

**BiGi**

Microbial Bioinformatics

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## de.NBI service center BiGi

The BiGi Bioinformatics Resource Center combines bioinformatics expertise and facilities at Bielefeld University (UBI) and Gießen Justus-Liebig University (JLU) providing bioinformatics support, compute resources and software tools for the field of microbial genome research. Since 2016, the partner project MetaProtServ at Magdeburg Otto-von-Guericke-University (OGM) complements our microbial genome analysis portfolio for metaproteome data analysis.

BiGi-UBI, in particular, maintains tools and web services specifically for metagenomics and postgenomics data analysis, integration and visualization. Particular emphasis is being placed on first-level user support and the provision of high-performance computing services for different user profiles.

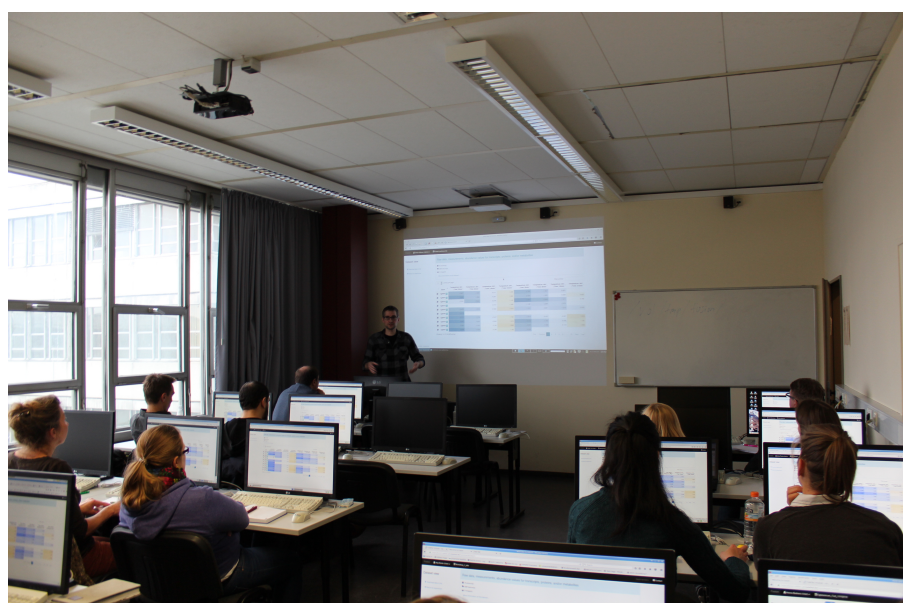
Application User	Expert Data Analyst	Developer
<ul style="list-style-type: none"> <li>Ready-to-use bioinformatics software</li> <li>Web- and client/server-based applications</li> <li>Guidance on applicable analysis methods</li> <li>Workflows for PolyOmics</li> </ul>	<ul style="list-style-type: none"> <li>Access to bioinformatics software tools</li> <li>Up-to-date data sources</li> <li>Access to compute and storage resources</li> <li>Possibility to install and execute own scripts and</li> </ul>	<ul style="list-style-type: none"> <li>HPC resources for development of bioinformatics analysis methods</li> <li>Access to the BiGi HPC infrastructure</li> <li>Virtual machine support and cloud computing re-</li> </ul>

The BiGi Bioinformatics Resource Center supports different levels of user competence.

Project lead: J. Stoye; de.NBI employees: N. Kleinbölting (research scientist, BiGi services), S. Jünemann (research scientist, BiGi training), A. Walender (research scientist, BiGi cloud), C. Henke (research scientist, BiGi cloud); further involved scientists: A. Sczyrba, S. Albaum, J. Krüger, B. Weisshaar; administration and support team: B. Fischer, T. Kasch, A. Neumann, R. Nolte, R. Orth, V. Tölle (group as of Feb 2020)

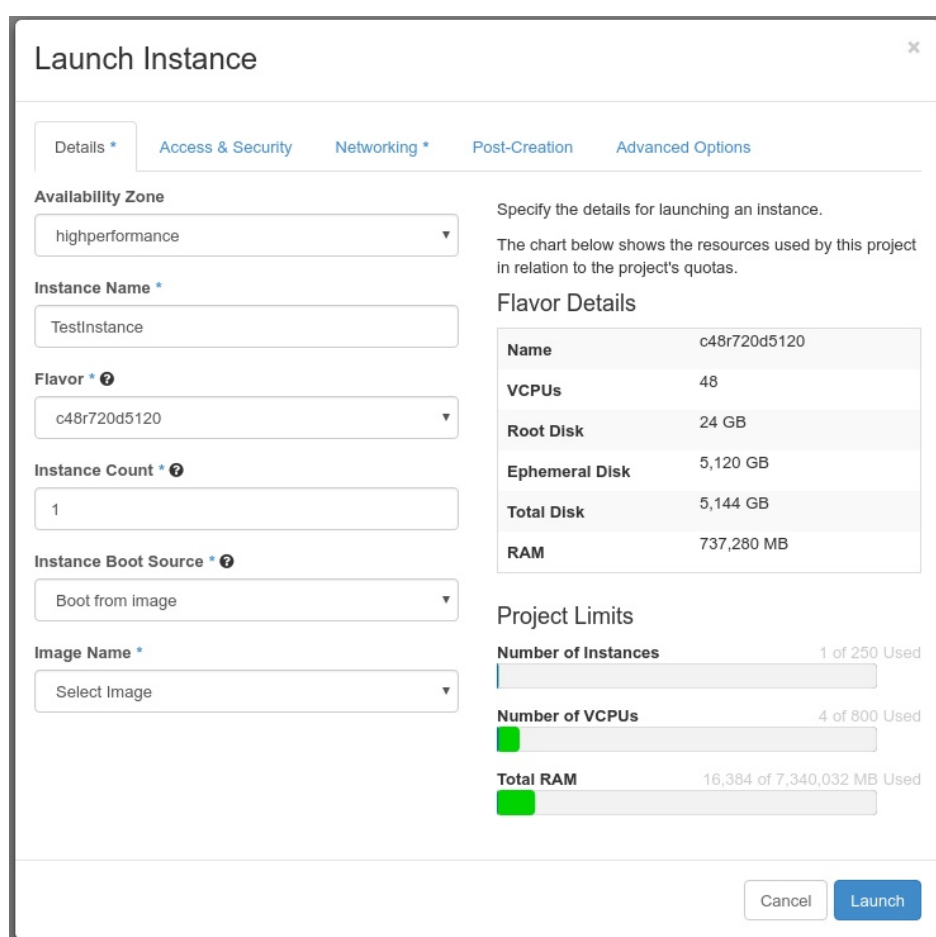
## de.NBI training and education

- Targeted and un-targeted metagenomics (Nov 23-25, 2015, 15 participants; Aug 29 - Sep 2, 2016, 25 part., in cooperation with DZIF; Mar 27-29, 2018, 17 part., at the ECCB 2018 in Athens: Sept 8th, 2018, 20 part.; Oct 9-11, 2019, 11 part.)
- Cloud computing workshops, i.a. at the GCB 2016 Berlin and 2018 Vienna (Sep 12, 2016, 45 part.; March 8th, 2018, 8 part., Sep 25, 2018, 20 part.; Sep 16, 2019, 20 part.)
- Polyomics data integration and analyses (Oct 13, 2016, 14 part.; Sep 7, 2017, 6 part.; Nov 13, 2018, 8 part.)
- de.NBI summer schools (Microbial Bioinformatics: Sep 20-25, 2015, Giessen; From Big Data to Big Insights: Sep 26-30, 2016, Castle Dagstuhl; On cloud computing: Jun 26-30, 2017, Giessen)
- Nanopore best practice (Nov 22-24, 2017, 20 part.; Sep 19-21, 2018, 14 part.; Sep 24-27, 2019, 15 part.)

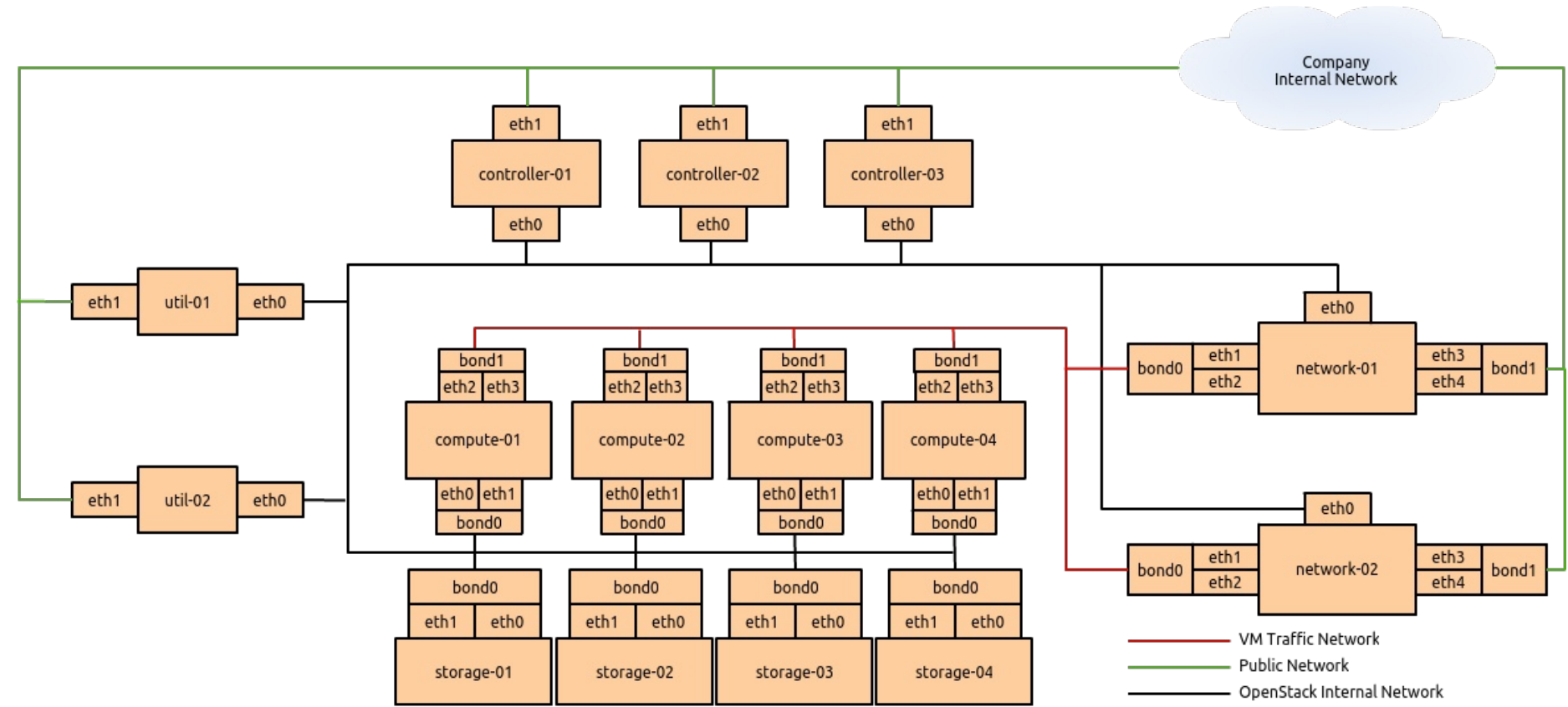


## de.NBI cloud activities

As part of the de.NBI cloud, BiGi-UBI is one of the centers providing cloud infrastructure to the life science community. In the present configuration, together with the next extension, the cloud comprises 3,680 + ~2,500 cores, highly interconnected (HA-Setup, 10 GbE), and 10 + ~6 PB gross storage capacity (Ceph Mimic, 40 GbE). Bielefeld, particularly, provides high memory servers (up to 3TB RAM) as well as GPU servers (10 + 20 + ~30 Nvidia Tesla P100 / V100 / T4).



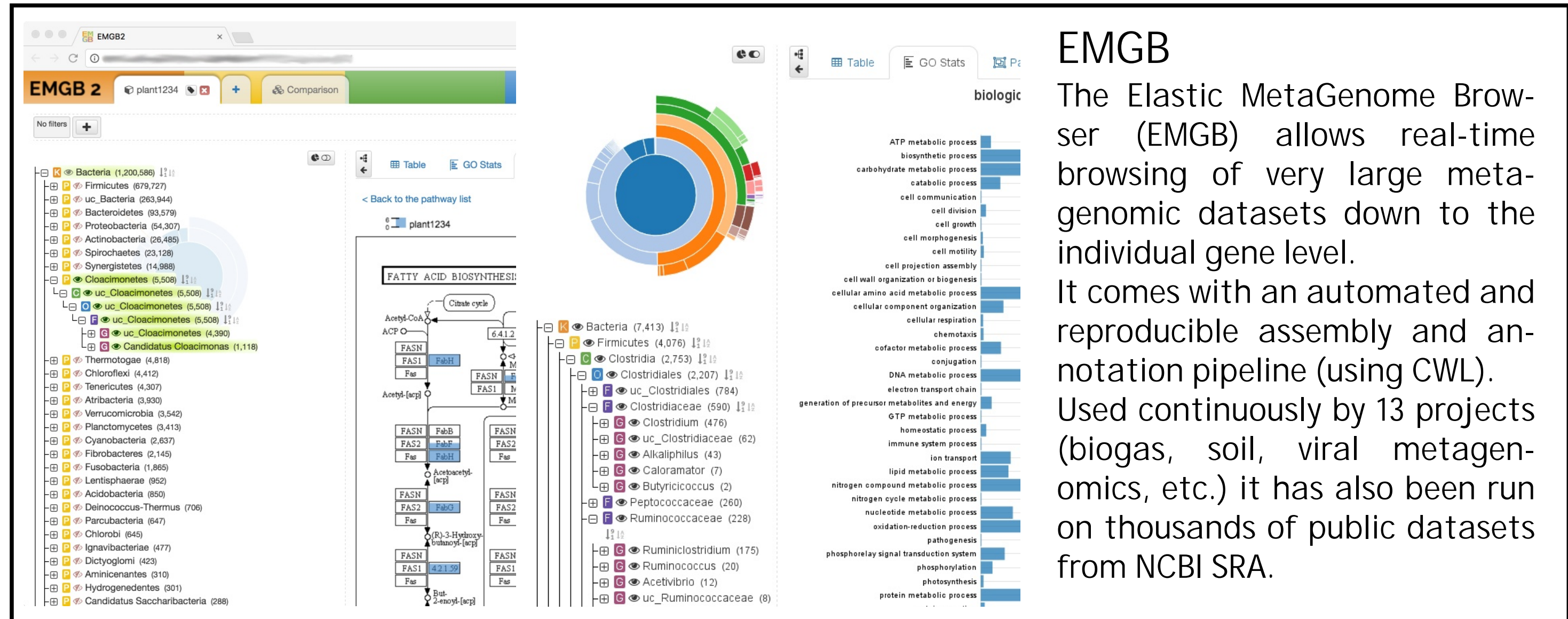
Start and manage your resources.



Bielefeld OpenStack cloud utilizes high interconnectivity maximizing the network bandwidth.

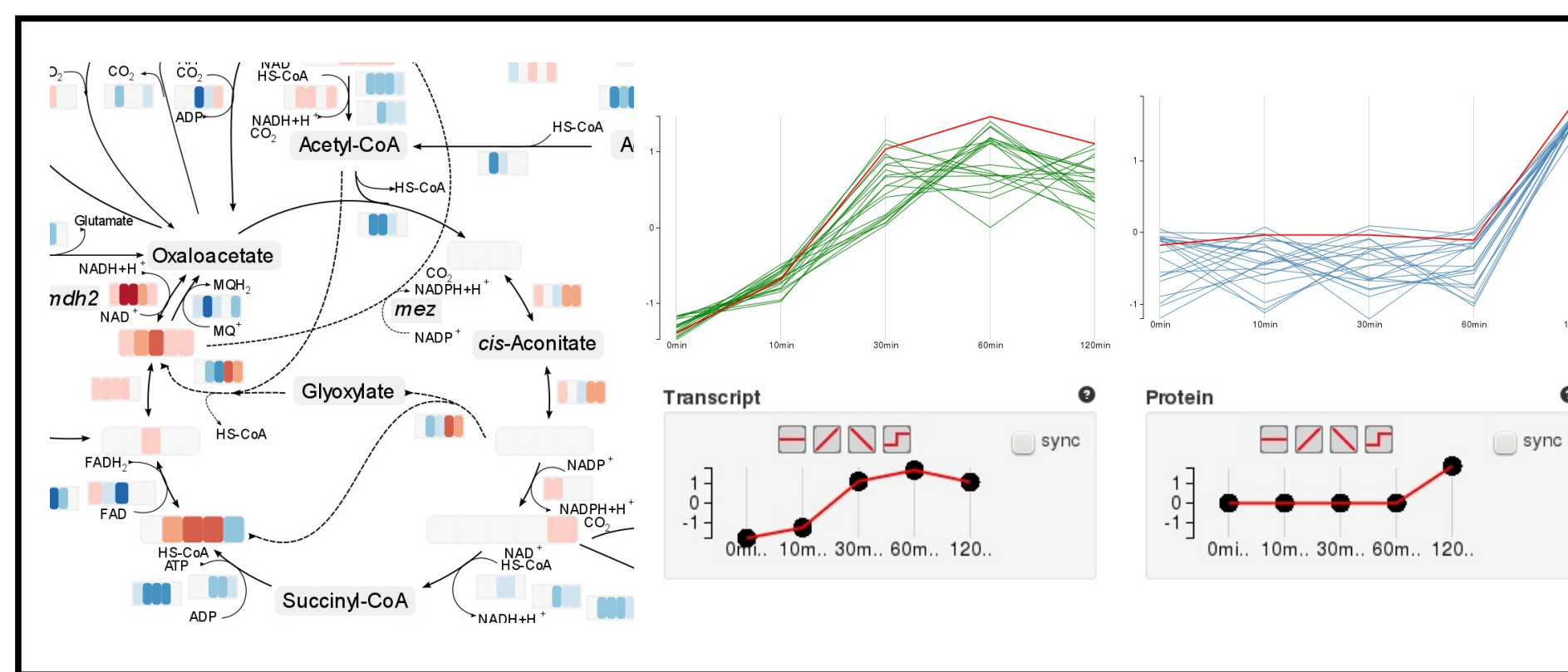
## de.NBI services and progress report

BiGi-UBI operates, maintains and supports a wide range of software tools and applications providing solutions for microbial analytics. Service requests range from project requests to comprehensive consultancy requests.



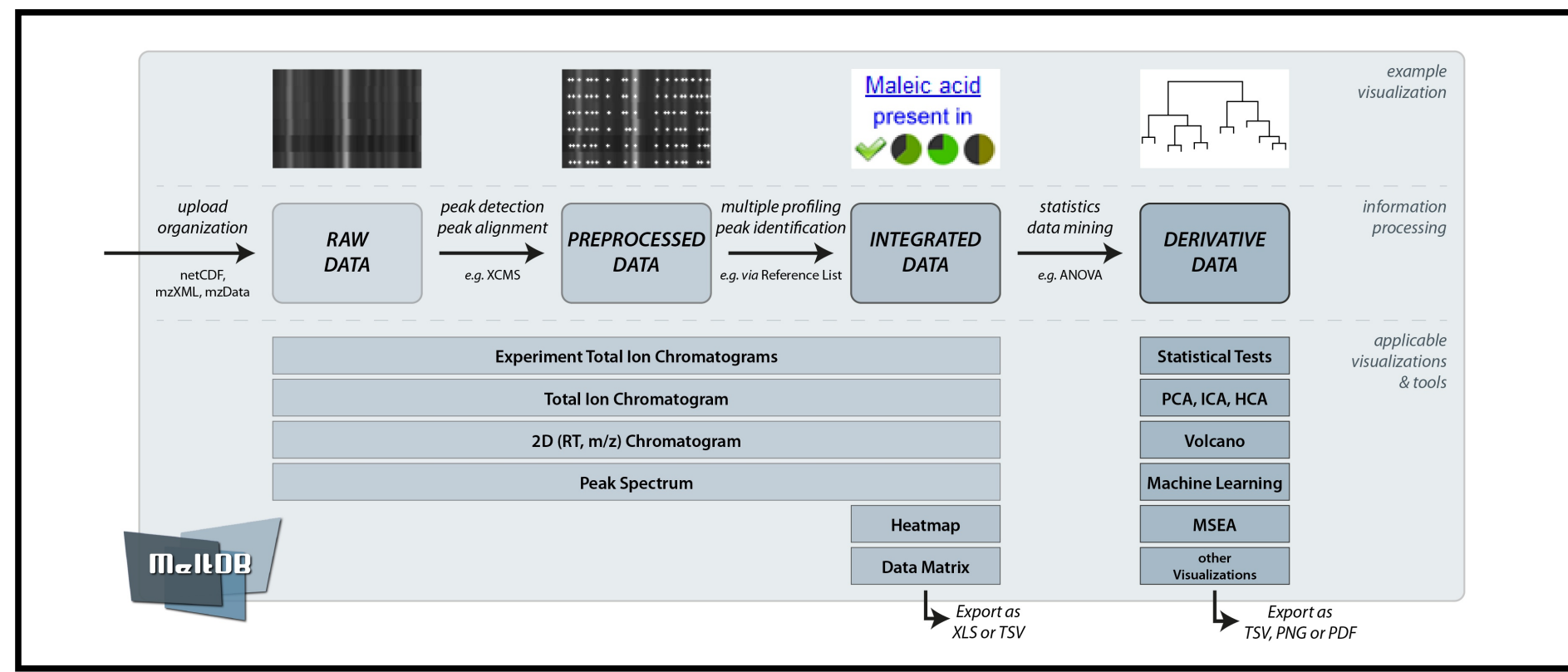
### EMGB

The Elastic MetaGenome Browser (EMGB) allows real-time browsing of very large metagenomic datasets down to the individual gene level. It comes with an automated and reproducible assembly and annotation pipeline (using CWL). Used continuously by 13 projects (biogas, soil, viral metagenomics, etc.) it has also been run on thousands of public datasets from NCBI SRA.



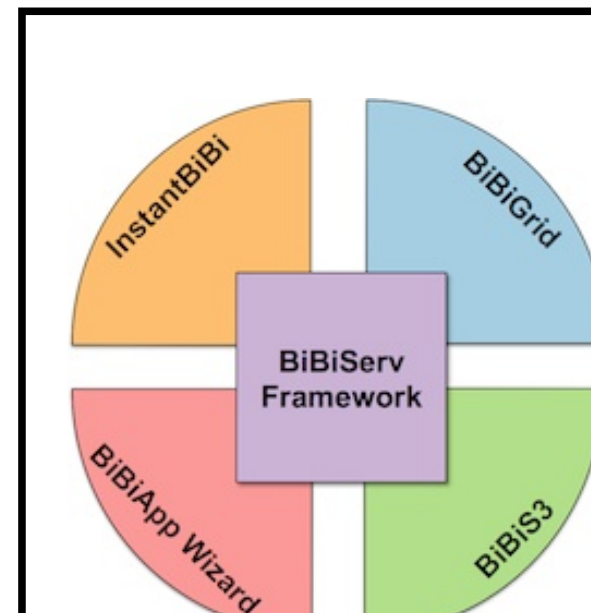
### Fusion

Omics Fusion is a web-based tool for the integration, analysis and interactive visualization of Multi-omics datasets. Since its public release in 09/2016 Fusion is used by 50-100 users each month who overall conducted more than 700 experiments with over 7000 processed jobs.



### MeltDB

The web-based software MeltDB is our solution for the storage and analysis of metabolomic datasets. It supports different peak detection and identification methods as well as several methods for the statistical analysis of multiple chromatograms.



### BibiServ

The BibiServ Framework provides a persistent service to the life-science community by hosting several bioinformatics tools developed in Bielefeld or in close collaboration. These tools include among others methods for alignment, evolutionary relationships, genome comparisons, and RNA structure prediction. The BibiServ continuously provides tools and software to the community (~2200 downloads & ~80k tool executions in 2019). Developments targeted the setup of the cloud environment and BibiGrid support for OpenStack.



### Compute & Storage resources

Compute and storage resources can be accessed in multiple ways: via direct login (ssh or Thinlinc remote desktop) and cluster usage based on UNIVA grid engine or via cloud computing resources based on OpenStack. Within the last year, compute and storage resources were, for example, provided to de.NBI users, e.g. at the Ruhr-Universität Bochum and the University Duisburg-Essen, as well as to other de.NBI partners, i.a., to MASH, MetaProtServ and SILVA. Developments and future activities at BiGi-UBI are continuously focussing on the provision of cloud computing and storage resources as well as on training courses in this regard.



### Elixir Activities

BiGi is involved in ELIXIR EXCELERATE implementation studies (Subtask 4.3.1 AAI, F1000Research 2018; Subtask 4.3.3 Storage and data transfer). As part of these, ~280TB of ENA metagenomics data are mirrored in the BiGi UBI cloud for local access. BiGi also participated in ELIXIR meetings (Future of Metabolomics, 2017; Compute Platform F2F Meeting, 2018; All Hands Meeting, 2018; Tools Platform F2F meeting, 2020) and is also a member of the TeCG for the ELIXIR Germany node.



### Administer Service Operations

All user driven service request are being tracked in a dedicated ticket system (request tracker) and the revised monitoring of key performance indicators have been implemented (matomo) as suggested by the SIG2 guidelines. Members of the BiGi center actively participated in all SIGs.

## Publications

Nelkner et al. (2019). "Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes". *Genes*  
Belmann et al. (2019) "de.NBI Cloud federation through ELIXIR AAI". *F1000Research*  
Jünemann et al. (2017). "Bioinformatics for Metagenomics and the Application to Biogas Research". *J Biotechnol*