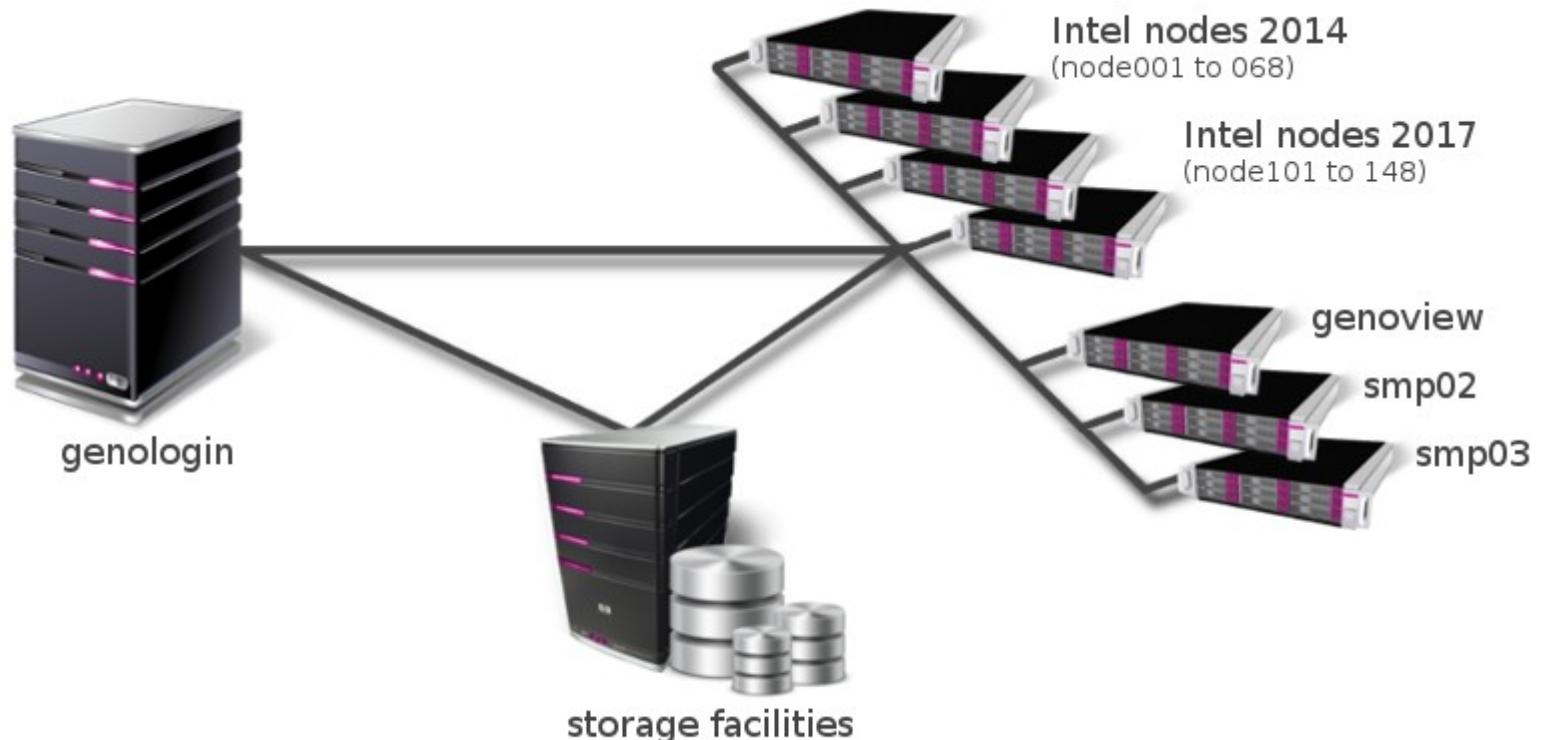
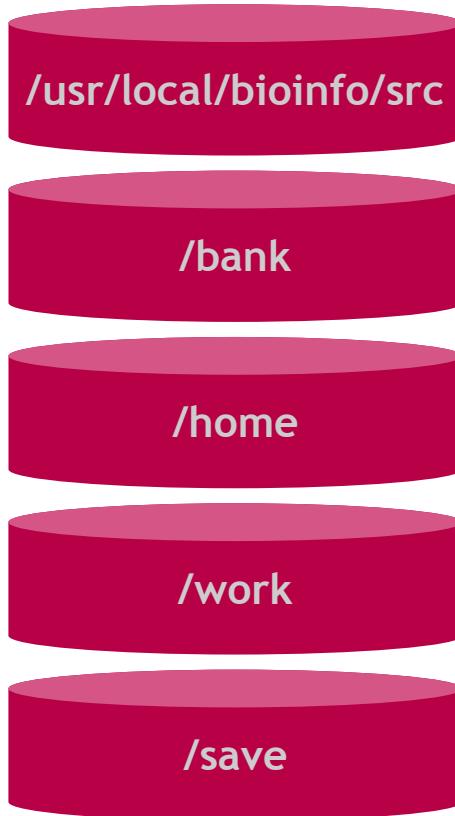


Revision cluster

Cluster



Disk spaces



Bioinformatics Software

International genomics Databanks

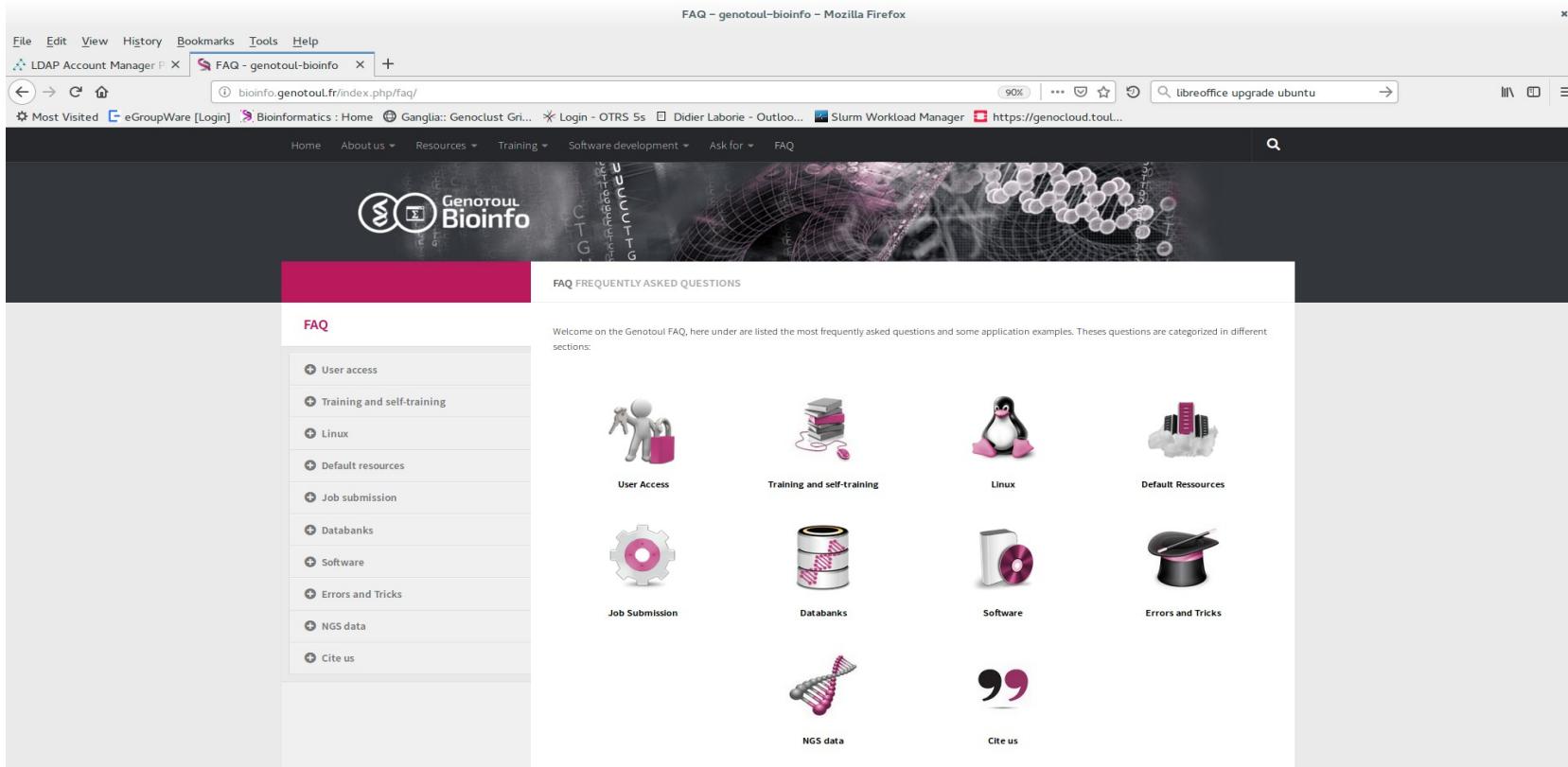
User configuration files (ONLY)
(1 GB user quota)

HPC computational disk space (TEMPORARY)
(1 TB user quota)

User disk space (with BACKUP)
(250 GB user quota + replication)

FAQ & Support

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

A screenshot of a Mozilla Firefox browser window showing the Genotoul Bioinfo FAQ page. The title bar says "FAQ - genotoul-bioinfo - Mozilla Firefox". The address bar shows the URL "bioinfo.genotoul.fr/index.php/faq". The page itself has a dark header with the Genotoul Bioinfo logo and navigation links for Home, About us, Resources, Training, Software development, Ask for, and FAQ. The main content area is titled "FAQ FREQUENTLY ASKED QUESTIONS". On the left is a sidebar with a "FAQ" heading and a list of categories: User access, Training and self-training, Linux, Default resources, Job submission, Databanks, Software, Errors and Tricks, NGS data, and Cite us. To the right of the sidebar are several icons with corresponding labels: "User Access" (a person opening a padlock), "Training and self-training" (books and a computer mouse), "Linux" (a penguin), "Default Ressources" (a stack of cylinders), "Job Submission" (a gear), "Databanks" (a database icon), "Software" (a CD/DVD), "Errors and Tricks" (a top-hat), "NGS data" (a DNA helix), and "Cite us" (two purple quotation marks).

FAQ - genotoul-bioinfo - Mozilla Firefox

bioinfo.genotoul.fr/index.php/faq

FAQ FREQUENTLY ASKED QUESTIONS

FAQ

- User access
- Training and self-training
- Linux
- Default resources
- Job submission
- Databanks
- Software
- Errors and Tricks
- NGS data
- Cite us

User Access

Training and self-training

Linux

Default Ressources

Job Submission

Databanks

Software

Errors and Tricks

NGS data

Cite us



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

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.

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.

Link to soft website

Not installed on SLURM Cluster- link to ask for

Availability/Use
(SLURM Cluster available on 16/03/2018)

Slurm Cluster: Ask for Install
SGE Cluster: /usr/local/bioinfo/src/ADMIXtools

SLURM Cluster: How to use
SGE Cluster: How to use

Installed on SLURM Cluster- link to help

- **Installation paths**

- Bioinfo -> /usr/local/bioinfo/src/
- Compilers → /tools/compilers
- Libraries → /tools/librairies
- Others system tools → /tools/others_tools
- Languages (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)

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.

- **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

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