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Computation in Bioinformatics: Multidisciplinary Applications

Chapter 14

## Basic Concepts in Proteomics and Applications

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### Summary

Compared to genomics or transcriptomics, proteomics is often regarded as an “emerging technology,” i.e., as not having reached the same level of maturity. While the successful implementation of proteomics workflows and technology still requires significant levels of expertise and specialization, great strides have been made to make the technology more powerful, streamlined, and accessible. In 2014, two landmark studies published the first draft versions of the human proteome. We aim to provide an introduction specifically into the background of mass spectrometry (MS)–based proteomics. Within the field, MS has emerged as a core technology. Coupled to increasingly powerful separations and data processing and bioinformatics solution, it allows the quantitative analysis of whole proteomes within a matter of days, a timescale that has made global comparative proteome studies feasible at last. We present and discuss the basic concepts behind proteomics MS and the accompanying topic of protein and peptide separations, with a focus on the properties of datasets emerging from such studies.

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## Basic Concepts in Proteomics and Applications

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### Abstract

Compared to genomics or transcriptomics, proteomics is often regarded as an "emerging technology" i.e., as not having reached the same level of maturity. While the successful implementation of proteomics workflows and technology still requires significant levels of expertise and specialization, great strides have been made to make the technology more powerful, streamlined, and accessible. In 2014, two landmark studies published the first draft versions of the human proteome. We aim to provide an introduction specifically into the background of mass spectrometry (MS)-based proteomics. Within the field, MS has emerged as a core technology. Coupled to increasingly powerful separations and data processing and bioinformatics solution, it allows the quantitative analysis of whole proteomes within a matter of days, a timescale that has made global comparative proteome studies feasible at last. We present and discuss the basic concepts behind proteomics MS and the accompanying topic of protein and peptide separations, with a focus on the properties of datasets emerging from such studies.

**Keywords:** Proteomics, mass spectrometry, data formats

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