MetaProtServ: Providing a standardized bioinformatics solution for metaproteomics data analysis

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Short description of the project

Targeting cellular functions metaproteomics complements metagenomics and metatranscriptomics as tools widely applied in microbial ecology (e.g., human gut microbiome, biogas plants). Bioinformatics data evaluation in metaproteomics diverges from typical proteomics approaches and faces unique challenges. In order to exploit more information from current metaproteome datasets, the MetaProteomeAnalyzer (MPA) software was developed. Within MetaProtServ, the GUI based MPA (www.mpa.ovgu.de) [Fig. 1] will be deployed as a powerful web service convincing more scientists from benefits of metaproteomics.

![Figure 1: The MPA software provides an intuitive graphical user interface, which enables researchers without a background in bioinformatics to run the data analysis easily.](image)

**de.NBI services**

The MetaProteomeAnalyzer (MPA) is provided to the research community as a centralized remote server solution and as a download for local installation. Users can access the server and its resources by creating an account. Currently 60 (previous period: 30) individual users are registered, of which at least twenty continuously use the software for their ongoing projects. With respect of the small size of the metaproteomics community, this constitutes a major increase in the user numbers. The acquired data volume exceeds 12 TB (previous period: 5).

**General information on the project**

The MetaProtServ partner project currently employs two staff members paid from de.NBI (Kay Schallert and Robert Heyer). Two staff members are project leaders (Dirk Benndorf and Gunter Saake). Furthermore, several staff are involved in consulting (David Broneske, Sebastian Püttker). We also established a industry partnership with Bruker Daltonik GmbH (Heiko Neuweger, Sven Bremer).

**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 software. 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.

![Figure 2: The new MPA-Cloud Website currently hosted on the de.NBI cloud. The picture shows part of the finished Prophane section of the page, allowing users to submit analysis jobs.](image)

**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**

