



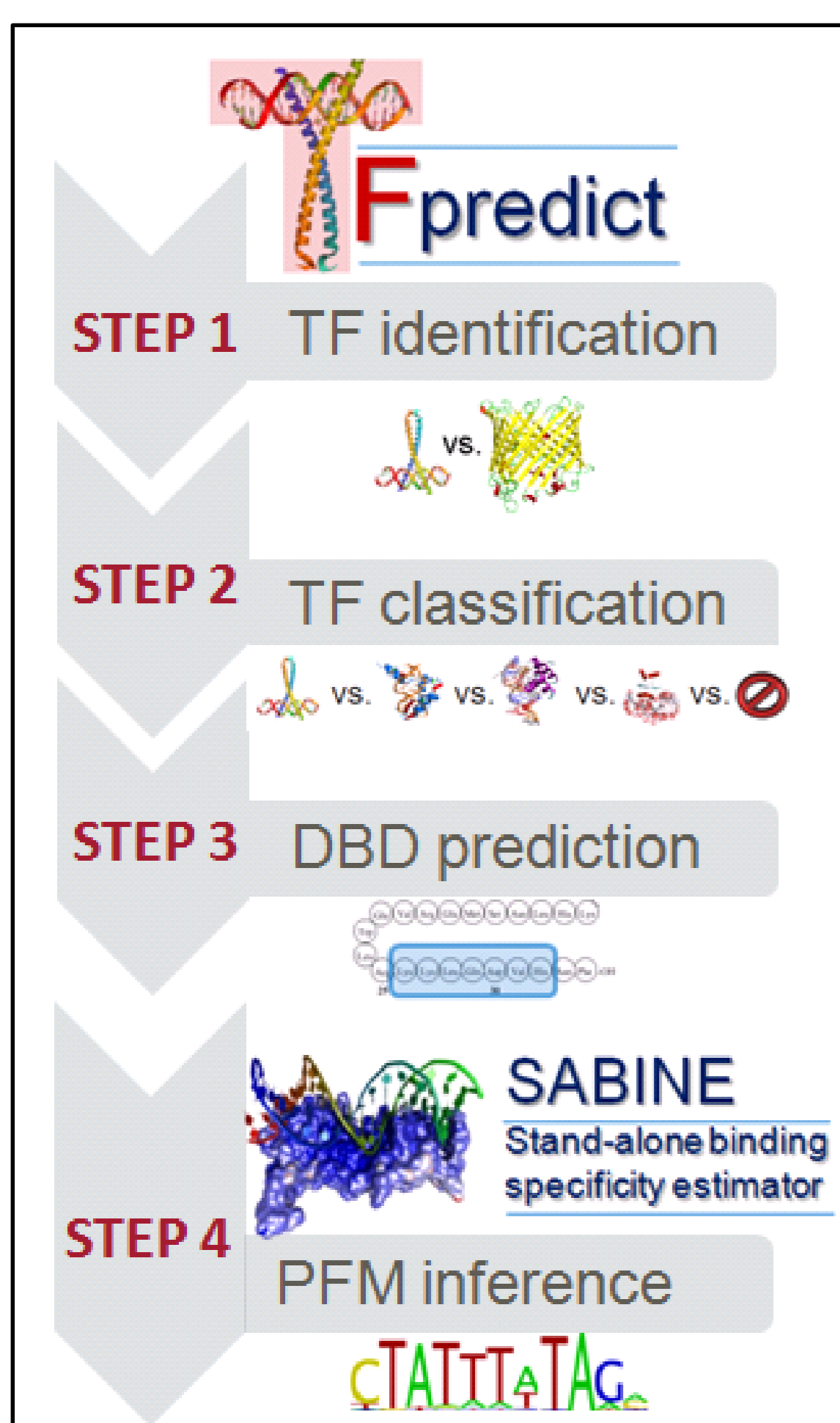
# ZBIT Bioinformatics Toolbox

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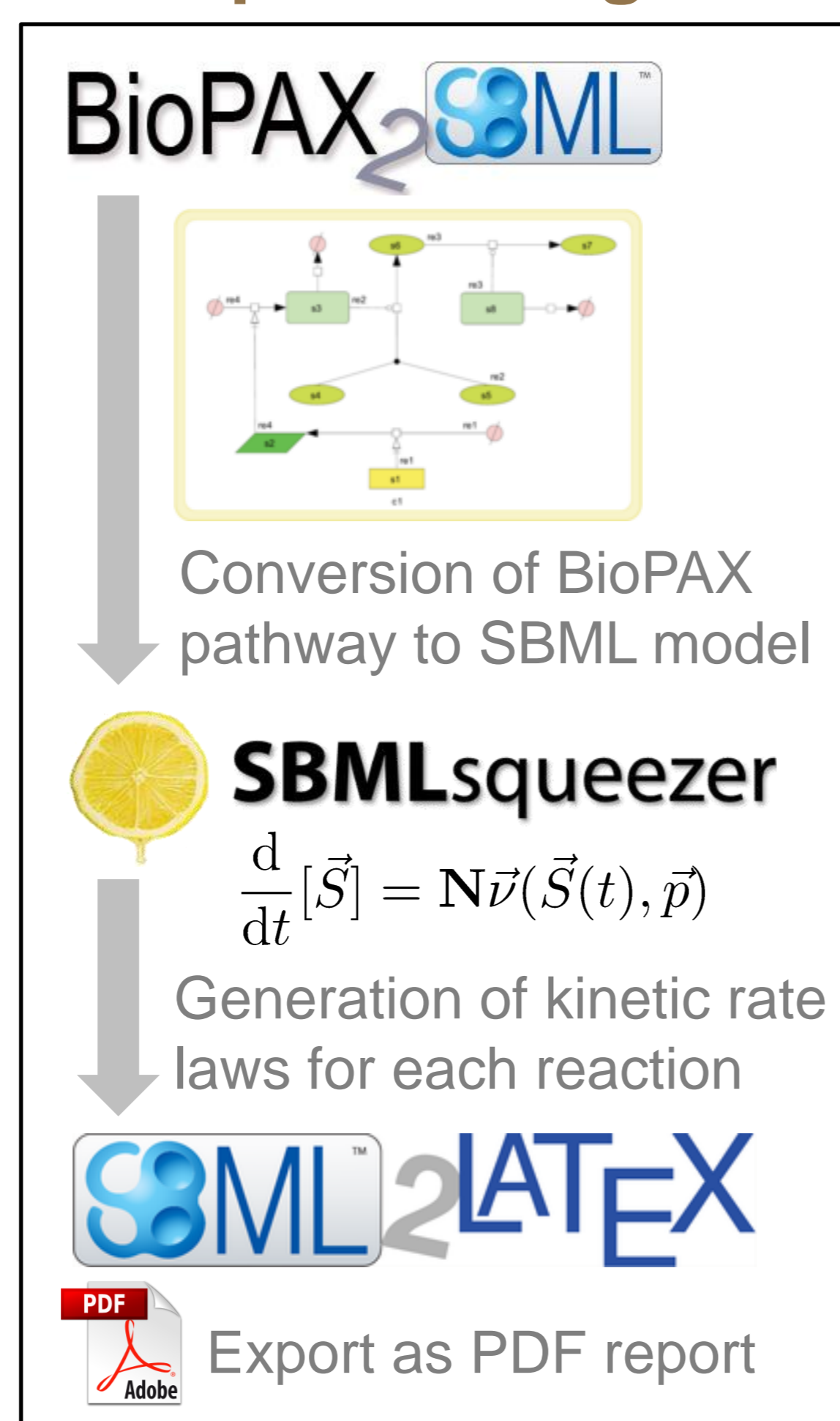
The ZBIT Bioinformatics Toolbox [1] provides web-based access to various software applications which have been developed in the Cognitive Systems group. The offered tools can be used for the conversion or extension of biochemical models provided in SBML format (BioPAX2SBML, SBML2LaTeX, SBMLsqueezer, ModelPolisher), the structural and functional annotation of transcription factors (TFpredict, SABINE), and analysis of gene and protein expression data (RPPApipe, ToxDBScan).

The bioinformatics tools are publicly available from our website (<https://webservices.cs.uni-tuebingen.de>) and can be applied either individually or jointly as consecutive steps of custom-built workflows.

## Transcription factor annotation



## SBML model processing



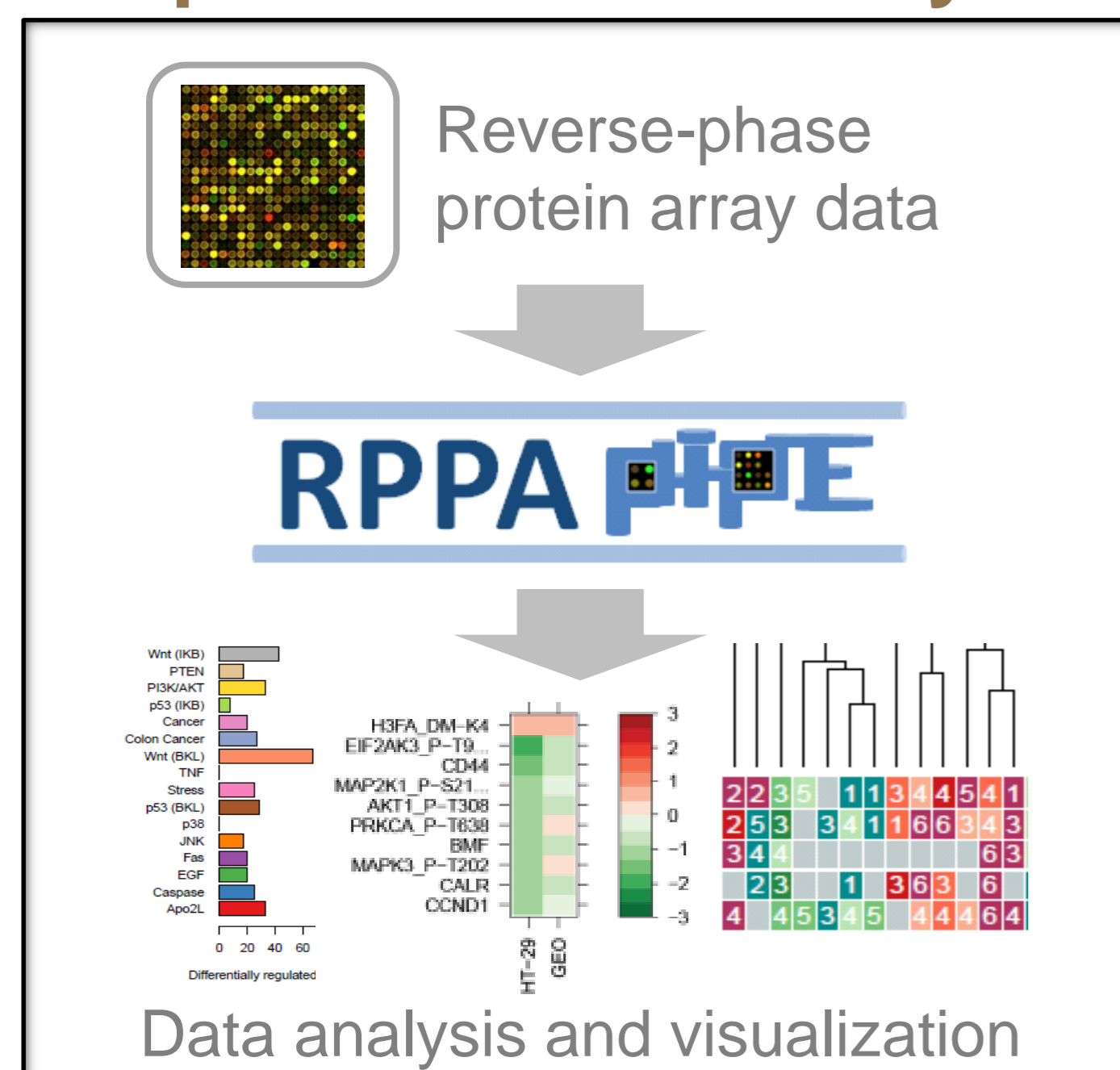
## Key Features

- **User management system** with private history providing access to uploaded datasets and results of performed analyses
- **Jobs** are submitted to a cluster and processed in parallel
- **Results** are reproducible and can be shared between users
- **Workflow editor** which allows to create custom-built workflows for the sequential execution of tools with compatible formats

## Analysis Tools

- **SBML2LaTeX** converts a given SBML file into a human-readable PDF report [2].
- **BioPAX2SBML** converts BioPAX level 2 and level 3 files into SBML files including the Qualitative Models extension [3].
- **SBMLsqueezer** automatically generates kinetic rate equations for biochemical networks given in SBML format [4].
- **ModelPolisher** annotates and enriches models using information from the BiGG Models database [5].
- **TFpredict** identifies transcription factors (TF), predicts their structural superclass, and detects their DNA-binding domains (DBD) given a protein sequence of interest [6].
- **SABINE** predicts the DNA motif of a TF in the form of a position frequency matrix (PFM), based on its amino acid sequence, DBD, superclass and species [6].
- **RPPApipe** offers predefined and custom-built workflows for the preprocessing, annotation, statistical analysis, clustering, pathway analysis and visualization of Reverse-Phase Protein Array (RPPA) data [7].
- **ToxDBScan** scans the TG-GATEs and DrugMatrix databases for similar chemicals, given the deregulated genes after short-term treatment with a chemical in male rats [8].

## Expression data analysis



## References

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