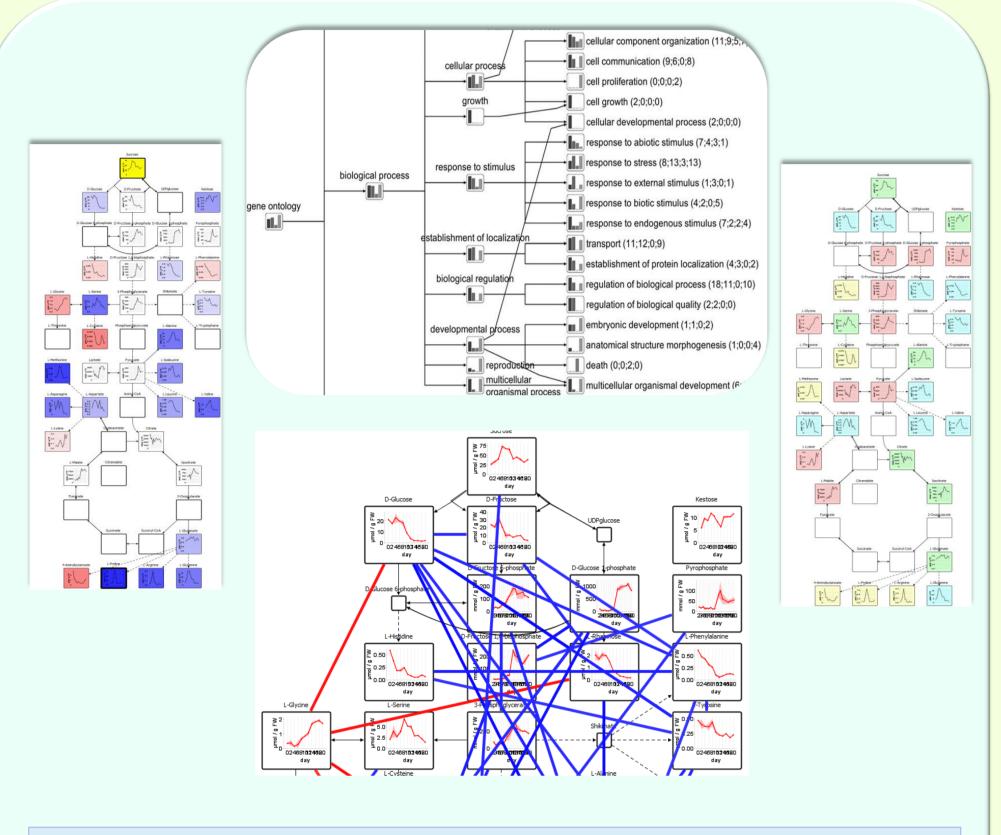
PLANT BIOINFORMATICS

Tools

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VANTED FRAMEWORK

The VANTED framework aims at the integration, analysis and visual exploration of experimental data in the context of biological networks. The main functions of VANTED can be divided into the six areas (i) Visualization and exploration, (ii) Data integration, (iii) Data analysis, (iv) Simulation, (v) Data handling, and (vi) Knowledge representation. These areas implement a sophisticated analysis pipeline for scientific data. The VANTED framework comprises the VANTED core as well as a framework for various extensions, denoted as add-ons. Those add-ons are being developed for the needs of life scientists and extend the functionality of the VANTED core towards various tasks and topics in the field of systems biology.



VANTED provides a rich set of analysis methods, regarding network analysis and data analysis.

- Network analysis (Identification of Centralities, shortest paths, clusters and circles; Motif based search)
- Statistics (1:n Correlation, n:n Correlation, SOM Clustering, T-/U-Test, Scatter matrix)
- Enrichment analysis (Hierarchy creation based on KEGG / GO hierarchy)

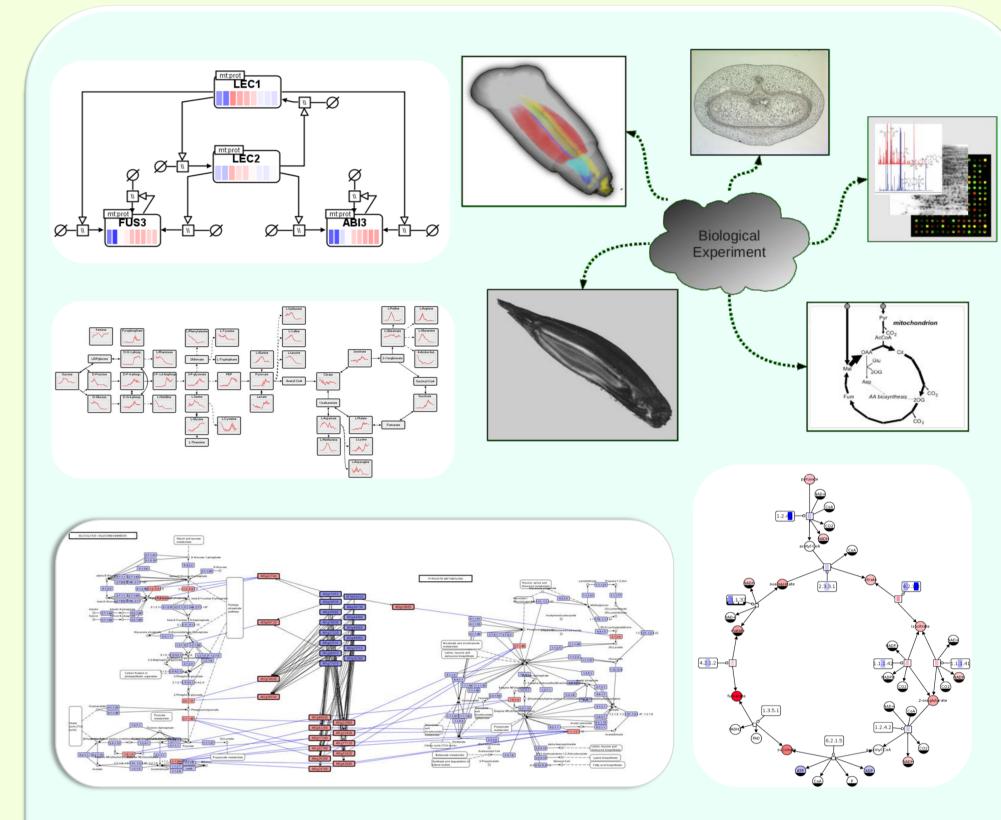
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The VANTED framework comprises a fully featured graph editor with features like

- Charts on nodes/edges (bar charts, pie charts, line charts, box plots, heat maps)
- Automated layout algorithms (Force-directed, Tree-layout, ...)
- Interactive exploration (Zoom, Panning, Search, Selection, Details, Cluster Overview Graph)

VISUALIZATION AND EXPLORATION



VANTED strongly supports mapping and integration methods, including

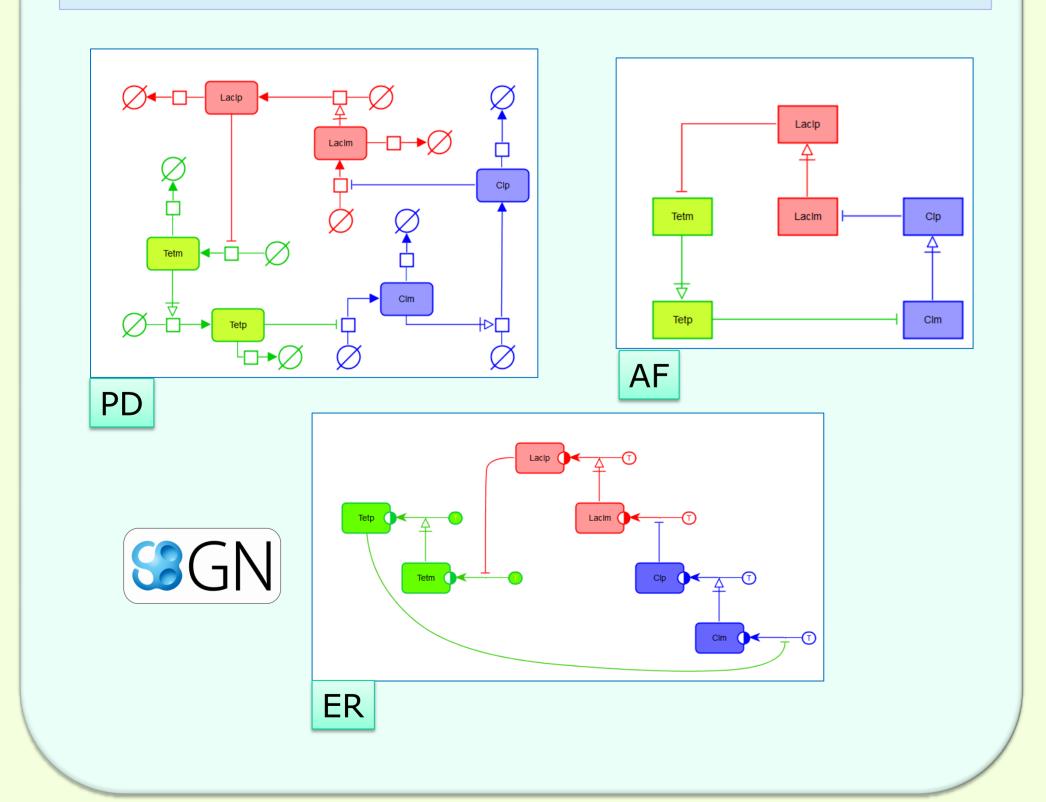
- Data mapping (Exploration of experiment data in the context of networks)
- Network integration (Combination of networks from different domains of life science)
- Data integration of multi-modal data (Networks, Volumes, Experiment data)

DATA AND NETWORK ANALYSIS

KNOWLEDGE REPRESENTATION

The VANTED framework supports different formats and levels of knowledge representation using SBGN. This standard provides visual representations of biochemical and cellular processes in an unambiguous way. Support for

- SBGN-PD (representing the transitions of entities from one form or state to another)
- SBGN-ER (representing the influences of entities upon the behavior of others)
- SBGN-AF (representing the activity flow from one entity to another or within the same entity)



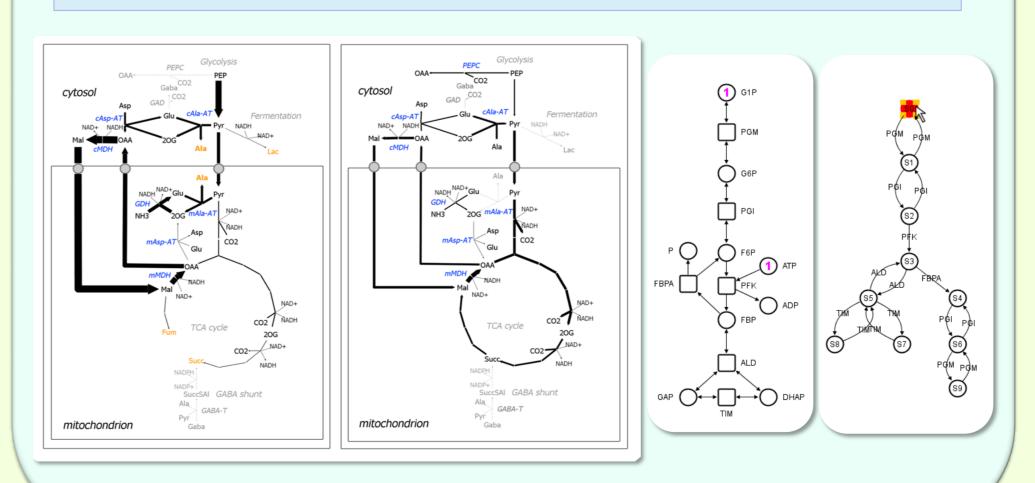
SIMULATION

VANTED

VANTED supports simulation techniques with focus on flux simulation and token distribution on biological networks.

Simulation results can be interactively explored, aiming at an intuitive data interpretation.

- Optimization based network analysis (Flux Balance Analysis (FBA), Flux Variability Analysis (FVA), Knockout Analysis, Robustness Analysis)
- Rule based network analysis (Petri nets)



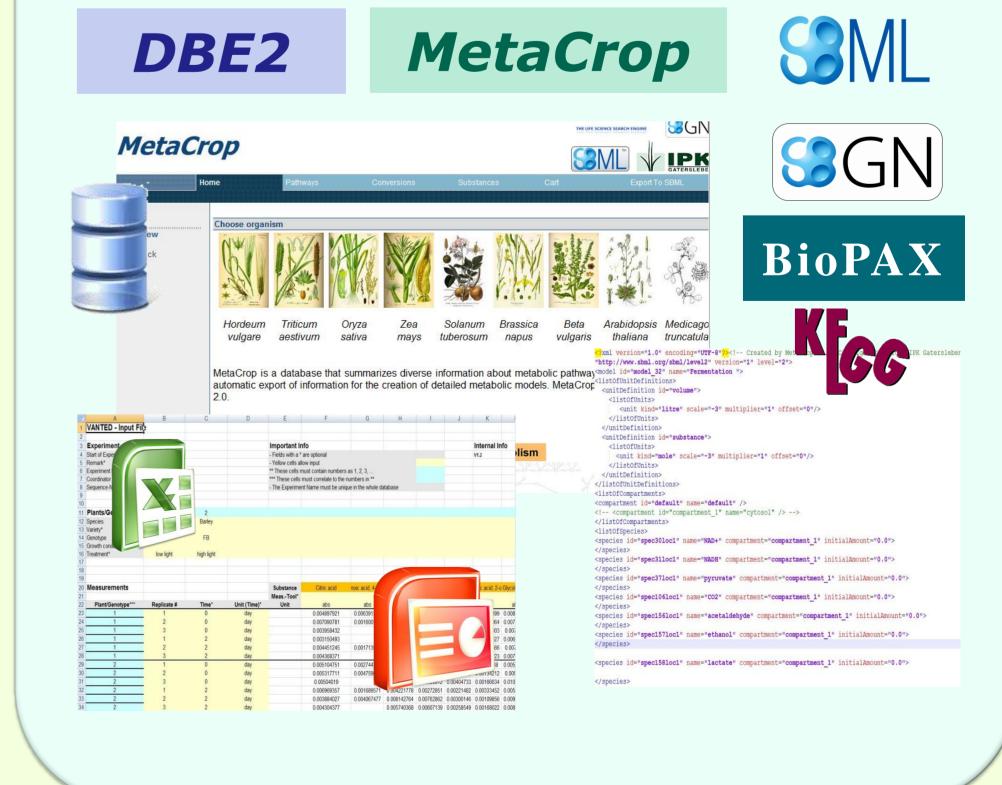
DATA HANDLING

DATA MAPPING

AND INTEGRATION

VANTED supports a variety of import and export methods to handle scientific data and networks.

- Load and save experiment data as special formatted Excel sheets, CSV files or using DBE2
- Load and save networks using SBML, SBGN, BioPAX, GML, GraphML, and MetaCrop
- Export networks as images in JPEG, PNG, and PDF format
- Export analysis results (Correlation, Clustering, Network properties)



References:

- 1. Klaus Hippe, Christian Colmsee, Tobias Czauderna, Eva Grafahrend-Belau, Björn H Junker, Christian Klukas, Uwe Scholz, Falk Schreiber and Stephan Weise, Novel Developments of the MetaCrop Information System for Facilitating Systems Biological Approaches, Journal of Integrative Bioinformatics, 7(3):125, 2010
- 2. Tobias Czauderna, Christian Klukas and Falk Schreiber, Editing, Validating, and Translating of SBGN Maps, Bioinformatics 26 (18):2340-2341, 2010
 3. Hendrik Rohn, Christian Klukas and Falk Schreiber, Creating views on integrated multidomain data, Bioinformatics 27 (13):1839-1845, 2011
- Björn H Junker, Christian Klukas and Falk Schreiber, VANTED: A system for advanced data analysis and visualization in the context of biological networks, BMC Bioinformatics, 7:109, 2006
- 5. Hendrik Mehlhorn and Falk Schreiber, DBE2 Management of experimental data for the VANTED system, Journal of Integrative Bioinformatics, 8(2):162, 2011 5. Johannes Gräßler, Dirk Koschützki and Falk Schreiber, CentiLib: Comprehensive Analysis and Exploration of Network Centralities, Bioinformatics, 2012 (in press)
- 7. Eva Grafahrend-Belau, Christian Klukas, Björn H. Junker and Falk Schreiber, FBA-SimVis: interactive visualization of constraint-based metabolic models, Bioinformatics 25 (20):2755-2757, 2009