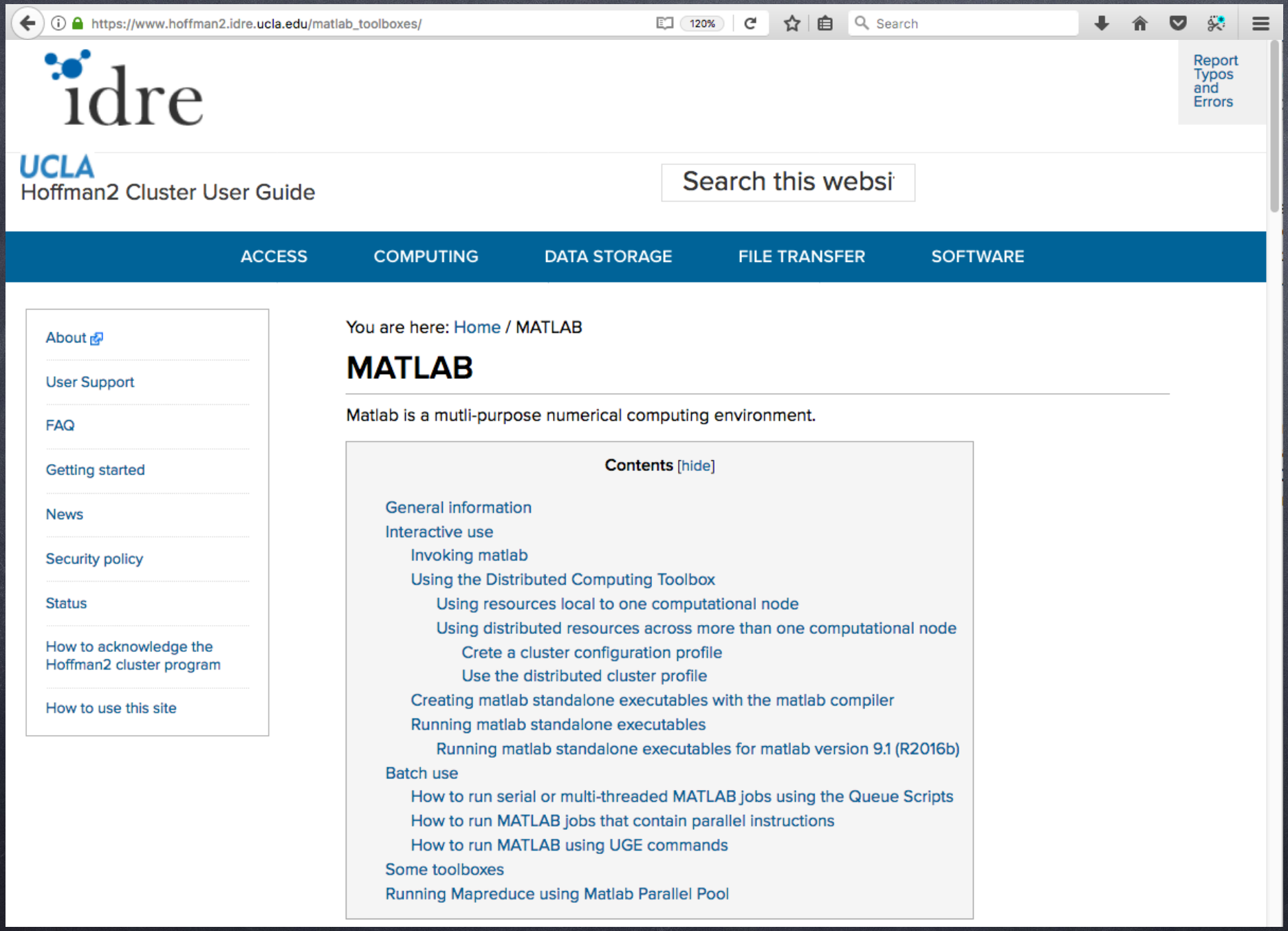
Matlab stand-alone executables



Matlab stand-alone executables



Matlab stand-alone executables



How to generate matlab stand-alone executables

```
[rdtest@login1 ~]$ qrsh -l h_data=3g,h_rt=1:00:00
[rdtest@n9860 ~]$ module load matlab
[rdtest@n9860 ~]$ cat myInverseMatrix.m
% Compute the inverse of a N-by-N random matrix

X = rand(4)
Y = inv(X)
X*Y  % check
[rdtest@n9860 ~]$ mcc -m myInverseMatrix.m
[rdtest@n9860 ~]$ ls -lt
total 124
-rwxr--r-- 1 rdtest systems 92207 Oct 11 18:06 myInverseMatrix
-rwxr--r-- 1 rdtest systems   883 Oct 11 18:06 run_myInverseMatrix.sh
-rw-r--r-- 1 rdtest systems  3801 Oct 11 18:06 readme.txt
-rw-r--r-- 1 rdtest systems    12 Oct 11 18:06 requiredMCRProducts.txt
-rw-r--r-- 1 rdtest systems  1277 Oct 11 18:06 mccExcludedFiles.log
-rw-r--r-- 1 rdtest systems   369 Oct 11 18:00 myInverseMatrix.m
[rdtest@n9860 ~]$ ./myInverseMatrix
```

How to run matlab stand-alone executables

matlab.q

Runs single or multi-processor in two steps: compile and execute

mcc.q

Use the MATLAB compiler to create a stand-alone executable. If you are using mcc.q interactively, it will ask you if you want the executable produced by mcc to use a single processor or not. If you are using mcc.q in command line mode, to create an executable that will run on a single processor specify this argument:

-R -singleCompThread

matexe.q

Run a MATLAB stand-alone executable created with mcc

How to generate matlab stand-alone executables w/ explicit parallel instructions

```
[rdtest@login1 ~]$ qrsh -l h_data=3g,h_rt=1:00:00
[rdtest@n9860 ~]$ module load matlab/9.1_MCR
[rdtest@n9860 ~]$ cat myparpoolexample.m
n=4;
p = parpool('local',n);

tic
ticBytes(gcp);
n = 1024;
A = zeros(n);
parfor (i = 1:n)
    A(i,:) = (1:n) .* sin(i*2*pi/1024);
end
tocBytes(gcp)
toc

delete(p)
[rdtest@n9860 ~]$ mcc -m -R -singleCompThread myparpoolexample.m
[rdtest@n9860 ~]$ ./myparpoolexample
```

How to run matlab stand-alone executables when parallel instructions are explicitly used

/u/local/apps/submit_scripts/**matlab_compile_and_submit.sh**

- Generates and submits a batch job that builds and runs a matlab standalone application out of one or more matlab functions
- Matlab standalone executables support the use of the Distributed Computing Toolox. The maximum number of parallel workers supported on hoffman2 is 16.
- If any part of your matlab code includes a parfor loop you will need to include the following lines:

```
%before the parfor loop, for example for 5 workers and the local
profile:

   p = parpool('local',5);

%after the parfor loop:

   delete(p)
```

How to run matlab stand-alone executables when parallel instructions are explicitly used

```
[rdtest@n9860 ~]$ cp /u/local/apps/submit_scripts/matlab_compile_and_submit.sh ./
[rdtest@n9860 ~]$ ls -l matlab_compile_and_submit.sh
-rwxr--r-- 1 rdtest systems 4783 Oct 11 18:54 matlab_compile_and_submit.sh
[rdtest@n9860 ~]$ ./matlab_compile_and_submit.sh

Usage:
 ./matlab_compile_and_submit.sh  [-t time in hours]
   [ -s number of processes ] [-m memory per process (in GB)]
   [-p parallel environment: 1 for shared 2 for distributed]
   [-f main matlab function] [-f matlab function 2] ... [-f matlab function n]
   [-ns (to build a submission script without submitting the job)]
   [ --help ]

[rdtest@n9860 ~/matlab]$ ./matlab_compile_and_submit.sh -t 1 -s 4 -m 2 -p 1 -f
myparpoolexample.m
Running myparpoolexample on 4 processes each with 2 GB of memory for 1 hour
[rdtest@n9860 ~/matlab]$
```

Abaqus python scripts

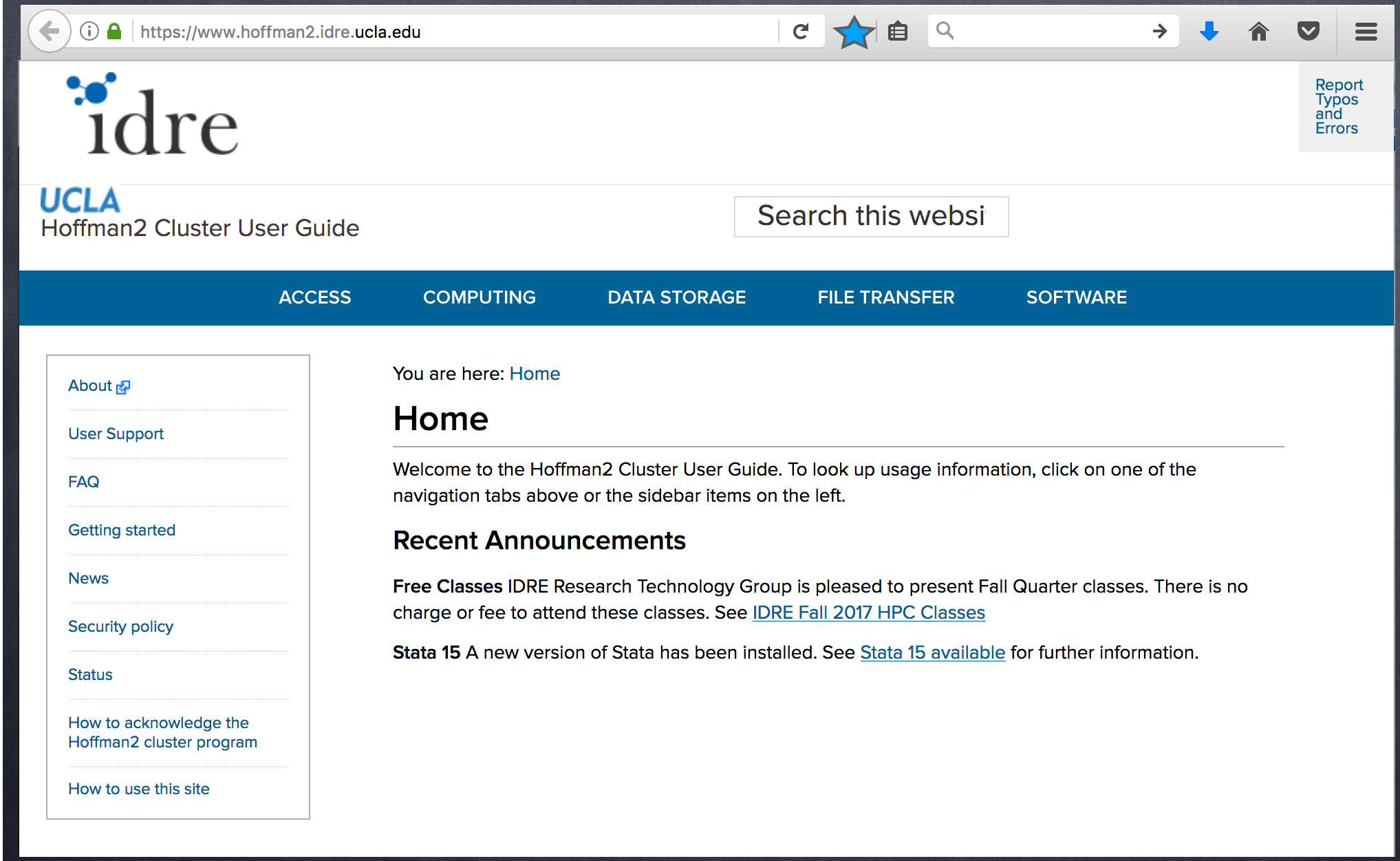
```
[rdtest@login1 ~]$ qrsh -l h_data=3g,h_rt=1:00:00
[rdtest@n9860 ~]$ module load abaqus
[rdtest@n9860 ~]$ abaqus cae &
```

This will open the Abaqus desktop from which you can do pre/post processing.

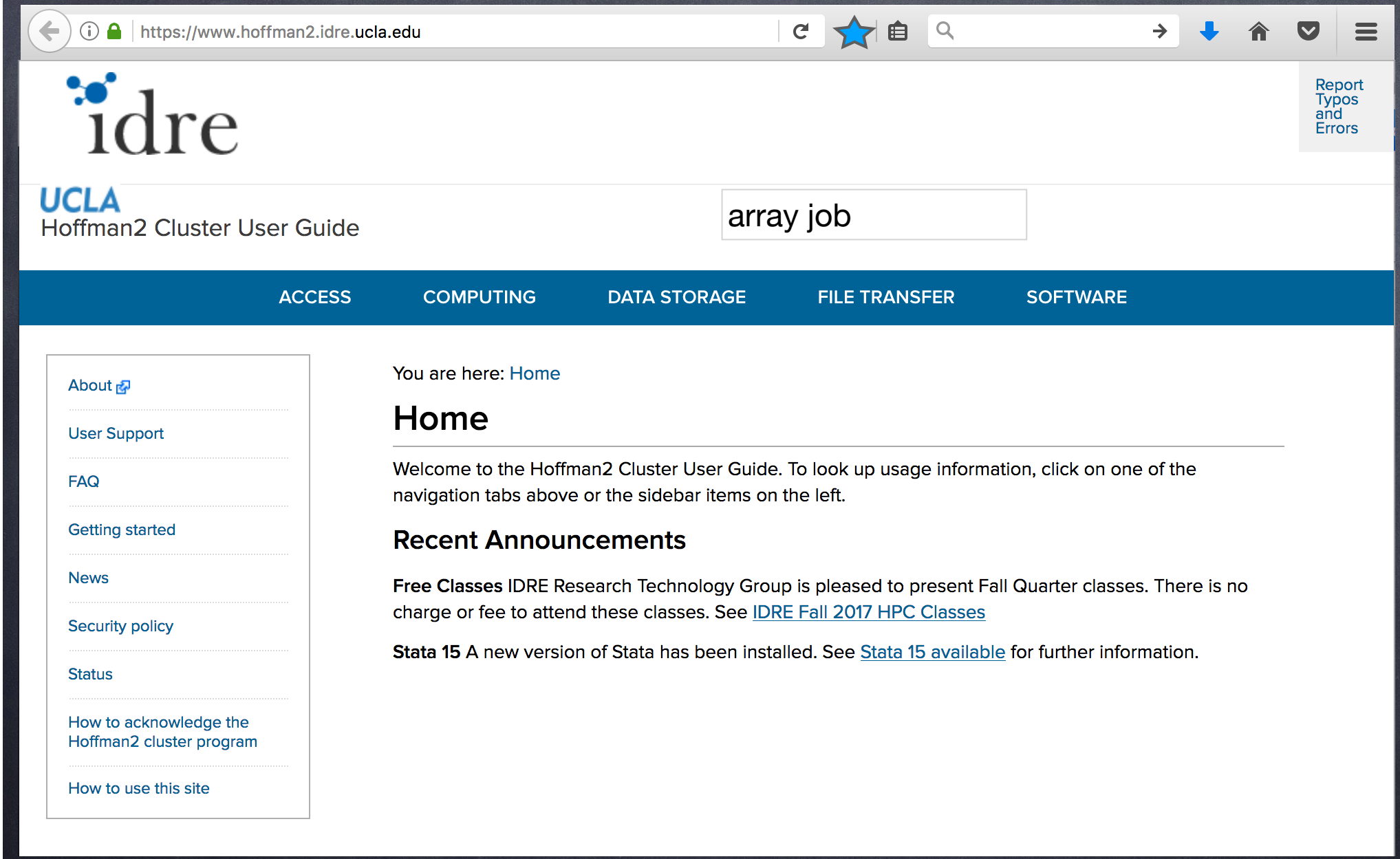
If you already have your abaqus python script:

```
[rdtest@login1 ~]$ qrsh -l h_data=3g,h_rt=1:00:00
[rdtest@n9860 ~]$ module load abaqus
[rdtest@n9860 ~]$ abaqus cae noGUI=test.py -- <input 1> <input 2> ... >> test.output
```

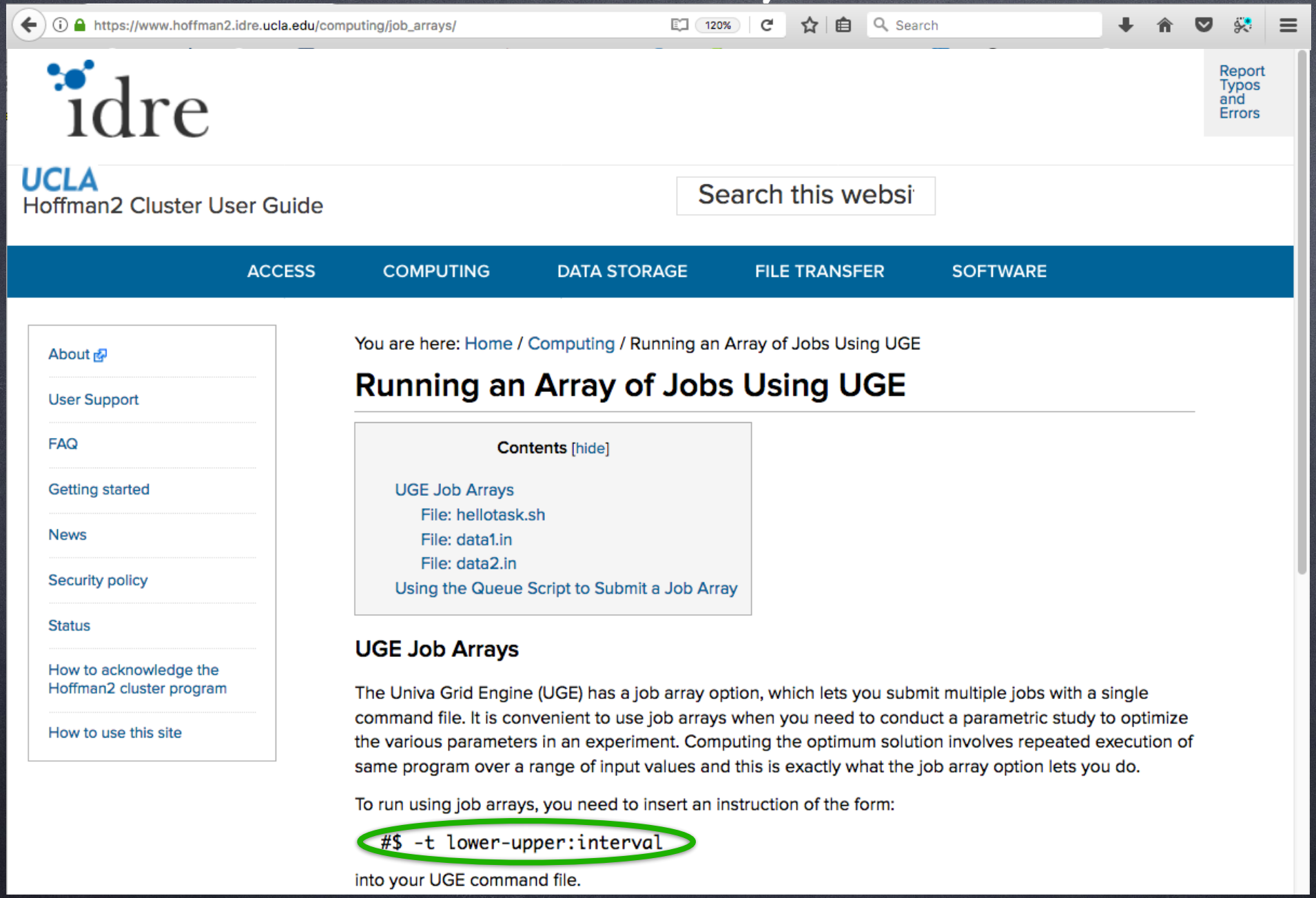
Job Arrays


https://www.hoffman2.idre.ucla.edu
idre
Report Typos and Errors
UCLA
Hoffman2 Cluster User Guide
Search this websi
ACCESS
COMPUTING
DATA STORAGE
FILE TRANSFER
SOFTWARE
About
User Support
FAQ
Getting started
News
Security policy
Status
How to acknowledge the Hoffman2 cluster program
How to use this site
You are here: Home
Home
Welcome to the Hoffman2 Cluster User Guide. To look up usage information, click on one of the navigation tabs above or the sidebar items on the left.
Recent Announcements
Free Classes IDRE Research Technology Group is pleased to present Fall Quarter classes. There is no charge or fee to attend these classes. See IDRE Fall 2017 HPC Classes
Stata 15 A new version of Stata has been installed. See Stata 15 available for further information.

Job Arrays


https://www.hoffman2.idre.ucla.edu
idre
Report Typos and Errors
UCLA
Hoffman2 Cluster User Guide
array job
ACCESS
COMPUTING
DATA STORAGE
FILE TRANSFER
SOFTWARE
About
User Support
FAQ
Getting started
News
Security policy
Status
How to acknowledge the Hoffman2 cluster program
How to use this site
You are here: Home
Home
Welcome to the Hoffman2 Cluster User Guide. To look up usage information, click on one of the navigation tabs above or the sidebar items on the left.
Recent Announcements
Free Classes IDRE Research Technology Group is pleased to present Fall Quarter classes. There is no charge or fee to attend these classes. See IDRE Fall 2017 HPC Classes
Stata 15 A new version of Stata has been installed. See Stata 15 available for further information.

Job Arrays


https://www.hoffman2.idre.ucla.edu/computing/job_arrays/
120%
Search
idre
Report Typos and Errors
UCLA
Hoffman2 Cluster User Guide
Search this websi
ACCESS
COMPUTING
DATA STORAGE
FILE TRANSFER
SOFTWARE
About
User Support
FAQ
Getting started
News
Security policy
Status
How to acknowledge the Hoffman2 cluster program
How to use this site
You are here: Home / Computing / Running an Array of Jobs Using UGE
Running an Array of Jobs Using UGE
Contents [hide]
UGE Job Arrays
File: hellotask.sh
File: data1.in
File: data2.in
Using the Queue Script to Submit a Job Array
UGE Job Arrays
The Univa Grid Engine (UGE) has a job array option, which lets you submit multiple jobs with a single command file. It is convenient to use job arrays when you need to conduct a parametric study to optimize the various parameters in an experiment. Computing the optimum solution involves repeated execution of same program over a range of input values and this is exactly what the job array option lets you do.
To run using job arrays, you need to insert an instruction of the form:
#$ -t lower-upper:interval
into your UGE command file.

Array jobs: submit multiple jobs with a single command file

- can your job be broken down in a series of tasks that are totally independent one from the other?
  - generally not if you are predicting tomorrows weather...
  - great if you are doing a parametric study

```
#!/bin/sh
echo “Task id is $SGE_TASK_ID”
if [ -e $HOME/JOBARRAY/data$SGE_TASK_ID.in ]; then
while read file
do
echo “hello $file”
done < $HOME/JOBARRAY/data$SGE_TASK_ID.in
fi
```

Array jobs: submit multiple jobs with a single command file

```
[rdtest@login1 ~]$  mkdir $HOME/JOBARRAY
[rdtest@login1 ~]$  cd $HOME/JOBARRAY
[rdtest@login1 ~/JOBARRAY]$  cp /u/local/apps/submit_scripts/array_jobs/hellotask.sh ./
[rdtest@login1 ~/JOBARRAY]$  cp /u/local/apps/submit_scripts/array_jobs/data*.in ./
[rdtest@login1 ~/JOBARRAY]$  jobarray.q

Enter to continue.

jobarray Serial UGE job script
Functions (acceptable abbreviations are shown in CAPS)
  Menu:      Display this menu
  Info:      Display help information
  Build:     Build   a UGE .cmd file for jobarray
  Submit:    Submit  a UGE .cmd file for execution
  STatus:    Display the status of UGE jobs for rdtest
  SYsstat:   Display the status of UGE jobs for the system
  Hold:      Hold    a UGE job
  RELease:   Release a UGE job that is held
  RESet      Reset   the priority of a UGE job
  Cancel:    Cancel  a UGE job
  Quit:      Exit    this script

Command:  b

Enter the name of the Job array program or script to be executed
<or quit>:  hellotask.sh
[…]
```

Array jobs

```
[rdtest@login1 ~/JOBARRAY]$  head nn 35 hello task.sh.cmd
#!/bin/csh -f
#  hellotask.sh.cmd
#
#  UGE job for hellotask.sh built Wed Oct 11 20:51:21 PDT 2017
#
#  The following items pertain to this script
#  Use current working directory
#$ -cwd
#  input           = /dev/null
#  output          = /u/home/r/rdtest/matlab/ARRAYJOBS/hellotask.sh.joblog.$JOB_ID.$TASK_ID
#$ -o /u/home/r/rdtest/matlab/ARRAYJOBS/hellotask.sh.joblog.$JOB_ID.$TASK_ID
#  error           = Merged with joblog
#$ -j y
#  The following items pertain to the user program
#  user program    = /u/home/r/rdtest/matlab/ARRAYJOBS/hellotask.sh
#  arguments       =
#  program input   = Specified by user program
#  program output  = Specified by user program
#  Resources requested
#
#$ -l h_data=1024M,h_rt=1:00:00
# #
#  Name of application for log
#$ -v QQAPP=job
#  Email address to notify
#$ -M rdtest@mail
#  Notify at beginning and end of job
#$ -m a
#  Job is not rerunable
#$ -r n
#
#  Job array indexes
#$ -t 1-2:1
[…]
```

Array jobs

```
[rdtest@login1 ~/JOBARRAY]$  ls -lt
total 24
-rw-r--r-- 1 rdtest systems  547 Oct 11 20:52 hellotask.sh.joblog.868129.2
-rw-r--r-- 1 rdtest systems  149 Oct 11 20:52 hellotask.sh.output.868129.2
-rw-r--r-- 1 rdtest systems  544 Oct 11 20:52 hellotask.sh.joblog.868129.1
-rw-r--r-- 1 rdtest systems  149 Oct 11 20:52 hellotask.sh.output.868129.1
-rwxr--r-- 1 rdtest systems 3165 Oct 11 20:51 hellotask.sh.cmd
-rw-r--r-- 1 rdtest systems   13 Oct 11 20:50 data2.in
-rw-r--r-- 1 rdtest systems   13 Oct 11 20:50 data1.in
-rwxr--r-- 1 rdtest systems  183 Oct 11 20:50 hellotask.sh
[rdtest@n9860 ~/JOBARRAY]$ head -n3 hellotask.sh.output.868129.1
"Task id is 1"
"hello first"
"hello second"
```

If your job can be broken in 100s, or 1000s or 10,000s independent tasks you are in business!!!

Array jobs R example

```
[rdtest@login3 R]$ cp /u/local/apps/submit_scripts/array_jobs/R/test_array.R ./
[rdtest@login3 R]$ cp /u/local/apps/submit_scripts/array_jobs/R/submit_R_array.sh./
[rdtest@login3 R]$ cat test_array.R
```

```
options(echo=TRUE) # if you want see commands in output file
args <- commandArgs(trailingOnly = TRUE)
print(args)
n <- length(args)
print(n)
suff <- args[n]
outputfile <- paste("myout", ".",suff, sep="")
write(args, file=outputfile,ncolumns = n,
       append = FALSE, sep = " ")
Sys.sleep(120)
```

Array jobs R example

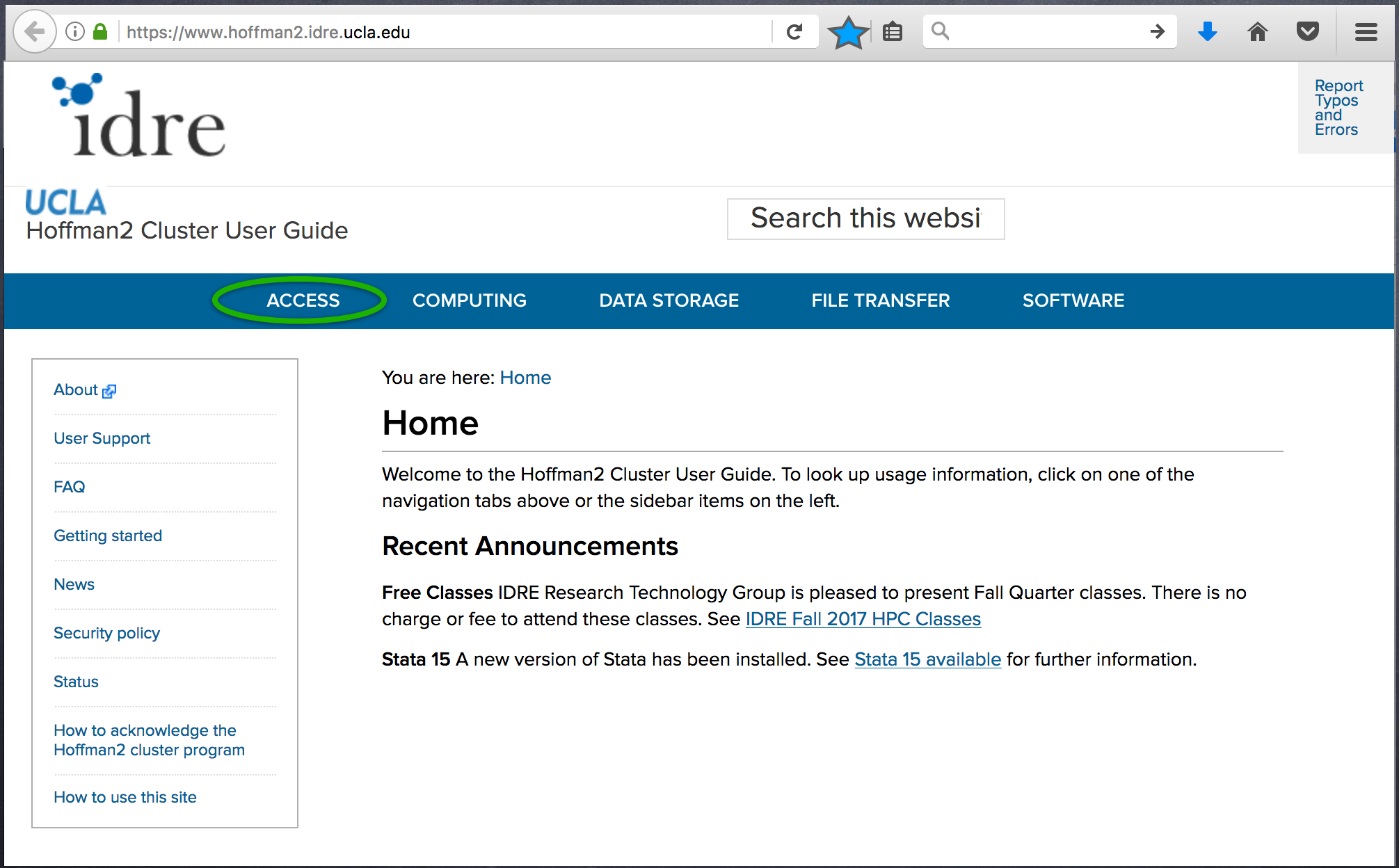
[rdtest@login3 R]$ cat submit_R_array.sh

```
#!/bin/bash
#$ -cwd
#$ -o  test.joblog.$JOB_ID.$TASK_ID
#$ -j y
#  Resources requested:
#$ -l h_data=1g,h_rt=2:00:00
#  Email address to notify
#$ -M $USER@mail
#$ -m bea
#$ -t 1-3:1


  echo ""
  echo "test started on:   "` hostname -s `
  echo "test started at:   "` date `
  echo ""
#
  . /u/local/Modules/default/init/modules.sh
  module load R

  echo “Task id is $SGE_TASK_ID”

#
# Run the user program
#

R CMD BATCH --no-save --no-restore "--args $SGE_TASK_ID" ./test_array.R \
 test_array.out.${JOB_ID}.$SGE_TASK_ID
```

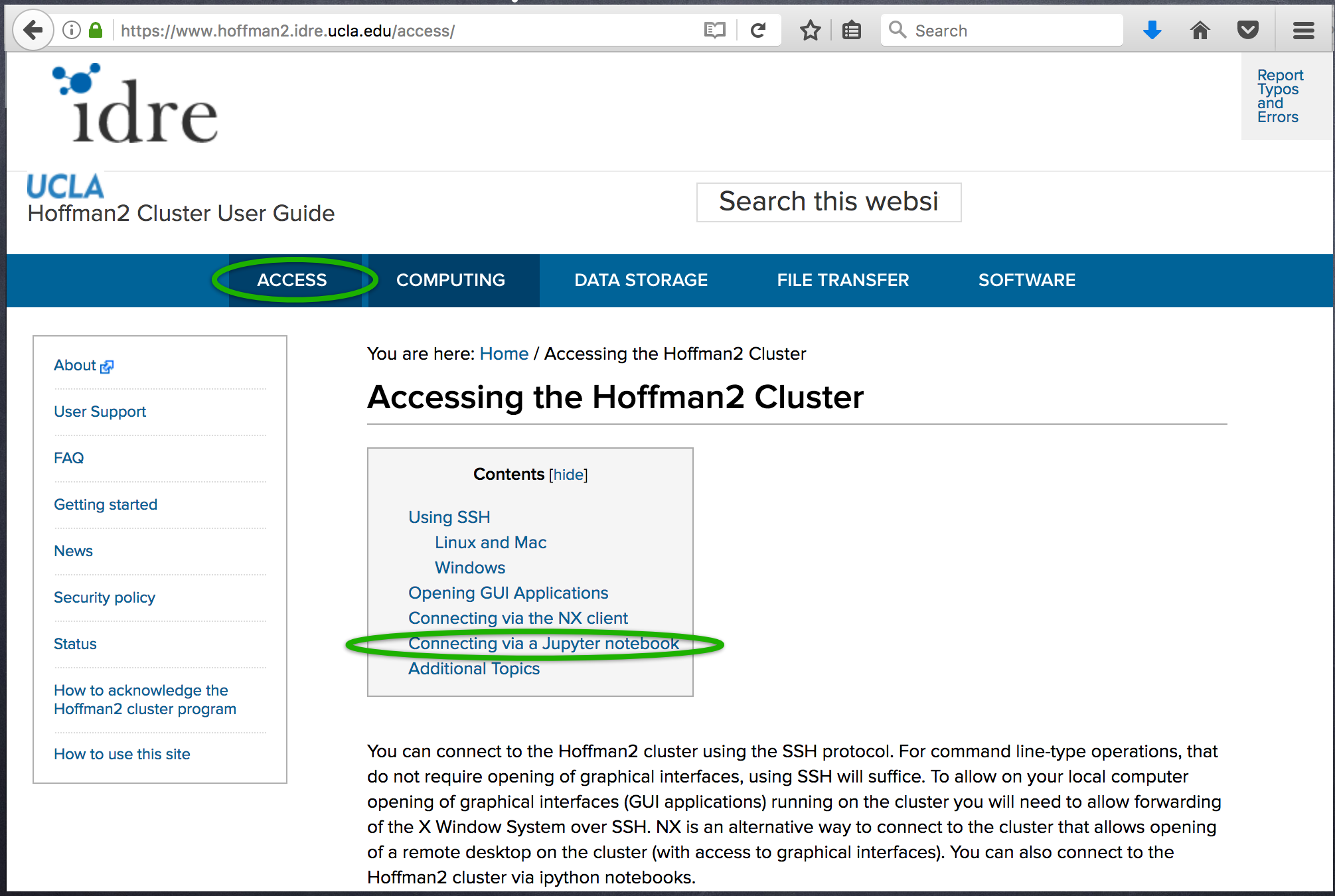
Array jobs in R

```
[rdtest@login3 R]$ chmod u+x submit_R_array.sh
[rdtest@login3 R]$ qsub submit_R_array.sh
Your job-array 868598.1-3:1 ("submit_R_array.sh") has been submitted
[rdtest@login3 R]$ ls -lt
total 32
-rw-r--r-- 1 rdtest systems 1093 Oct 11 21:40 test_array.out.868598.3
-rw-r--r-- 1 rdtest systems 1093 Oct 11 21:40 test_array.out.868598.2
-rw-r--r-- 1 rdtest systems 1093 Oct 11 21:40 test_array.out.868598.1
-rw-r--r-- 1 rdtest systems    2 Oct 11 21:38 myout.3
-rw-r--r-- 1 rdtest systems    2 Oct 11 21:38 myout.1
-rw-r--r-- 1 rdtest systems    2 Oct 11 21:38 myout.2
-rw-r--r-- 1 rdtest systems   94 Oct 11 21:38 test.joblog.868598.3
-rw-r--r-- 1 rdtest systems   94 Oct 11 21:38 test.joblog.868598.2
-rw-r--r-- 1 rdtest systems   94 Oct 11 21:38 test.joblog.868598.1
-rwxr--r-- 1 rdtest systems  529 Oct 11 21:29 submit_R_array.sh
-rw-r--r-- 1 rdtest systems  295 Oct 11 21:28 test_array.R
```

Jupyter notebooks



Jupyter notebooks



Jupyter notebooks

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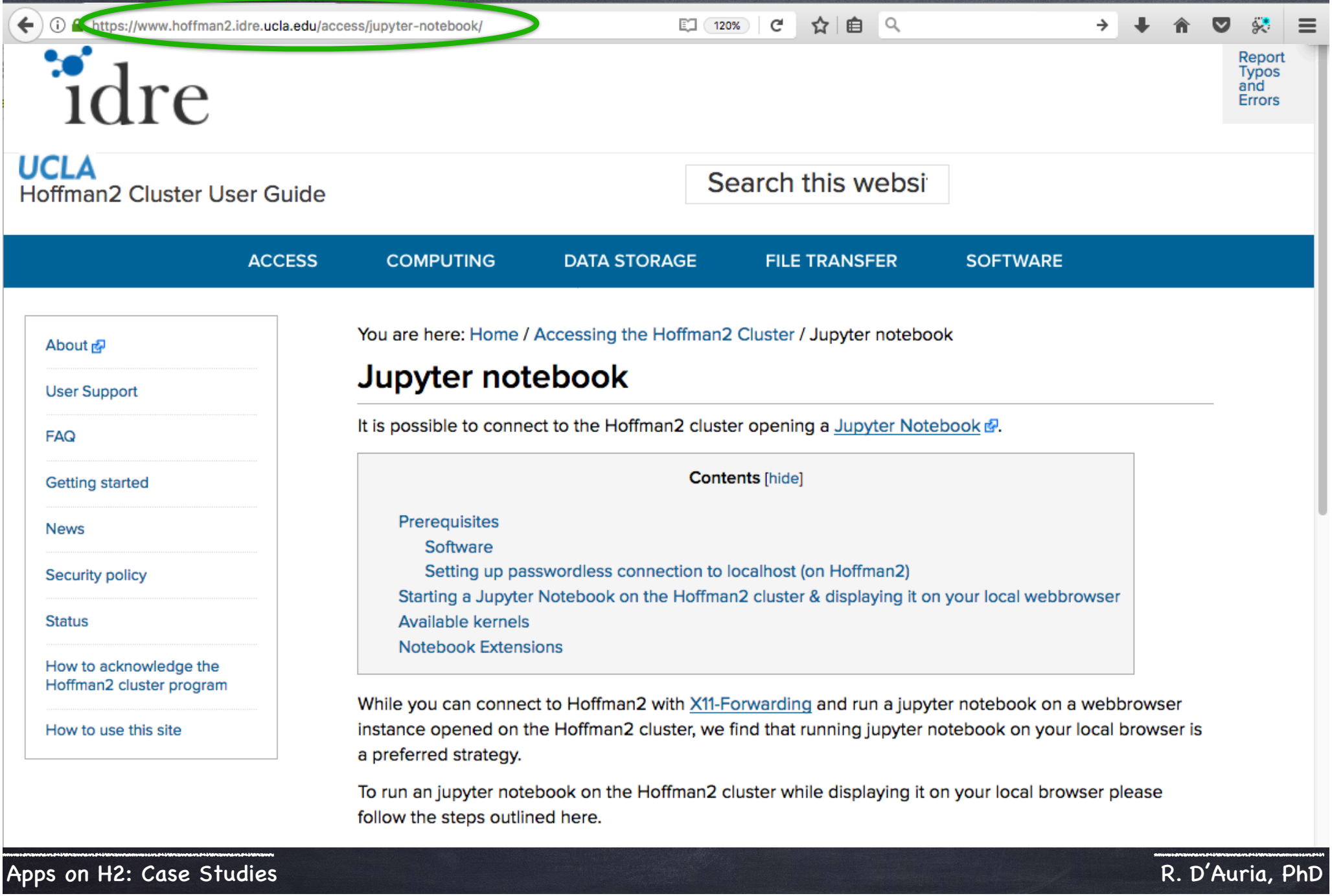
Accessing the Hoffman2 Cluster

Contents [hide]

You can connect to the Hoffman2 cluster using the SSH protocol. For command line-type operations, that do not require opening of graphical interfaces, using SSH will suffice. To allow on your local computer opening of graphical interfaces (GUI applications) running on the cluster you will need to allow forwarding of the X Window System over SSH. NX is an alternative way to connect to the cluster that allows opening of a remote desktop on the cluster (with access to graphical interfaces). You can also connect to the Hoffman2 cluster via ipython notebooks.

Jupyter notebooks



Running R on the Hoffman2 cluster

- for interactive use:
  - ssh -X <youruserid>@hoffman2.idre.ucla.edu
  - qrsh -l h_data=1g,h_rt=2:00:00 -pe shared 8
  - export OMP_NUM_THREADS=8
  - module load R/3.3.3
  - R
- for batch use:
  - ssh <youruserid>@hoffman2.idre.ucla.edu
  - R333.q
- for notebook use:
  - you will need:
    - a terminal (cygwin if on windows)
    - a local installation of python (version 2.6 or greater)
    - a web browser
  - navigate to:
  - https://www.hoffman2.idre.ucla.edu/access/jupyter-notebook/
  - download the script: h2jupynb
  - run:
    - python h2jupynb
  - run R from your web browser…

Running python on the Hoffman2 cluster

- for interactive use:
  - `ssh -X <youruserid>@hoffman2.idre.ucla.edu`
  - `qrsh -l h_data=1g,h_rt=2:00:00 -pe shared 8`
  - `export OMP_NUM_THREADS=8`
  - `module load python/2.7.13`
  - `python`
- for batch use:
  - `ssh <youruserid>@hoffman2.idre.ucla.edu`
  - `Write a submission script or use multithread.q`
- for notebook use:
  - `python h2jupynb`

Jupyter notebooks

```
dauria@alba:~> jupyter-notebook/h2jupynb --help
Usage:

      h2jupynb [-u <Hoffman2 user name>] [-t <time in hours>] [-m <memory in GB>]
               [-s <number of slots>] [-v <python-version>] [-p <port>] [-d <dir>]

If no arguments are given to this script it is assumed that:
      your Hoffman2 user name is the same as on your client machine
      the time duration for your session is of 2 hours
      the memory per slot for your session is of 1GB
      the number of slots for your session is of 1
      the python version for your notebook is 2.7.13
      the port on which the server is started is 8789
      the starting directory on Hoffman2 is your $HOME

      python versions currently available are 2.7.13 or 3.6.1

      python versions: 2.7.3 or 3.4 are available but deprecated.
```

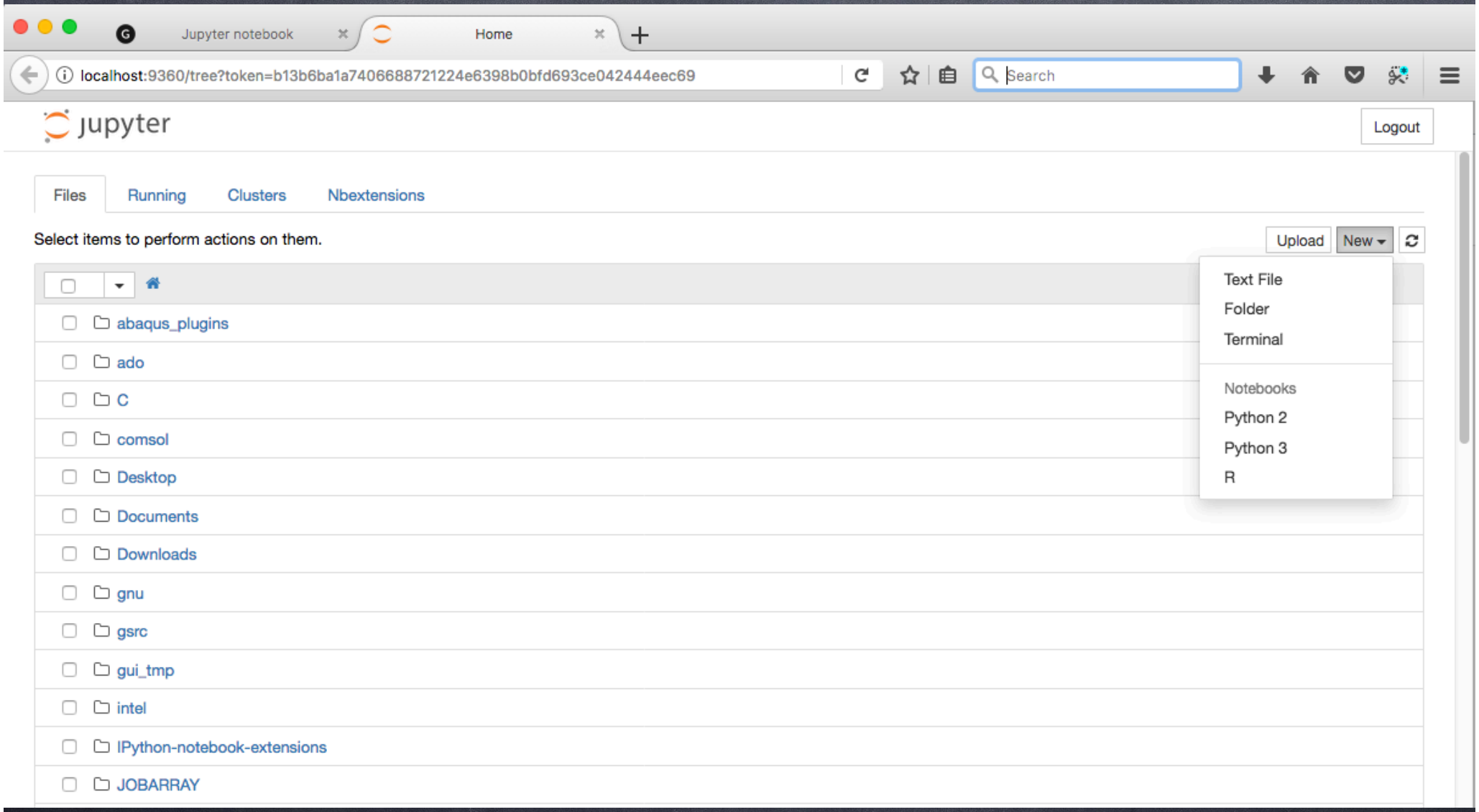
Jupyter notebooks

```
dauria@alba:~> jupyter-notebook/h2jupynb -u rdtest

Your Hoffman2 user name is rdtest
The time in hours is 2
The memory in GB per slots is 1
The number of slots is 1
The version of python for the notebook is 2.7.13
The port is 9360
The directory on Hoffman2 is $HOME
rdtest@hoffman2.idre.ucla.edu's password:  <- enter password here

Last login: Sat Oct  7 17:05:00 2017 from cpe-76-91-252-105.socal.res.rr.com

Welcome to the Hoffman2 Cluster!
[...]

qrsh -N JUPYNB -l i,h_rt=2:00:00,h_data=1g -pe dc\* 1
module load python/2.7.13
echo HOSTNAME=`hostname`
[rdtest@login4 ~]$ qrsh -N JUPYNB -l i,h_rt=2:00:00,h_data=1g -pe dc\* 1
```

Jupyter notebooks

```
module load python/2.7.13
echo HOSTNAME=`hostname`
[rdtest@n2188 ~]$ module load python/2.7.13

[...]

[rdtest@n2188 ~]$ echo HOSTNAME=`hostname`

HOSTNAME=n2188
[rdtest@n2188 ~]$ jupyter notebook --port=9360

[...]

        http://localhost:9360/?token=b13b6ba1a7406688721224e6398b0bfd693ce042444eec69

ssh -4 -t -Y rdtest@hoffman2.idre.ucla.edu -L 9360:localhost:9360 ssh -t -Y n2188 -L 9360:localhost:9360
Pseudo-terminal will not be allocated because stdin is not a terminal.
rdtest@hoffman2.idre.ucla.edu's password:          <- enter password here
Warning: No xauth data; using fake authentication data for X11 forwarding.
Pseudo-terminal will not be allocated because stdin is not a terminal.
Warning: no access to tty (Bad file descriptor).
Thus no job control in this shell.
TUNNEL
Succesfully opened notebook!
Kill this process to end your notebook connection.
```

Jupyter notebooks



localhost:7114/notebooks/jupyter_R_example_approx_of_pi.ipynb

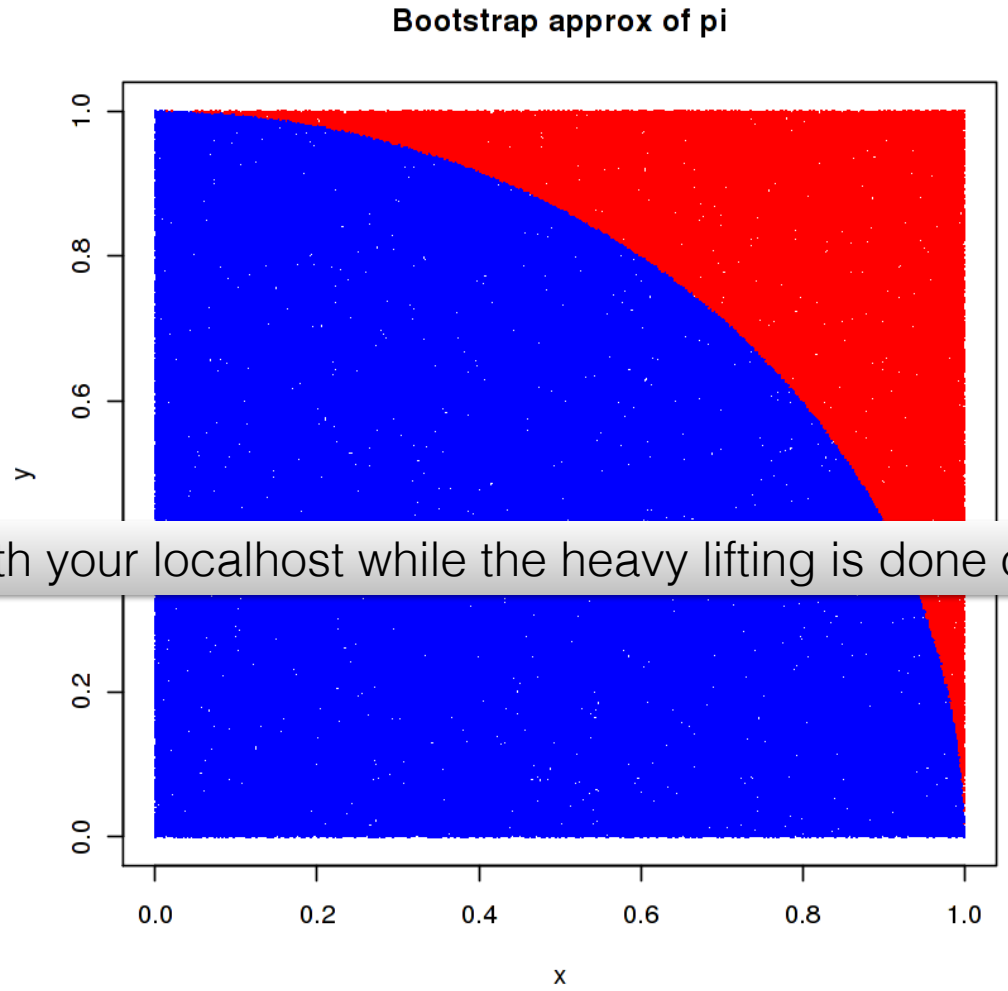
jupyter jupyter_R_example_approx_of_pi Last Checkpoint: 04/07/2017 (autosaved) Logout

File Edit View Insert Cell Kernel Help

Code CellToolbar

In [2]:
```
n <- 9000000
x <- runif(n); y <- runif(n)
inside <- x^2+y^2 <= 1
pi <- 4*sum(inside)/n
idx <- sample.int(trunc(n/(log(n))), replace=FALSE)
x <- x[idx]; y <- y[idx]; inside <- inside[idx]
plot(x,y, col=ifelse(inside,"blue","red"), cex = 0.5, pch = ".", main = sprintf("Bootstrap approx of pi", n, pi))
print(pi)
```

```
[1] 3.141733
```



You interact with your localhost while the heavy lifting is done on the cluster!!!

localhost:7432/notebooks/plot_w_jupyter_nb.ipynb

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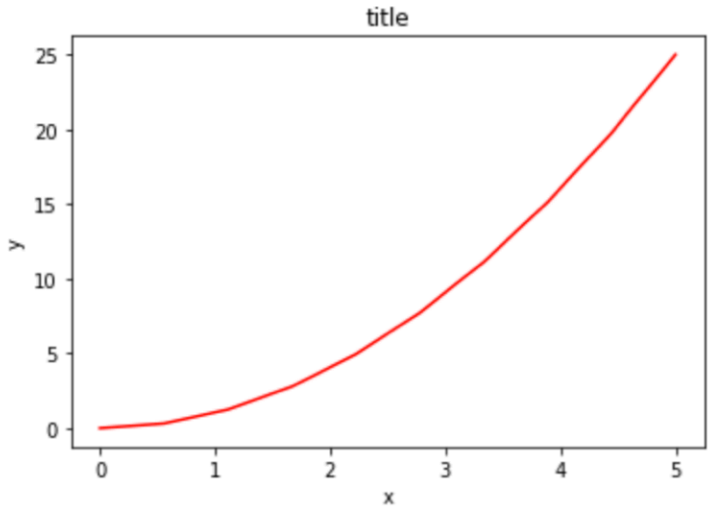
jupyter plot_w_jupyter_nb (autosaved) Logout

File Edit View Insert Cell Kernel LaTeX_envs Help Python 2

Code CellToolbar

In [1]:
```
%pylab inline
from pylab import *
import matplotlib.pyplot as plt
from pylab import *
x = linspace(0, 5, 10)
y = x ** 2
figure()
plot(x, y, 'r')
xlabel('x')
ylabel('y')
title('title')
show()
```

```
Populating the interactive namespace from numpy and matplotlib
```



In [ ]:

Jupyter notebook

```
Warning: No xauth data; using fake authentication data for X11 forwarding.
Pseudo-terminal will not be allocated because stdin is not a terminal.
Warning: no access to tty (Bad file descriptor).
Thus no job control in this shell.
TUNNEL
Succesfully opened notebook!
Kill this process to end your notebook connection.
^C Traceback (most recent call last):
  File "jupyter-notebook/h2jupynb", line 242, in <module>
    time.sleep(timeinhours*3600)
KeyboardInterrupt
Killed by signal 2.
```