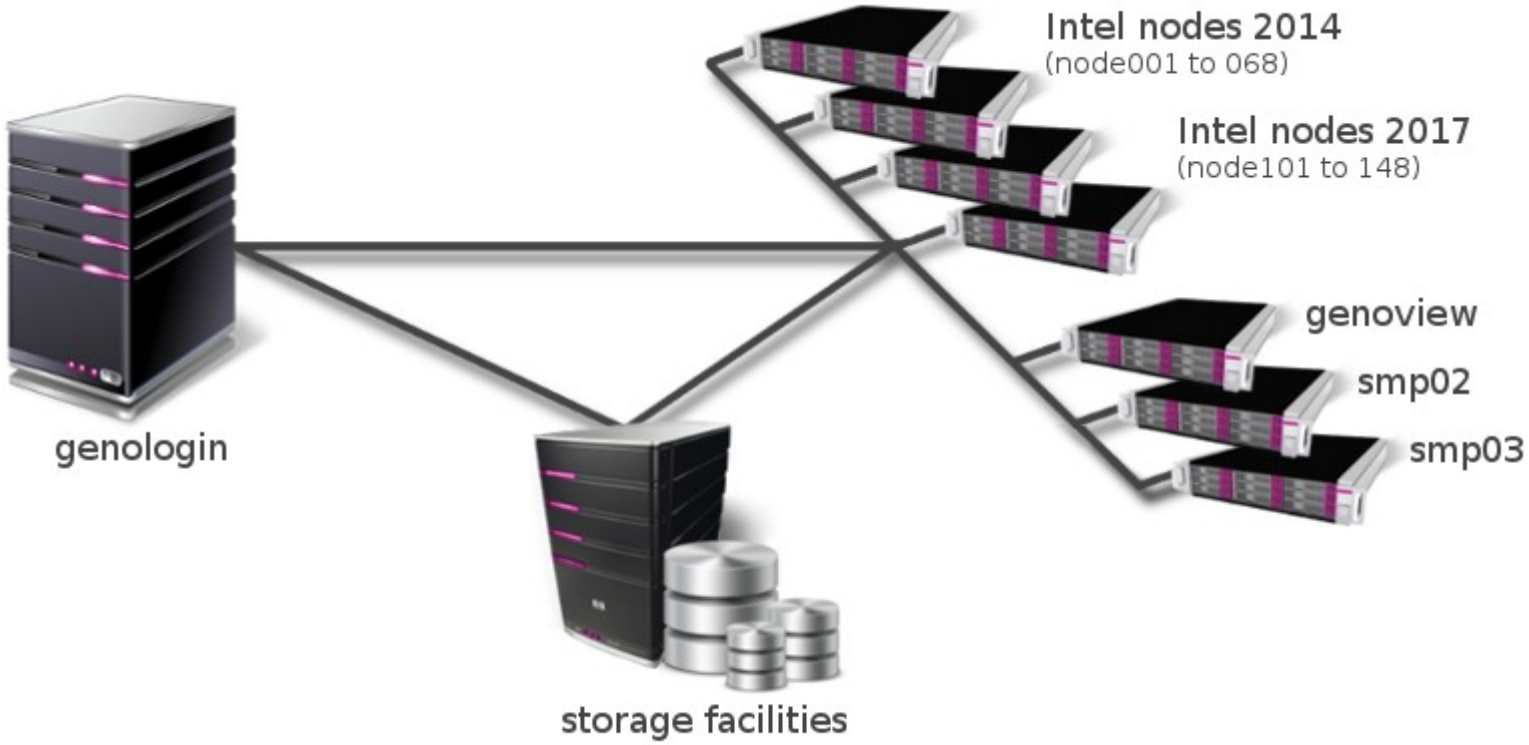
Revision cluster

Cluster

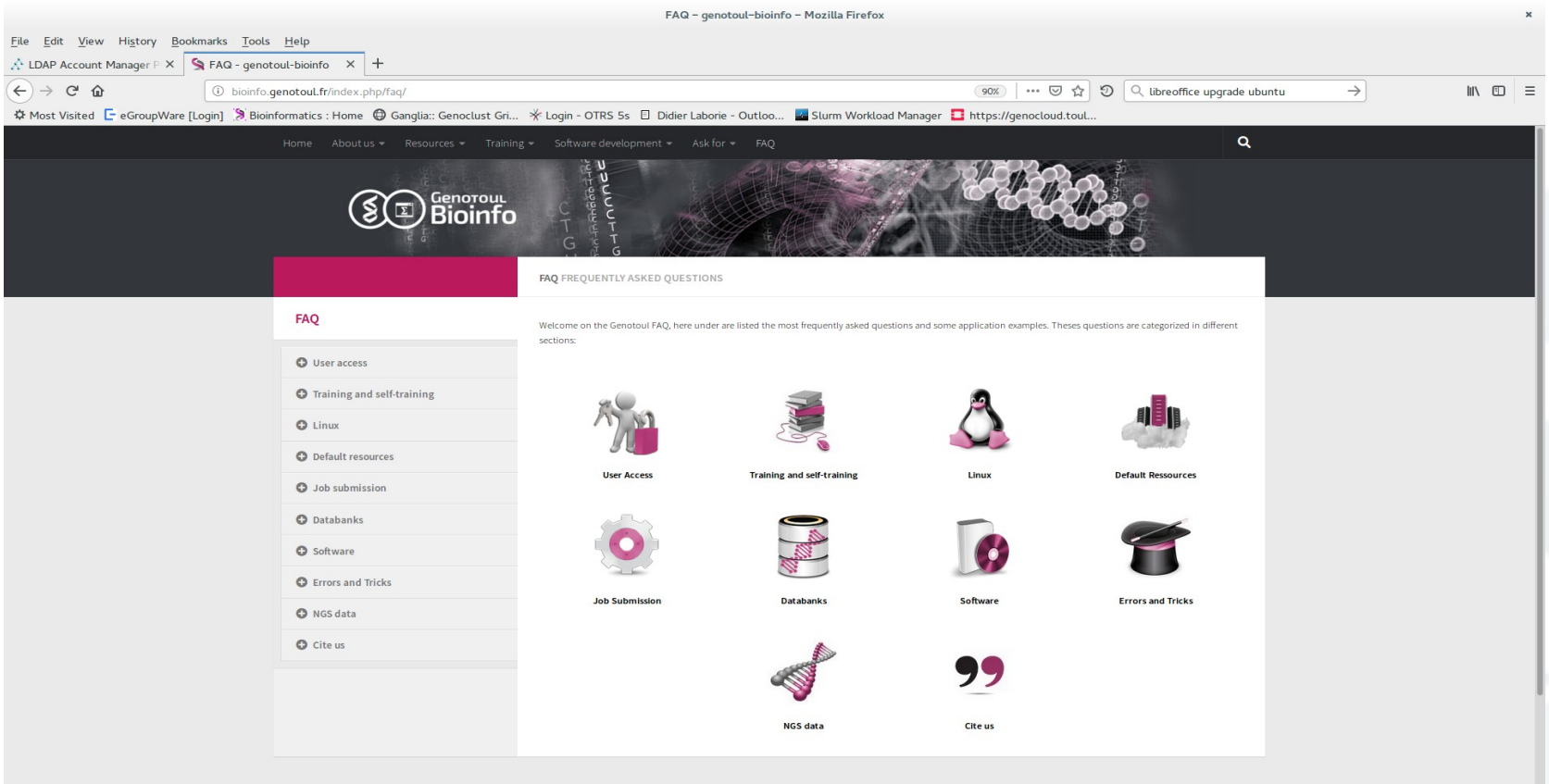

Intel nodes 2014
(node001 to 068)
Intel nodes 2017
(node101 to 148)
genoview
smp02
smp03
genologin
storage facilities

Disk spaces

/usr/local/bioinfo/src	Bioinformatics Software
/bank	International genomics Databanks
/home	User configuration files (ONLY) (1 GB user quota)
/work	HPC computational disk space (TEMPORARY) (1 TB user quota)
/save	User disk space (with BACKUP) (250 GB user quota + replication)

FAQ & Support

- *Questions=> support.genopole@inrae.fr*



Environment : Search/Find a soft

Website (Resources/Software): http://bioinfo.genotoul.fr/index.php/resources-2/softwares/

Select a category:

All software

Search a software:

Search Go

Search Results for "Admixture"

Application	Description	Avaibility/Use (SLURM Cluster available on 16/03/2018)
Admixtools	ADMIXTOOLS (Patterson et al. 2012) is a software package that supports formal tests of whether admixture occurred, and makes it possible to infer admixture proportions and dates.	**Slurm Cluster:** Ask for Install **SGE Cluster:** /usr/local/bioinfo/src/ADMIXtools
Admixture	ADMIXTURE is a software tool for maximum likelihood estimation of individual ancestries from multilocus SNP genotype datasets. It uses the same statistical model as STRUCTURE but calculates estimates much more rapidly using a fast numerical optimization algorithm.	**SLURM Cluster:** How to use **SGE Cluster:** How to use

Not installed on SLURM Cluster- link to ask for

Link to soft website

Installed on SLURM Cluster- link to help

Environment : Search/Find a soft

- **Installation paths**
  - Bioinfo -> /usr/local/bioinfo/src/
  - Compilers → /tools/compilers
  - Libraries → /tools/librairies
  - Others system tools → /tools/others_tools
  - Langages (Python, R , Java..) → /tools
  - Useful scripts → /tools/bin (sarray, squota_cpu, saccount_info…). In user's default PATH.
- **Commands**
  - **module avail**: display all available software installed on the cluster
  - **module avail <category/soft_name>**: display available versions for a specific application (with category in bioinfo,compiler,mpi or system) (case sensitive)
  - **search_module <soft_name>**: display available versions for a specific application (case insensitive)

SLURM
Job submission commands

- BATCH
  - **sbatch** : submit a batch script to slurm.
  - **sarray** : submit a batch job-array to slurm
  - **scancel** : kill the specified job

- INTERACTIVE
  - **srun --pty bash** : submit an interactive session with a compute node (default workq partition).
  - **srun --x11 --pty bash** : submit an interactive session with X11 forwarding (default workq partition)

    For the first time, create your public key as below (onto genologin server)

    $ ssh-keygen

    $cat .ssh/id_rsa.pub >> .ssh/authorized_keys
  - **runVisuSession.sh** : submit a TurboVNC / VirtualGL session with the graphical node (interq partition). Just for graphics jobs.

SLURM
Monitoring commands

- **sinfo** : display nodes, partitions, reservations
- **squeue** : display jobs and state
- **sacct** : display accounting data
- **scontrol show** : get informations on jobs, nodes, partitions
- **sstat** : show status of running jobs
- **sview** : graphical user interface

SLURM
Default parameters

- workq partition -p workq
- 1 thread -c 1
- 2GB RAM memory -mem=2GB

- 100,000H annually compute time (more on demand)
- 10,000: max jobs for all users
- 2500: max jobs per user inside the queue
- 2500 : max tasks array per job