

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.**

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Having the de.NBI Cloud, we can easily crunch through some large-scale metabolomics 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.**

de.NBI Cloud Federation



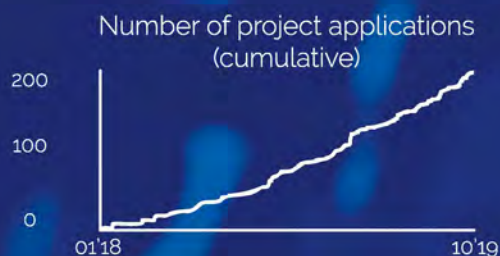
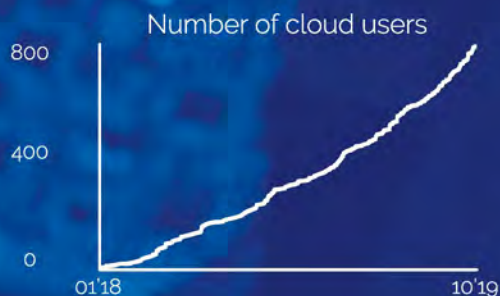
The de.NBI Cloud is a federation consisting of six academic cloud sites. The whole system is accessible through single sign-on which allows the user to reuse their existing university or research institution account.



Cloud

Cloud Computing for Life Sciences

Trend of usage



<https://cloud.denbi.de>

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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:

Apply for cloud resources



Monitor the status of your project



Manage your project members



Get de.NBI Cloud specific news



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 entrypoint in cloud computing.



scalability



configurability



API access

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.



ease of use



flat learning curve



remote desktop possibility

SaaS: Software as a Service

PaaS: Plattform as a Service

IaaS: Infrastructure as a Service

SaaS

Use state of the art workflows for your research

Ready to use scientific service:
 - 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: An application to create documents containing code and visualizations
- RStudio: Integrated development environment for R
- TheiaIDE: 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

Spezialized Hardware:

- High Memory nodes
- GPU nodes
- FPGAs

Hosted Databases:

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