OmicScope unravels systems-level insights from quantitative proteomics data

Guilherme Reis-de-Oliveira[1,2], Victor Corasolla Carregari[2], Daniel Martins-de-Souza[2]

[1.] CPB, Boldrini Research Center, R. Márcia Mendes, 506;
[2.] LNP, Laboratory of Neuroproteomics, Rua Monteiro Lobato;

Mass spectrometry-based proteomics has become a crucial tool for decoding the complex molecular mechanisms behind diseases and biological processes. After identifying and quantifying proteins, obtaining comprehensive information from proteomics data requires using multiple software tools. These tools cover differential proteomics, enrichment analysis, protein-protein interaction searches, and other applications, depending on the study's complexity. However, the diversity of tools in the proteomics field poses a significant challenge, particularly for non-programmers and newcomers, due to the steep learning curve required to master each tool's functions, capabilities, and limitations.

To address this challenge and introduce a new era of computational tools in proteomics, we conducted a comprehensive survey of the available tools. We evaluated them based on input format acceptance, pre-processing steps, differential proteomics workflows, enrichment analysis capabilities, meta-analysis features, figure options, and graphical user interfaces. Based on our results, we developed Omicscope—an integrative solution designed to streamline proteomics data analysis from differential expression to system-level integration. It provides a unique environment capable of handling and integrating quantitative proteomics data, enrichment outcomes, and comparing independent studies.

Omicscope performs differential analysis across various platforms and experimental designs, conducts enrichment analysis using 224 Enrichr libraries, and integrates independent studies to enhance biological insights. Additionally, it offers a comprehensive suite of graphical outputs, including gold-standard proteomics figures and unique plots tailored to enhance comprehension in individual experiments and systems-level analyses. Our tool also provides a versatile array of output files for integration with third-party software, including tables, vectorized images, network files, and its own output format. Aiming democratizing and widespread proteomics data analysis, OmicScope is available both as a Python package and a web application (https://omicscope.ib.unicamp.br/).

In conclusion, OmicScope has been carefully designed to assist experimentalists in analyzing and interpreting proteomics datasets. Our tool aims to support proteomics researchers in tackling complex biological questions and understanding molecular pathways associated with various disorders.

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