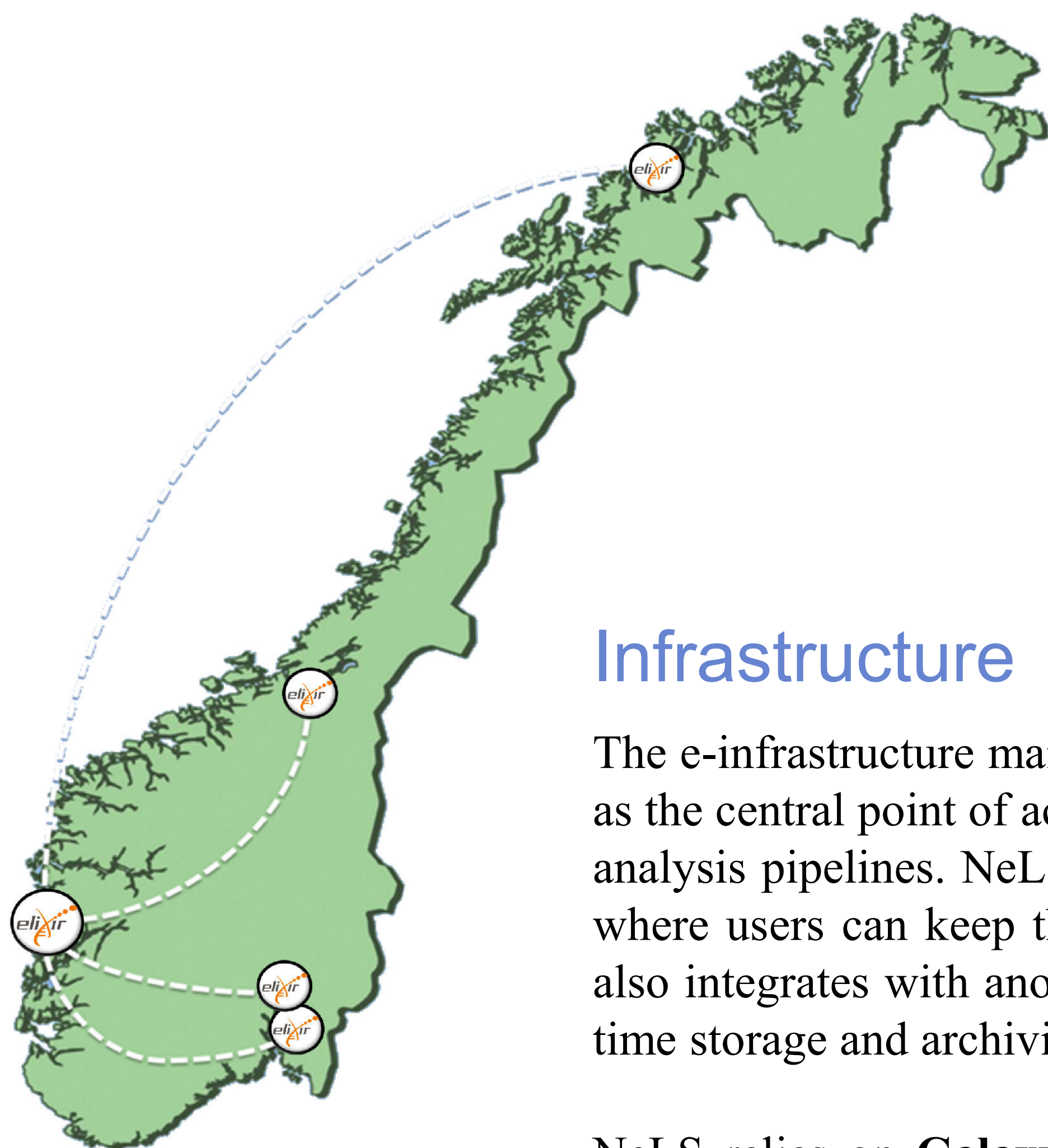


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Introduction

NeLS is one of the packages of the ELIXIR.NO project which aims to provide a national Norwegian e-infrastructure allowing users within the life sciences community to efficiently and safely *store*, *share*, *analyse* and *publish* their genomics scale data. The project is funded by the Norwegian Research Council and involves a collaboration between bioinformatics research groups at five Norwegian universities led by the University of Bergen.

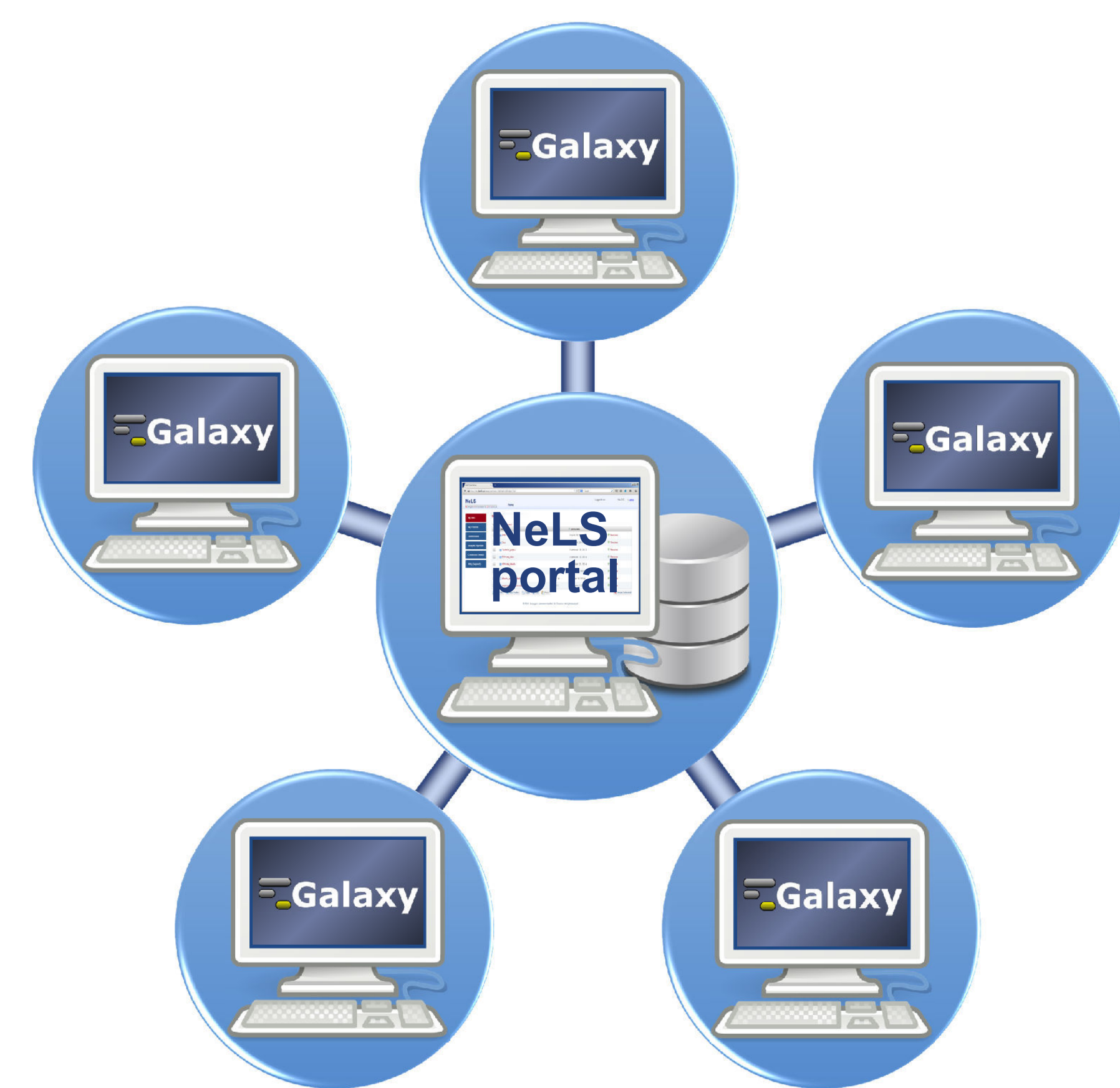


Infrastructure

The e-infrastructure maintains a **web portal** at <https://nels.bioinfo.no> that functions as the central point of access to the NeLS resources, which include data storage and analysis pipelines. NeLS currently offers about 300TB of short-term storage space where users can keep their data while working on projects, and the infrastructure also integrates with another storage provider called StoreBioInfo to facilitate long-time storage and archiving of data after a project has ended.

NeLS relies on **Galaxy** – a web-based workbench developed at Penn State and Johns Hopkins University – as its primary platform for data analysis. Each of the five participating universities hosts its own Galaxy server, either running on dedicated hardware or as a front-end to shared computer clusters. The open-source code of Galaxy has been modified with NeLS-specific enhancements, such as tools to export and import data to and from the NeLS Storage.

Other systems integrated with NeLS include **The Genomic Hyperbrowser** – a system for statistical analysis of genomic data tracks, and **MotifLab** – a JAVA-based application for analysing gene regulatory regions.



User authentication

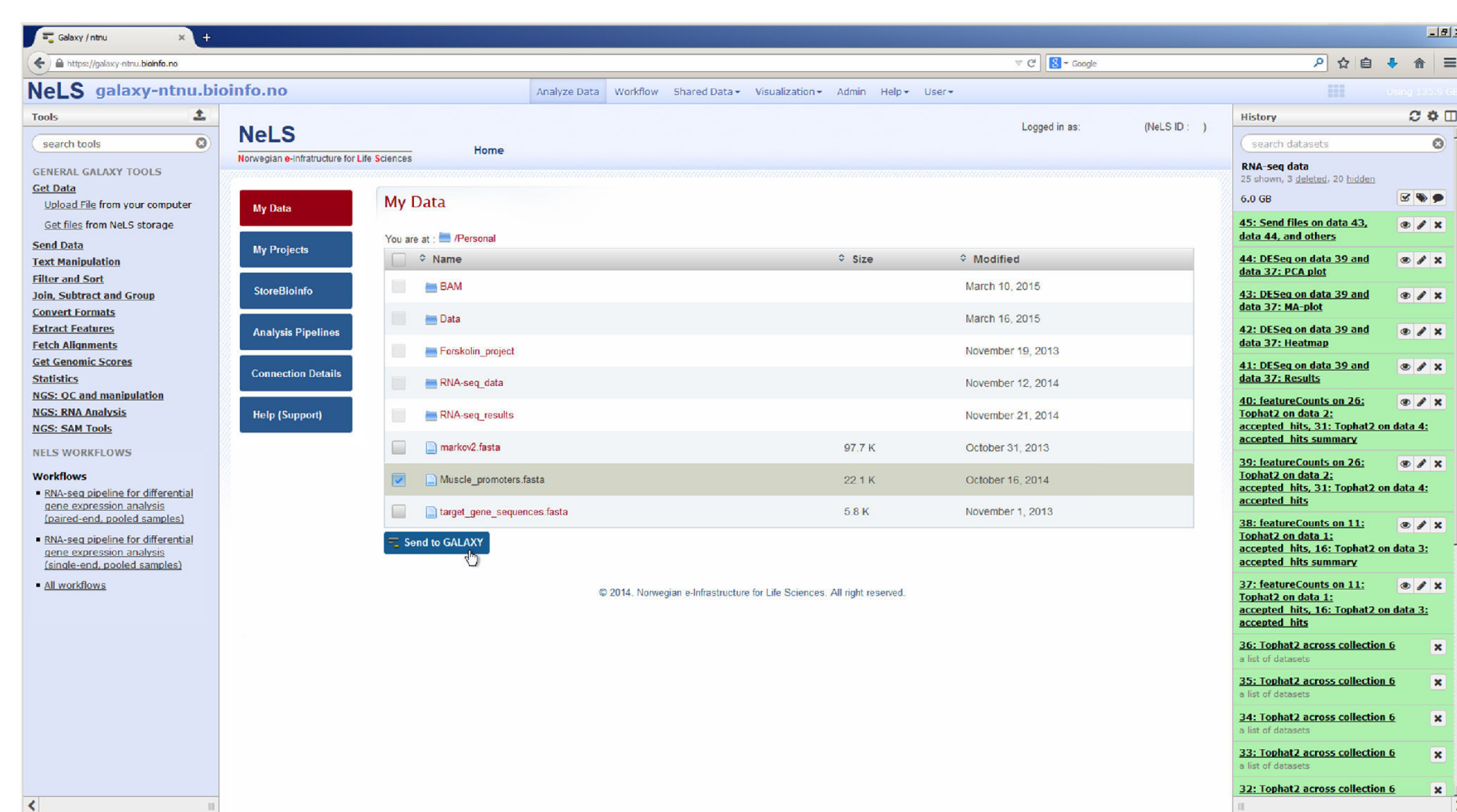


Authentication of users is done with the common electronic identity provider for the Norwegian educational sector (FEIDE), which means that all students, researchers and overall university users can log into NeLS with their institution provided credentials. Development is well underway to provide an alternative identity provider for users outside of the education sector as well as international project collaborators. All of the browser-based NeLS resources support *single sign-on* which allows users to move freely between the portal and the different Galaxy servers without the need for re-authentication. For advanced users, NeLS provides API and SSH access through credentials that can be accessed from inside the NeLS portal.

Services

The five Galaxy servers are each configured with different types of analysis tools reflecting the research focus of the hosting groups, primarily within the areas of marine genomics and human medicine. Part of the responsibilities of these groups will also be to develop domain-specific analysis pipelines that will be published as workflows in Galaxy. Currently, NeLS offers workflows for differential gene expression analysis of RNA-seq data, variant calling in somatic and germline cells, and taxonomic classification of shotgun metagenomic sequences. For analysis of human patient data, NeLS collaborates closely with the Norwegian “services for sensitive data (TSD)” project to provide access to relevant Galaxy workflows within a high-security environment.

In addition, the Norwegian Elixir node also operates a bioinformatics help desk with highly qualified personnel that can assist the user community with anything from small practicalities to long-term research collaboration on large projects.



This screenshot from the NeLS Galaxy server at NTNU shows a user accessing the NeLS Portal in the middle to import data files from the storage into their Galaxy history.