Satoru Miyano   Jill Mesirov
Simon Kasif   Sorin Istrail
Pavel Pevzner   Michael Waterman   (Eds.)

Research in Computational Molecular Biology

9th Annual International Conference, RECOMB 2005
Cambridge, MA, USA, May 2005
Proceedings

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Research in Computational Molecular Biology Satoru Miyano,Jill Mesirov,Simon Kasif,Sorin Istrail,Pavel Pevzner,Michael Waterman,2005-04-28 This volume contains the papers presented at the 9th Annual International Conference on Research in Computational Molecular Biology RECOMB 2005 which was held in Cambridge Massachusetts on May 14 18 2005 The RECOMB conference series was started in 1997 by Sorin Istrail Pavel Pevzner and Michael Waterman The list of previous meetings is shown below in the s tion Previous RECOMB Meetings RECOMB 2005 was hosted by the Broad Institute of MIT and Harvard and Boston University s Center for Advanced nomic Technology and was excellently organized by the Organizing Committee Co chairs Jill Mesirov and Simon Kasif This year 217 papers were submitted of which the Program Committee lected 39 for presentation at the meeting and inclusion in this proceedings Each submission was refereed by at least three members of the Program Committee After the completion of the referees reports an extensive Web based discussion took place for making decisions From RECOMB 2005 the Steering Committee decided to publish the proceedings as a volume of Lecture Notes in Bioinf matics LNBI for which the founders of RECOMB are also the editors The prominent volume number LNBI 3500 was assigned to this proceedings The RECOMB conference series is closely associated with the Journal of Compu tional Biology which traditionally publishes special issues devoted to presenting full versions of selected conference papers The RECOMB Program Committee consistedof42members aslistedonaseparatepage Iwouldliketothank the RECOMB 2005 Program Committee members for their dedication and hard work   **Computational Systems Bioinformatics** Peter Markstein,Ying Xu,2006 This volume contains about 40 papers covering many of the latest developments in the fast growing field of bioinformatics The contributions span a wide range of topics including computational genomics and genetics protein function and computational proteomics the transcriptome structural bioinformatics microarray data analysis motif identification biological pathways and systems and biomedical applications There are also abstracts from the keynote addresses and invited talks The papers cover not only theoretical aspects of bioinformatics but also delve into the application of new methods with input from computation engineering and biology disciplines This multidisciplinary approach to bioinformatics gives these proceedings a unique viewpoint of the field Sample Chapter s Chapter 1 Exploring the Ocean s Microbes Sequencing the Seven Seas 122 KB Contents Exploring the Ocean s Microbes Sequencing the Seven Seas M E Frazier et al Protein Network Comparative Genomics T Ideker Bioinformatics at Microsoft Research S Mercer Protein Fold Recognition Using Gradient Boost Algorithm F Jiao et al Efficient Annotation of Non Coding RNA Structures Including Pseudoknots via Automated Filters C Liu et al Efficient Generalized Matrix Approximations for Biomarker Discovery and Visualization in Gene Expression Data W Li et al Sorting Genomes by Translocations and Deletions X Qi et al Detection of Cleavage Sites for HIV 1 Protease in Native Proteins L You Identifying Biological Pathways via Phase Decomposition and Profile Extraction Y Zhang Complexity and Scoring Function of MS MS

Peptide De Novo Sequencing C Xu Simulating In Vitro Epithelial Morphogenesis in Multiple Environments M R Grant et al and other papers Readership Research and application community in bioinformatics systems biology medicine pharmacology and biotechnology A useful reference for graduate researchers in bioinformatics and computational biology

Mathematical Foundations of Computer Science 2005 Joanna Jedrzejowicz,2005-08-17 This book constitutes the refereed proceedings of the 30th International Symposium on Mathematical Foundations of Computer Science MFCS 2005 held in Gdansk Poland in August September 2005 The 62 revised full papers presented together with full papers or abstracts of 7 invited talks were carefully reviewed and selected from 137 submissions All current aspects in theoretical computer science are addressed ranging from quantum computing approximation automata circuits scheduling games languages discrete mathematics combinatorial optimization graph theory networking algorithms and complexity to programming theory formal methods and mathematical logic   Pattern Recognition in Computational Molecular Biology Mourad Elloumi,Costas Iliopoulos,Jason T. L. Wang,Albert Y. Zomaya,2015-12-24 A comprehensive overview of high performance pattern recognition techniques and approaches to Computational Molecular Biology This book surveys the developments of techniques and approaches on pattern recognition related to Computational Molecular Biology Providing a broad coverage of the field the authors cover fundamental and technical information on these techniques and approaches as well as discussing their related problems The text consists of twenty nine chapters organized into seven parts Pattern Recognition in Sequences Pattern Recognition in Secondary Structures Pattern Recognition in Tertiary Structures Pattern Recognition in Quaternary Structures Pattern Recognition in Microarrays Pattern Recognition in Phylogenetic Trees and Pattern Recognition in Biological Networks Surveys the development of techniques and approaches on pattern recognition in biomolecular data Discusses pattern recognition in primary secondary tertiary and quaternary structures as well as microarrays phylogenetic trees and biological networks Includes case studies and examples to further illustrate the concepts discussed in the book Pattern Recognition in Computational Molecular Biology Techniques and Approaches is a reference for practitioners and professional researches in Computer Science Life Science and Mathematics This book also serves as a supplementary reading for graduate students and young researches interested in Computational Molecular Biology   *Parallel Computing for Bioinformatics and Computational Biology* Albert Y. Zomaya,2006-05-24 Discover how to streamline complex bioinformatics applications with parallel computing This publication enables readers to handle more complex bioinformatics applications and larger and richer data sets As the editor clearly shows using powerful parallel computing tools can lead to significant breakthroughs in deciphering genomes understanding genetic disease designing customized drug therapies and understanding evolution A broad range of bioinformatics applications is covered with demonstrations on how each one can be parallelized to improve performance and gain faster rates of computation Current parallel computing techniques and technologies are examined including distributed computing and grid computing Readers are provided with a mixture of

algorithms experiments and simulations that provide not only qualitative but also quantitative insights into the dynamic field of bioinformatics Parallel Computing for Bioinformatics and Computational Biology is a contributed work that serves as a repository of case studies collectively demonstrating how parallel computing streamlines difficult problems in bioinformatics and produces better results Each of the chapters is authored by an established expert in the field and carefully edited to ensure a consistent approach and high standard throughout the publication The work is organized into five parts Algorithms and models Sequence analysis and microarrays Phylogenetics Protein folding Platforms and enabling technologies Researchers educators and students in the field of bioinformatics will discover how high performance computing can enable them to handle more complex data sets gain deeper insights and make new discoveries **Research in Computational Molecular Biology** S. Cenk Sahinalp,2017-04-13 This book constitutes the proceedings of the 21th Annual Conference on Research in Computational Molecular Biology RECOMB 2017 held in Hong Kong China in May 2017 The 22 regular papers presented in this volume were carefully reviewed and selected from 184 submissions 16 short abstracts are included in the back matter of the volume They report on original research in all areas of computational molecular biology and bioinformatics **Algorithms and Computation** Xiaotie Deng,Dingzhu Du,2005-12-03 This book constitutes the refereed proceedings of the 16th International Symposium on Algorithms and Computation ISAAC 2005 held in Sanya Hainan China in December 2005 The 112 revised full papers presented were carefully reviewed and selected from 549 submissions The papers are organized in topical sections on computational geometry computational optimization graph drawing and graph algorithms computational complexity approximation algorithms internet algorithms quantum computing and cryptography data structure computational biology experimental algorithm mehodologies and online algorithms randomized algorithms parallel and distributed algorithms graph drawing and graph algorithms computational complexity combinatorial optimization computational biology computational complexity computational optimization computational geometry approximation algorithms graph drawing and graph algorithms computational geometry approximation algorithms graph drawing and graph algorithms and data structure Current Topics in Human Genetics Hong-wen Deng,2007 Analogies play a fundamental role in science To understand how and why at a given moment a certain analogy was used one has to know the specific historical circumstances under which the new idea was developed This historical background is never presented in scientific articles and quite rarely in books For the general reader the undergraduate or graduate student who learns the subject for the first time but also for the practitioner who looks for inspiration or who wants to understand what his colleague working in another field does these historical circumstances can be fascinating and useful This book discusses a series of analogy effects in subatomic physics the prediction and theory of which the author has contributed to in the last 50 years These phenomena are presented at a level accessible to the non specialist without formulae but with emphasis on the personal and historical background memoirs of meetings discussions and correspondence with collaborators and colleagues

As such besides its scientific aspects the book constitutes an absorbing witness account of a holocaust survivor who subsequently illegally crossed the Iron Curtain to escape communist persecution **Ad-Hoc, Mobile, and Wireless Networks** Evangelos Kranakis,Jaroslav Opatrny,2007-09-05 This book constitutes the refereed proceedings of the 6th International Conference on Ad Hoc Networks and Wireless ADHOC NOW 2007 held in Morelia Mexico in September 2007 The 21 revised full papers were carefully reviewed and selected from 50 submissions The papers are organized in topical sections on routing topology control security and privacy protocols as well as quality of service and performance **Data Classification** Charu C. Aggarwal,2014-07-25 Comprehensive Coverage of the Entire Area of ClassificationResearch on the problem of classification tends to be fragmented across such areas as pattern recognition database data mining and machine learning Addressing the work of these different communities in a unified way Data Classification Algorithms and Applications explores the underlyi **Research in Computational Molecular Biology** Alberto Apostolico,Concettina Guerra,Sorin Istrail,Pavel Pevzner,Michael Waterman,2006-08-12 This volume contains the papers presented at the 10th Annual International Conference on Research in Computational Molecular Biology RECOMB 2006 which was held in Venice Italy on April 2 5 2006 **Reconstructing Evolution** Olivier Gascuel,Mike Steel,2007-06-28 Evolution is a complex process acting at multiple scales from DNA sequences and proteins to populations of species Understanding and reconstructing evolution is of major importance in numerous subfields of biology For example phylogenetics and sequence evolution is central to comparative genomics attempts to decipher genomes and molecular epidemiology Phylogenetics is also the focal point of large scale international biodiversity assessment initiatives such as the Tree ofLife project which aims to build the evolutionary tree for all extant species Since the pioneering work in phylogenetics in the 1960s models have become increasingly sophisticated to account for the inherent complexity of evolution They rely heavily on mathematics and aim at modelling and analyzing biological phenomena such as horizontal gene transfer heterogeneity of mutation and speciation and extinction processes This book presents these recent models their biological relevance their mathematical basis their properties and the algorithms to infer them fromdata A number of subfields from mathematics and computer science are involved combinatorics graph theory stringology probabilistic and Markov models information theory statistical inference Monte Carlo methods continuous and discrete algorithmics This book arises from the Mathematics of Evolution Phylogenetics meeting at the Mathematical Institute Henri Poincar Paris in June 2005 and is based on the outstanding state of the art reports presented by the conference speakers Ten chapters based around five themes provide a detailed overview of key topics from the underlying concepts to the latest results some of which are at the forefront of current research

Optimization for Machine Learning Suvrit Sra,Sebastian Nowozin,Stephen J. Wright,2012 An up to date account of the interplay between optimization and machine learning accessible to students and researchers in both communities The interplay between optimization and machine learning is one of the most important developments in modern computational

science Optimization formulations and methods are proving to be vital in designing algorithms to extract essential knowledge from huge volumes of data Machine learning however is not simply a consumer of optimization technology but a rapidly evolving field that is itself generating new optimization ideas This book captures the state of the art of the interaction between optimization and machine learning in a way that is accessible to researchers in both fields Optimization approaches have enjoyed prominence in machine learning because of their wide applicability and attractive theoretical properties The increasing complexity size and variety of today s machine learning models call for the reassessment of existing assumptions This book starts the process of reassessment It describes the resurgence in novel contexts of established frameworks such as first order methods stochastic approximations convex relaxations interior point methods and proximal methods It also devotes attention to newer themes such as regularized optimization robust optimization gradient and subgradient methods splitting techniques and second order methods Many of these techniques draw inspiration from other fields including operations research theoretical computer science and subfields of optimization The book will enrich the ongoing cross fertilization between the machine learning community and these other fields and within the broader optimization community

Research in Computational Molecular Biology ,2005 **Handbook of Computational Molecular Biology** Srinivas Aluru,2005-12-21 The enormous complexity of biological systems at the molecular level must be answered with powerful computational methods Computational biology is a young field but has seen rapid growth and advancement over the past few decades Surveying the progress made in this multidisciplinary field the Handbook of Computational Molecular Biology of *Bioinformatics Algorithms* Ion Mandoiu,Alexander Zelikovsky,2008-03-11 Presents algorithmic techniques for solving problems in bioinformatics including applications that shed new light on molecular biology This book introduces algorithmic techniques in bioinformatics emphasizing their application to solving novel problems in post genomic molecular biology Beginning with a thought provoking discussion on the role of algorithms in twenty first century bioinformatics education Bioinformatics Algorithms covers General algorithmic techniques including dynamic programming graph theoretical methods hidden Markov models the fast Fourier transform seeding and approximation algorithms Algorithms and tools for genome and sequence analysis including formal and approximate models for gene clusters advanced algorithms for non overlapping local alignments and genome tilings multiplex PCR primer set selection and sequence network motif finding Microarray design and analysis including algorithms for microarray physical design missing value imputation and meta analysis of gene expression data Algorithmic issues arising in the analysis of genetic variation across human population including computational inference of haplotypes from genotype data and disease association search in case control epidemiologic studies Algorithmic approaches in structural and systems biology including topological and structural classification in biochemistry and prediction of protein protein and domain domain interactions Each chapter begins with a self contained introduction to a computational problem continues with a brief review of the existing literature on the subject

and an in depth description of recent algorithmic and methodological developments and concludes with a brief experimental study and a discussion of open research challenges This clear and approachable presentation makes the book appropriate for researchers practitioners and graduate students alike **Research in Computational Molecular Biology** Bonnie Berger,2010-05-09 This volume contains the papers presented at RECOMB 2010 the 14th Annual International Conference on Research in Computational Molecular Biology held in Lisbon Portugal during April 25 28 2010 The RECOMB conference series was started in 1997 by Sorin Istrail Pavel Pevzner and Michael Waterman RECOMB 2010 was hosted by INESC ID and Instituto Superior Tecnico or nized by a committee chaired by Arlindo Oliveira and took place at the Int national Fair of Lisbon Meeting Centre This year 36 papers were accepted for presentation out of 176 submissions The papers presented were selected by the Program Committee PC assisted by a number of external reviewers Each paper was reviewed by three members of the PC or by external reviewers and there was an extensive Web based discussion over a period of two weeks leading to the nal decisions RECOMB 2010 also introduced a Highlights Track in which six additional presentations by senior authors were chosen from papers published in 2009 The RECOMB conferenceseriesiscloselyassociatedwiththeJournalofComputational Biology which traditionally publishes special issues devoted to presenting full versions of selected conference papers **Bioinformatics Research and Applications** Zhipeng Cai,Oliver Eulenstein,Daniel Janies,Daniel Schwartz,2013-05-13 This book constitutes the refereed proceedings of the 9th International Symposium on Bioinformatics Research and Applications ISBRA 2013 held in Charlotte NC USA in May 2013 The 25 revised full papers presented together with 4 invited talks were carefully reviewed and selected from 46 submissions The papers cover a wide range of biomedical databases and data integration high performance bio computing biomolecular imaging high throughput sequencing data analysis bio ontologies molecular evolution comparative genomics and phylogenomics molecular modeling and simulation pattern discovery and classification computational proteomics population genetics data mining and visualization software tools and applications **Comparative Genomics** Aoife McLysaght,Daniel H. Huson,2005-12-17 This volume contains the papers presented at the 3rd RECOMB Comparative Genomics meeting which was held in Dublin Ireland on September 18 20 2005 **Computational Science - ICCS 2006** Vassil N. Alexandrov,G. Dick van Albada,Peter M.A. Sloot,J. J. Dongarra,2006-05-12 This is Volume II of the four volume set LNCS 3991 3994 constituting the refereed proceedings of the 6th International Conference on Computational Science ICCS 2006 The 98 revised full papers and 29 revised poster papers of the main track presented together with 500 accepted workshop papers were carefully reviewed and selected for inclusion in the four volumes The coverage spans the whole range of computational science

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