

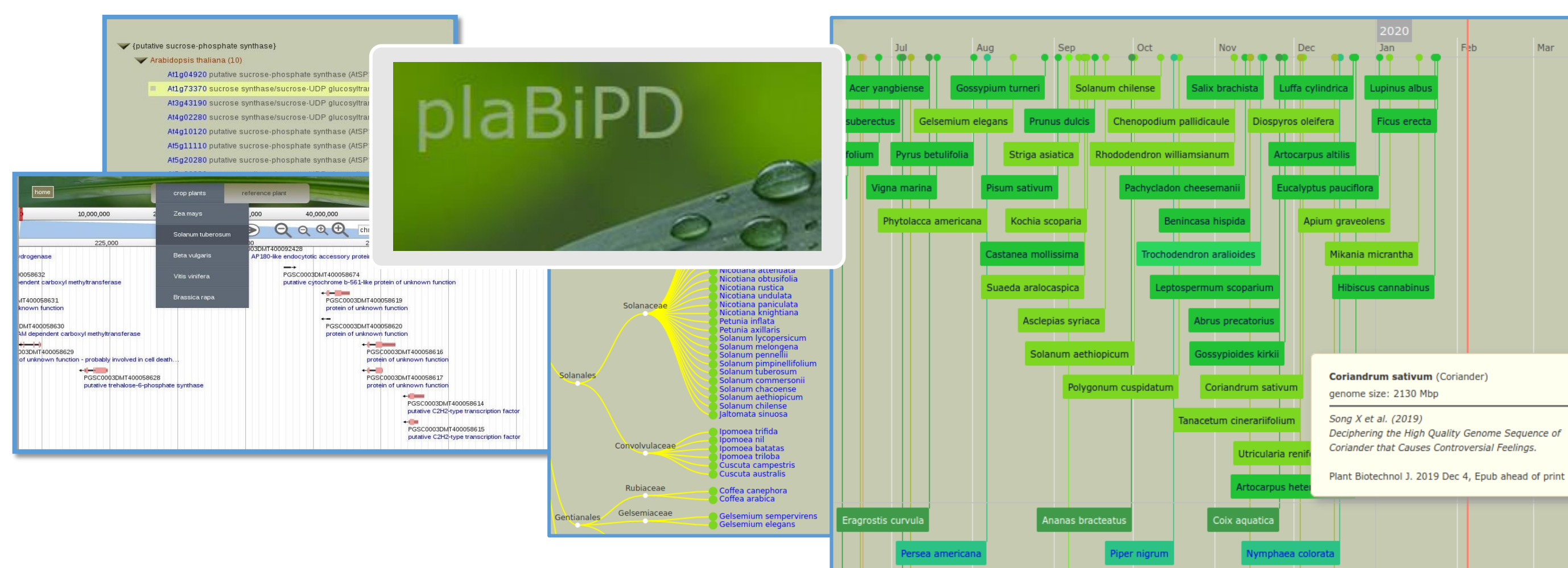
GCBN German Crop Bio Greenformatics Network @ FZJ

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Short description of the project

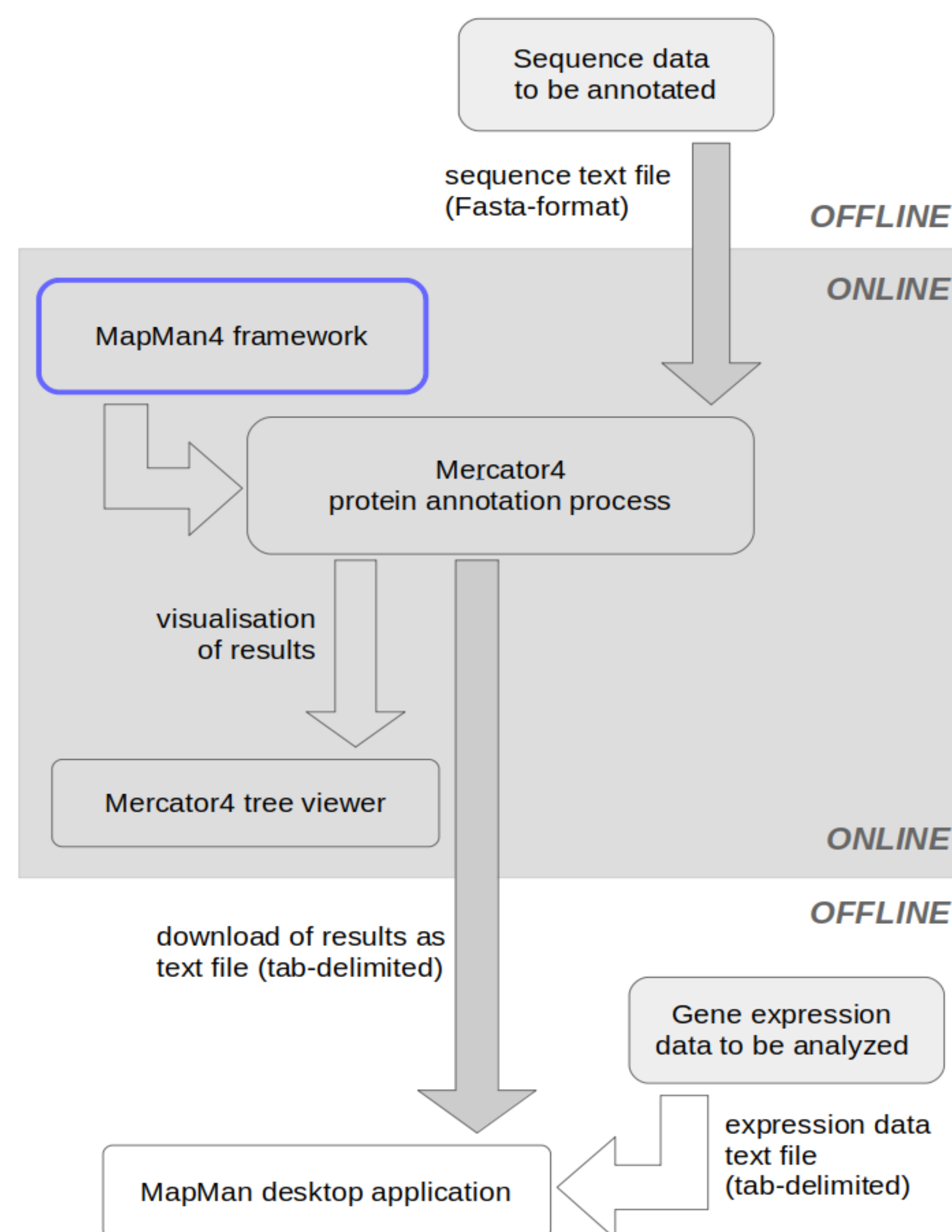
The Forschungszentrum Jülich (FZJ) node of GCBN provides tools and resources tailored to the plant research community. With a particular focus on crop plants, the web resource www.plabipd.de serves as the access point. FZJ tracks advances in published sequenced plant genomes and develops algorithms for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



Screenshots of some resources available at www.plabipd.de

de.NBI services

The **Mercator4** online annotation service allows users to submit plant protein or DNA sequences for classification into **MapMan4** categories. The results from Mercator4 can be compared online to reference plant species or other submitted user jobs. They can also be downloaded and directly used to explore RNAseq data in the MapMan desktop application on pathway diagrams.



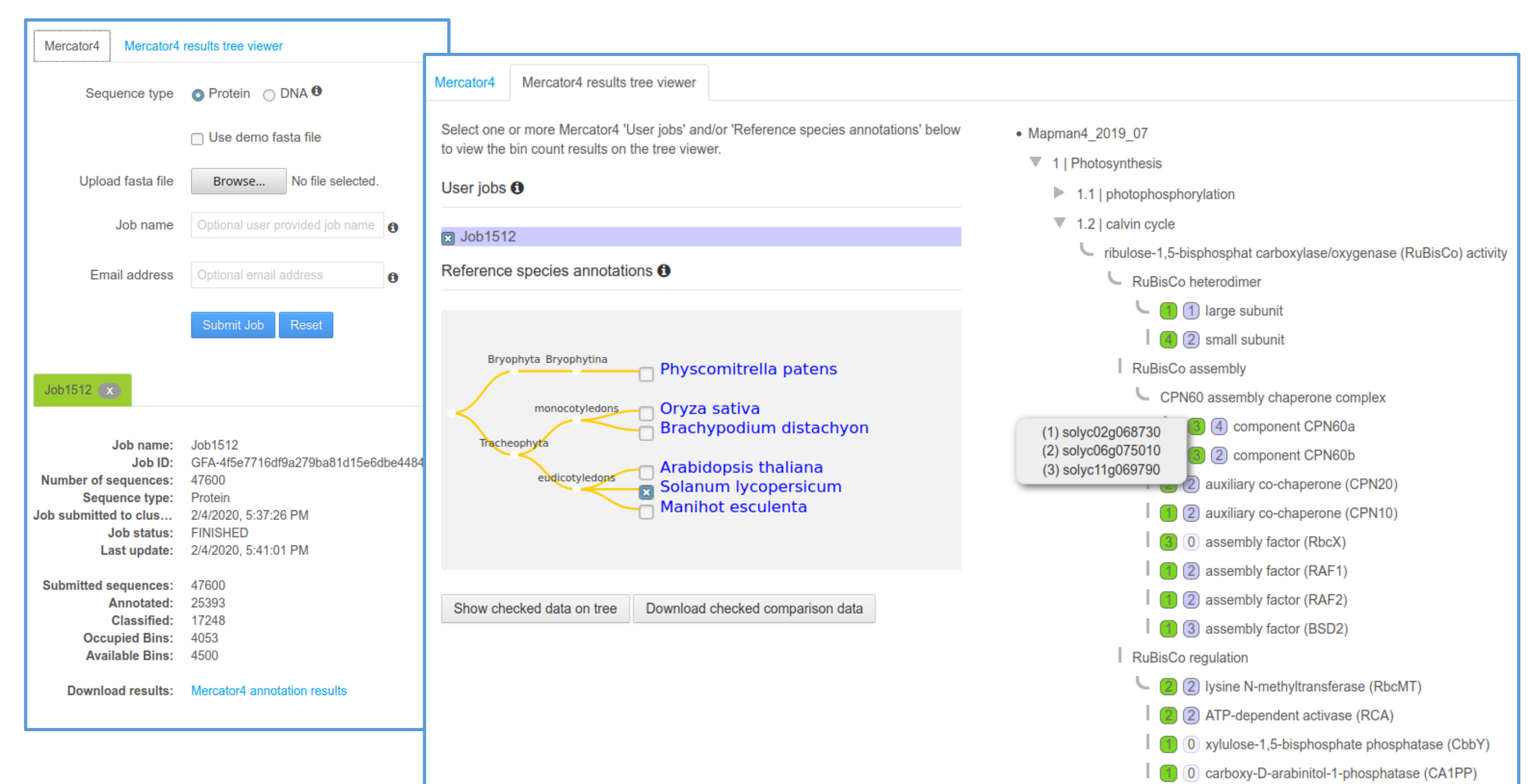
Overview of the Mercator4 plant protein annotation process.

General information on the project

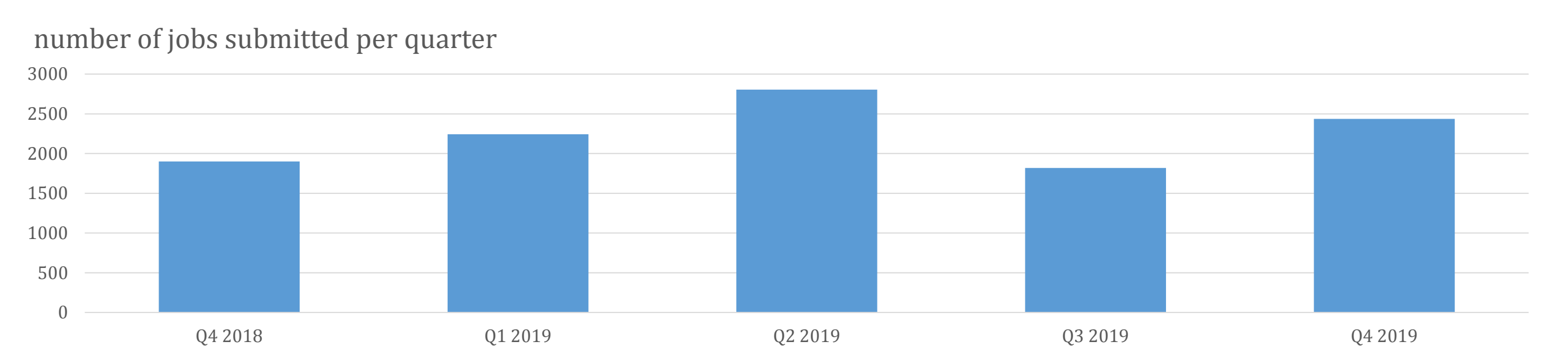
Core group Björn Usadel (PI), Rainer Schwacke (0.5x de.NBI-position, Mapman4, www.plabipd.de) and Marie E. Bolger (Mercator4, www.plabipd.de). The project is supported by Anthony M. Bolger (HPC cluster and programming).

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 v.2, 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.



Screenshots of the Mercator4 online annotation service.



Usage of the Mercator4 online annotation service.

Additionally, FZJ maintains a selection of bioinformatics tools (**MapMan desktop application**, **RobiNA** and **Trimmomatic**) 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 RNAseq 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.

de.NBI Training and education

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

Publications

Schwacke R, Ponce-Soto GY, Krause K, Bolger AM, Arsova B, Hallab A, Gruden K, Stitt M, **Bolger ME**, **Usadel B** (2019)
Mapman4: a refined protein classification and annotation framework applicable to multi-omics data analysis.
Mol Plant. 2019 Jun 3, 12(6): 879-892

Bolger AM, Poorter H, Dumschott K, **Bolger ME**, Arend D, Osorio S, Gundlach H, Mayer KFX, Lange M, Scholz U, **Usadel B** (2019)
Computational aspects underlying genome to phenome analysis in plants.
Plant J. 2019 Jan, 97(1): 182-198