



PRIME: Platform for RIKEN Metabolomics

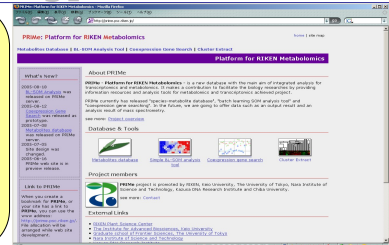
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<http://prime.psc.riken.jp/>

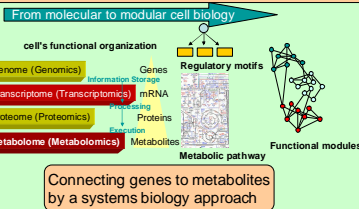
SUMMARY

We have developed a web-based database, "PRIME (Platform for RIKEN Metabolomics)," which contains powerful tools for researchers to analyze gene co-expression data and mass spectral data. PRIME has been developed with the main aim of facilitating integrated analysis for transcriptomics and metabolomics. We have already available are (1) Metabolite Database (KNpSACK), (2) BL-SOM Analysis Tool (Batch-Learning Self-Organizing Map), (3) Coexpression Gene Search (coexpression database), and (4) Tree extracting tool (data from AtGenExpress) which are the major constituents of PRIME. The contribution of PRIME is that it assists the biologists by providing information resources and analysis tools for metabolomics and transcriptomics projects. We are motivated to build a research platform with an aim to improve plant production capabilities in both quantitative and qualitative terms, based on integrated genome sciences founded on metabolome research.



What is Metabolomics?

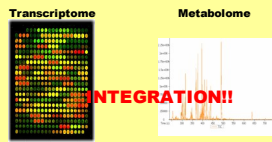
Metabolomics can be defined as the quantitative and qualitative analysis of all low molecular weight metabolites in an organism's cells.



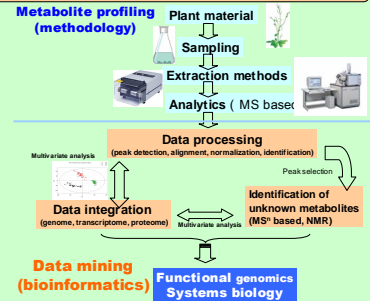
OUR GOAL

PRIME

A framework for understanding the mechanism of plants by integration of transcriptome and metabolome data



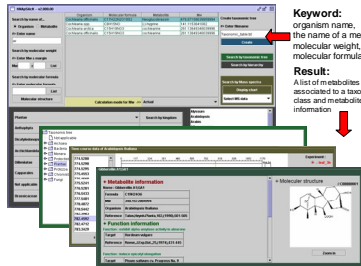
Plant Metabolomics (non-target analysis)



TOOLS

(1) Metabolite database

Metabolite database, "KNpSACK," is for the analysis of metabolites. Information on natural products is amassed, giving special emphasis on their biological origins. User can retrieve information on metabolites by entering the organism name, the name of a metabolite, molecular weight, and molecular formula.

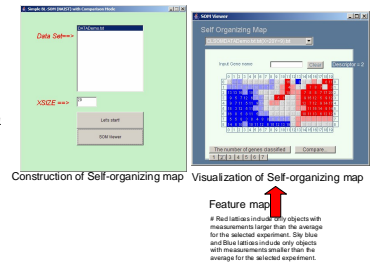


Keyword: organism name, the name of a metabolite, molecular weight, and molecular formula
Result: A list of metabolites that are associated to a taxonomic class and metabolite information

free downloadable tool

(2) BL-SOM

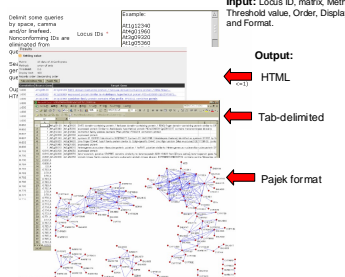
For visualization of multivariate data (e.g. gene expression) we modified the conventional self-organizing map (SOM) and introduced batch-learning self-organizing map (BL-SOM), to make the learning process and resulting map independent of the order of input data.



free downloadable tool

(3) Coexpression gene search

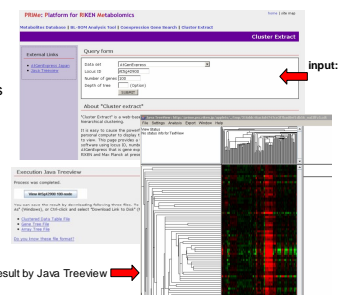
Coexpression Gene Search is a web application system to search for coexpressed genes based on correlation value from some gene expression data by ATTED (*Arabidopsis thaliana* trans-factor and cis-element prediction database).



web-based tool

(4) Cluster Extract

Cluster Extract is a web-based tool to extract a part of tree by locus id (AGI code) as key from result of hierarchical clustering. The dataset is AtGenExpress that is gene expression analysis project using Affymetrix GeneChip *Arabidopsis* ATH1, produced by RIKEN and Max Planck at present.



web-based tool

FUTURE DIRECTIONS

- Metabolomic analysis and technology development by mass spectrometry and NMR
- Metabolomics analysis of mutants and transgenic lines of *Arabidopsis* and rice
- Discovery of gene-to-metabolite networks by integrated analysis with transcriptomics
- Development of software for metabolome analysis and network analysis
- Construction of metabolome and related database
- Analytical databases of standard metabolites by mass spectrometry and NMR
- Database of isolated metabolites from *Arabidopsis thaliana*

