

## INVITED LECTURE H9

### MS analysis: Imaging and protein identification tools

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Proteomics experiments produce up to thousands of mass spectra per day that must be analyzed on efficient proteome informatics platforms in order to extract pertinent biological knowledge. We have been developing several platforms for high-confidence analysis of proteomics data. Melanie is a software architecture for image analysis that served as the basis for two software packages. One is MSight, a comprehensive package for the analysis of MS data obtained after protein or peptide separation, such as LC-MS or electrophoresis-MS. The software allows for differential analysis as well as for quality control of experimental design, data exploration and linking to identification results. Phenyx, a search engine developed at GeneBio in collaboration with the Swiss Institute of Bioinformatics provides efficient identification of proteins from MS-MS data. A new platform, swissPIT, is designed for the analysis of MS-MS data using two identification engines (Phenyx and X!Tandem) and two characterization software (Popitam and InsPecT), giving access to automated protein identification and characterization through a unique Web portal. The platform runs on the SwissBioGrid environment for high-throughput usage. The various tools offer tight integration among themselves and with external data sources.