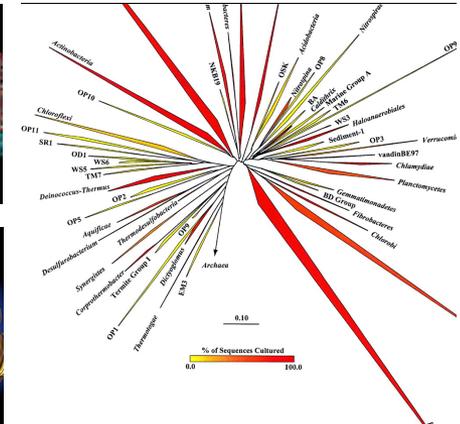
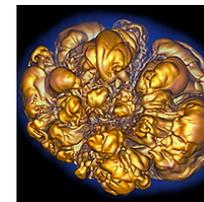
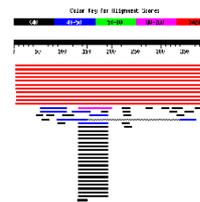
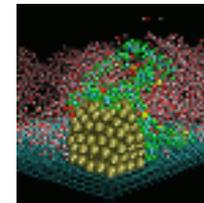
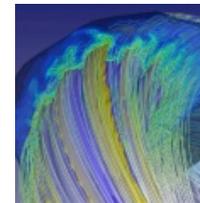
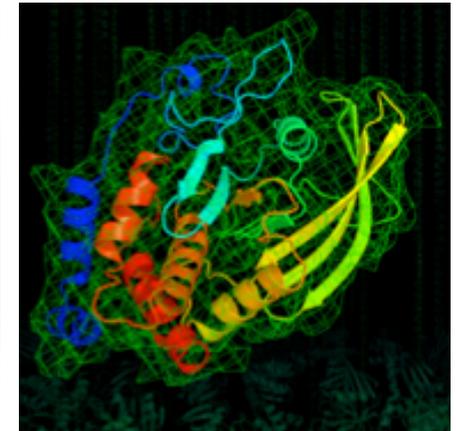


Working Remotely on NERSC Systems (genepool focus)



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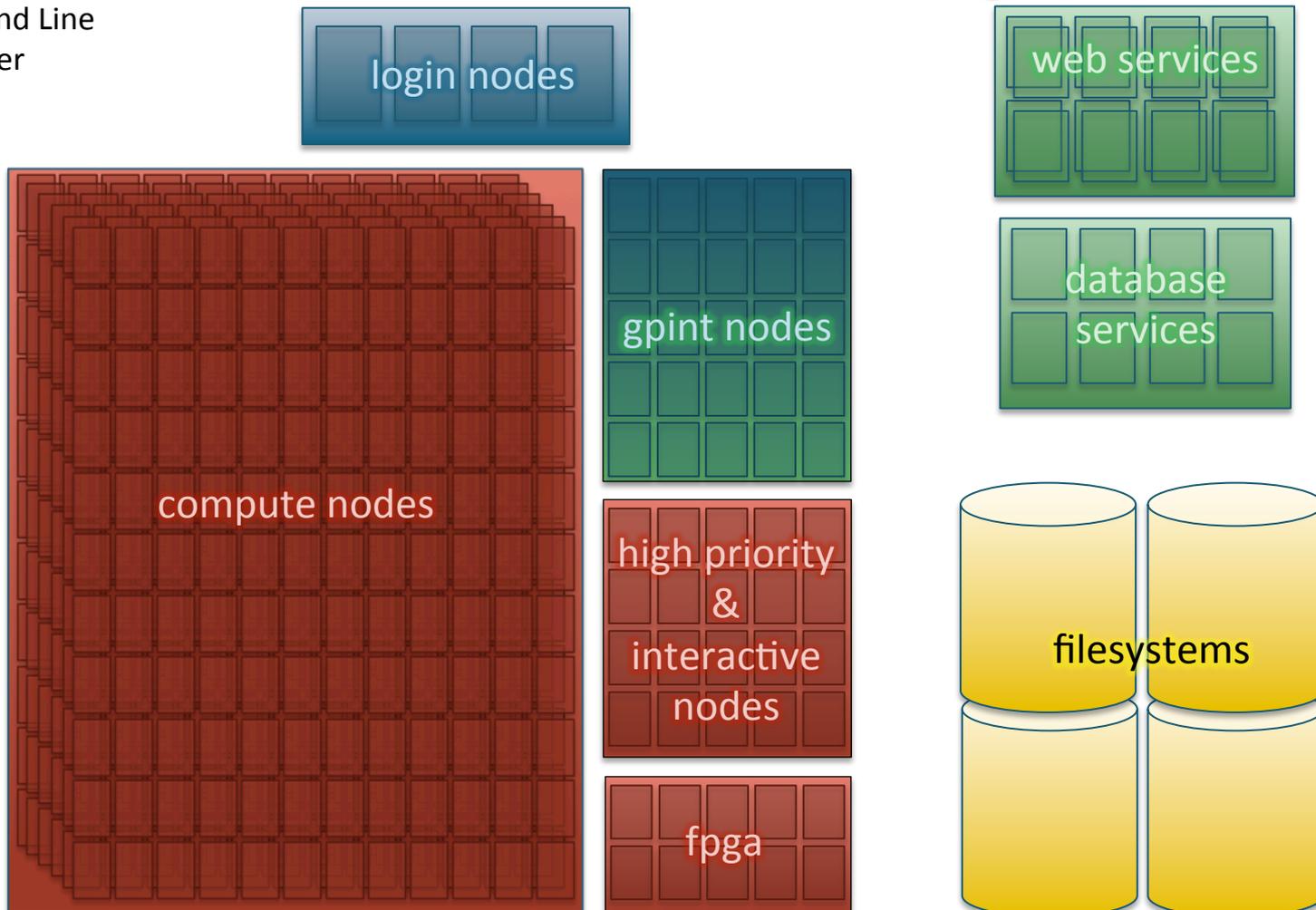
Structure of the Genepool System

User Access

- Command Line
- Scheduler
- Service

`ssh genepool.nersc.gov`

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



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

Working interactively?

- **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 qsub` with `stdin` input:**

```
genepool% qsub -v -cwd -l high.c  
find ./myDataDir -type f -name \*.frag -exec cat {} >> $BSCRATCH/large_dataset.complete  
<ctrl-d>  
Your job 347292 ("STDIN") has been submitted.  
genepool%
```

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
```

TCPKeepAlive is on by default

helps with network issues

ServerAlive needs to be configured by you

Keeps long running connections alive through firewalls and such

- 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 iterm2 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

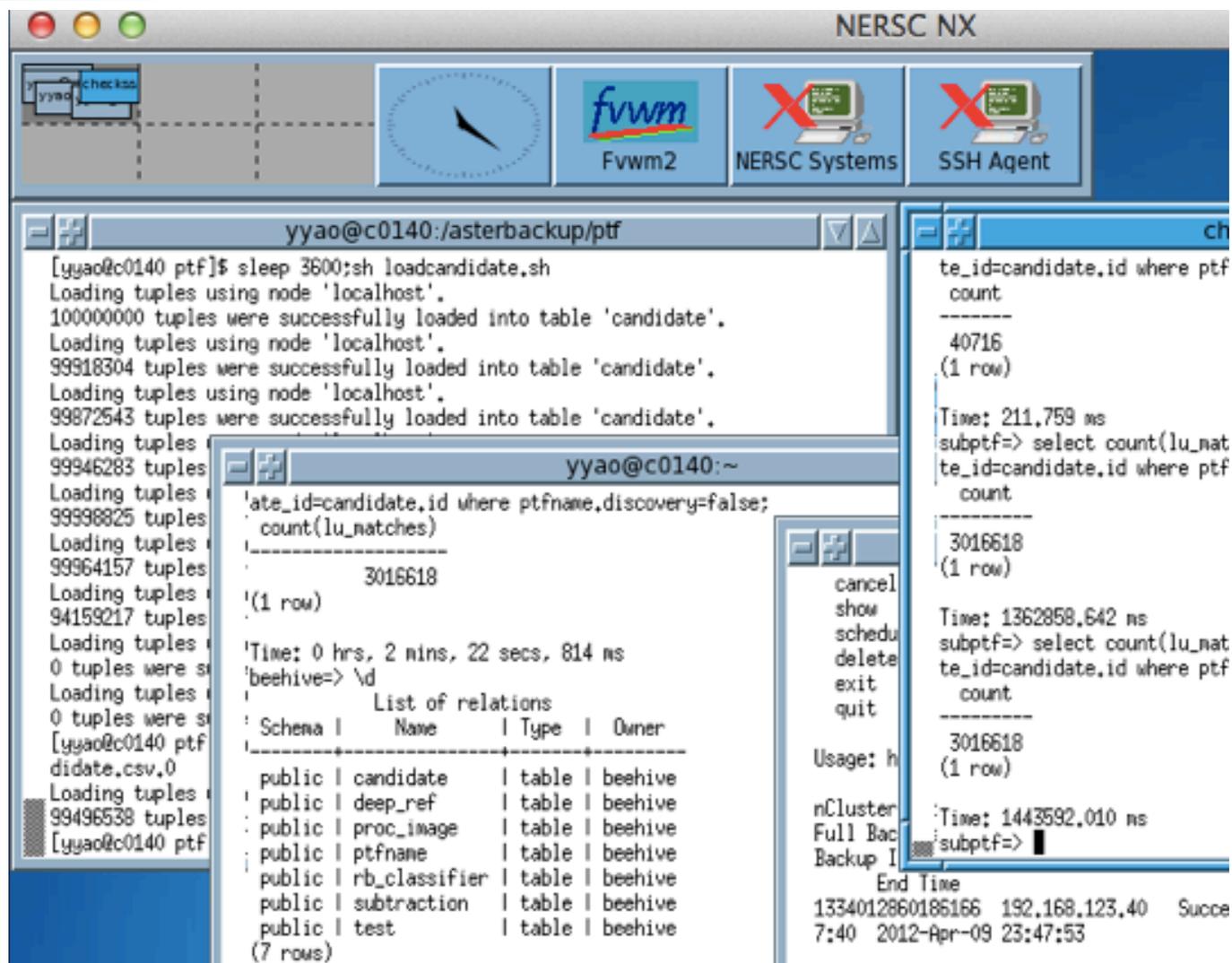
Options for graphical applications

- **Problem:** I need to use a graphical analysis tool or integrated development environment, or xemacs
- **Answer 2: use accelerated X → NX**
 - <http://www.nersc.gov/users/data-and-networking/connecting-to-nersc/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



The screenshot shows the NERSC NX desktop environment. The top bar includes system icons for 'yyao@checks', a clock, 'Fvwm2', 'NERSC Systems', and 'SSH Agent'. Three terminal windows are open:

- Terminal 1 (yyao@c0140:/asterbackup/ptf):** Shows a script execution with the command `sleep 3600;sh loadcandidate,sh`. It reports loading 1,000,000, 999,183,04, and 998,725,43 tuples into the 'candidate' table.
- Terminal 2 (yyao@c0140:~):** Shows a SQL query: `'ate_id=candidate.id where ptfname.discovery=false; count(lu_matches)`. The result is a single row with the value 3016618. Below the query is a 'List of relations' table:

Schema	Name	Type	Owner
public	candidate	table	beehive
public	deep_ref	table	beehive
public	proc_image	table	beehive
public	ptfname	table	beehive
public	rb_classifier	table	beehive
public	subtraction	table	beehive
public	test	table	beehive

- Terminal 3 (yyao@c0140:~):** Shows a SQL query: `te_id=candidate.id where ptf count`. The result is a single row with the value 40716. Below the query is a menu with options: cancel, show, schedu, delete, exit, quit. The usage is shown as 3016618 (1 row).

At the bottom right, a status bar shows: `Time: 1443592,010 ns`, `subptf=>`, `1334012860186166 192.168.123.40 Succes`, and `7:40 2012-Apr-09 23:47:53`.

- **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`

