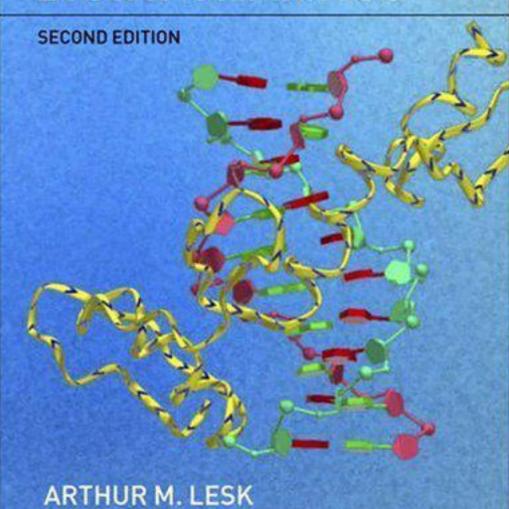
OXFORD

# BIOINFORMATICS



# Introduction to Bioinformatics

SECOND EDITION

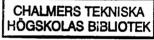
Arthur M. Lesk

The Pennsylvania State University

In nature's infinite book of secrecy A little I can read.

- Antony and Cleopatra





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## Plan of the book

- Chapter 1 sets the stage and introduces all of the major players: DNA and protein sequences and structures, genomes and proteomes, databases and information retrieval, the World Wide Web, computer programming. Before developing individual topics in detail it is important to see the framework of their interactions.
- Chapter 2 presents the nature of individual genomes, including the Human Genome, and the relationships among them, from the biological point of view.
- Chapter 3 imparts basic skills in using the Web in bioinformatics. It
  describes archival databanks, and leads the reader through sample sessions
  involving information retrieval from some of the major archival databases
  in molecular biology.
- Chapter 4 treats the analysis of relationships among sequences—alignments and phylogenetic trees. These methods underlie some of the major computational challenges of bioinformatics: detecting distant relatives, understanding relationships among genomes of different organisms, and tracing the course of evolution at the species and molecular levels.
- Chapter 5 moves into three dimensions, treating protein structure and folding. Sequence and structure must be seen as full partners, with bioinformatics developing methods for moving back and forth between them as fluently as possible. Understanding protein structures in detail is essential for determining their mechanisms of action, and for clinical and pharmacological applications.
- Chapter 6 treats proteomics and systems biology, including new highthroughput sources of information about the expression and distribution of proteins in cells, and attempts to synthesize the information to reveal patterns of organization.