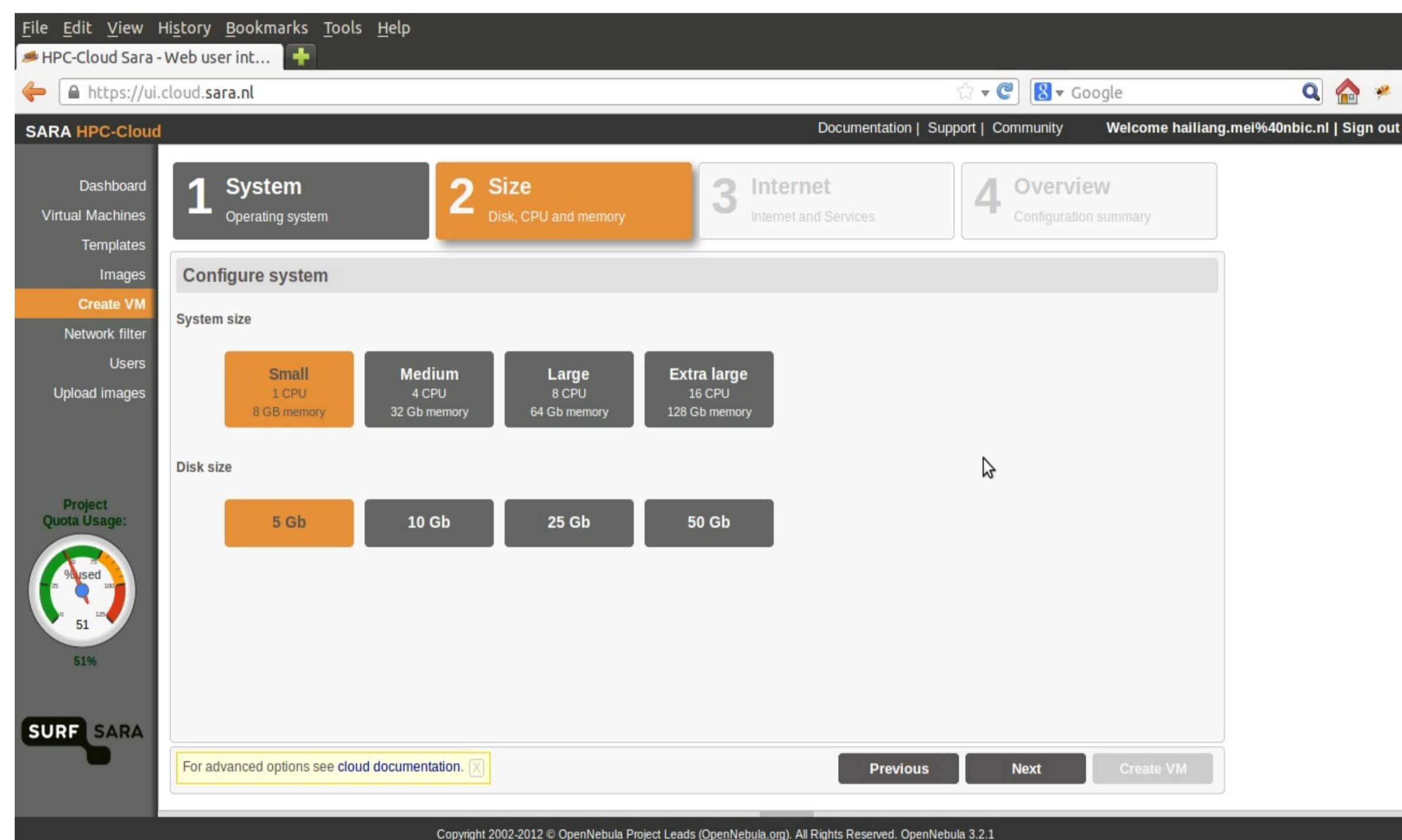


NBIC Galaxy @ SURFsara HPC Cloud

Mattias de Hollander, David van Enckevort, Leon Mei, Marc van Driel, Rob Hooft

→ SURFsara HPC Cloud

- 19 nodes, 32 cores and 256 GB RAM each
- 400 TB storage in total
- Maximum 40 Gb access to storage



→ Installation Automation

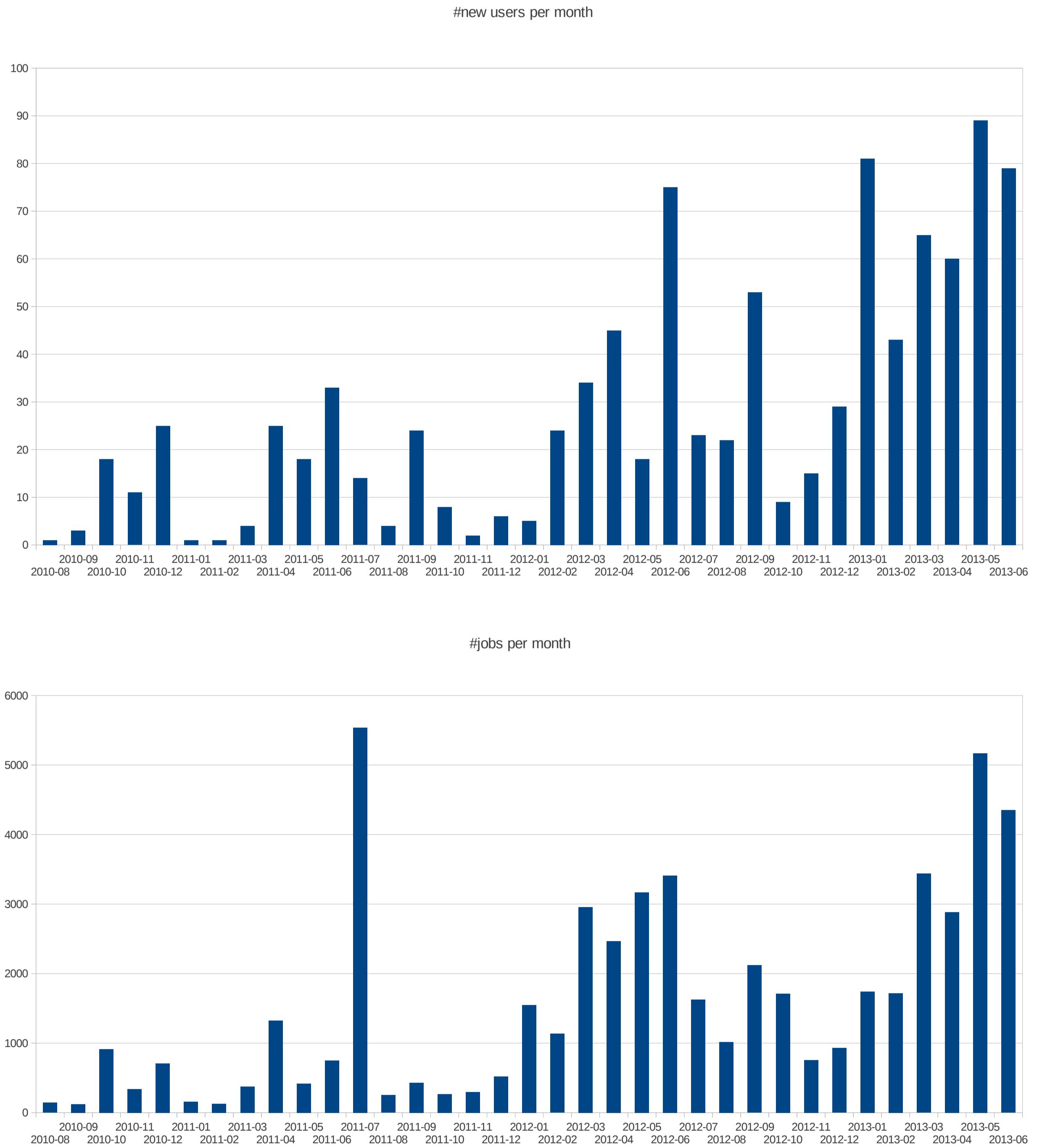
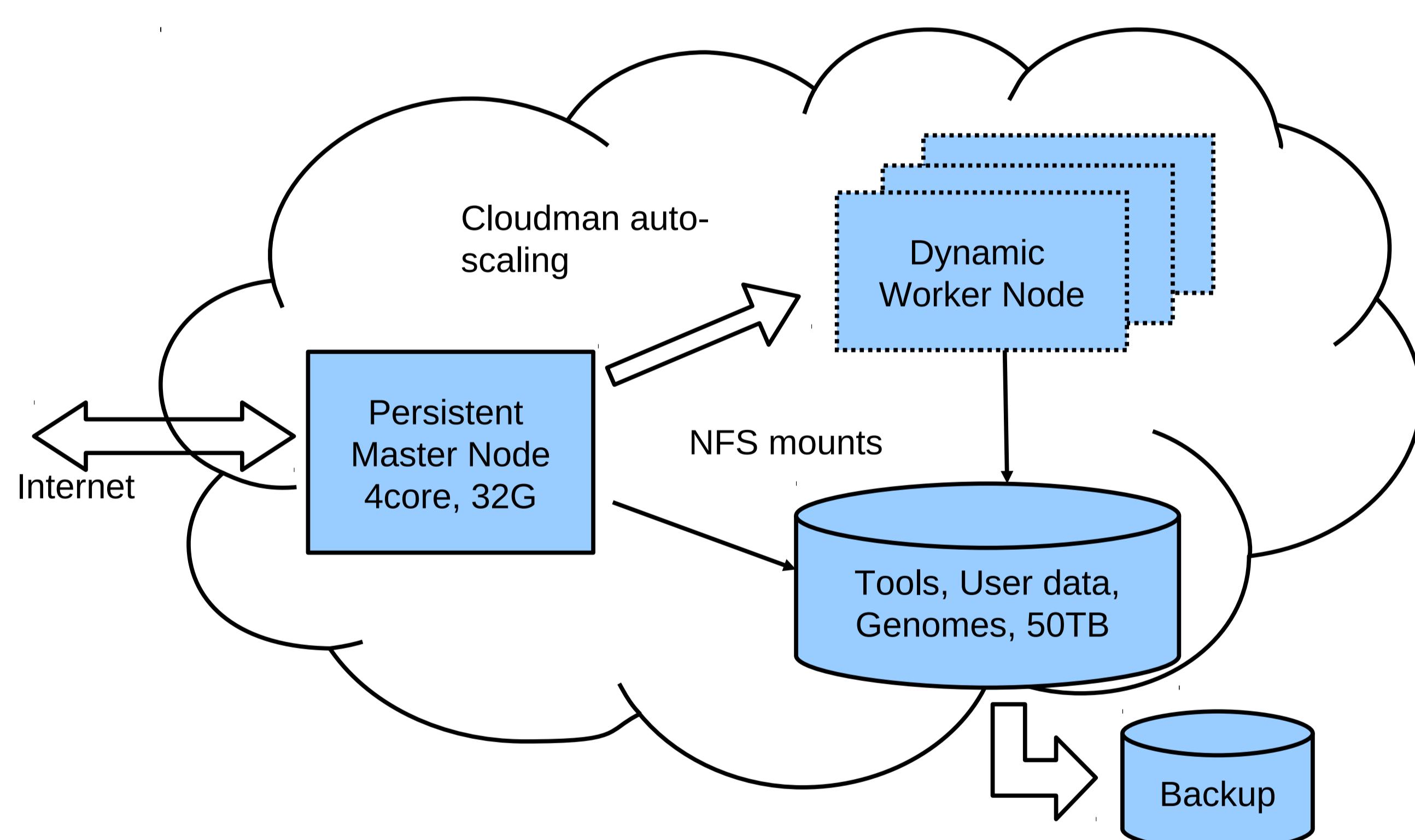
- Automatic tool installation
 - Cloudman script with opennebula support
 - Galaxy codebase
 - PostgreSQL DB & Sun Grid Engine
 - Common NGS tools, e.g., BWA, bowtie, samtools, etc.
- Automatic reference dataset installation
 - Cloudbiolinux script
 - Common genome builds, hg18, hg19, mm9, tair10, etc.
 - Tool specific genome indexes for bowtie, BWA, etc.

→ Usage

- Used successfully in a number of NGS courses organized by NBIC
- Base image was used by several project specific Galaxy instances running at SURFsara HPC Cloud

→ System Architecture

- Implemented using Cloudman script
- NFS shared file system
- /mnt/galaxyTools: galaxy, 3rd party tools,
- /mnt/galaxyData: galaxy user data, postgres DB
- /mnt/galaxyIndices: genomes, liftover chains



→ Acknowledgement

- Enis Afgan and the members of NBIC Galaxy administration team
- NIOO, SURFsara, CTMM-Trait

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