Preface

This book discusses the latest developments in clinical omics research and describes in detail a subset of the algorithms used in publicly available software tools. The book should be considered as an omics-bioinformatics resource. However, it is not just a pure bioinformatics resource filled with complex equations; it describes to some extent the biological background and also discusses experimental methods. The advantages and drawbacks of the various experimental methods in relation to data analysis will be reviewed as well. In other words, the intention is to establish a bridge between theory and practice. Practical examples showing methods, results, and conclusions from data mining strategies will be given in some cases. It is not possible to cover all areas of omics techniques and bioinformatics algorithms in one book. However, an important subset is described and discussed from both the experimental and the bioinformatics views. The book starts out by discussing various successful examples in which omics techniques have been used in a clinically related study. An important buzz word in omics is biomarkers. The word “biomarker” has different meanings depending on the context in which it is used. Here, it is used in a clinical context and should be interpreted as “a substance whose specific level indicates a particular cellular or clinical state.” In theory, one could easily imagine cases where one biomarker is found at different levels, at different intervals that indicate various states. An even more complex example would be a set of biomarkers and their corresponding set of concentration levels, which could be used for classifying a specific cellular or clinical state. In complex cases, more elaborate models based on machine learning and statistics are essential for identifying interrelationships between biomarkers.

The introduction chapter is therefore followed by an introductory overview of machine learning, which can be and has been extensively applied to many omics data analysis problems. The subsequent chapter discusses statistics, algorithms, and experimental consideration in genomics, transcriptomics, proteomics, and metabolomics. One of the challenges for bioinformatics in the future is to incorporate and integrate information from all omics subareas to obtain a unified view of the biological samples. This is exactly the aim of systems biology. Systems biology is a broad field involving data storage, controlled vocabulary, data mining, interaction studies, data correlation, and modeling of biochemical pathways. The data input comes from various “omics” fields such as genomics, transcriptomics, proteomics, interactomics, and metabolomics. Metabolomics can be further divided into subcategories such as peptidomics, glycomics, and lipidomics. The term “systems biology” has raised some discussion since more conservative scientists prefer a strict usage where prediction and mathematical modeling should, at a minimum, be part of a systems biology study.

The last chapters mainly concentrate on automatic ways to retrieve information for a biological study. Chapter 15 describes automated ways to correlate experimental findings with annotated features in publicly available databases. It describes how automated methods can help in experimental design and in setting the final results from omics studies into a larger context. Chapter 16 focuses on text mining to retrieve more extended information about the system under study.
It is true that many omics techniques are currently not cost-effective enough to be clinical applicable, but that is very likely going to change in the near future, which means that integrated bioinformatics solutions will be highly valuable.

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