Analysis of complex protein sets by mass spectrometry

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Proteomics assumes qualitative and quantitative analysis of complex protein sets – proteomes or subproteomes. At the qualitative level identification of thousands of proteins and their posttranslational modifications in a typical sample can efficiently be carried out using existing software (for instance MASCOT database search program). At the quantitative level, however, data analysis becomes more complex and existing bioinformatic tools fulfill their purposes only to a limited degree. In a quantitative analysis mass spectra of peptide mixtures after chromatographic separation in one or several dimensions are generated. These datasets contain tens of thousands of signals bearing quantitative information on the relative peptide/protein level in the series of samples. At the first steps of the analysis appropriate feature selection, retention time correction, amplitude normalization etc. algorithms have to be applied. To fulfill the purposes of differential proteomics the lists of quantitated features have to be next subjected to statistical analysis tailored to a specific project. Further on efficient informatic tools linking the results of the differential proteomic experiment with protein interaction networks are necessary to allow for streamlined global analyses of proteomes at systems level.