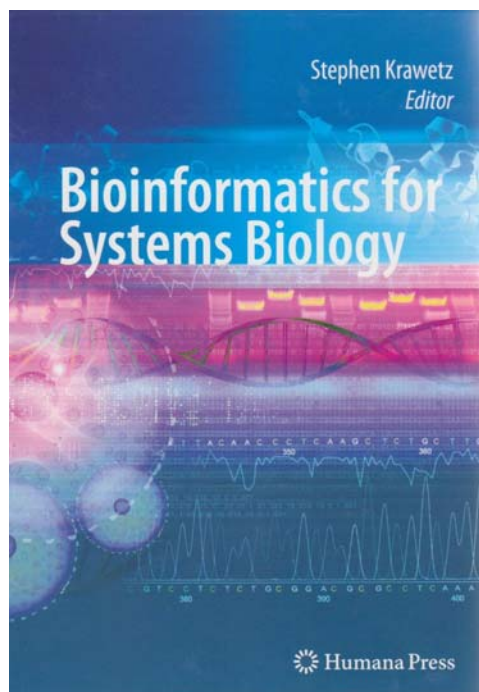


STEPHEN KRAWETZ (EDITOR) BIOINFORMATICS FOR SYSTEMS BIOLOGY



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The biological sciences are now in the midst of a true life sciences revolution akin to what physics experienced just after the turn of the last century. We are now in a phase of unparalleled growth that is reflected by the amount of data generated from each experiment. At the time of this writing, the rate of data acquisition was approaching 2 terabytes over the course of 5 days with first pass analysis proceeding over the following 2-3 week period. This fundamental shift has provided unprecedented opportunities that for the first time afford us the ability, i.e., means, breadth, and depth of data, to truly address human biology at the systems level. This wealth of information from seemingly disparate datasets and its integration is being realized through bioinformatics. It is with this philosophy that the text *Bioinformatics for Systems Biology* was born. This revolution has spawned true personalized medicine that encompasses diagnostics and treatment through to cure.

For the physical and computer scientist, this text provides an introduction to the basic biological principles governing a cell. This quickly moves from the fundamentals to exploring the underlying genetic processes. While providing a rudimentary and necessary overview for the life scientist, the physical and computer scientist will be apprised of various nuances within the field reflecting the reality of “wet-bench” science. For those in the life sciences, it is rapidly becoming appreciated that we are progressing from examining our favorite “pet” gene to the system. Statistics is now an essential component to understand the vast datasets and this is emphasized throughout the text.

The majority of the text is devoted to the common ground that these groups share. It provides rich examples of tools, databases, and strategies to mine the databases to reveal novel insights. A host of examples of parsing the data into a series of overlays that use various presentation systems are reviewed. The goal is to provide a representation most comfortable to the user to enable the user to thoroughly explore the data. The text concludes with examples of how the systems information is used to inform personalized medicine in a true “bench to bedside” manner.

Bioinformatics for Systems Biology bridges and unifies many disciplines. It presents the life scientist, computational biologist, and mathematician with a common framework. Only by linking the groups together may the true life sciences revolution move forward in mostly uncharted and emerging field of Systems Biology.



Table of Contents

Part I	Life of a Cell and Its Analysis	1		
Part II	Statistical Tools and Their Application	137	Part V	Literature Mining for Association and Meaning 367
Part III	Transcriptome Analysis	207	Part VI	Genomic Databases 435
Part IV	Structural and Functional Sequence Analysis	281	Part VII	Biological Networks 515
			Part VIII	Bridging the Gap 579