



News from the MapMan Family of Omics Tools



MAX-PLANCK-GESELLSCHAFT

MapMan

Robin

PageMan

Mercator

Resources

Help

Axel Nagel¹, Marc Lohse¹, Dirk Walther¹, Birgit Kersten¹, Joachim Selbig², Bjoern Usadel¹, Mark Stitt¹
Contact: mapman@mpimp-golm.mpg.de Web: <http://mapman.gabipd.org>

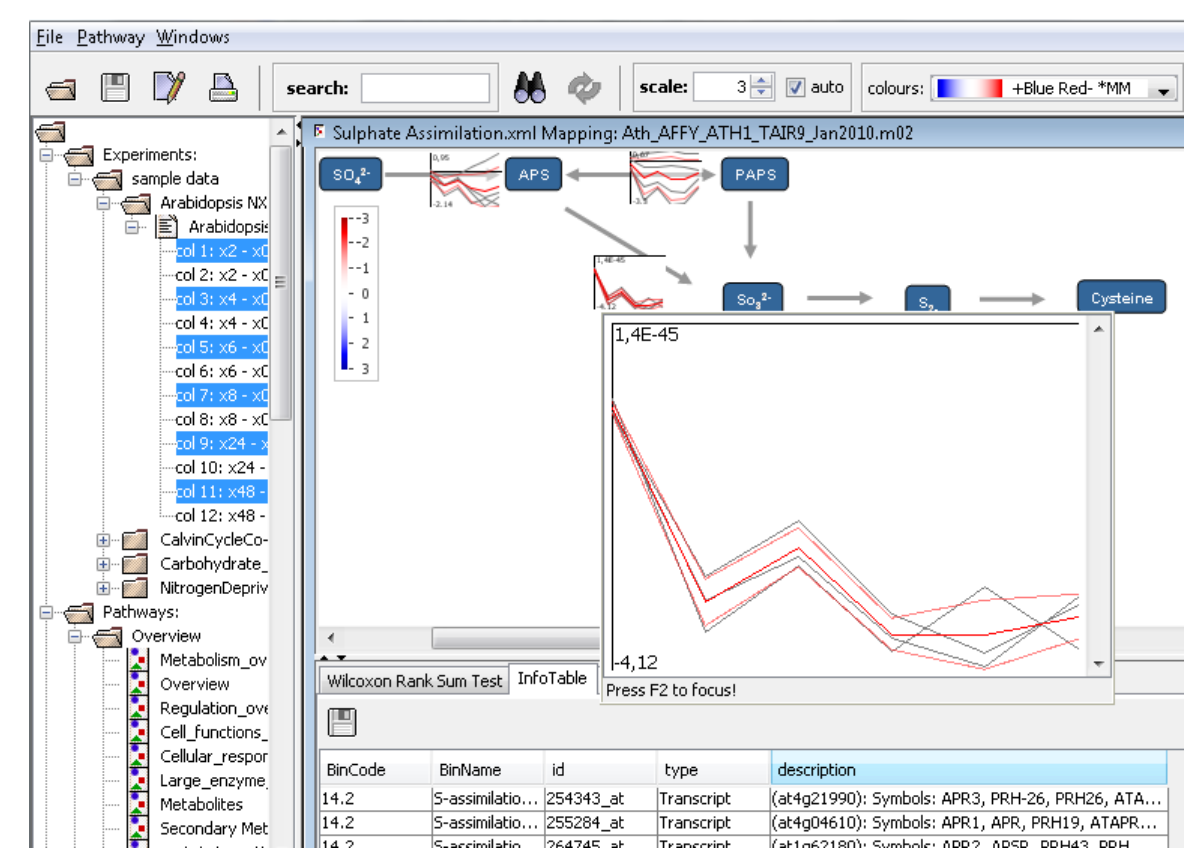
¹ Max Planck Institute of Molecular Plant Physiology, Am Mühlenberg 1, 14476 Potsdam, Germany
² University of Potsdam, c/o MPIMP, Am Mühlenberg 1, 14476 Potsdam, Germany

Overview

The MapMan family of omics tools was first developed for the reference species *Arabidopsis*. Here we describe:

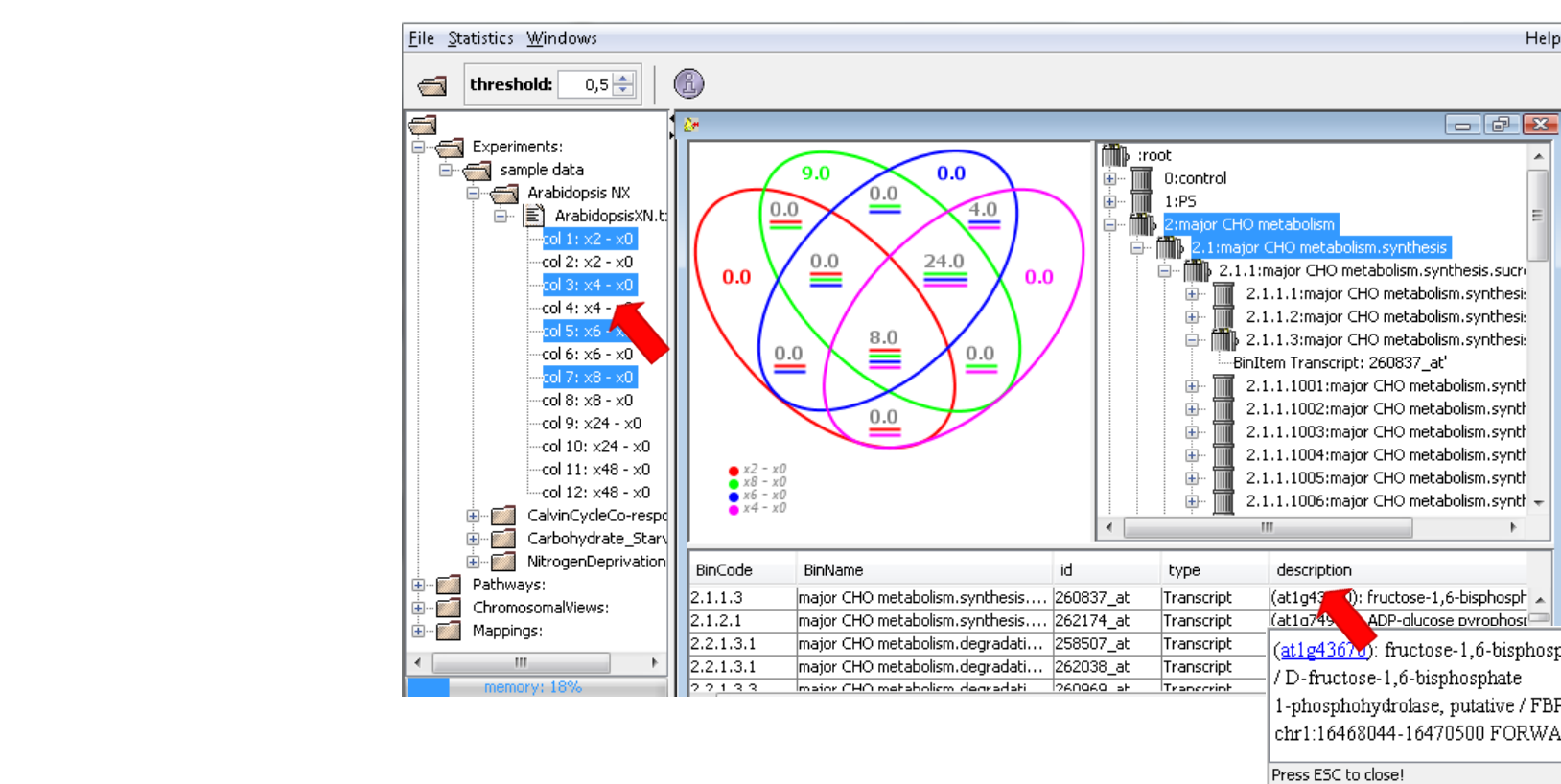
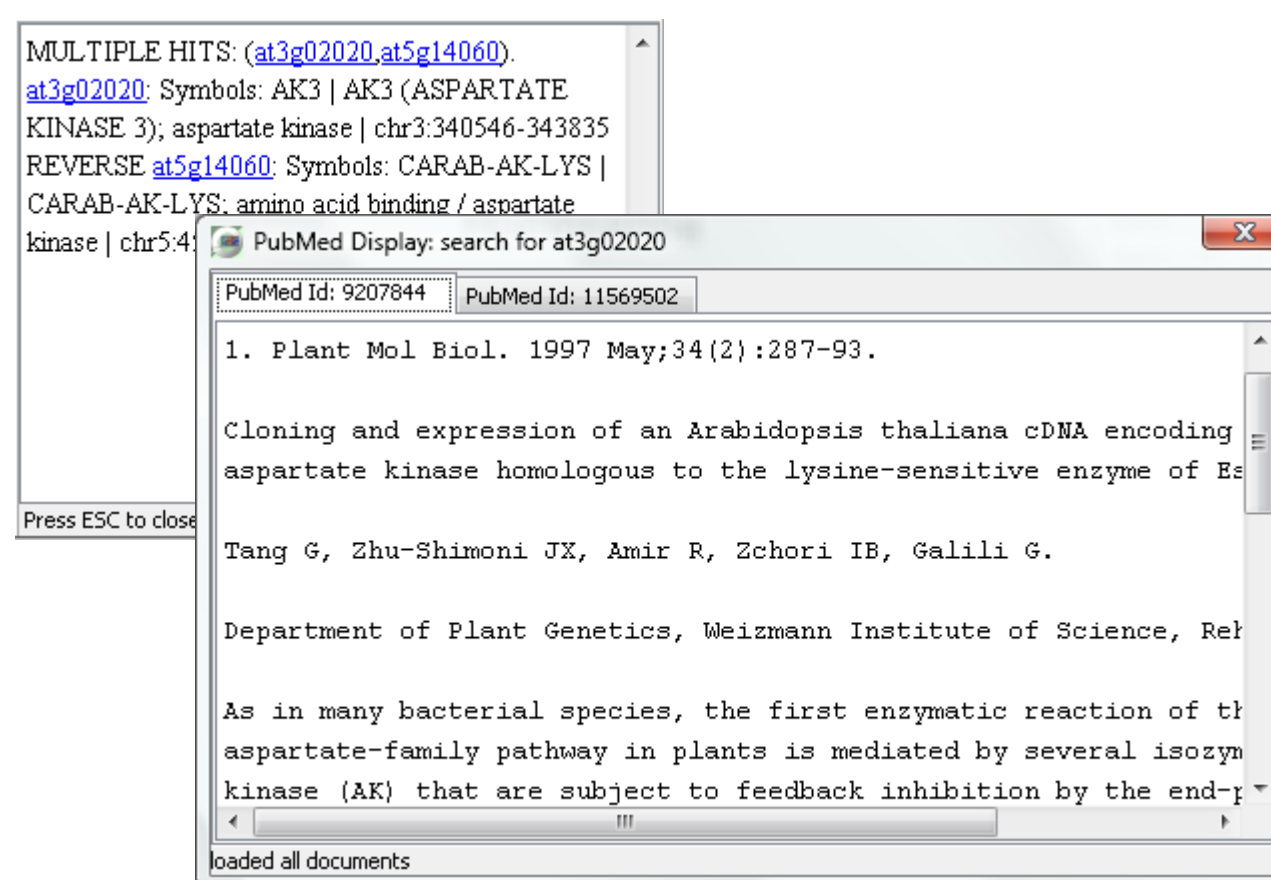
- (i) How the flexibility and functions in the user interfaces have been extended.
- (ii) Extensions to crop plants. As crop specific data has become available we have applied the concept of the MapMan functional classes (BINS) to crop sequence data. This allowed us to visualize and analyze crop data sets, drawing on a generic software and supported by the *Arabidopsis* reference genome.

MapMan Extensions



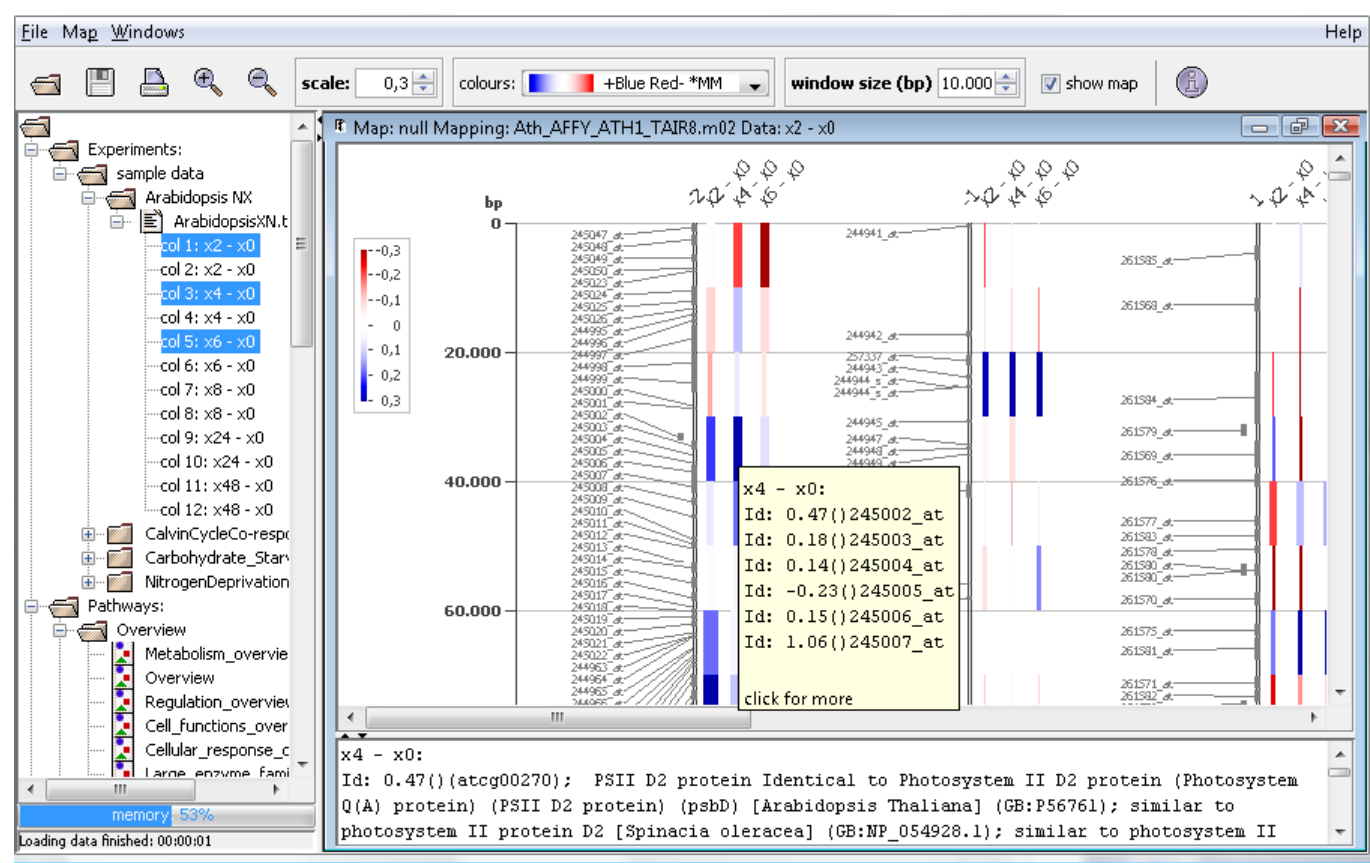
Visualize time series data:

- See multiple experiments in parallel while having the whole MapMan annotation at your fingertips
- including interactive tool tips which get you straight to publications mentioning the gene of interest.



View your data in Venn diagrams:

- Compare multiple experiments and group the elements by providing a threshold which marks them to be present
- Either see all features, or filter for a free selection of paths within the MapMan annotation (e.g. look for genes only in 2.1 major CHO metabolism.synthesis).

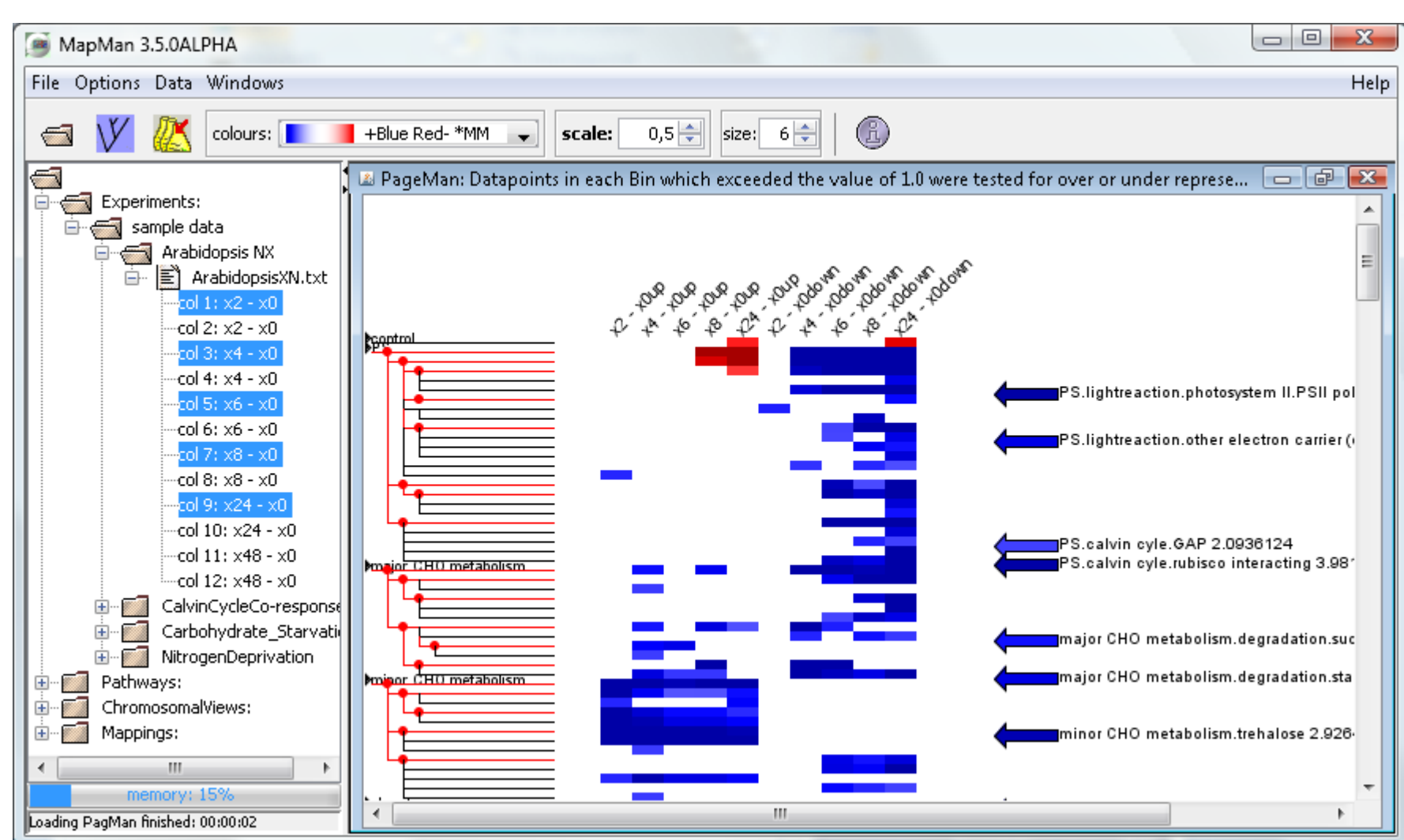


Chromosomal Display:

- View your transcript profiling data in the context of their location on the chromosome.
- Add a file containing additional markers to be shown on the map in parallel to the experimental data
- Devalue the window size to group experimental values by their location to easily see hot spots.

PageMan

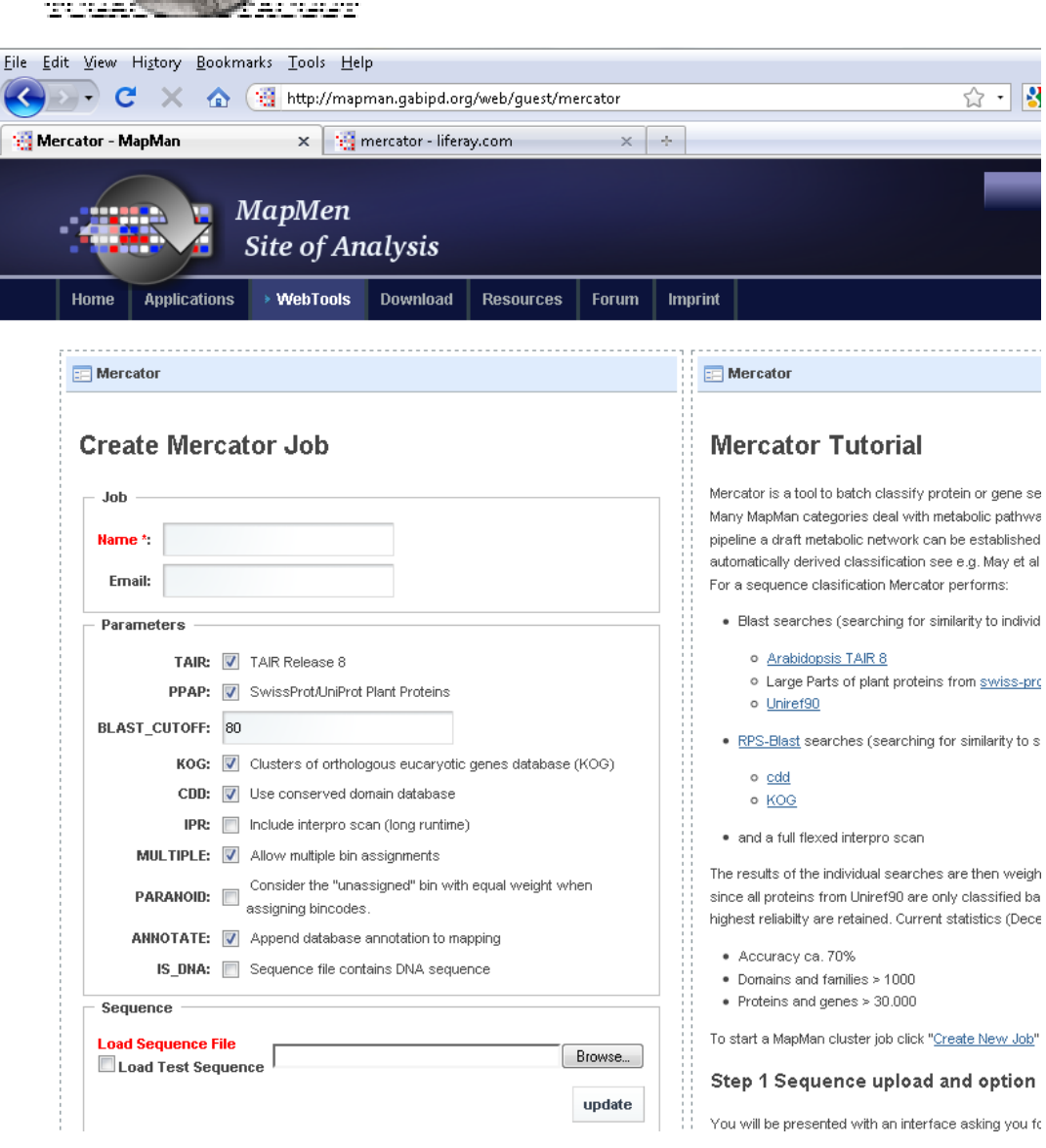
The PageMan functionality has now been fully integrated into the MapMan application:



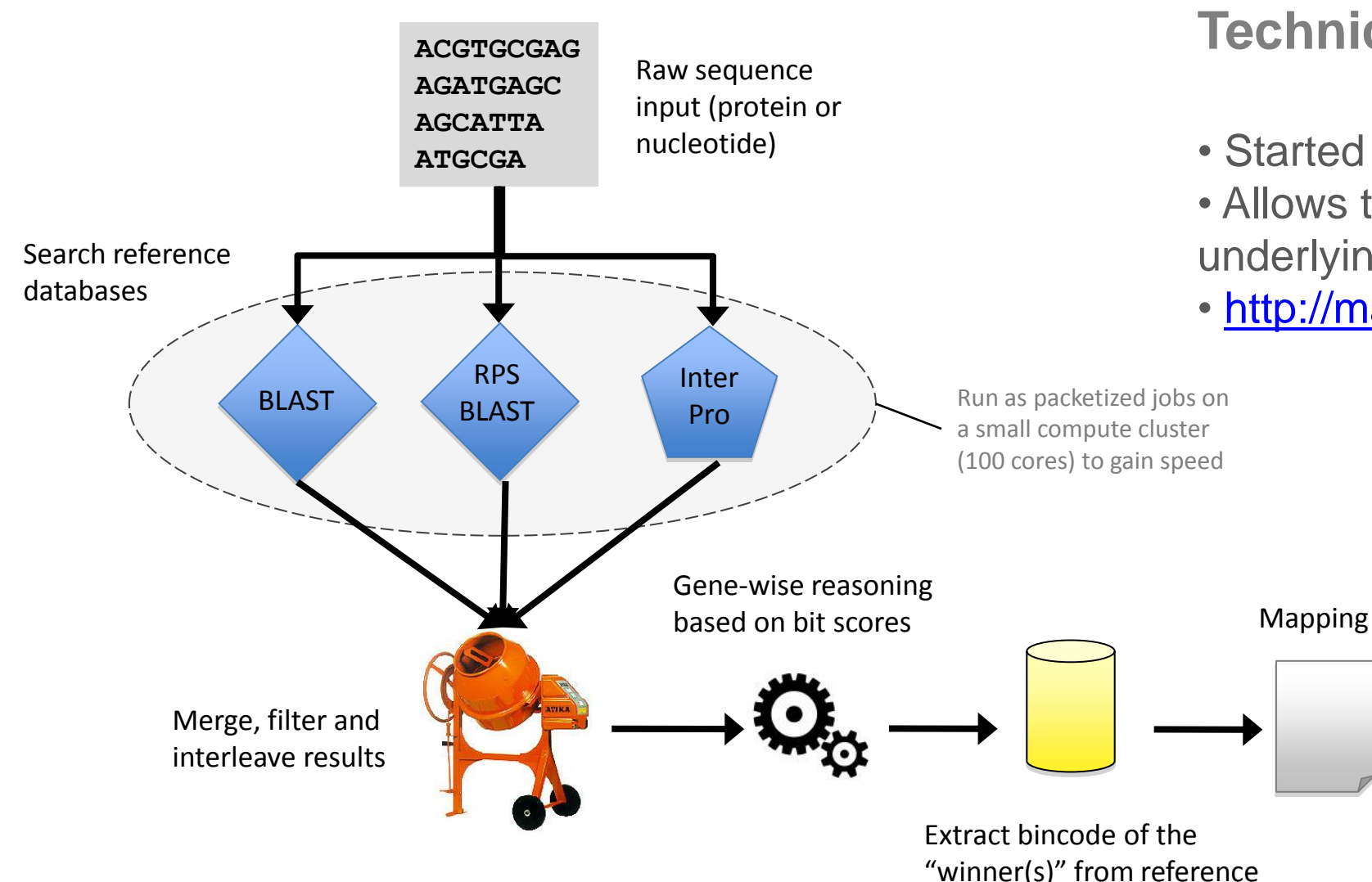
We used the MapMan ontology to compress the data to several hundred features, of which most have a biological meaning. To do this, either an enrichment analysis or a Wilcoxon test is performed for every BIN. Thus the question asked is, if there are more genes up or down regulated within each BIN than expected by chance. Finally the user is presented with a graphical overview of the BIN hierarchy as well as of individual statistical tests which are colour coded.

Mercator

Mercator pipeline for automated sequence annotation based on manually curated references:



Mercator Workflow



Technical details:

- Started and monitored through a web interface
- Allows the annotation of sequences (e.g. sequences underlying a transcript profiling chip)
- <http://mapman.gabipd.org/web/guest/mercator>

Robin



ROBIN, a User Friendly Graphical Interface to Powerful Open Source Microarray Processing

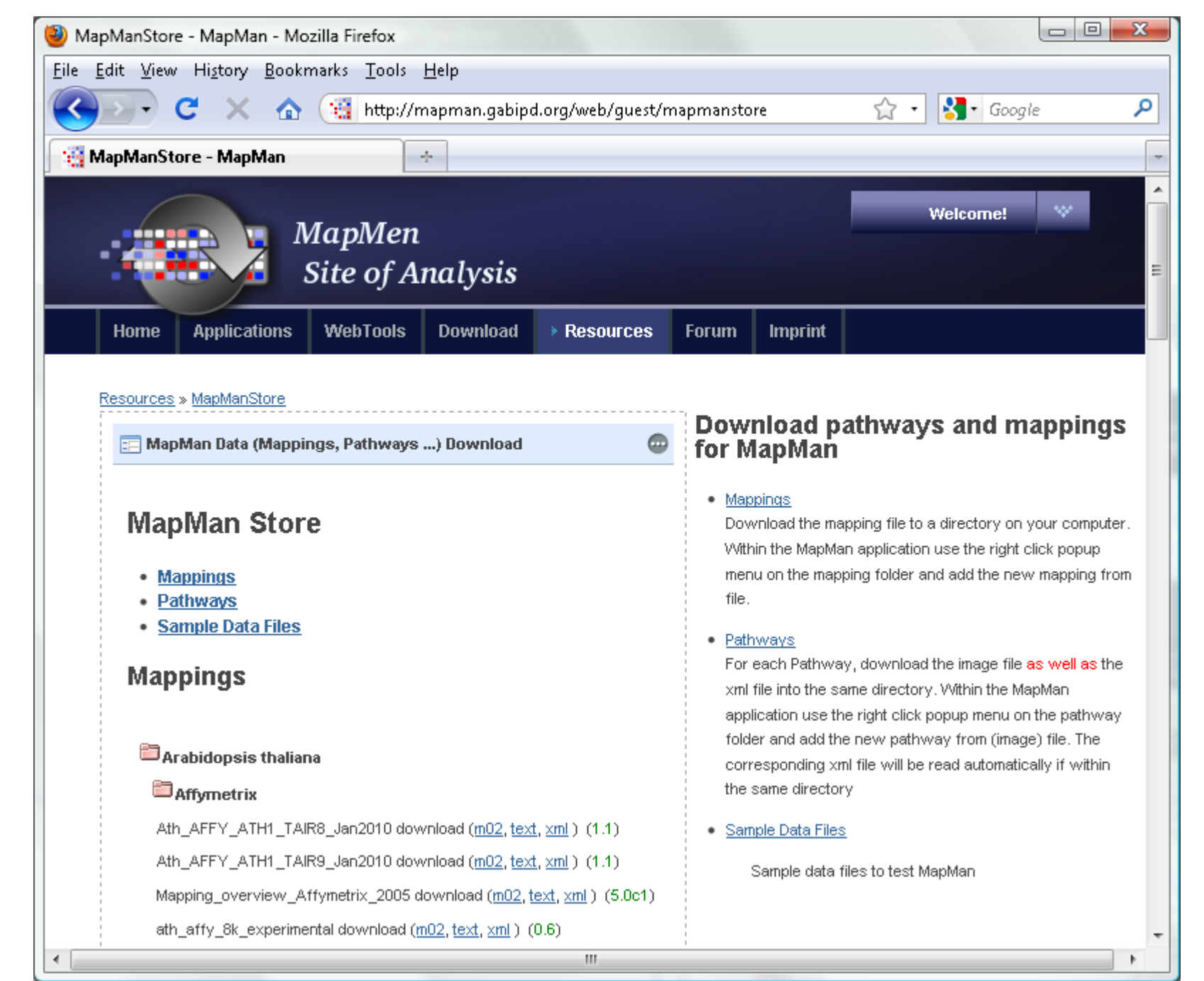
Robin is the raw experimental data preprocessor of MapMan. Thorough quality assessment and customizable statistical analysis of Affymetrix, Agilent and other single channel and two-color microarray data. For further details see poster: P086

Resources

Online access to up to date MapMan Mappings and Pathways Mappings(Annotation Data) available for :

- *Arabidopsis thaliana*
- *Chlamydomonas reinhardtii*
- *Glycine max*
- *Hordeum vulgare*
- *Medicago truncatula*
- *Oryza sativa Japonica Group*
- *Populus trichocarpa*
- *Saccharum officinarum*
- *Solanum lycopersicum*
- *Solanum tuberosum*
- *Triticum aestivum*
- *Vitis vinifera*
- *Zea mays*

<http://mapman.gabipd.org/web/guest/mapmanstore>



Help

Get help and support online, using our web forum or contact us directly by email: <http://mapman.gabipd.org/web/guest/forum>



References

- Usadel B, Poree F, Nagel A, Lohse M, Czedik-Eysenberg A, Stitt M. A guide to using MapMan to visualize and compare Omics data in plants: a case study in the crop species, Maize. *Plant Cell Environ.* 2009 Sep;32(9):1211-29.
- Sreenivasulu N, Usadel B, Winter A, Radchuk V, Scholz U, Stein N, Weschke W, Strickert M, Close TJ, Stitt M, Graner A, Wobus U. Barley grain maturation and germination: Metabolic pathway and regulatory network commonalities and differences highlighted by new MapMan/PageMan profiling tools. *Plant Physiol.* 2008, 146:1734-1761
- Telstrom V, Usadel B, Thimm O, Stitt M, Kuster H, Niehaus K. The Lipopolysaccharide of *Sinorhizobium meliloti* Suppresses defense-associated Gene Expression in Cell Cultures of the Host Plant *Medicago truncatula*. *Plant Physiol.* 2007, 143:825-37
- Usadel B, Nagel A, Steinhauser D, Gibon Y, Bläsing OE, Redestig H, Sreenivasulu N, Krall L, Hannah MA, Poree F, Fernie AR, Stitt M. PageMan: an interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. *BMC Bioinformatics.* 2006, 7:535
- Usadel B, Urbanczyk-Wochniak E, Thimm O, Nunes-Nesi A, Carrari F, Davy M, Bläsing OE, Kowalczyk M, Weicht D, Polincus A, Meyer S, Stitt M, Fernie AR. Conversion of MapMan to allow the analysis of transcript data from Solanaceous species: effects of genetic and environmental alterations in energy metabolism in the leaf. *Plant Molecular Biology* 2006, 60:773-92.
- Usadel B, Nagel A, Steinhauser D, Gibon Y, Bläsing OE, Redestig H, Sreenivasulu N, Krall L, Hannah MA, Poree F, Fernie AR, Stitt M. PageMan: an interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. *BMC Bioinformatics* 2006, 7:535
- Usadel B, Nagel A, Thimm O, Redestig H, Bläsing OE, Palacios-Rojas N, Selbig J, Hannemann J, Piques MC, Steinhauser D, Scheible WR, Gibon Y, Morcuende R, Weicht D, Meyer S, Stitt M. Extension of the Visualization Tool MapMan to Allow Statistical Analysis of Arrays, Display of Corresponding Genes, and Comparison with Known Responses. *Plant Physiology* 2005, 138:1195-1204.

For a full list of publications see: <http://mapman.gabipd.org/web/guest/publications>

Funding

This study was supported by a grant from the German Federal Ministry of Education and Research (BMBF grant 0315049A) and by the Max-Planck-Society.

