
Preface

This book discusses the multiple facets of “Bioinformatics for Omics Data,” an area of research that intersects with and integrates diverse disciplines, including molecular biology, applied informatics, and statistics, among others. Bioinformatics has become a default technology for data-driven research in the Omics realm and a necessary skill set for the Omics practitioner. Progress in miniaturization, coupled with advancements in readout technologies, has enabled a multitude of cellular components and states to be assessed simultaneously, providing an unparalleled ability to characterize a given biological phenotype. However, without appropriate processing and analysis, Omics data add nothing to our understanding of the phenotype under study. Even managing the enormous amounts of raw data that these methods generate has become something of an art.

Viewed from one perspective, bioinformatics might be perceived as a purely technical discipline. However, as a research discipline, bioinformatics might more accurately be viewed as “[molecular] biology involving computation.” Omics has triggered a paradigm shift in experimental study design, expanding beyond hypothesis-driven approaches to research that is basically explorative. At present, Omics is in the process of consolidating various intermediate forms between these two extremes. In this context, bioinformatics for Omics data serves both hypothesis generation and validation and is thus much more than mere data management and processing. Bioinformatics workflows with data interpretation strategies that reflect the complexity of biological organization have been designed. These approaches interrogate abundance profiles with regulatory elements, all expressed as interaction networks, thus allowing a one-step (descriptive) embodiment of wide-ranging cellular processes. Here, the seamless transition to computational Systems Biology becomes apparent, the ultimate goal of which is representing the dynamics of a phenotype in quantitative models capable of predicting the emergence of higher order molecular procedures and functions that arise from the interplay of basic molecular entities that constitute a living cell.

Bioinformatics for Omics data is certainly embedded in a highly complex technological and scientific environment, but it is also a component and driver of one of the most exciting developments in modern molecular biology. Thus, while this book seeks to provide practical guidelines, it hopefully also conveys a sense of fascination associated with this research field.

This volume is structured in three parts. Part I provides central analysis strategies, standardization, and data management guidelines, as well as fundamental statistics for analyzing Omics profiles. Part II addresses bioinformatics approaches for specific Omics tracks, spanning genome, transcriptome, proteome, and metabolome levels. For each track, the conceptual and experimental background is provided, together with specific guidelines for handling raw data, including preprocessing and analysis. Part III presents examples of integrated Omics bioinformatics applications, complemented by case studies on biomarker and target identification in the context of human disease.

I wish to express my gratitude to all authors for their dedication in providing excellent chapters, and to John Walker, who initiated this project. As for any omissions or errors, the responsibility is mine. In any case, enjoy reading.

Vienna, Austria

Bernd Mayer



<http://www.springer.com/978-1-61779-026-3>

Bioinformatics for Omics Data

Methods and Protocols

Mayer, B. (Ed.)

2011, XII, 584 p., Hardcover

ISBN: 978-1-61779-026-3

A product of Humana Press