High Performance Computing for Genomics

Part I: High Performance Computing

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Overview

- Login
- Storage
- Credit system
- Module system
- HardwarePBS
- Job Submission

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Login

Login is possible through various methods.

Command line example (Linux/Mac):

\$ ssh vsc3XXXX@login.hpc.kuleuven.be

Or via putty (Windows)

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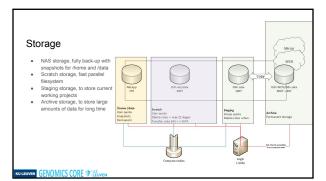
If you are not logged in yet, Now is the moment

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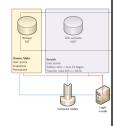
Personal Storage

Personal Storage, only accessible by the owner Fully Backup

- Home Directory
 SVSC_HOME or /user/leuven/3XX/vsc3XXXX
 - 25GB
 - Important data, configuration files
- Data Directory
 - \$VSC_DATA or /data/leuven/3XX/vsc3XXXX

 - 75GB Important data, biger then Home
- Scratch Space
 - \$VSC_SCRATCH or /scratch/leuven/3XX/vsc3XXXX

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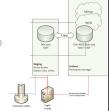


Project Storage

Permissions are managed per group (usually the group of the project)

- Staging Space
 - Storage for project files (while working at the project)
 Size is project dependable (per 1TB)
- Archive Storage

 Long term storage and backup for project files (or staging)
- Size is project dependable (per 1TB)
 Only accessible from the login node



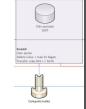
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Temporary Storage

Scratch: fast storage, used during the processing of the data

- Node Scratch
 - \$VSC_SCRATCH_NODE
 - Size is machine dependable, min 150 GB
 Is NOT accessible from the login node
- Site Scratch
- \$VSC_SCRATCH_SITESimilar as \$VSC_SCRATCH_NODE
- Personal Scratch
 - · \$VSC_SCRATCH
 - Personal scratch, 100GB
 - Accessible from the login node
- Data will be deleted within 21 days

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Exercise 1			
Exercise i			
Find the path for the following locations:			
\$VSC_HOME			
• \$VSC_DATA			
\$VSC_SCRATCH\$VSC_SCRATCH_NODE			
- \psi \psi \cdo \cdo \cdo \cdo \cdo \cdo \cdo \cdo			
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Copy Data			
s rsync -ahrprogress /stagin	ad/leuwen/eta 00019/workehon/*		
rsyncprogress -ahr filename targetDire	ectory		
progress	Show the progress of the copy		
-a	Preserve almost everything		
-h	Output numbers must be Human readable		
-r	Copy directories recursively		
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		-	
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Exercise 1b			
Make a tutorial directory in your data dire	ctory		
Copy the workshop data into this directory:			
/staging/leuven/stg_00019/workshop			
CENOMICS CODE (IN)			
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Overview Login Credit systemModule system Hardware • PBS Job Submission GENOMICS CORE TELEUVEN Credit System VSC ~ regular bank Each job costs a certain number of credits Each job belongs to a project Each project account has its own credits Users have access to one or multiple project accounts (multiple users can have access to the same project account) GENOMICS CORE WILLEUVEN Credit System: balance Load the accounting module \$ module load accounting Check the amount of credits at your disposal \$ gbalance

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Credit System: statement Get an overview of the transactions

\$ gstatement

Get an overview of the transactions of a certain project, over a certain time

gstatement -g lp_projectname -s 2015-09-01 -e 2015-09-30

-g	groupname
-u	username
-S	start
-е	end

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Credits System: quotes

Estimating the cost of a job is possible by requesting a quote:

gquote -1 nodes=3:ppn=4:ivybridge,pmem=2gb,walltime=48:00:00

- nodes=3:ppn=4:ivybridge
- 3 nodes, with 4 processors per node of the ivybridge type
- pmem=2gb
- 2GB of memory (RAM)
- walltime=48:00:00

The job will run for maximum 48 hours

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Job Cost Calculation

The effective cost of the job is calculated using this formula:

(0.000278*nodes*walltime + startup)*nodetype

nodes	The number of nodes that were reserved
walltime	The effective duration of the job (in seconds)
startup	0.1, it is added for the overhead of scheduling
nodetype	A representation of the node type's performance

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Exercise 2 • Get a quote for 5 minutes computing on 1 node, 5 processors of the ivybridge Get a quote for 20 minutes computing on 2 nodes, 4 processors of the haswell type, using 100Gb of memory Get a quote for 1 hour for both the ivybridge and the haswell processor GENOMICS CORE PLEUVEN Overview Login Storage Module system Hardware PBS Job Submission GENOMICS CORE PLEUVEN Module System For many programs, multiple versions are installed, and each version requires specific libraries. Toolchains consists of compilers and libraries, together with software depending on those libraries. The $\ensuremath{\mathsf{module}}$ system inside the toolchain is used to manage the $\ensuremath{\mathsf{environment}}$ variables, and all dependencies to resolve possible conflicts.

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Module System: Module av Many software packages are installed as modules: \$ module av ----- /apps/leuven/thinking/2014a/modules/all ------ Autoconf/2.69-GCC-4.8.2 Autoconf/2.69-intel-2014a Automake/1.14-GCC-4.8.2 Automake/1.14-intel-2014a BEAST/2.1.2 ... pyTables/2.4.0-intel-2014a-Python-2.7.6 timedrun/1.0.1 worker/1.4.2-foss-2014a zlib/1.2.8-foss-2014a zlib/1.2.8-intel-2014a GENOMICS CORE PLEUVEN Module System: load and unload Load a module \$ module load BEAST \$ module load BEAST/2.1.2

Module System: list

View all loaded modules

Unload a module

Unload all modules

GENOM \$ module purge

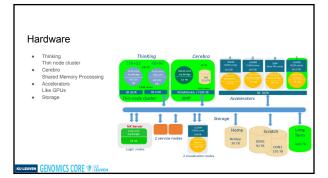
ew all loaded modules

\$ module list
Currently Loaded Modulefiles:
1) /thinking/2014a
2) 3wav1.7.0.51
3) icc/2013.5.192
4) ifort/2013.5.192
5) impi/4.1.3.045
6) imkl/11.1.1.06
1) intal/2014
8) beagle-lib/20140304-intel-2014a
9) BEAST/2.1.2
111 | OpenMEI/2.1.2
112 | openFile/2.1.2
113 | OpenMEI/3.6.5-CGC-4.8.2
120 | openFile/2.014a
130 | OpenBEAS/0.2.8-gompi-2014a-LAFACK-3.5.0
14) FFTW/3.3-3-gompi-2014a
15) SCALAPACK/2.0.2-gompi-2014a-OpenBLAS-0.2.8-LAFACK-3.5.0
16) foss/2014a
17) z1ib/1.2.8-foss-2014a

\$ module load BEAST/2.1.2 zlib/1.2.8-foss-2014a

\$ module unload BEAST

Overview Login Storage Credit system Module system Hardware PBS Job Submission



Hardware: Thinking

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- Thinking
 - Thin, powerful nodes2 processor types:
 - Processor type
 Haswell
 - 208 nodes, 24 cores/node High computing power, low I/O
 - Ivybridge 144 nodes, 20 cores/node
 - Lots of I/O

 2 versions of RAM: 64GB and 128GB
- Cerebro

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Hardware: Cerebro • Thinking • Cerebro • Shared Memory • 2 partitions: ■ Smp1 48 nodes, 10 cores/node (lvybridge) 250 GB shared (max 11.77 TB) ■ Smp2 16 nodes, 10 cores/node (lvybridge) 124 GB shared (max 1.79 TB)

Hardware: Overview

Cluster	Partition	#cores (threads) per node	Usable Memory	#Credits/hour
ThinKing	Ivybridge	20	60-124GB	4.76
ThinKing	Haswell	24	60-124GB	6.68
Cerebro	Smp1	10	Shared 250GB	3.45
Cerebro	Smp2	10	Shared 124GB	3.45

The Operating System also needs some RAM, good practice is to reserve 4GB.

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Hardware: which task on which cluster? Cluster Partition Task Description Task Example Alignment Read Mapping Variant Calling Read Counting Memory low jobs, with lots of I/O ThinKing Ivybridge Memory low jobs, low I/O, high computing power needed Model Calculations Star Discovering ... ThinKing Haswell De Novo Assemblies Reference-based Assemblies High memory jobs, computing power less important Cerebro Smp1 and Smp2 GENOMICS CORE W LEUVEN

Overview Login Storage Credit system Module system Hardware PBS Job Submission ROLLINYON GENOMICS CORE ♣ 100000000000000000000000000000000000	
Portable Batch System (PBS) Portable Batch System (or simply PBS) is the name of computer software that performs job scheduling. Its primary task is to allocate computational tasks, i.e., batch jobs, among the available computing resources. It is often used in conjunction with UNIX cluster environments. PBS is supported as a job scheduler mechanism by several meta schedulers by Wikipedia	
PBS script Every shell script (.sh) can be turned into a PBS script (.pbs). A typical scripts will need the following adjustments: 1. Include PBS headers 2. Load the software modules 3. Optimize I/O using a scratch node 4. Check if results are copied/stored in a data or staging directory	
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PBS header

Headers contain the run parameters
Each line starts with #PBS then the parameter and the value

```
#!/bin/bash -1
#PBS -1 walltime=12:00:00
#PBS -1 mem=100gb
#PBS -1 nodes=1:ppn=20:ivybridge
#PBS -M mail@mail.com
#PBS -m aeb
#PBS -N jobname
#PBS -A lp_projectname
```

PBS header: job description

Walltime: the maximum time the job can run

#PBS -l walltime=12:00:00

Mem: the maximum memory available for the job

#PBS -1 mem=100gb

Number of nodes, processors per node (ppn) and the processor type

#PBS -l nodes=1:ppn=20:ivybridge

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PBS header: notifications

You can send a mail @ certain conditions

-M specifies the mail adres

#PBS -M mail@mail.com

#PBS -m aeb

m the conditions when a mail has to be send:

b	When the job begins
е	When the job ends
а	When the job is aborted

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PBS header: billing The name of the job, this will be visible for other users #PBS -N jobname The project that will be used for the billing #PBS -A lp_projectname GENOMICS CORE PLEUVEN PBS script Every shell script (.sh) can be turned into a PBS script (.pbs). A typical scripts will need the following adjustments: 1. Include PBS headers 2. Load the software modules module load BEAST/2.1.2 3. Optimize I/O using a scratch node 4. Check if results are copied/stored in a data or staging directory GENOMICS CORE W LEUVEN PBS script Every shell script (.sh) can be turned into a PBS script (.pbs). A typical scripts will need the following adjustments: 1. Include PBS headers 2. Load the software modules 3. Optimize I/O using a scratch node \$VSC_SCRATCH, \$VSC_SCRATCH_NODE

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Scratch is fast temporary storage

4. Check if results are copied/stored in a data or staging directory

PBS script Every shell script (.sh) can be turned into a PBS script (.pbs). A typical scripts will need the following adjustments: 1. Include PBS headers 2. Load the software modules 3. Optimize I/O using a scratch node 4. Check if results are copied/stored in a data or staging directory Scratch is temporary, when the job is finished, data will be lost GENOMICS CORE PLEUVEN Overview • Login Storage Credit system Module system Hardware • Job Submission GENOMICS CORE W LEUVEN Job submission Thinking \$ qsub run-job.pbs \$ module load cerebro/2014a \$ qsub run-job.pbs When a job is submitted, the job id is returned. jobIDs are unique. Thinking jobs starts with 2

rebro jobs starts with 3

Jobs progress An overview of all your jobs: \$ qstat -u vsc3XXXX hpc-p-svcs-5: Elap Username Queue Req'd Req'd Job ID Jobname SessID NDS TSK Memory Time S Time $\tt 30017323.hpc-p-svcs-5 \qquad vsc3XXXX \qquad q21d \qquad jobname$ 1gb 480:00:00 R 00:04:16 10 197071 GENOMICS CORE PLEUVEN

Job estimated start

Get the estimated start of a job:

showstart 30017323.hpc-p-svcs-5

job 30017323 requires 10 procs for 20:00:00:00

00:00:00 on Mon Apr Estimated Rsv based start in

18 16:29:10

Estimated Rsv based completion in 20:00:00:00 on Sun May

8 16:29:10

Best Partition: smpl NOTE: job is running

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Job overview

An overview of every parameter and all used resources can be requested: \$ checkjob 30017323.hpc-p-svcs-5 job 30017323

AName: jobname State: Running

Creds: user:vsc3XXXX group:vsc3XXXX account:lp_projectname class:q21d qos:normal WallTime: 00:02:43 of 20:00:00:00

WallTime: 00:02:43 of 20:00:00:00 SubmitTime: Mon Apr 18 16:28:56 (Time Queued Total: 00:00:14 Eligible: 00:00:14) StartTime: Mon Apr 18 16:29:10 TemplateSets: DEFAULT

Total Requested Tasks: 10

Req[0] TaskCount: 10 Partition: smp1 Memory >= 1024M Disk >= 0 Swap >= 0 Dedicated Resources Per Task: PROCS: 1

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Job stop/kill/delete Sometimes a job has to be killed. qdel 30017323.hpc-p-svcs-5 GENOMICS CORE TELEUVEN Exercise 3 1. Open paths.pbs Edit the PBS header (change the mail, and accounting information) 2. Ask a quote based on the PBS header 3. Start the job on thinking 4. Check the start time and status of the job 5. Check the output of the job GENOMICS CORE PLEUVEN Coffee break