

An introduction to the visualization of experimental data from genomics, proteomics and metabolomics with VANTED for interested users from biology and bioinformatics

In this introduction especially targeted to interested users from biology and bioinformatics I will give a live software demonstration on the following topics:

- Use of the VANTED software system for the visualization of gene expression data in context of KEGG Pathways
- Visualization of protein data in context of pathways from the IPK crop plant pathway database MetaCrop
- Visualization and statistical analysis of metabolite data in context of user drawn pathways

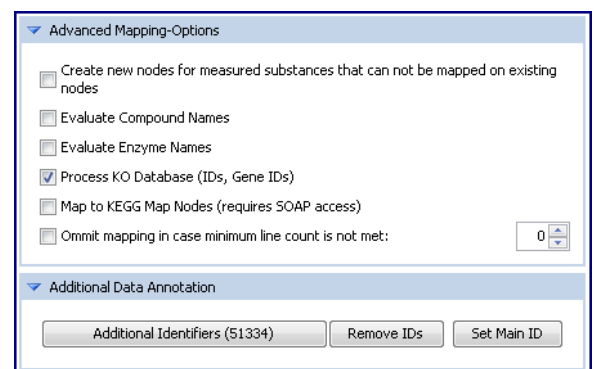
Installation

- Go to <http://vanted.ipk-gatersleben.de>, click 'Installation'
- Click Java Web Start Link (if it does not work, download Java and try again)
- Download database files (Menu Help/Database Status), restart VANTED after download is completed

Task 1: Gene expression data → KEGG pathways

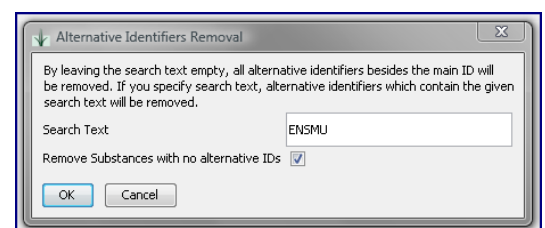
1. Access KEGG pathways

- Select organism or reference maps from Network side panel
- Download desired pathway(s)



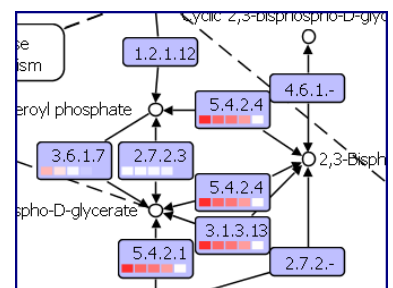
2. Prepare dataset file

- Prepare CSV data file (save as Text from Excel)
- Load data file
- Provide and load alternative identifier table



3. Perform data-mapping

- Change mapping options
- Perform mapping
- Change visualization settings
- Exchange KO IDs by Enzyme No.



Task 2: Protein data → MetaCrop pathways

1. Access MetaCrop pathways

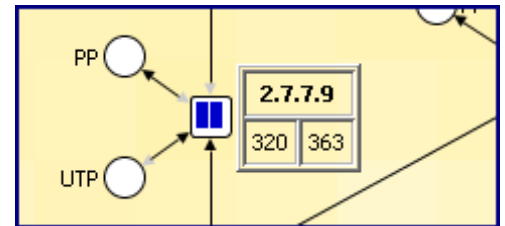
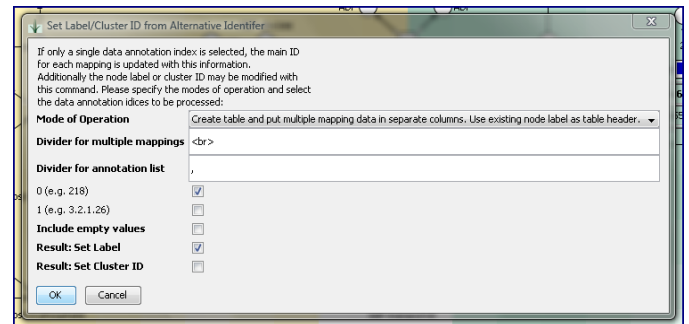
- Download desired pathway (Sucrose breakdown pathway (monocots))
- Replace labels with EC Number (Elements/Table based...)

2. Prepare dataset file

- Using "0" values if no "real" values are available

3. Perform data-mapping

- Perform mapping
- Undo label replacement
- Set label from alternative identifiers to display mapped spot list



Task 3: Metabolite data → user drawn pathways, statistical analysis

1. Draw pathway

- Show how to draw a network and modify edge and node styles

2. Prepare dataset file

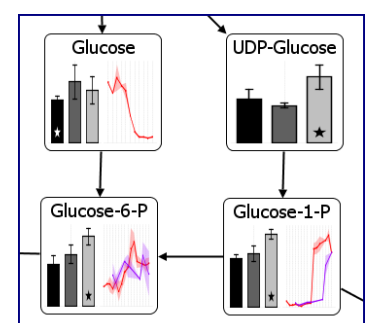
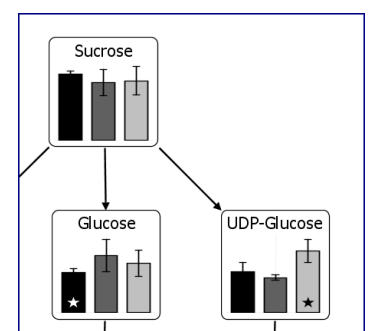
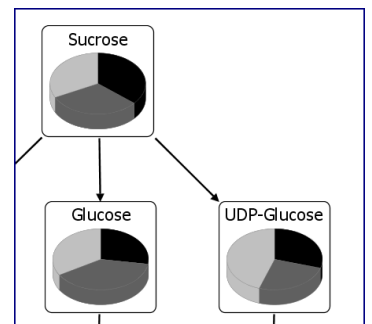
- Using VANTED template

3. Perform data-mapping

- No alternative identifiers used here
- Show how to use line-, bar- and pie-charts

4. (Statistical) data analysis

- Perform t-test
- Correlation analysis
- Data clustering



Example data from...

Gene expression: Rüdiger Horstkorte, Wenke Weidemann
 MetaCrop pathways: Eva Grafarend-Belau
 Proteins: Stephanie Kaspar, Hans-Peter Mock
 Metabolite data and pathway: Hardy Rolletschek