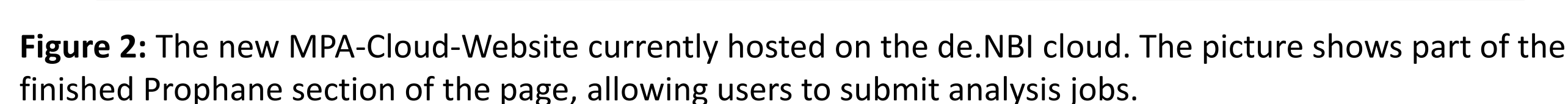
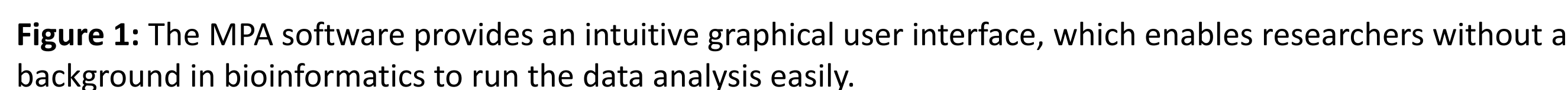


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2 Otto-von-Guericke University Magdeburg, Chair of Database and Software Engineering

Progress report

We continue to offer the MPA software to the scientific community and constantly grow our user base. Furthermore, we developed the back end for a new fully cloud compliant version of the MPA software³. Currently, the front end for this cloud compliant version is finished. Furthermore, the Prophane software, that offers orthogonal functional and taxonomic annotation, was recently added to the cloud version and is productively deployed on the de.NBI cloud, accessible through www.prophane.de [Fig. 2]. A publication that highlights the combined workflow of MPA and Prophane is currently under review.



de.NBI Training and education

We gave two official de.NBI courses. The first course was conducted in June over a week, and included a two day laboratory preparation of the participants samples for the following three day MPA software training course. The second course was conducted in September, as part of the GCB2019 conference. It focused on talks on the theoretical background of metaproteomics. Furthermore, users are continuously supported. In addition, the activities of de.NBI will be presented at the 4th International Metaproteome Symposium which is co-organized by Dirk Benndorf as a member of the scientific committee.

Publications

[1] "Challenges and perspectives of metaproteomic data analysis"; R. Heyer & K. Schallert et al. (2017)
Journal of Biotechnology; 261, 24-36, 2017, <https://doi.org/10.1016/j.jbiotec.2017.06.1201>

[2] "A robust and universal Metaproteomics Workflow for Research Studies and Routine Diagnostics
Within
24 h Using Phenol Extraction, FASP Digest, and the MetaProteomeAnalyzer"; R. Heyer & K. Schallert et al.
(2019)

[3] "MSDataStream - Connecting a Bruker Mass Spectrometer to the Internet"; R. Zoun et al. (2019)

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