

Algorithms for Label-Free Protein Quantification Across Hundreds of LC-MS Data Sets

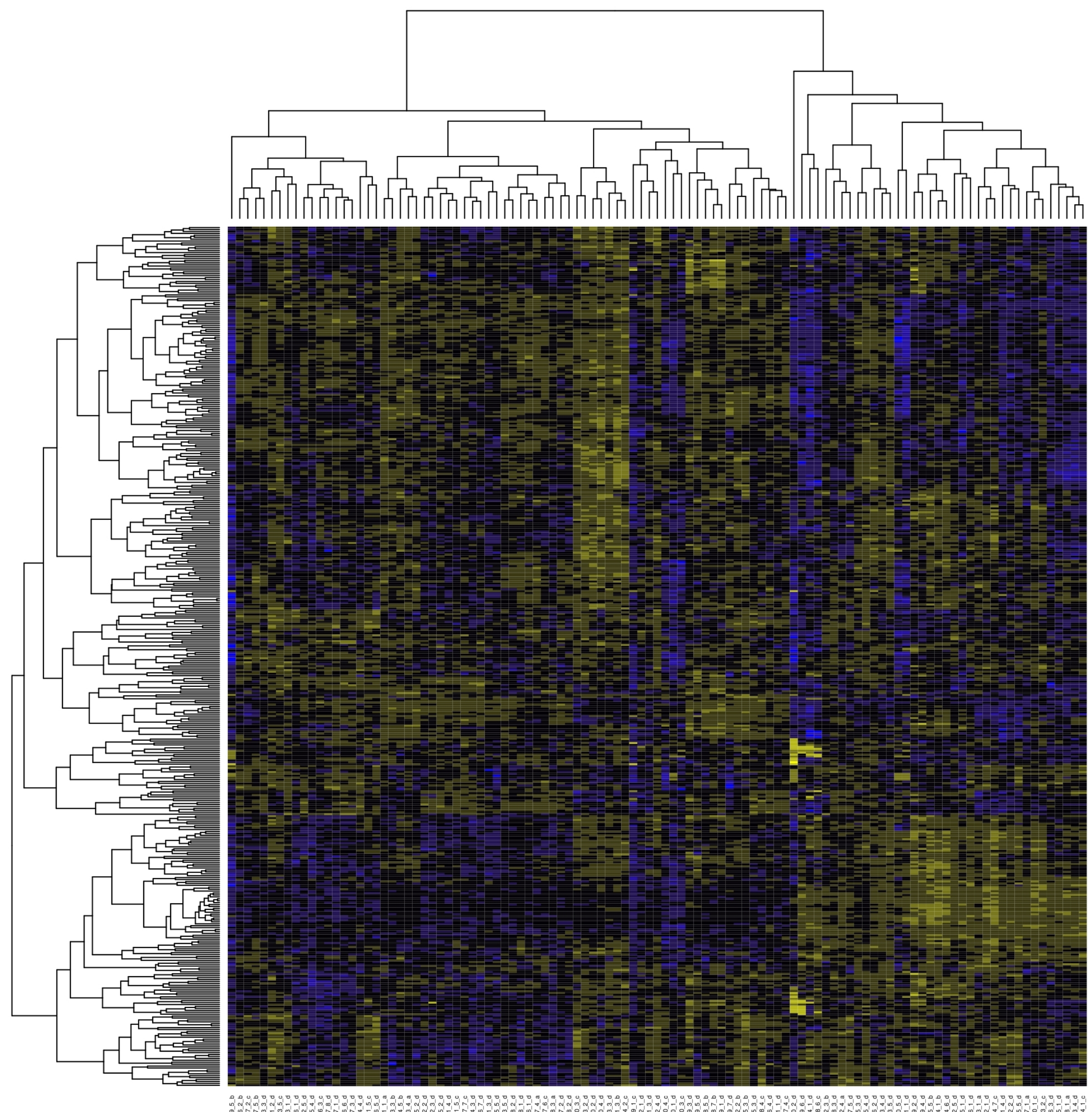
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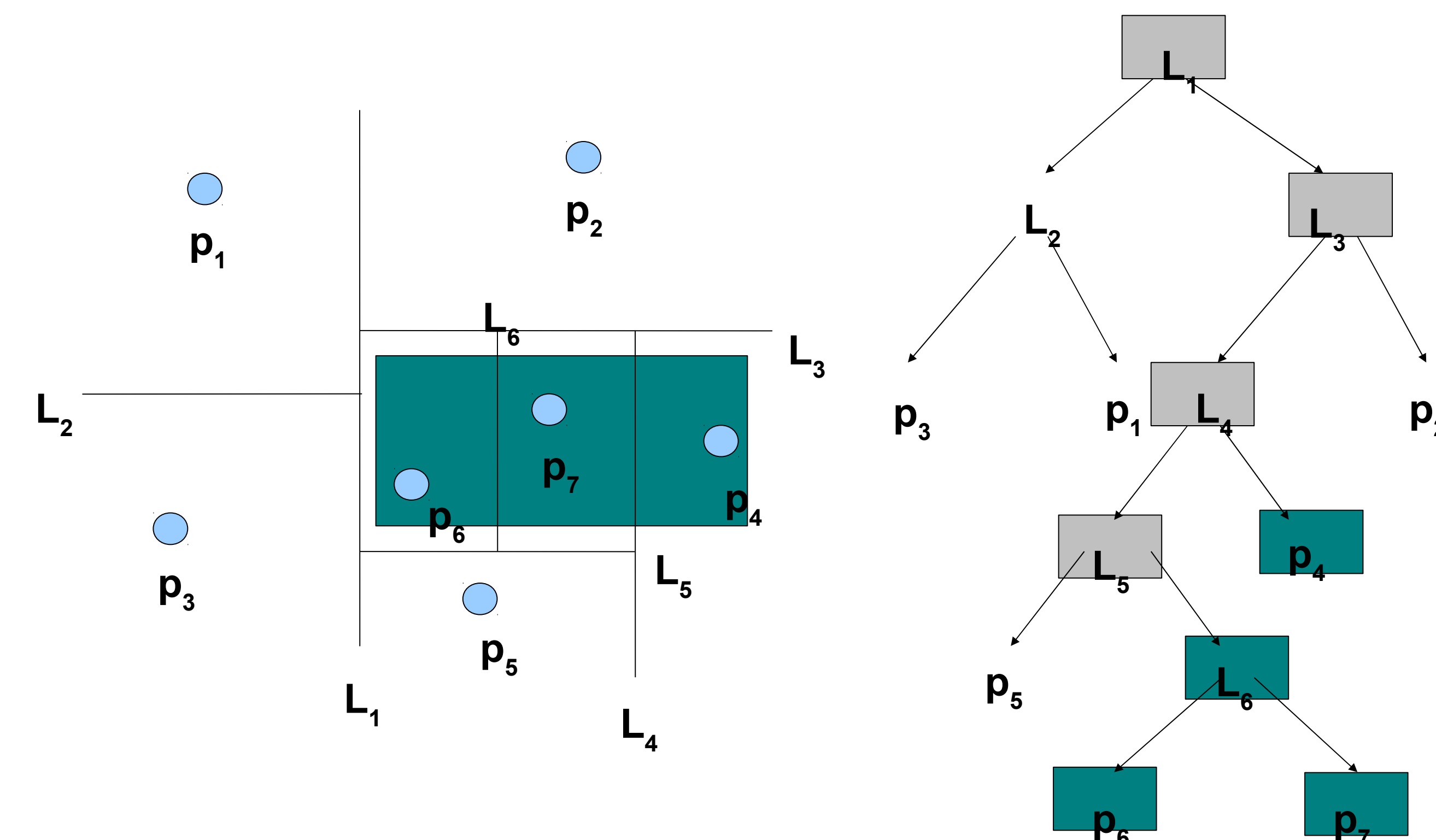
Poster 039

Label-Free Protein Quantification



- ♦ total unfractionated proteins from 102 genotype progeny from a cross between *S. cerevisiae* strains BY4716 and RM11-a
- ♦ 472 total scans including parent strains and gas phase fractionation data
- ♦ 27 minutes 20 second processing time for quantitative data 4-core 2.8Ghz AMD 2220, 13GB max memory
- ♦ 0.9535 biological replicate correlation
- ♦ 635 unique proteins in 40 or more progeny

Key Idea: Use space partitioning data structures and planar orthogonal range queries. Full precision and faster algorithms.



Full GUI. Demonstration available on request.

C++ cross-platform (Linux, Windows, Mac)

Isotope Labelled Data Processing with better proteome coverage than MaxQuant!!!

