We use the de.NBI Cloud since 2017 to serve the MetaProteomeAnalyzer software to the metaproteomics community. [...] The initialization of the cloud project was easily possible.

Roman Zoun
Otto von Guericke University of Magdeburg

Having the de.NBI Cloud, we can easily crunch through some large-scale metaproteomics data sets using the containerized workloads we have developed in the PhenoMeNaL-H2020.EU project [...] In the future, we are going to use the de.NBI cloud even more.

The de.NBI Cloud is a federation consisting of six academic cloud sites. The whole system is accessible through single sign-on which allows the user to reuse their existing university or research institution account.

Trend of usage

Number of cloud users

0 400 800
01'18 10'19

Number of project applications (cumulative)

0 100 200
01'18 10'19

https://cloud.denbi.de
cloud@denbi.de
@denbiCloud
Mission

The de.NBI Cloud is a cloud federation, providing compute and storage resources free of charge for academics. The vast capacity of the de.NBI Cloud enables developers to operate science gateways with thousands of users such as usegalaxy.eu and researchers to run their bioinformatic tools and workflows for life science projects of any size. The de.NBI Cloud is, besides de.NBI Tools and de.NBI Training, a service offered by the German Network for Bioinformatics Infrastructure.

**de.NBI Cloud Access**

The de.NBI Cloud can be accessed through the de.NBI Cloud Portal. The browser-based portal allows principal investigators of any German university or research institution to submit a simple web form which is then reviewed by a cloud access committee. Once approved, the requested resources are allocated and further project management functions are unlocked.

**Project Types**

- **OpenStack**
  
  OpenStack lets you manage your storage, compute and network resources and thereby start frameworks for parallel processing of large data. This is suited for experienced power users wanting full control over their computing environment and offers an easy to use entry point in cloud computing.

- **SimpleVM**
  
  SimpleVM allows you to start a virtual machine with a few clicks. This project type fits your needs, if you are not familiar with cloud computing and simply want to use the tools and workflows known to you in a self-customizable environment.

- **SaaS**
  
  Use state of the art workflows for your research

  - Workflows for sequence analysis, including Illumina and Oxford Nanopore
  - Fully established software packages and workflow systems

- **PaaS**
  
  access to fully configured infrastructure for running tools and pipelines

  State of the art research environments can be started with few clicks to ease and streamline your work in the cloud.

  - Jupyter Notebook: Application to create documents containing code and visualizations
  - RStudio: Integrated development environment for R
  - TheliaIDE: Integrated development environment framework for desktop and web applications

- **IaaS**
  
  Full control over compute environment - plain access to virtualized infrastructure

  Distributed Workflows:
  - Easy setup of virtual clusters using BibiGrid, Terraform, Butler
  - Ready made and proven workflows for genomics, metagenomics, metabolomics etc.
  - UNICORE, Arvados

  Big Data Analysis:
  - Use Hadoop or Spark based solutions for big data analysis

Apply for cloud resources

Monitor the status of your project

Manage your project members

Get de.NBI Cloud specific news

Spezialized Hardware:

- High Memory nodes
- GPU nodes
- FPGAs

Hosted Databases:

Mirrors for lightning fast access to databases for your analysis (e.g. SRA, ICGC, ...)