# MapMan
## Visualize your pathways in crops

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http://www.gabipd.org/projects/MapMan

http://mapman.mpimp-golm.mpg.de

## ■ Introduction

The MapMan family of software was first developed for the reference species Arabidopsis. In this poster we describe:
(i) How the flexibility and functions in the user interface 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 array data sets, drawing on a generic software and supported by the Arabidopsis reference genome.

## ■ Annotations (Fig 2/3)

MapMan was originally developed for Arabidopsis ATH1 arrays. More than 10k non-trivial associations were made between genes and BINS (functions). Due to improvements in the Arabidopsis genome annotation, it was possible to map more and more transcripts, to refine the given associations or to correct these where new functional evidence was published. Given the relative stability of Arabidopsis gene models, a new Arabidopsis genome release usually does not require too many changes, as these are made continuously.

To adapt the MapMan ontology to crops, the associations were transferred using BLAST followed by extensive manual checks. As assignments are usually made on unigene builds, which are not stable, extensive quality control is needed for each new unigene set release. To partly circumvent this problem and to build a more stable basis, plant proteins from SwissProt were associated with BINS as well, currently covering some 8000 proteins. Further annotation of protein domains has been started. This is developed into an automated pipeline in the GABI-FUTURE program.
Currently mapped crops include:
*Barley* Sreenivasulu, IPK-Gatersleben
*Tomato* Fernie, MPI Golm
*Medicago* Niehaus, Tellström, Bielefeld
*Potato,Grapevine* Rotter, NIB Slovenia
*Maize* Poree, MPI Golm

## ■ PageMan (Fig 4)

Whereas MapMan -so far- can only display one contrast (treatment vs. control) at a time, the need to visualize several treatments (e.g. a time series) has become pressing, as array technology is used increasingly in the plant field. It is not feasible to display both (almost) all genes in all experiments. 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 upregulated within each BIN than expected by chance.

The user is presented with a wizard based interface that guides through the selection of files, and shows the compression statistics and multiple testing procedures that are available. Finally the user is presented with a graphical overview of the BIN hierarchy as well as of individual statistical tests which are colour coded.

At the same time a functional classification, incorporating this statistics is also included in a web-based tool.

## ■ MapMan Cluster Edition (Fig 1)

Within MapMan it is now possible to cluster data. The results of this biologically-abstract mathematical clustering procedures can be viewed in the context of our knowledge of the structure of biological processes via the MapMan functional annotation (BINS). Elements of the cluster or clusters of interest can be highlighted in the pathway view by simply dragging them onto the pathway. This allows interpretation of the clusters in the context of automated analysis and hand curated ontologies.
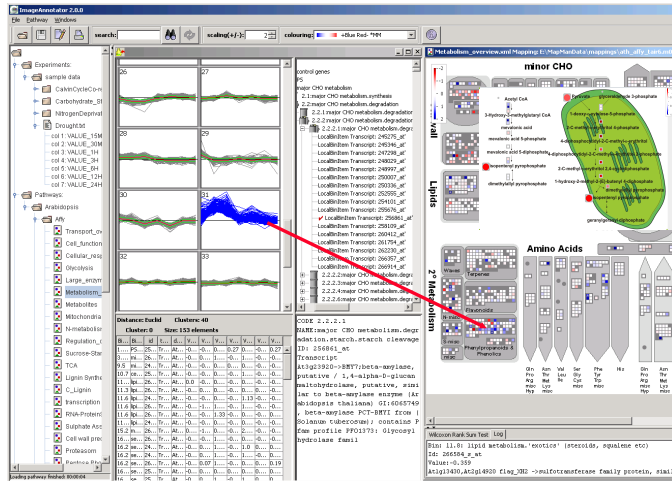


**Figure 1:** MapMan Cluster Edition
Clusters can be dragged into pathways. The inset shows a combined profiling experiment using transcript data [squares] and metabolites [circles]
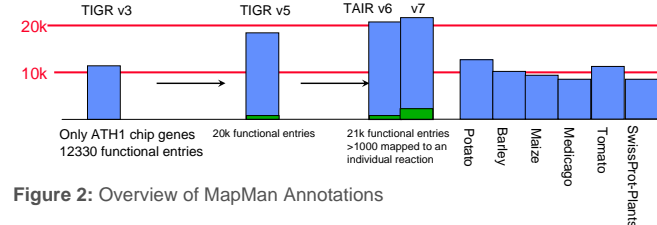


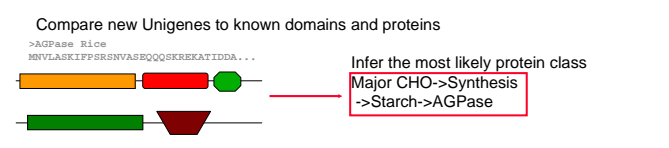**Figure 2:** Overview of MapMan Annotations



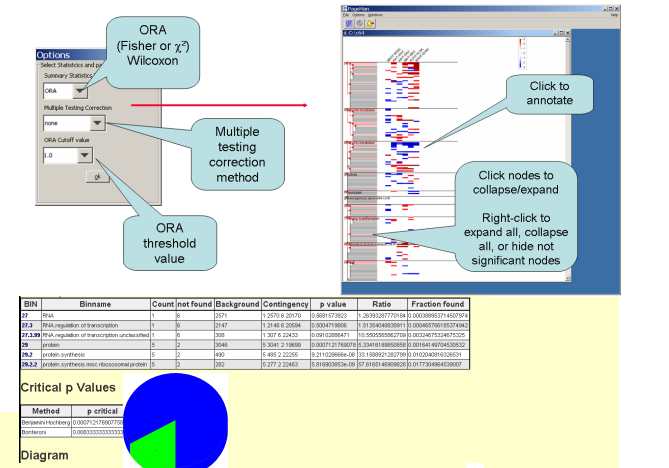**Figure 3:** Annotation of contigs based on known genes



**Figure 4:** PageMan
upper panel: Stand-alone tool showing changed BINs
lower panel: Webtool showing classification results of gene lists

## ■ MapScavenger (Fig 5)

PageMan has been extended to work with annotation data coming from MIPS (FunCat), Kegg (KeggOrthology and Pathways) and GO. Existing annotations can be converted into MapMan mapping files which are used by PageMan.
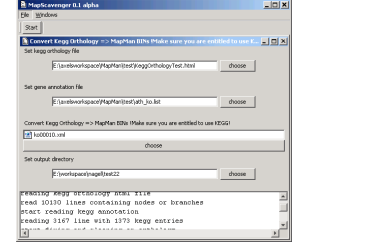


**Figure 5:** MapScavenger

## ■ MapManWeb (Fig 6)

To facilitate the web based publishing of gene expression data we have developed a web version of the ImageAnnotator. Currently 21 experiments with more that 160 single or duplicate hybridisations are accessible. In addition, data to be visualised can also be transferred from other sites like CSBDB http://csbdb.mpimp-golm.mpg.de) which interfaces with MapManWeb (http://www.gabipd.org/projects/MapMan).
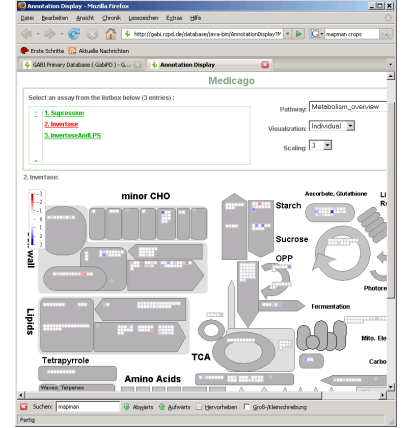


**Figure 6:** MapManWeb
Displayed is a medicago experiment viewed in a webbrowser

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