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

(i) How the flexibilities 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 pathways 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 chromosomes
- Add a file containing additional markers to be shown on the map in parallel to the experimental data
- Devise 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)

References

Asel Nagele, Marc Lohse, Dirk Walther, Birgit Kersten, Joachim Selbig, Bjorn Udadel, Mark Stitt

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Online access to up to date MapMan Mappings and Pathways Mapping(Annotation Data) available for:
- Arabidopsis thaliana
- Citrullus colocynthis
- Glycine max
- Hordeum vulgare
- Medicago truncatula
- Oryza sativa
- Populus trichocarpa
- Sinorhizobium meliloti
- Vitis vinifera
- Zea mays

Technical details:
- Started and monitored through a web interface
- Allows the annotation of sequences (e.g. sequences, underlying a transcript profiling chip)

Resources

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Further details see poster: P086

Help

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

Helpful resources are:
- MapMan overview http://mapman.gabipd.org
- MapMan news https://news.mapman.org
- PageMan http://mapman.gabipd.org/web/guest/mapmanstore
- MapMan Robin: a User Friendly Graphical Interface to Powerful Open Source Microarray Processing
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