

Preface

Translational bioinformatics is to bridge clinical application and methodology development and translate the analysis and visualization of complex medical datasets to clinical informatics. The volume *Bioinformatics of Human Proteomics* as one of the serial books entitled *Translational Bioinformatics* more focuses on the application of bioinformatics in human sample-based proteomic studies. The present volume aims to introduce new concepts and methodologies of human proteomics-based bioinformatics and present a number of outstanding studies. We hope clinicians and clinical researchers will find the volume helpful in medical practice, the selection of appropriate software to analyze the protein microarray data for medical decision-making, the development of disease-specific biomarkers, and in drug target identification and clinical validation. With increasing numbers of clinical studies on human tissue-based proteomics, translational bioinformatics integrates omics technology, metabolic and signaling pathways, biomarker discovery and development, computational biology, high-throughput image analysis, human tissue bank, mathematical medicine and biology, protein expression and profiling and systems biology together. Bioinformatics of human proteomics is a critical tool to discover and develop protein-based diagnostics and therapies for diseases.

The serial book *Translational Bioinformatics* is an effort to match disease complexity with patient information, clinical data, standard laboratory evaluations, imaging data and omic data obtained from molecular profiling experiments, in order to improve medical care, patient prognosis, and human health. We created the *Journal of Clinical Bioinformatics* (www.jclinbioinformatics.com) to elucidate how biological and medical information can be applied to the development of personalized healthcare, medication, and therapies, and translate bioinformatics and computational methods into clinical and medical applications as well as the advancement of our understanding of the molecular and cellular mechanisms of diseases. To further accelerate the translational process to clinical practice, new journals *Clinical and Translational Medicine* (www.clintransmed.com) and *Translational Respiratory Medicine* (www.transrespmed.com) were expected to foster a predictive, preventive, personalized, and practical approach toward precision medicine, and exchange

ideas between basic and clinical scientists on molecular and cellular mechanisms of disease and potential therapies, leading to improved patient prognosis.

The first part of the volume starts with the chapter “Clinical Bioinformatics in Human Proteomics Research” to describe the concept and importance of bioinformatics in human proteomics combining clinical informatics, bioinformatics, medical informatics, information technology, mathematics, and addresses clinically relevant challenges in early diagnosis, efficient therapies, and predictive prognosis of patients with disease. The chapter “Clinical Bioinformatics in Human Proteomics Research” explains how to analyze protein-protein interactions, understand the regulation of signal pathways, select different approaches discovering the interaction, and characterize protein complexes. The chapter entitled “Protein Function Microarrays: Design, Use and Bioinformatic Analysis in Cancer Biomarker Discovery and Quantization” describes available methodologies relevant to human proteomics and provides a simple approach to the design and fabrication of cancer antigen arrays suitable for cancer biomarker discovery through serological analysis of cancer patients, including raw data extraction, pre-processing, and analysis. The chapter “Proteomics and Cancer Research” discusses disease-specific biomarkers to detect early-stage cancer, predict prognosis, determine therapy efficacy, identify novel drug targets, and ultimately develop personalized medicine. The chapter “Towards Development of Novel Peptide-Based Cancer Therapeutics: Computational Design and Experimental Evaluation” demonstrates peptides as a novel class of drugs for cancer therapy and discusses three novel bioactive peptide analogues designed using the Resonant Recognition Model.

The second part of the volume focuses more on “Advances in Proteomic Methods” to introduce new technologies for sample processing, protein identification, quantification, structure, and function for the further improvement of accuracy, precision, and reproducibility. The chapter “Clinical and Biomedical Mass Spectrometry: New Frontiers in Drug Developments and Diagnosis” states the importance of protein biomarkers in drug discovery and development, high throughput multiplexed biomarker assay in clinical health care and targeted medicine, and new biomarkers in the early identification of disease and disease progression. The chapter “Disease Biomarkers: Modeling MR Spectroscopy and Clinical Applications” introduces the reference technique for evaluating the metabolism of different tissues in vivo, with special application to brain and prostate lesion characterization and tumor follow-up. Such technology with spectroscopic imaging, higher spatial resolution, lower acquisition times, and the automation of the spectra processing analysis can be also applied in many degenerative and oncologic diseases. The chapter “Processing of Mass Spectrometry Data in Clinical Applications” provides specific bioinformatic tools to assist researchers in the management of large-scale proteomic data and identify biomarkers for clinical practice with a specific focus on the identification of proteotypic peptides and the classification of proteomic data. The chapter “Bioinformatics Approach for Finding Target Protein in Infectious Disease” elaborates the systems biology approaches for identification of novel drug targets for various infectious diseases and highlights some in silico experiments and effective systems biology strategies.

The third part of the volume calls special attention from clinicians and researchers on biomarkers, network biomarkers, or dynamic network biomarkers and emphasizes the importance of dynamic interactions between proteins. The chapter “Identification of Network Biomarkers for Cancer Diagnosis” explains the reasons that the complexity and heterogeneity of carcinogenesis should be explored and validated from individual marker discovery to a systems-oriented paradigm. Network-based biomarker discovery can be one of new strategies to monitor the efficacy and efficiency of cancer intervention. The chapter “Software Development for Quantitative Proteomics Using Stable Isotope Labeling” demonstrates a technique to identify and validate protein-based biomarkers by stable isotope labeling coupled with liquid chromatography and high resolution tandem mass spectrometry. UNiquant as a quantification program is introduced to analyze quantitative proteomics data. Another alternative for “Clinical Translation of Protein Biomarkers Integrated with Bioinformatics” can be achieved by maturely quantitative proteomics methods such as stable isotope labeling by amino acids in cell culture, isobaric peptide tags for relative and absolute quantification, and label-free. Targeted quantitative measurements of selected proteins can be applied for the further validation in a large population of patients. The chapter “Proteomic Approaches for Urine Biomarker Discovery in Bladder Cancer” offers a practical example to analyze urinary protein patterns of bladder cancer with the proteomic approach. The chapter “Antibody Microarray and Multiplexing” highlights statistical methods for data normalization and analysis of antibody-based microarray and the implementation of each technique to the technology and suitability on basis of sample types and experiment designs. Last but not least, the chapter “Proteomics in Anesthesia and Intensive Care Medicine” presents a vision of clinical proteomic application from the clinician.

Bioinformatics in human proteomics becomes more and more important in identification and development of disease-specific biomarkers, to diagnose various phases of diseases, monitor severities of diseases and responses to therapies, and predict prognoses and responses of patients to therapy. The application of bioinformatics in clinical proteomics benefits disease-associated specificity, sensitivity, traceability, stability, repeatability, and reliability. Integration of clinical proteomics with bioinformatics can bridge identification and validation of gene or protein-based biomarkers, network biomarkers, dynamic network biomarkers with human diseases, patient phenotypes, and clinical applications. The book intends to accelerate the discovery and development of human disease-specific biomarkers for the early diagnosis, monitoring, and evaluation of diseases and predictions of responses to therapy.

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<http://www.springer.com/978-94-007-5811-7>

Bioinformatics of Human Proteomics

Wang, X. (Ed.)

2013, XIV, 394 p.,

ISBN: 978-94-007-5811-7