UPPMAX Basics

What even is UPPMAX?

What about SNIC?

How do I submit jobs to the queue?
UPPMAX Basics

- Organisation
  - What is what
  - What does UPPMAX do
- How a cluster works
- How to use UPPMAX clusters
Organisational orienteering

- VR/SRC and a consortium of universities funds **SNIC** — Swedish National Infrastructure for Computing
- SNIC and Uppsala University funds **UPPMAX** — UU’s supercomputing centre
- NBIS, a part of SciLifeLab, has a facility called **Compute and Storage**, which is hosted by UPPMAX
UPP MAX

• Mission for SNIC: to provide a quality high-performance computing environment nationally
  – General purpose
  – Data intensive
  – Sensitive data (human sequences)
• Mission for UU: to provide relevant services to the university
• Mission for NBIS/SciLifeLab: to provide the best possible resources for data-driven life science, especially bioinformatics
UPPMAX (more concretely)

• Computer infrastructure
  – Clusters
  – Storage
  – Cloud

• Support staff
  – System administrators
  – Application experts
High Performance Computing

Calculation nodes

Login nodes

Storage
## UPPMAX Clusters

<table>
<thead>
<tr>
<th></th>
<th>Rackham</th>
<th>Snowy</th>
<th>Bianca</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Purpose</strong></td>
<td>General-purpose</td>
<td>General-purpose</td>
<td>Sensitive</td>
</tr>
<tr>
<td><strong># Nodes</strong></td>
<td>486</td>
<td>228-ish</td>
<td>200</td>
</tr>
<tr>
<td><strong>Memory/node</strong></td>
<td>128 GB</td>
<td>128 GB</td>
<td>128 GB</td>
</tr>
<tr>
<td><strong>Fat nodes</strong></td>
<td>512 GB - 1 TB</td>
<td>512 GB – 4 TB</td>
<td>256 GB</td>
</tr>
<tr>
<td><strong>Local disk</strong></td>
<td>2 TB</td>
<td>4 TB</td>
<td>4 TB</td>
</tr>
<tr>
<td><em>(scratch)</em></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Login nodes</strong></td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td><strong>Storage</strong></td>
<td>Crex, Lutra</td>
<td>Crex, Lutra</td>
<td>Castor, Cygnus</td>
</tr>
</tbody>
</table>
Storage systems

- Domus — Home directories for Rackham/Snowy
- Crex — Project storage for Rackham/Snowy
- Castor — Project storage for Bianca
- Cygnus — “New” project storage for Bianca
- Lutra — Paid-for storage on Rackham/Snowy
Exercise

• Open a web browser to http://uppmax.uu.se.
• Find articles about how to best use the storage systems and good data practices.
• Look at Support -> User Guides and Support -> FAQ
• Find and discuss articles in Breakout Rooms
Solution

- Disk Storage Guide
- How to use a node’s own disk
- How does automatic backup of project areas work at UPPMAX?
- File compression guide
- How can I compress my files as quickly and efficiently as possible?
- How should I compress FastQ-format files?
- Which compression format should I use for NGS-related files (FastQ, Fasta, VCF, GFF, etc.)?
Storage Basics

• All nodes can access:
  • your home directory on Domus or Castor
  • a project directory on Crex or Castor
  • Its own local disk (2-3 TB)
• If you’re reading/writing a file once, use a directory on Crex or Castor
• If you’re reading/writing a file many times...
• copy to the file to "scratch", the node local disk
• "cp myFile $SNIC_TMP"
Other systems

- Dis — part of the SNIC Science Cloud
- Grus — NGI data delivery
- Da Vinci — GPU resource
Bianca

- Login:
  - First 2FA login to Bianca portal
  - Second regular login to private cluster
- Data import/export:
  - SFTP from “outside”
  - Data in non-backed up “wharf” directory
  - NGI delivery via SUPR
Bianca Has No Internet

• We have “solutions”
  - Data transfers:
    • NGI Deliver through SUPR
    • Transit server (transit.uppmax.uu.se)
  - Software
    • Almost the same software library as Rackham
    • Local Conda repository
    • Local Perl modules
    • Local R packages
ThinLinc

- Both Rackham and Bianca offer graphical login
- On web: https://rackham-gui.uppmax.uu.se
- Or use the client (only for Rackham)
- Try it now!
Slurm, `sbatch`, the job queue

- Problem: 1000 users, 500 nodes, 10k cores
  - Need a queue:
Slurm, `sbatch`, the job queue

- Easiest to schedule single-threaded, short jobs
Jobs

- Job = what happens during booked time
- Described in a Bash script file
  - Slurm parameters
  - Load software modules
  - Move around file system
  - Run programs
  - Collect output
- ...and more
Slurm parameters

• 1 mandatory setting for jobs:
  • Which compute project? (\texttt{-A})

• 3 settings you really should set:
  • Less than one node? (\texttt{-p})
  • How many cores? (\texttt{-n})
  • How long at most? (\texttt{-t})

• If in doubt:
  • \texttt{-p core}
  • \texttt{-n 1}
  • \texttt{-t 10-00:00:00}
Slurm parameters

- Where should it run?  (-p node or -p core)
  - Use a whole node or just part of it?
    - 1 node = 20 cores (16 on Bianca & Snowy)
    - 1 hour walltime = 20 core hours = expensive
    - Waste of resources unless you have a parallel program or need all the memory

- Default value: core
How long is the job

• How long is it? (-t)
  • Always overestimate with ~50%
    • Jobs killed when timelimit reached
    • Only charged for time used
  • -t = time (hh:mm:ss)
    • 78:00:00 or 3-6:00:00
• Default value: 7-00:00:00
Efficient jobs

• Use your booked cores or memory
  – (at least 50%)

• Runtime longer than 1 hour
  – Combine shorter jobs

• Ask UPPMAX support for help!
Interactive jobs

• Most work is most effective as submitted jobs, but e.g. development needs responsivity
• Interactive jobs are high-priority but limited in –n and –t
• Quickly give you a job and logs you in to the compute node
• Require same Slurm parameters as other jobs
• Try it:
  - $ interactive -A g2020018 -p core -n 1 -t 10:00
  - Which node are you on?
  - Logout with Ctrl-D or logout
A simple job script template

```bash
#! /bin/bash -l
#SBATCH -A g2020018  # Project name
#SBATCH -p core  # Asking for cores (as opposed to multiple nodes)
#SBATCH -n 1  # Number of cores
#SBATCH -t 00:10:00  # Ten minutes
#SBATCH -J Template_script  # Name of the job

go to some directory
cd /proj/g2020018/marcus1

load software modules
module load bioinfo-tools

do something
echo Hello world!
```
Exercise (1)

- Copy the template from the previous slide
- Put it into a file named “jobtemplate.sh”
- Make the file executable (chmod)
Exercise (2)

- Submit the job:
  - $ sbatch jobtemplate.sh

- Note the job id!

- Check the queue:
  - $ jobinfo -u yourusername

- When it’s done, look for the output:
  - $ ls

- Check the output file to see if it ran correctly
Other Slurm tools

- Squeue — quick info about jobs in queue
- Jobinfo — detailed info about jobs
- Finishedjobinfo — summary of finished jobs
- Jobstats — efficiency of booked resources
Software at UPPMAX

- 800+ programs and packages installed
- Managed by a 'module system'
  - Everything already installed, but hidden
  - Manually loaded before use
  - Bioinformatics tools require loading the “bioinfo-tools” module first

- `module spider <name>` — search for modules
- `module load <module name>` — Loads the module
- `module unload <module name>` — Unloads the module
- `module list` — Lists loaded modules
Software exercise

- Use `module spider` to find a software you like to use.
- Try to run the software, e.g. “$ samtools”
- Load the latest version of the module
  - `load bioinfo-tools` first if necessary
  - You can write “module load samtools” and then TAB-complete to see the available modules
- Now try to run the software again
Wrap-up

- In breakout rooms, ask for help:
  - Finding software
  - Writing job scripts
  - Basic Linux