PROPOSITIONS

belonging to the thesis

Towards High Throughput Spatiotemporal Proteomics:

Analytical Workflows and Quantitative Label-Free Mass Spectrometry

1. Despite recent progress in “single-run proteomics”, more than one dimension of fractionation will remain indispensable for many types of samples (this thesis).

2. All fractionation techniques provide additional information on the analytes, which may be of considerable biological interest (this thesis).

3. An FTICR-ion trap cluster can achieve similar performance and sample throughput as multiple hybrid ion trap-FTMS instruments, but at a lower cost (this thesis).

4. Temporally and spatially resolved proteomics is feasible using a quantitative label-free approach (this thesis).

5. Taverna is a powerful tool for processing, analysis, interpretation and visualization of proteomics data (this thesis).

6. Mass spectrometry supports hypothesis- as well as data-driven research.

7. Rapidly improving mass spectrometry technology demands development of fast and robust ways of data processing for confident peptide/protein identification and quantitation in large data sets.

8. History is cyclical. First we divide large scale molecular biology into sub-disciplines (genomics, proteomics, metabolomics, etc.) and then create a new field to combine them.

9. Great things are not done by impulse, but by a series of small things brought together (Vincent van Gogh, 1853-1890).

10. Talking isn’t doing (William Shakespeare, 1564-1616).

11. Life is too short to waste it on things which do not make you happy.

12. Time flies when you are having fun.