Short description of the project

The Forschungszentrum Jülich (FZJ) node of GCBN provides tools and resources tailored to the plant research community. With a particular focus on crop plants, the web resource www.plabipd.de serves as the access point. FZJ tracks advances in published sequenced plant genomes and develops algorithms for functional annotation of plant proteins.

Screenshots of some resources available at www.plabipd.de

Progress report

The FZJ node of GCBN has further developed the MapMan4 annotation framework for protein function predictions as the foundation of the Mercator4 service. This is driven by clustering and analysis of proteins from publicly available plant proteomes and has led to the generation of more than 5900 protein categories (MapMan4 v2, July 2019). In order to increase annotation speed, the back-end high performance computing (HPC) cluster has been further upgraded and extended. The high quality annotations together with the cluster upgrades enable protein function prediction for whole plant proteomes and transcriptomes within minutes.

Usage of the Mercator4 online annotation service.

Additionally, FZI maintains a selection of bioinformatics tools ([MapMan desktop application](https://www.plabipd.de), [RobiNA](https://www.plabipd.de) and [Trimmomatic](https://www.plabipd.de)) for the analysis and interpretation of sequencing data. The command line tool Trimmomatic is used for trimming Illumina data sets and has been incorporated into automated cluster pipelines and Galaxy pipelines. RobiNA allows the visual analysis of large microarray or small RNA-seq data sets and provides the input for the MapMan desktop application, a tool to analyse plant functional pathways and visualize transcriptomics, metabolomics and proteomics quantitative data.

Screenshots of the Mercator4 online annotation service.

de.NBI Training and education

de.NBI – CeBiTec Nanopore Best Practice Workshop 2019
Bielefeld, 25. - 27. Sep. 2019

Publications


MapMan 4: a refined protein classification and annotation framework applicable to multi-omics data analysis.


Computational aspects underlying genome to phenome analysis in plants.


General information on the project

Core group Björn Usadel (PI), Rainer Schwacke and Marie Bolger (www.plabipd.de). The project is supported by Anthony M. Bolger (HPC cluster and programming).

www.denbi.de