
Preface

Inspired by the enormous impact of Genomics and the hopes that came along with it, biochemistry and its methods slowly evolved into what is now widely known as Proteomics. Scientists dedicated to mass spectrometry and gel-based technologies became aware of the powerful tools they hold in hand, dreaming of the quantitative analyses of proteins in cells, tissues, and diseases. Thus, Proteomics soon went from a shooting-star in the life science field to a must-have in each larger wet-lab group.

Methods and technology developed rapidly, often much faster than the awareness of the special needs of the tools in use and even faster than standard protocols and standard formats could mature. Soon proteomics techniques created more and more data, while meaningful approaches for data handling, interpretation, and exchange sometimes were clearly behind, resulting in misinterpreted studies and frustrated colleagues from time to time.

However, the know-how generated and experiences made especially in the last several years caused a rethinking of strategy design and data interpretation. Moreover, the elaboration of standards by such voluntarily driven groups as Proteomics Standards Initiative within the Human Proteome Organisation or the US institutions, Institute of Systems Biology (ISB), and National Institute of Standards and Technology (NIST), ushered in a new era of understanding and quality, proving how powerful Proteomics is when the technology can be controlled through data generation, handling, and mining.

This book reflects these new insights within the Proteomics community, taking the historical evolution as well as the most important international standardization projects into account so that the reader gets a feeling for the dynamism and openness in this field. Basic and sophisticated overviews are given in regard to proteomics technologies, standard data formats, and databases – both local laboratory databases and public repositories. There are chapters dealing with detailed information concerning data interpretation strategies, including statistics, spectra interpretation, and analysis environments. Other chapters describe the HUPO initiatives or are about more specialized tasks, such as data annotation, peak picking, phosphoproteomics, spectrum libraries, LC/MS imaging, and splice isoforms. This volume also includes in-depth description of tools for data mining and visualization of Proteomics data, leading to modeling and Systems Biology approaches. To look beyond the Proteomics tasks and challenges, some chapters present insights into protein interaction network evolution, text mining, and random matrix approaches.

All in all, we believe that this book is a well-balanced compendium for beginners and experts, offering a broad scope of data mining topics but always focusing on the current state-of-the-art and beyond. Enjoy!

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From Standards to Applications

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