

Introduction to Using the HD Human Neuroscience Institute (hd-hni) Cluster Cornell Center for Advanced Computing

hd-hni.cac.cornell.edu

http://www.cac.cornell.edu/wiki/index.php?title=HD_Human_Neuroscience_Institute_(HD-HNI)_Computing

www.cac.cornell.edu



/home



It is for your benefit to always use the scheduler.



ssh –Y netid@hd-hni.cac.cornell.edu



COMMON LINUX COMMANDS

ls	mkdir	diff	pushd
cd	fg	touch	popd
cat	bg	chmod	source
grep	ssh	alias	sort
find	if	umask	sleep
less	for	head	pushd
echo	export	tail	popd
pwd	cut	top	ps
exit	sed	tar	nohup
rm	awk	mv	time
logout	make	ln	date
man	xargs	expr	

Create your job script

Dear Scheduler,

I'd like you TODO

pwd

/home/fs01/netid

mkdir bin

vi bin/testjob.sh



sensible gedit programmer eclipse get-it-done nano do-it-all emacs did what? vi

PBS DIRECTIVES

Input - Program - Output

#!/bin/bash #PBS -1 walltime=00:05:00,nodes=1:ppn=4 #PBS -j oe **#PBS** -N testdefaultqueue #PBS -q default # Turn on echo of shell commands set -x # Because jobs start in the HOME directory, move to submit dir cd \$PBS O WORKDIR echo 'pwd' echo "PBS O WORKDIR is `pwd`" echo "env is `env`" # copy your binary that you want to run and any data files to a local directory on node job is executing on # this example assumes you have a binary file named helloworld.sh in your local bin directory cp \$HOME/bin/helloworld.sh \$TMPDIR cd \$TMPDIR # run the binary file from the local disk on the node the job was placed on ./helloworld.sh >&hello.stdout # Copy output files to your output folder cp -f \$TMPDIR/hello.stdout \$HOME/output



pwd

/home/fs01/netid

mkdir bin

vi bin/testjob.sh

qsub bin/testjob.sh





default







 qsub showq checkjob canceljob

Interactive –I

qsub -I jobscript.sh

Matlab

- R2012b
- R2013a: default
- module avail
 >module load matlab/R2012b
 >matlab

Ganglia Monitor: http://hd-hni.cac.cornell.edu/ganglia/

help@cac.cornell.edu http://www.cac.cornell.edu