Mass-Up and Decision Peptide-Driven:
two open-source applications for MALDI-TOF MS data analysis and protein quantification

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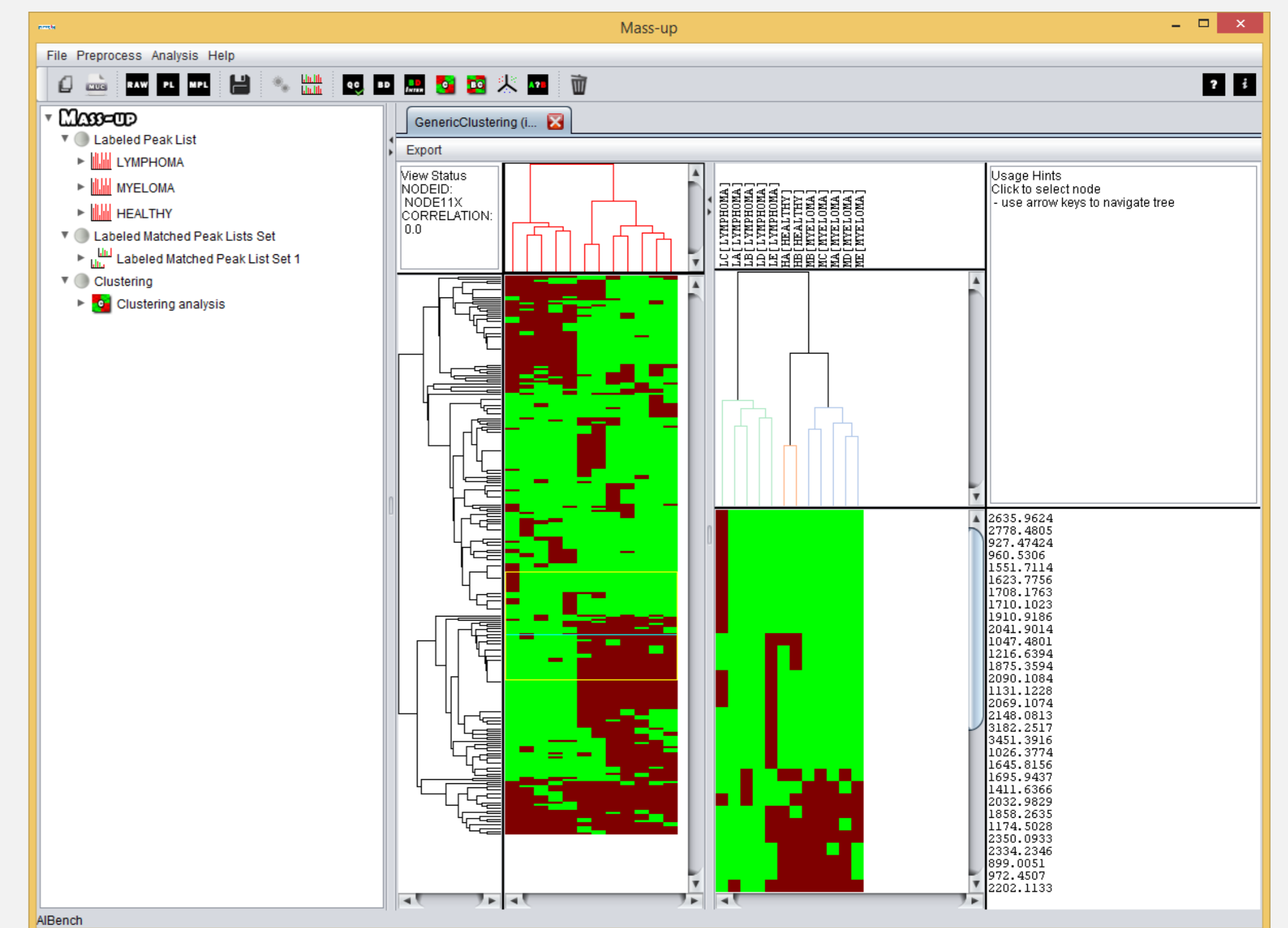
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Mass-Up

What is Mass-Up? Mass-Up is an open-source software for proteomics designed to support the preprocessing and analysis of MALDI-TOF mass spectrometry data.

Features: Mass-Up allows researchers to easily:
- Load and visualize raw spectra from mzML, mzXML or CSV files.
- Preprocess raw spectra using well-known R libraries (MALDIquant and MassSpecWavelet).
- Perform different types of analysis (quality control, biomarker discovery, principal component analysis, hierarchical clustering, biclustering, and classification analysis) on the aligned peak lists.
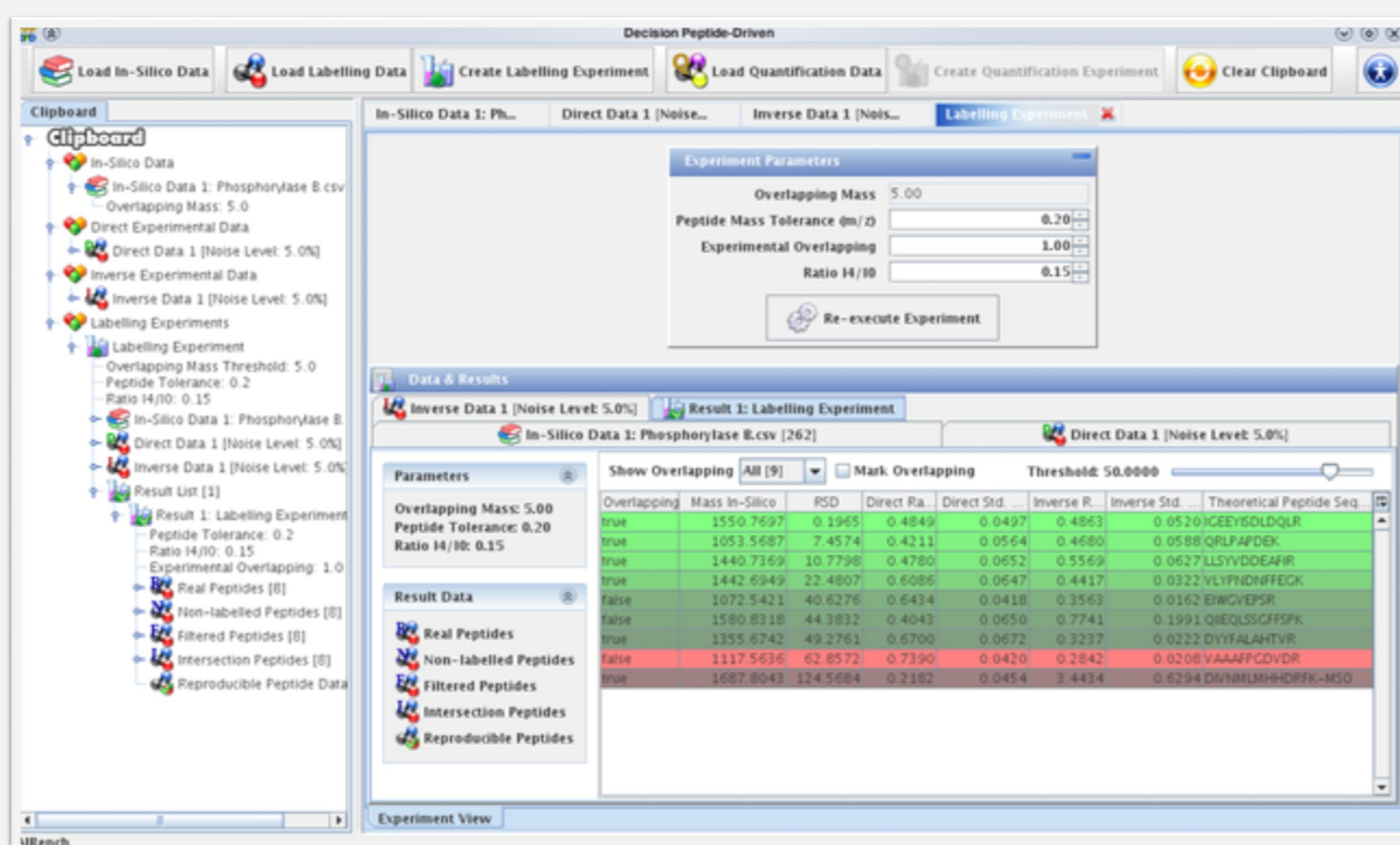
H. López-Fernández; H.M. Santos; J.L. Capelo; F. Fdez-Riverola; D. Glez-Peña; M. Reboiro-Jato (2015) *Mass-Up: an all-in-one open software application for MALDI-TOF mass spectrometry knowledge discovery*. BMC Bioinformatics. 16:318. ISSN: 1471-2105. DOI: 10.1186/s12859-015-0752-4

DPD

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What is Decision Peptide-Driven? The DPD tool assists the user in the application of a specific protocol for protein quantification based on 18O direct and inverse labeling followed by MALDI-TOF MS analysis.

Features. DPD uses MALDI-TOF MS spectra and allows users to:
- Compare direct and inverse labeling experiments in order to determine the most reproducible peptides.
- Calculate the O16/O18 ratio from a mixture of unknown amount of protein and an internal standard labeled (reproducible peptides) with O18.
- Consequently determine the unknown amount of protein.

H.M. Santos; M. Reboiro-Jato; D. Glez-Peña; M.S. Diniz; F. Fdez-Riverola; R. Carvalho; C. Lodeiro; J.L. Capelo (2010) *Decision peptide-driven: a free software tool for accurate protein quantification using gel electrophoresis and matrix assisted laser desorption ionization time of flight mass spectrometry*. Talanta. Volume 82/4, pp. 1412-1420. ISSN: 0039-9140. DOI: 10.1016/j.talanta.2010.07.007