

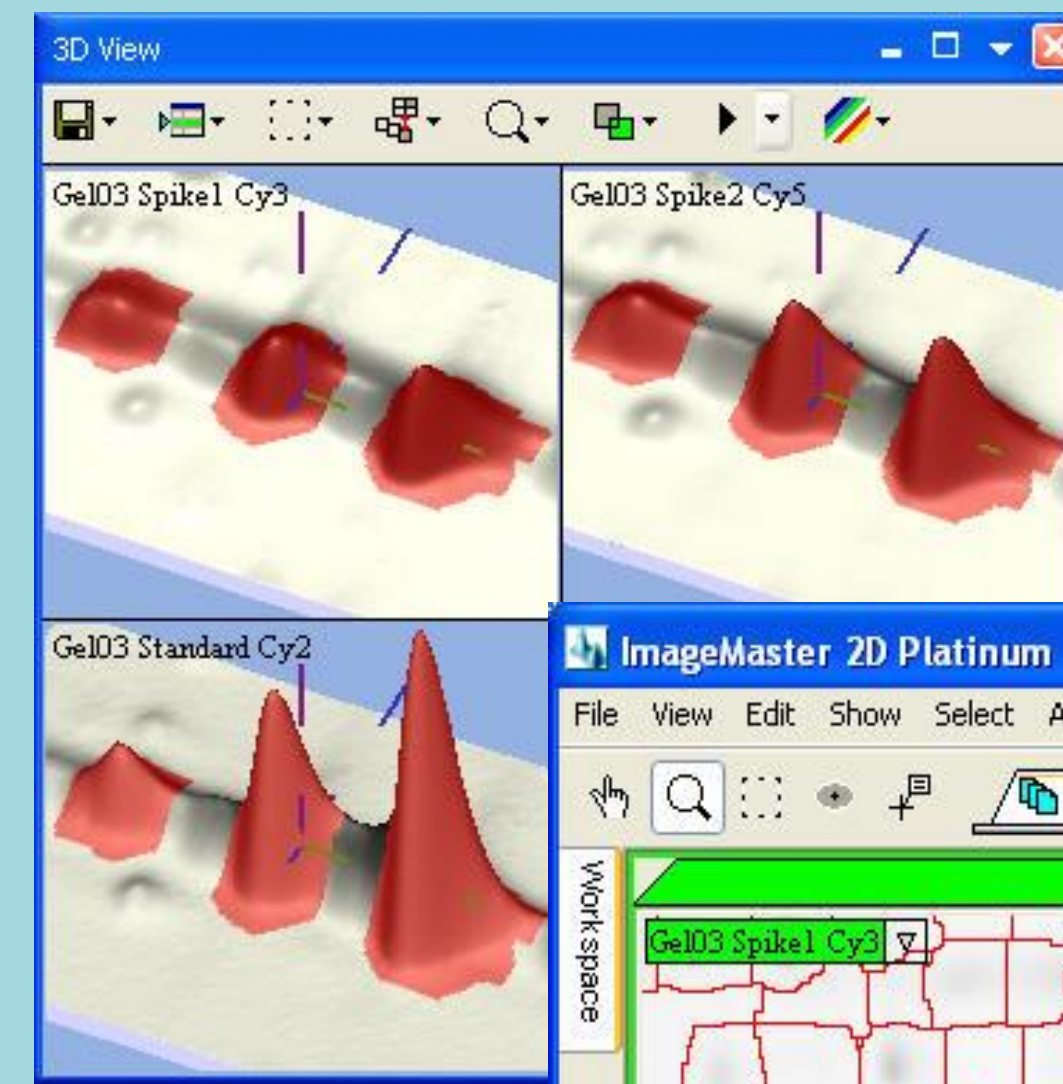
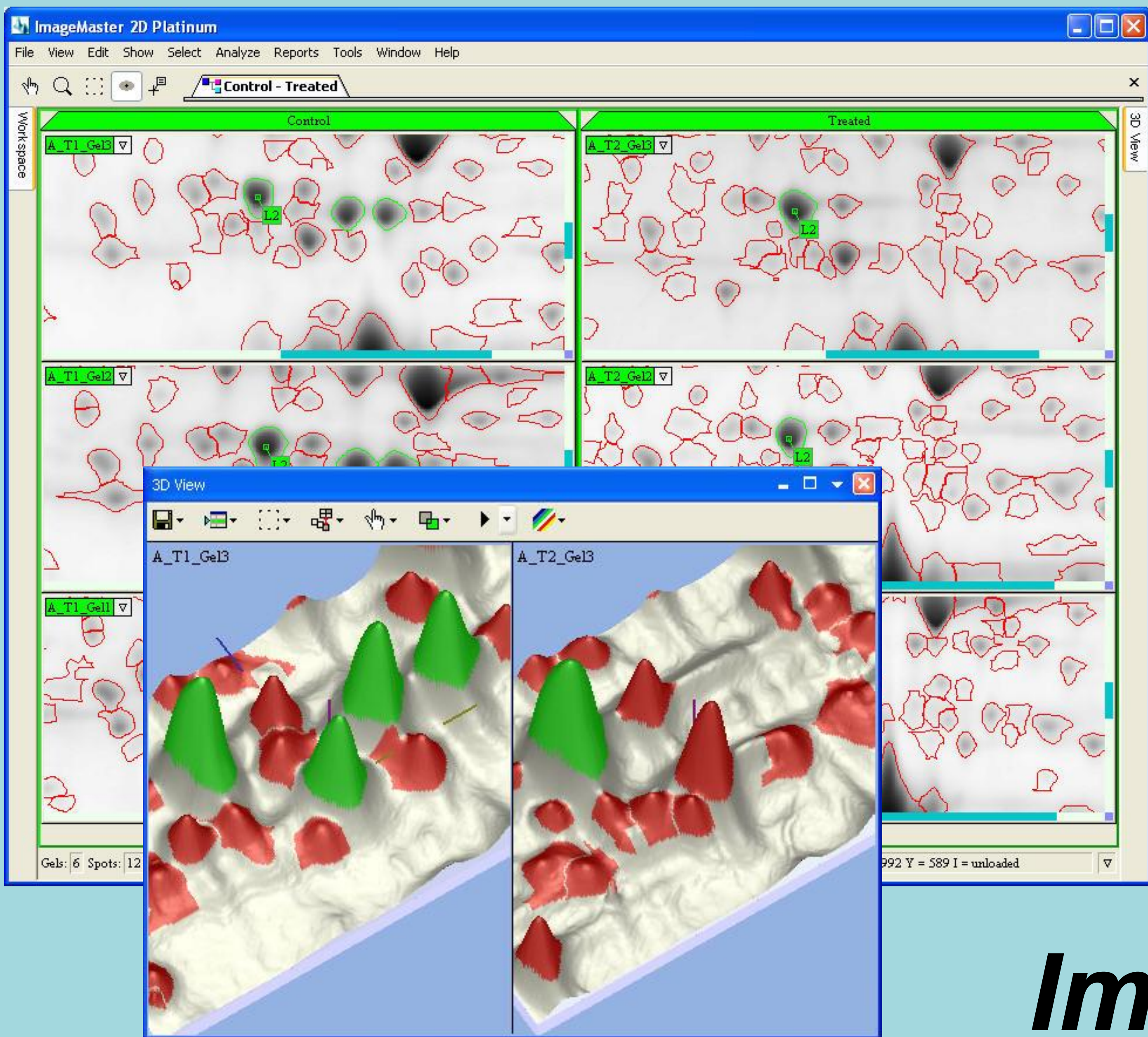
Melanie: analysis of proteomics data with ImageMaster and MSight

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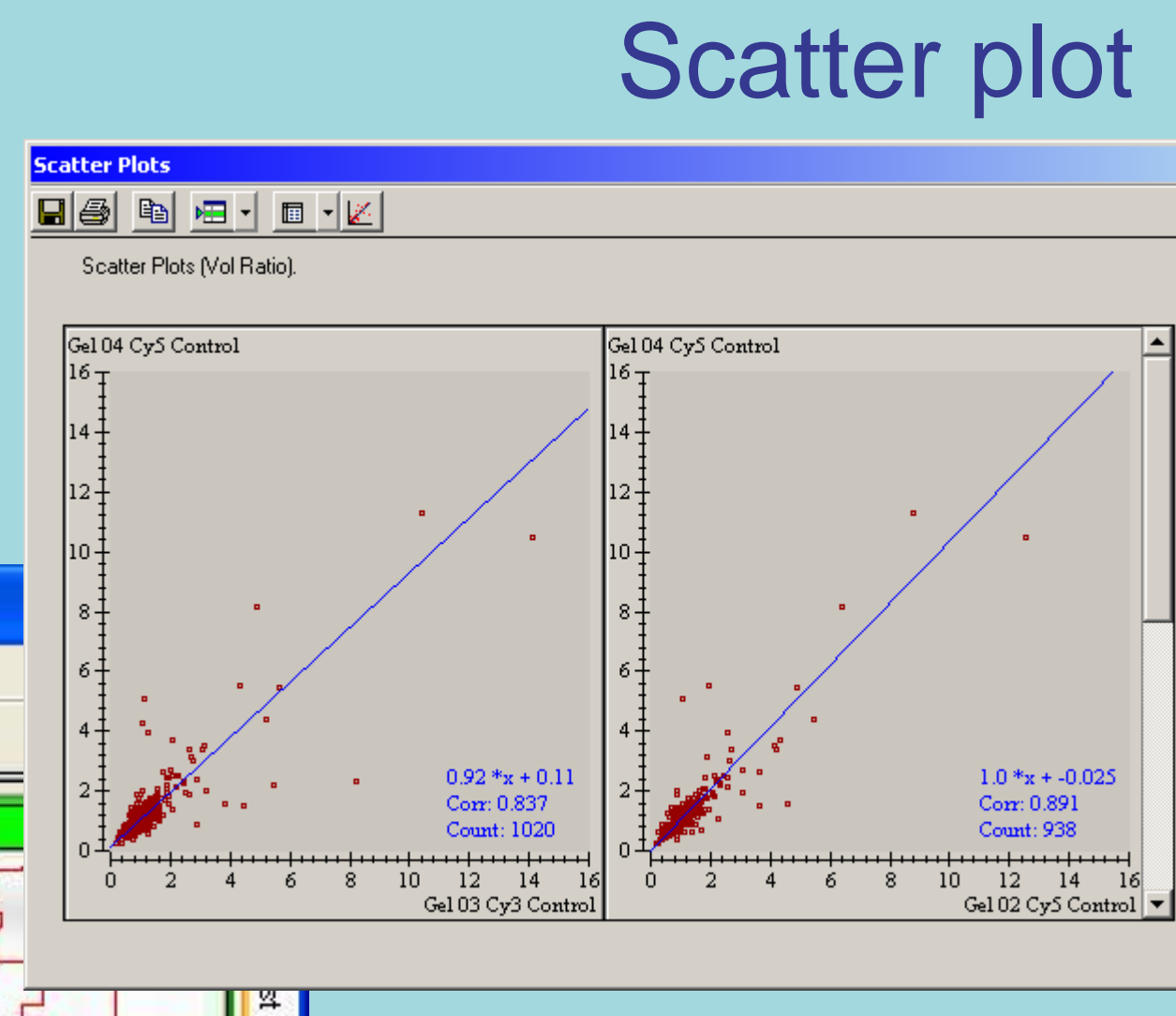
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Melanie's algorithms and interface, initially developed to analyse 2-DE gel images, were adapted to the visualisation and analysis of LC-MS datasets. These developments demonstrate that proteome imaging follows a general schema. Therefore, a general software framework can be developed that may then lead to software packages for various proteomics techniques where visualisation and data analysis are necessary, such as 2-D PAGE, LC-MS, CE-MS, SDS-MS, etc. Developments of algorithms (such as detection or matching) specific to the application or the type of data must of course be carried out, while the general framework and all the display, visualisation and manipulation tools, as well as the data and statistical analysis modules may be re-used as is. While software reusability has been a key problem in software development, our experience shows that partial solutions can be elaborated with little efforts for proteome informatics.

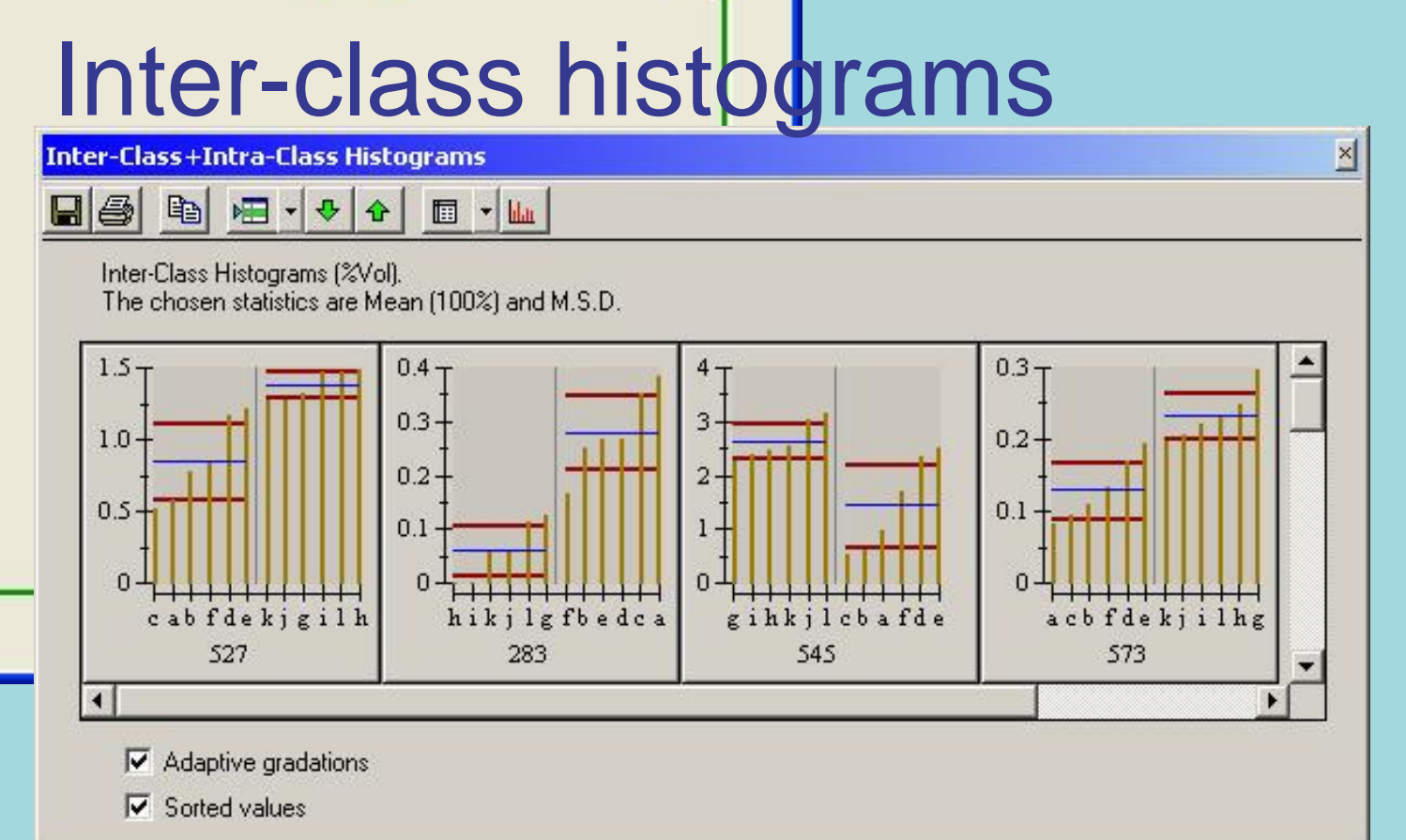
Differential proteome analysis



DIGE analysis



Scatter plot



Inter-class histograms

ImageMaster 2-DE Gel Analysis

melanie a general framework

MSight

LC-MS Data Analysis

Spot detection, Spot matching
Gel alignment
2D data handling
DIGE analysis
Data volume (~ 4MB / gel)

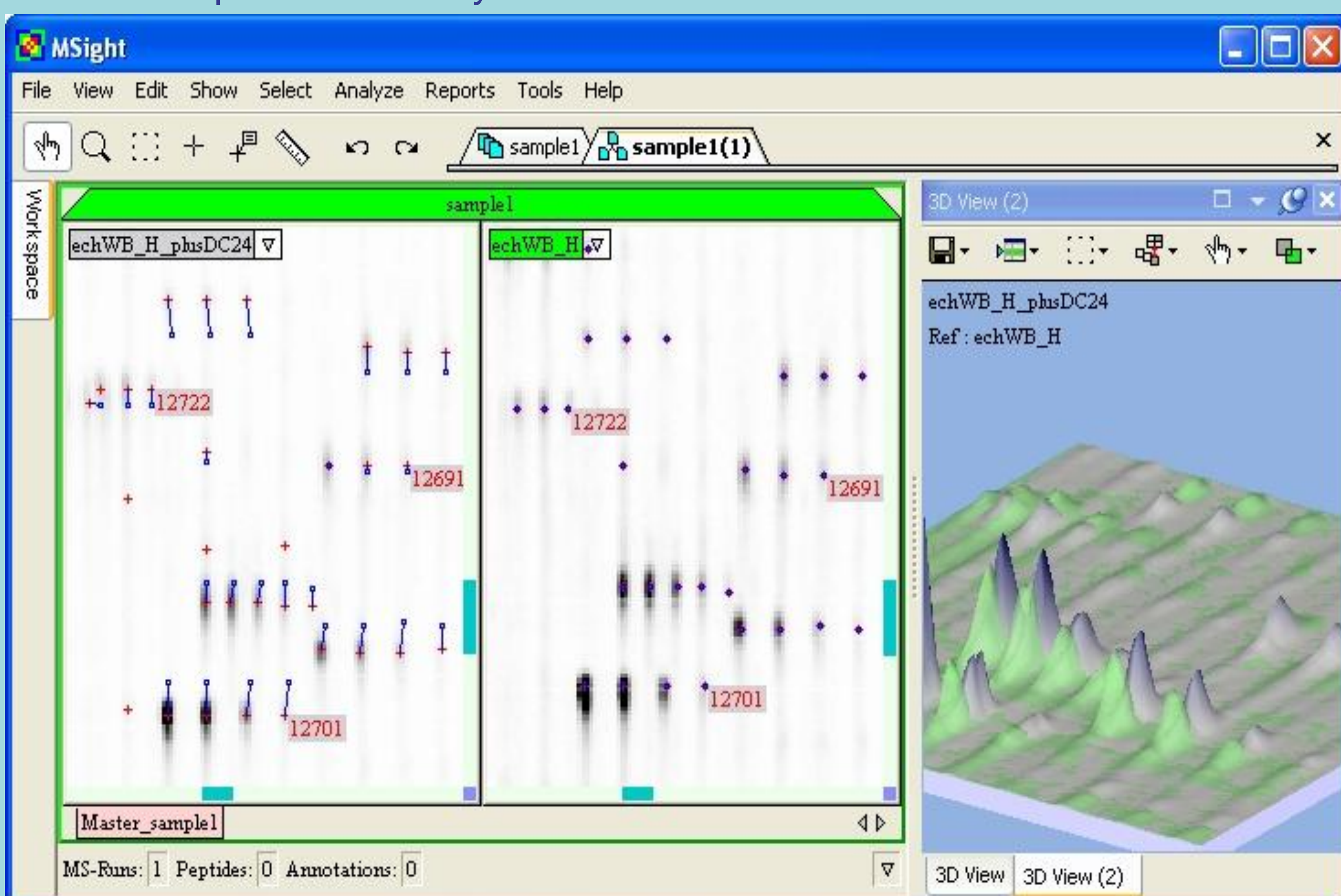
Distinct features

Peak detection, Peak matching
Time warping
2 x 1D data handling
Data volume (~ 100MB / LC-MS run)

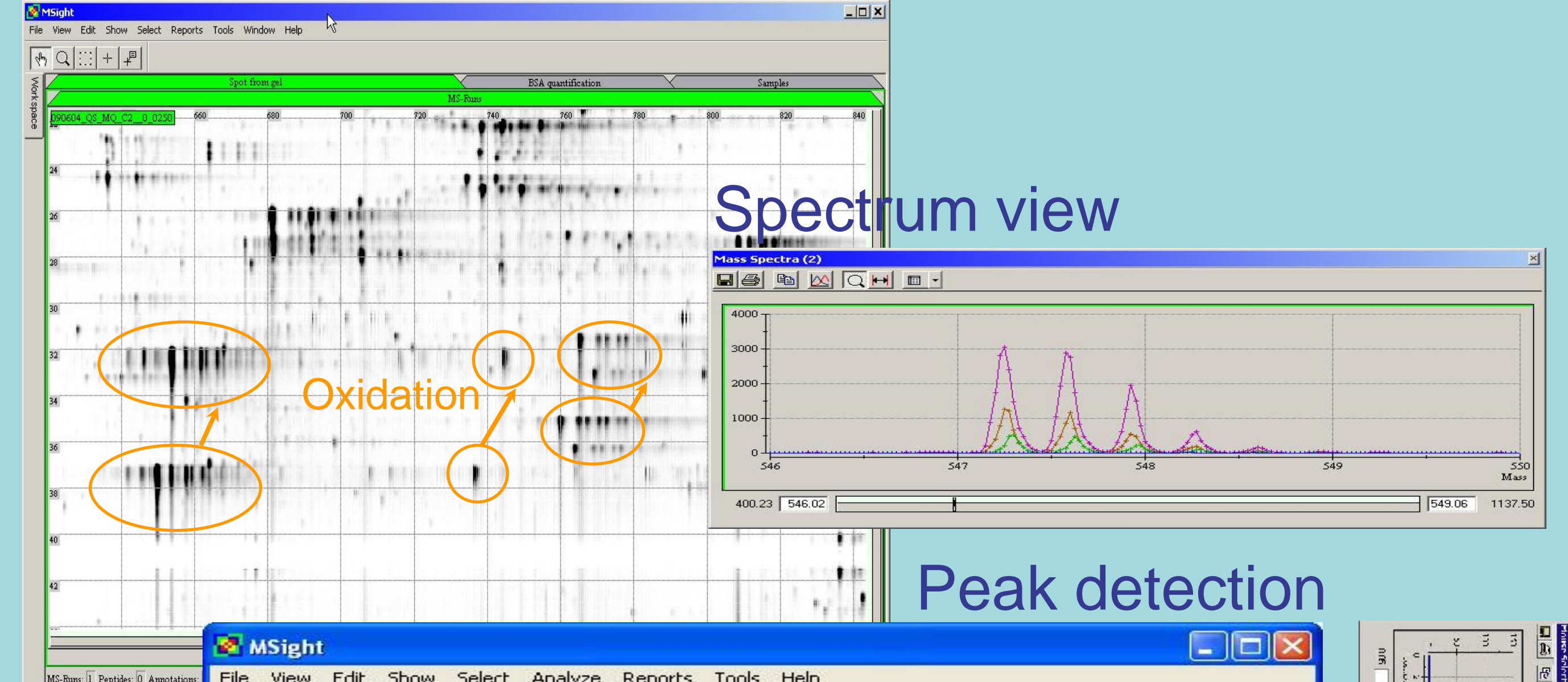
Shared features

Image navigation
Data management through the Workspace
Differential proteome analysis
Knowledge extraction

Differential proteome analysis



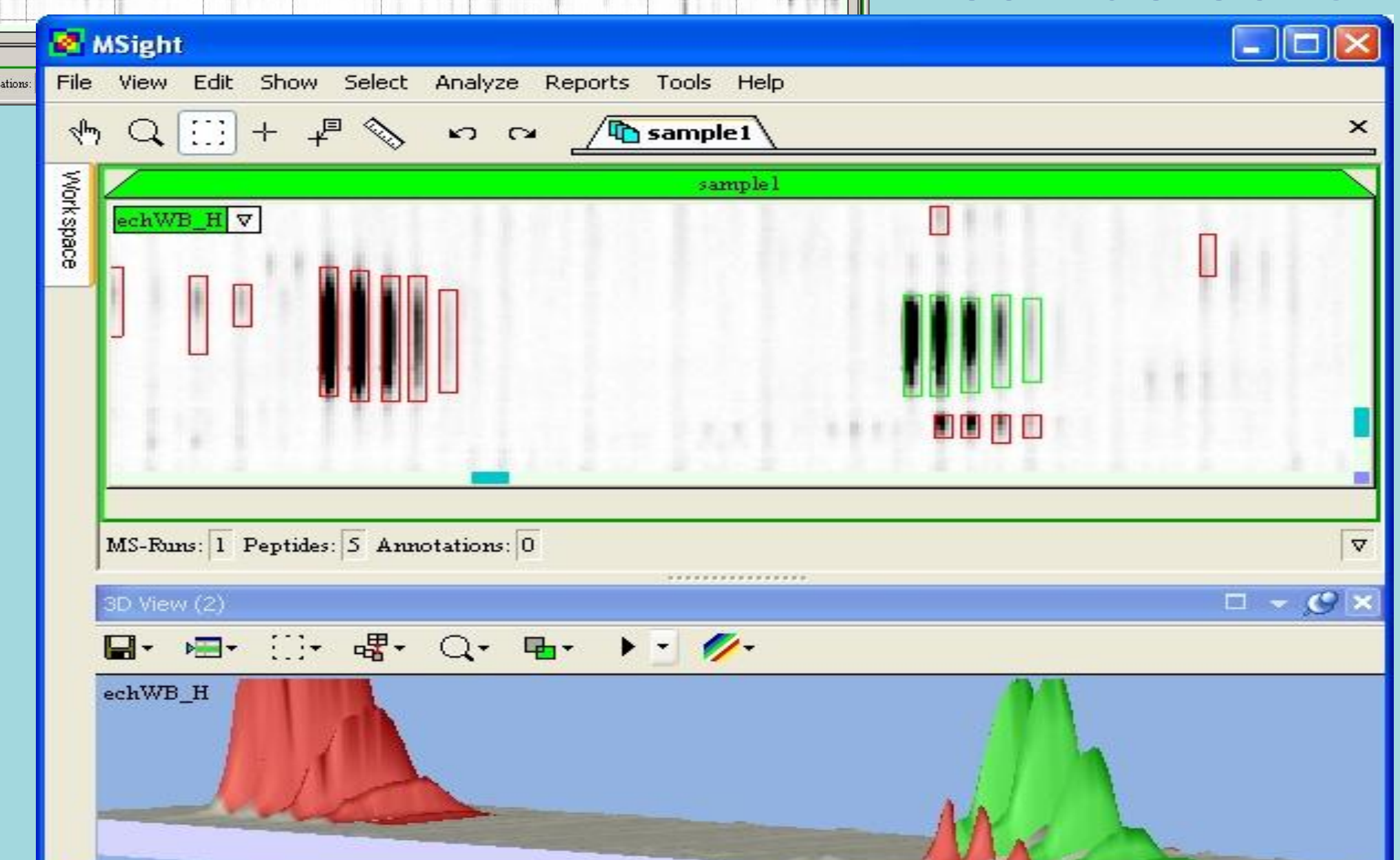
PTM analysis



Spectrum view

Oxidation

Peak detection



Chromatogram view