Solexa Data Crunching

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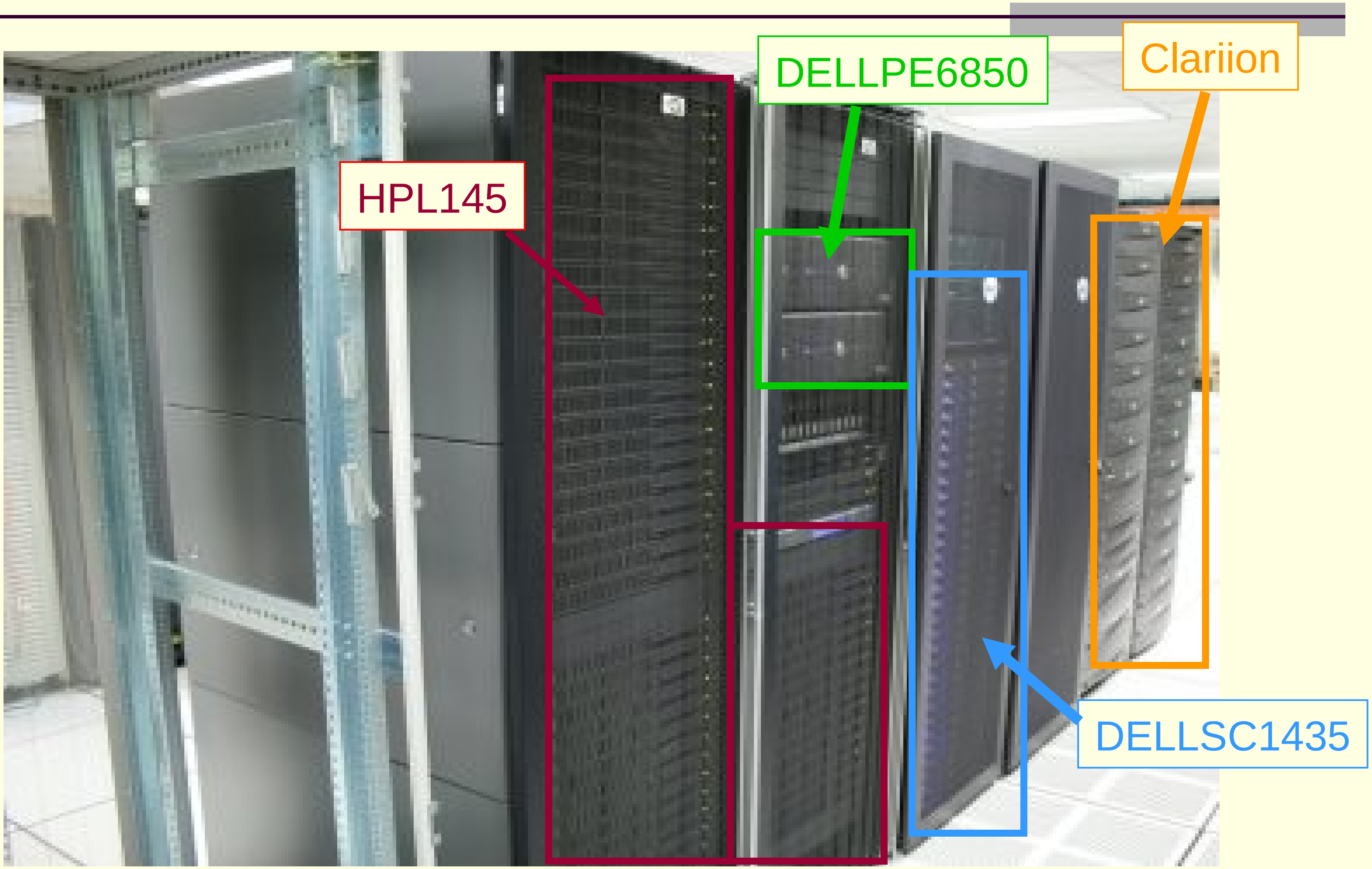
March 20, 2008

Data Crunching

- Binar – A Tour
- Resources on Binar
- How Data is Crunched
- Other Resources

Binar

Binar: Components



HPL145

DELLPE6850

Clariion

DELLSC1435

More Specs

- HPL145
  - 2 dual core Opteron/4 Gb mem
  - 55 nodes
- DELLPE6850
  - 4 quad core Intel/64 Gb mem
  - 2 nodes
- DELLSC1435
  - 2 dual core Opteron/4 Gb mem
  - 25 nodes
  - Infiniband capable

Cluster Use/Etiquette

- Use queue system to run jobs
  - Sun Grid Engine queueing
  - Fair share queueing is in use
- File space is not storage
  - Do not store data on the cluster
  - Cluster has 2.0 Tb only for workspace
  - 23 Active Users

Queues

$qsub script	basic form
$qstat	shows jobs in queue
$qstat |grep user	shows jobs for username

Info for Binar and Sun Grid Engine is online at

http://inside.umassmed.edu/is/acs/ResearchComputing/researchclusters.aspx

Script Template for Queue

```
#!/bin/bash
#$ -S /bin/bash      <- specify shell
#$ -cwd              <- use current working dir
#$  … other sge parameters
PATH=<path to your program>:$PATH
export PATH

…rest of script ….
```

Then submit script within working directory

```
$qsub –cwd script
```

Scripts

It is very important to set custom paths, esp for programs that you write, or using bioperl.

/share/… is common to all nodes.

/export/home/<user> (your home directory) is

available to remote nodes.

Important Directories

/share/apps/bin   commonly used programs

/share/apps/pipeline/… Solexa pipeline progs

/share/nemo/Genomes   contains genome directories formatted for Eland

/share/nemo/Genomes/hg18

/share/nemo/Genomes/mm9

Resources on Binar

- EMBOSS (similar to GCG, scriptable)
- Clustalw, T_Coffee - multiple alignment
- Phylip, MrBayes - phylogenetic
- BLAST, mpi-blast
- HMMER
- Bioperl, biopython

These have their own directories.

Current Genomes on Binar

hg18	Human (UCSC)
mm9, mm8	Mouse (UCSC)
dm5.5, dm5.4	Drosophila (Flybase)
yeast	SGD
z7v	Zebrafish
ceWS187	C.Elegans

/share/nemo/Genomes/xxxx

Creating a Genome file for Eland

You can run eland against a custom Genome.

2. Each piece (e.g. a chromosome) must be a separate fasta file.
3. Create a directory for the genome
   ```
     mkdir ~/mygenome
   ```
4. Run squashGenome
   ```
   /share/nemo/pileline/Eland/squashGenome \
   ~/mygenome  pathtoFasta/*.fasta
   ```
5. More detail in Pipeline docs

Pipeline processing

- Three phases
  - Image Analysis -Firecrest
  - Base Calling Bustard
  - Sequence Mapping –Gerald
- Initial Run to generate Cross-talk and offsets
- Run the first two by lane
  - If you specify Genome Gerald can be run
  - If we don’t have the genome, let us know what and where, then we can install it.

Post-processing

- When runs are done several files are available
  - quality files, base calls
  - sequences, remapping results
  - summary data
- These are packaged and delivered to you.
- Let me know if you need custom programs for analysis, i.e. ones not delivered with the pipeline

Resources

- Cluster info
  http://inside.umassmed.edu/is/acs/ResearchComputing/researchclusters.aspx
- Pipeline Info
  http://biotools.umassmed.edu/BIOCORE/pipeline
- Solexa Google Group
  http://groups.google.com/group/solexa
- Bioc-Seq (New bioconductor group)
  https://stat.ethz.ch/mailman/listinfo/bioc-sig-sequencing
- UNIX On-line Help
  http://biotools.umassmed.edu/unixhelp