Working Remotely on NERSC Systems (genepool focus)

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Structure of the Genepool System

User Access
- Command Line
- Scheduler
- Service

ssh genepool.nersc.gov

login nodes

compute nodes

gpint nodes

high priority & interactive nodes

fpga

web services

database services

filesystems

http://...jgi-psf.org

User Access
- Command Line
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- Service
Types of Jobs on genepool

• **Batch – Scheduled** (compute nodes, fpga)
  – 8,320 cores for 72,953,280 compute hours per year in genepool
  – use “qsub” to submit a job

• **Interactive – Scheduled** (compute nodes subset)
  – 80 cores presently, increasing size
  – use “qlogin” to submit a job

• **Interactive – Unscheduled** (login nodes, gpints)
  – 4 login nodes, 27 gpint nodes
  – ssh to the host, direct-use

• **Services – Unscheduled** (login nodes, gpints, gpweb, gpdb, gpodb)
  – Web services
  – Database services
  – Automated job submission / control
Working interactively?

• Not all work is appropriate for batch jobs
  – The production queues can have a several hour wait
  – For non-intensive, memory-limited operations
    • one time file copy, home directory organization, code compilation, development, process development (e.g. writing a batch script), high-priority one-off work
    • Use the genepool login nodes or your group’s gpint
  – For resource intensive interactive work
    • Use qlogin to schedule your interactive job
      – qlogin -l high.c -l ram.c=40G … [no script]
    • ssh to a bunch of gpints and login nodes until you find one lightly loaded and hope another user doesn’t interfere with your work
Tip: For an intensive job that needs to get done soon-ish but you don’t want to write a batch script, just use `qsub` with stdin input:

```
find . -type f -name *.frag -exec cat {} >> $BSCRATCH/large_dataset.complete <ctrl-d>
Your job 347292 ("STDIN") has been submitted.
```

"STDIN"
Options for command line work on gpints

Command Line: ssh to gpintXX

• Direct ssh access to gpints is only possible from LBL sites, or using LBL VPN (or JGI VPN)

• Dealing with connection disruptions:
  – Setup the connection keep-alive connections properly
  – Linux/MacOSX, edit $HOME/.ssh/config, add:
    ```
    Host *
      TCPKeepAlive "yes"
      ServerAliveInterval 120
      ServerAliveCountMax 30
    ```
  – Windows (putty):
    • Set “Session Properties → Connection → Sending of null packets to keep session active → Seconds between keepalives” to 120 (2 minutes)
Options for command line work on gpints

• **Problem:** interactive work is lost when terminal closed to go home, or network briefly interrupted

• *Use screen or tmux to keep your session*
  – screen/tmux allow you to disconnect from an ssh session and continue it later
  – Also allow multiple terminals
  – tmux has some nice features (color, scrollback, integration with term2 on Mac); but is less used than screen so your mileage may vary
Options for graphical applications

• **Problem:** I need to use a graphical analysis tool or integrated development environment, or xemacs

• **Answer 1:** use ssh with X forwarding
  – ssh -X genepool.nersc.gov
  – ssh -Y genepool.nersc.gov (if you get security warnings)
  – Just run the command. You will need an X client on your local system. Trivial with linux, MacOSX; harder with Windows.

• **Notes on X forwarding:**
  – X forwarding over ssh is robust, but often slow.
  – Your work will be lost if the ssh session is terminated. See earlier tips for keepalives.
  – If you are using windows and want X-forwarding, try installing cygwin/X with mintty and ssh; my experience is that this is often much better than Exceed or even using putty for X forwarding to a Windows X client
Options for graphical applications

• **Problem:** I need to use a graphical analysis tool or integrated development environment, or xemacs

• **Answer 2:** use accelerated X → NX
  – NX provides a full linux window manager (the NERSC window manager is rather old, this is being updated)
  – NX (like screen, tmux) allows *session reconnection*; so you can come back to your work later

• **Notes on NX with NERSC**
  – For security reasons, your NX session will be on an NX server without access to your data. You need to connect to genepool (and soon a gpint!) once you arrive on the NX server
Using NX

Run many terminals, save state!

Run graphical applications faster than X-forwarding
Eclipse

- **Problem:** I need to use Eclipse and X and NX are both too slow

- **Option 1)** Run eclipse locally on your computer, and use version control (git, svn, etc) to commit changes;

- **Option 2)** We are presently investigating Eclipse Remote System Explorer
  - Will allow direct editing of files on genepool
  - Will permit direct execution and debugging of executables on genepool (may need to use ssh tunnelling)
  - This service will hopefully be available by the end of February
Options for using gpint web-services

• Some groups have web services setup on the gpints
  – gpintXX aren’t directly accessible on the general internet
  – Option 1) LBL or JGI VPN to access the services directly
  – Option 2) tunnel access through ssh
    • ssh -L 50044:gpintXX.nersc.gov:50044 genepool.nersc.gov
    • Direct web browser to http://localhost:50044
  – Option 3) ssh SOCKS proxy (all web-browser traffic diverted through genepool)
    • ssh -D <portnum> genepool.nersc.gov
    • Configure web browser to use the localhost:portnum as a proxy
    • External HOWTO: http://www.mikeash.com/ssh_socks.html
    • Direct web browser to http://gpintXX.nersc.gov