

Suhai, S. (ed.): **Theoretical and Computational Methods in Genome Research.** - Plenum Press, New York - London 1997. 330 pp. Hard cover, US \$ 95.00. ISBN 0-306-45503-X.

Any large-scale genome project necessarily involves construction of genetic and physical maps finally completed to the form of whole-genome sequence in the first generation, followed by functional genome analysis in the second generation of the project. Selected hot research problems related to these developmental steps are reflected in this reviewed book, which combines 23 chapters (written altogether by 55 authors). Each chapter represents a plenary lecture held at the International Symposium on Theoretical and Computational Genome Research on March 24 - 27, 1996 at the Deutsches Krebsforschungszentrum (DKFZ) in Heidelberg.

First chapter discusses various statistical and algorithmic issues for estimation of the local similarity significance of multiple sequence regions not independently, as usual methods do, but in combination. Reported new statistical tests enable beforehand filtering of low complexity sequence regions evolving probably by gene slippage. Second chapter analyses the sequential structure of human genomic DNA by hidden Markov models (HMM). With HMM it was possible to rapidly recognise patterns of exons and splice sites. Chapter 3 is about the partial progress in the development of algorithm for identification of transcriptional regulatory region (TRR) able to drive skeletal-muscle specific expression. Chapter 4 is related to the analysis of gene functions performed by computerising the knowledge body of metabolic pathways using DBGET integrated database retrieval system, Kyoto encyclopedia of genes and genomes (KEGG) and deductive database for metabolic pathways. Chapter 5 reports about application of Monte-Carlo and Brownian models to describe structure and dynamics of DNA and chromatin. Chapter 6 answers the question about feasibility of sequencing of the whole human genome based on computer simulation studies. Chapter 7 and 8 deals with sequence pattern diagnostics and recognition of functional domains. Chapters 9, 10 and 12 address current problems related to enhancing productivity and accuracy of gene mapping and to advances in analysis of linkage data. Current innovations of electronic data storage in genomic databases, data management, development of comprehensive genome information systems, and application of visually oriented technologies are covered by chapters 11, 13, 14, and 15. Chapter 16 reports about computer data management for ligand-based drug design. Chapters 17 - 23 are related to protein level where following topics are discussed: picturing the working protein, computer-modelling of the structure of HIV 1 protease, neural network analysis for correlation of hydration effects, structure and spectroscopy of small peptides, computer-simulation of protein-DNA interaction, application of iterative double dynamic programming for protein sequence and structure comparisons. The one exception is the chapter 21 reviewing computerised evolutionary aspects of RNA molecules *in vitro*.

All papers are well written even if, necessarily, in various styles and illustrated with many explanatory diagrams and reprints of computer screens. Each chapter is appended with recent bibliographical references and includes surface and electronic addresses (personal links as well as links to [mostly WWW-based] databases and related documents accessible via Internet as is usual for computer literature). The part of 23 chapters is complemented with an index of subjects. Undoubtedly, this book, even if necessarily fragmental in covered topics, reflects current rapid advances in theoretical genomics achieved recently and offers new stimulating ideas both to advanced students and to researchers in biocomputing and molecular biology of the whole genomes.

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