Melanie: analysis of proteomics data with ImageMaster and MSight

D. Walther¹, G. Bouchet¹, S. Catherinet¹, S. Pelhatre¹, M. Tuloup¹, P. M. Palagi¹ and R. D. Appel¹,²,³

¹ PIQ, Swiss Inst. Bioinformatics (SIB), Geneva, ² Computer Sciences Department, Geneva Univ., ³ Geneva Univ. Hospital (Switzerland)

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.

**ImageMaster**

*2-DE Gel Analysis*

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

- Distinct features
  - Spot detection, Spot matching
  - Gel alignment
  - DIGE analysis
  - Data volume (~ 4MB / gel)

**MSight**

*LC-MS Data Analysis*

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

- Distinct features
  - PTM analysis
  - Spectrum view
  - Chromatogram view

MSight is freely available at http://www.expasy.org/MSight

ImageMaster 2D Platinum is commercialised by GeneBio and GE Healthcare