



ShowMEPATH: Automated Multi-Omics Comparative Analysis Tool Revealing Hidden Patterns in Large-Scale Fold-Change Data

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BACKGROUND

Volcano plots are used as a visualization and statistical analysis tool in the field of omics data analysis. It enables researchers to assess the significance and extent of changes in gene expression, protein abundance, metabolite levels, or other biological measurements between different conditions or groups. This tool enables researchers to map biological pathways and to understand the functional relationships and interactions within a pathway to gain insights into the overall biological significance of their experimental findings. With the increasing scale of research data and the need to compare multiple sample groups, there is a growing demand for new, efficient methods to analyze and interpret complex biological omics data.

BRIEF DESCRIPTION

The University of California, Riverside has developed a new omics software named, ShowMEPATH, employing a faster and easier approach to compare changes in metabolites within multiple sample groups, along with an automated algorithm to facilitate the process. The software introduces a novel tool to visualize volcano plots, called Parallel Fold Change (PFC) plot. Unlike current software solutions, PFC enables researchers to easily process their large omics data sets to compare various biological networks. The PFC plot is an efficient tool for analyzing and interpreting complex biological comparisons and it helps researchers to efficiently map omics pathways.

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OTHER INFORMATION

KEYWORDS

metabolomics, transcriptomics, proteomics, omics data, metabolite, transcript, proteome, statistical analysis, volcano plot, visualization, parallel fold change, plot, KEGG, multi-omics, software, automated, algorithm, fold-change, pattern,

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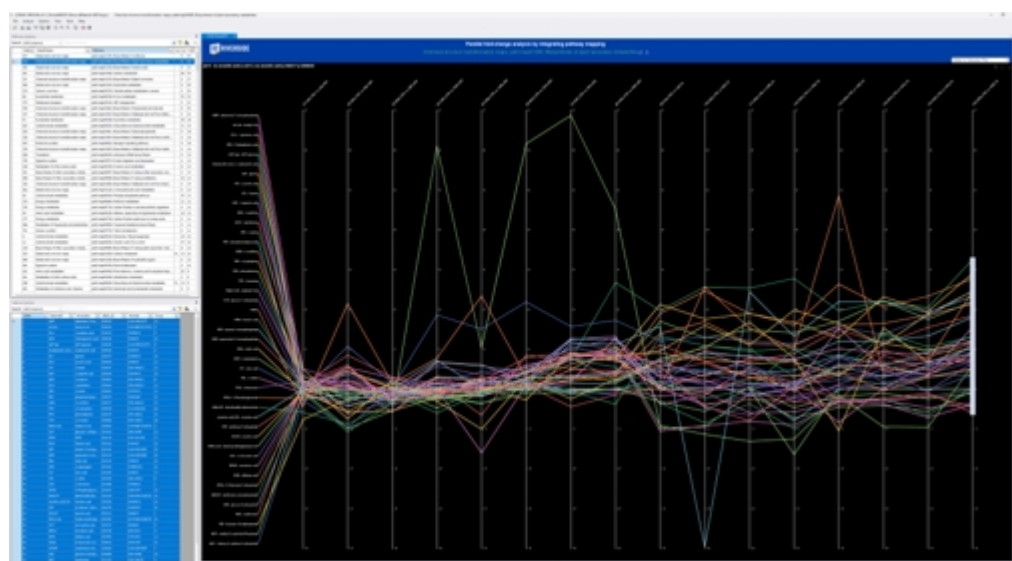


Fig 1: This figure illustrates a Parallel Fold Change (PFC) plot and demonstrates the parallel comparison of multiple samples in metabolomics. The tool

examines the fold-change patterns of 45 metabolites across 16 scenarios involving 8 genotypes and 3 treatments. Using ShowMEPATH, researchers can identify detailed patterns within biological experiments, with the ability to hover over lines in the PFC plots for seamless access to KEGG modules or pathways, thereby streamlining the exploration of related biological information

APPLICATIONS

- ▶ ShowMEPATH enables researchers to efficiently explore, interpret, and map complex biological data involving large data sets obtained from a large scale of samples, and to ultimately gain insights into the functional relationships and interactions among molecules within a biological pathway.

PATENT STATUS

Patent Pending

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