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Graphs And Genes

James J. Park,Albert Y. Zomaya,Sang-Soo Yeo,Sartaj Sahni

Graphs And Genes:

   Graphs and Genes B.G. Mirkin,S.N. Rodin,2011-11-08 This book is written by a mathematician and a theoretical biologist who have arrived at a good mutual understanding and a well worked out common notation The reader need hardly be convinced of the necessity of such a mutual understanding not only for the two investigators but also for the sciences they represent Like Moliere s hero geneticists are gradually beginning to understand that unknowingly they have been speaking in the language of cybernetics Mathematicians are unexpec tedly discovering that many past and present problems and methods of genetics can be naturally formulated in the language of graph theory In this way a powerful abstract mathematical theory suddenly finds a productive application Moreover in its turn such an application be gins to feed the mathematical theory by presenting it with a number of new problems The reader may judge for himself the fruitfulness of such mutual interaction At the same time several important circumstances need to be men tioned The formalization and rigorous formulation given here embraces not only the older problems known by geneticists for many decades the construction of genetic maps the analysis of complementation etc but also comparatively new problems the construction of partial com plementation maps phylogenetic trees of proteins etc   Graphs and Genes B.G. Mirkin,S.N. Rodin,1984 This book is written by a mathematician and a theoretical biologist who have arrived at a good mutual understanding and a well worked out common notation The reader need hardly be convinced of the necessity of such a mutual understanding not only for the two investigators but also for the sciences they represent Like Moliere s hero geneticists are gradually beginning to understand that unknowingly they have been speaking in the language of cybernetics Mathematicians are unexpec tedly discovering that many past and present problems and methods of genetics can be naturally formulated in the language of graph theory In this way a powerful abstract mathematical theory suddenly finds a productive application Moreover in its turn such an application be gins to feed the mathematical theory by presenting it with a number of new problems The reader may judge for himself the fruitfulness of such mutual interaction At the same time several important circumstances need to be men tioned The formalization and rigorous formulation given here embraces not only the older problems known by geneticists for many decades the construction of genetic maps the analysis of complementation etc but also comparatively new problems the construction of partial com plementation maps phylogenetic trees of proteins etc   *Graphs and Genes* Boris Grigor'evich Mirkin,Sergeĭ Nikolaevich Rodin,1984   Graphs and Genes B.G. Mirkin,Boris Grigor'evich Mirkin,S.N. Rodin,1984 This book is written by a mathematician and a theoretical biologist who have arrived at a good mutual understanding and a well worked out common notation The reader need hardly be convinced of the necessity of such a mutual understanding not only for the two investigators but also for the sciences they represent Like Moliere s hero geneticists are gradually beginning to understand that unknowingly they have been speaking in the language of cybernetics Mathematicians are unexpec tedly discovering that many past and present problems and methods of genetics can be

naturally formulated in the language of graph theory In this way a powerful abstract mathematical theory suddenly finds a productive application Moreover in its turn such an application be gins to feed the mathematical theory by presenting it with a number of new problems The reader may judge for himself the fruitfulness of such mutual interaction At the same time several important circumstances need to be men tioned The formalization and rigorous formulation given here embraces not only the older problems known by geneticists for many decades the construction of genetic maps the analysis of complementation etc but also comparatively new problems the construction of partial com plementation maps phylogenetic trees of proteins etc **Genetic Theory for Cubic Graphs** Pouya Baniasadi,Vladimir Ejov,Jerzy A. Filar,Michael Haythorpe,2015-07-15 This book was motivated by the notion that some of the underlying difficulty in challenging instances of graph based problems e g the Traveling Salesman Problem may be inherited from simpler graphs which in an appropriate sense could be seen as ancestors of the given graph instance The authors propose a partitioning of the set of unlabeled connected cubic graphs into two disjoint subsets named genes and descendants where the cardinality of the descendants dominates that of the genes The key distinction between the two subsets is the presence of special edge cut sets called cubic crackers in the descendants The book begins by proving that any given descendant may be constructed by starting from a finite set of genes and introducing the required cubic crackers through the use of six special operations called breeding operations It shows that each breeding operation is invertible and these inverse operations are examined It is therefore possible for any given descendant to identify a family of genes that could be used to generate the descendant The authors refer to such a family of genes as a complete family of ancestor genes for that particular descendant The book proves the fundamental although quite unexpected result that any given descendant has exactly one complete family of ancestor genes This result indicates that the particular combination of breeding operations used strikes the right balance between ensuring that every descendant may be constructed while permitting only one generating set The result that any descendant can be constructed from a unique set of ancestor genes indicates that most of the structure in the descendant has been in some way inherited from that very special complete family of ancestor genes with the remaining structure induced by the breeding operations After establishing this the authors proceed to investigate a number of graph theoretic properties Hamiltonicity bipartiteness and planarity and prove results linking properties of the descendant to those of the ancestor genes They develop necessary and in some cases sufficient conditions for a descendant to contain a property in terms of the properties of its ancestor genes These results motivate the development of parallelizable heuristics that first decompose a graph into ancestor genes and then consider the genes individually In particular they provide such a heuristic for the Hamiltonian cycle problem Additionally a framework for constructing graphs with desired properties is developed which shows how many known graphs that constitute counterexamples of conjectures could be easily found <u>Handbook of Research on Computational Methodologies in Gene Regulatory Networks</u> Das, Sanjoy,Caragea, Doina,Welch, Stephen,Hsu, William

H.,2009-10-31 This book focuses on methods widely used in modeling gene networks including structure discovery learning and optimization Provided by publisher **Mathematics of Bioinformatics** Matthew He,Sergey Petoukhov,2011-03-16 Mathematics of Bioinformatics Theory Methods and Applications provides a comprehensive format for connecting and integrating information derived from mathematical methods and applying it to the understanding of biological sequences structures and networks Each chapter is divided into a number of sections based on the bioinformatics topics and related mathematical theory and methods Each topic of the section is comprised of the following three parts an introduction to the biological problems in bioinformatics a presentation of relevant topics of mathematical theory and methods to the bioinformatics problems introduced in the first part an integrative overview that draws the connections and interfaces between bioinformatics problems issues and mathematical theory methods applications **Integer Linear Programming in Computational and Systems Biology** Dan Gusfield,2019-06-13 Integer linear programming ILP is a versatile modeling and optimization technique that is increasingly used in non traditional ways in biology with the potential to transform biological computation However few biologists know about it This how to and why do text introduces ILP through the lens of computational and systems biology It uses in depth examples from genomics phylogenetics RNA protein folding network analysis cancer ecology co evolution DNA sequencing sequence analysis pedigree and sibling inference haplotyping and more to establish the power of ILP This book aims to teach the logic of modeling and solving problems with ILP and to teach the practical work flow involved in using ILP in biology Written for a wide audience with no biological or computational prerequisites this book is appropriate for entry level and advanced courses aimed at biological and computational students and as a source for specialists Numerous exercises and accompanying software in Python and Perl demonstrate the concepts Graph-Based Representations in Pattern Recognition Donatello Conte,Jean-Yves Ramel,Pasquale Foggia,2019-06-10 This book constitutes the refereed proceedings of the 12th IAPR TC 15 International Workshop on Graph Based Representation in Pattern Recognition GbRPR 2019 held in Tours France in June 2019 The 22 full papers included in this volume together with an invited talk were carefully reviewed and selected from 28 submissions The papers discuss research results and applications at the intersection of pattern recognition image analysis and graph theory They cover topics such as graph edit distance graph matching machine learning for graph problems network and graph embedding spectral graph problems and parallel algorithms for graph problems Bioinformatics and Computational Biology Sanguthevar Rajasekaran,2009-03-27 This book constitutes the refereed proceedings of the First International on Bioinformatics and Computational Biology BICoB 2007 held in New Orleans LA USA in April 2007 The 30 revised full papers presented together with 10 invited lectures were carefully reviewed and selected from 72 initial submissions The papers address current research in the area of bioinformatics and computational biology fostering the advancement of computing techniques and their application to life sciences in topics such as genome analysis sequence analysis phylogenetics structural bioinformatics analysis of high throughput biological

data genetics and population analysis as well as systems biology **Multivariate Network Visualization** Andreas Kerren,Helen Purchase,Matthew O. Ward,2014-04-15 This book is the outcome of the Dagstuhl Seminar 13201 on Information Visualization Towards Multivariate Network Visualization held in Dagstuhl Castle Germany in May 2013 The goal of this Dagstuhl Seminar was to bring together theoreticians and practitioners from Information Visualization HCI and Graph Drawing with a special focus on multivariate network visualization i e on graphs where the nodes and or edges have additional multidimensional attributes The integration of multivariate data into complex networks and their visual analysis is one of the big challenges not only in visualization but also in many application areas Thus in order to support discussions related to the visualization of real world data also invited researchers from selected application areas especially bioinformatics social sciences and software engineering The unique Dagstuhl climate ensured an open and undisturbed atmosphere to discuss the state of the art new directions and open challenges of multivariate network visualization

Microbial Comparative Genomics and Pangenomics: New Tools, Approaches And Insights Into Gene and Genome Evolution Paulo Jorge Dias,Satyanarayana Tulasi ,Digvijay Verma,2024-11-11 Comparative Genomics is the field of knowledge dedicated to the analysis and comparison of genes and genomes The scientific areas comprised in this field include subjects as diverse as just naming a few 1 the development of algorithms for the alignment of genes whole genomes short and long sequencing reads 2 the search for remote sequence similarity 3 the discovery of motifs and sequence patterns 4 the identification of gene families 5 the detection of ortholog paralog groups 6 the reconstruction of evolutionary history of the genes 7 the detection of signs of selective forces exerted over genes and genomes 8 the reconstruction of ancestral DNA and genome sequences 9 the detection and analysis of genome synteny 10 the inference of ancestral gene order among others In addition an important new sub field of Comparative Genomics has emerged in the last decade referred to as Pangenomics making available improved tools to analyze the exponential genomic data accumulating since the development of Second and Third Generation Sequencing Technologies **Network and Parallel Computing** James J. Park,Albert Y. Zomaya,Sang-Soo Yeo,Sartaj Sahni,2012-12-09 This book constitutes the refereed post proceedings of the 9th IFIP International Conference on Network and Parallel Computing NPC 2012 held in Gwangju Korea in September 2012 The 38 papers presented were carefully reviewed and selected from 136 submissions The papers are organized in the following topical sections algorithms scheduling analysis and data mining network architecture and protocol design network security paralel distributed and virtualization techniques performance modeling prediction and tuning resource management ubiquitous communications and networks and web communication and cloud computing In addition a total of 37 papers selected from five satellite workshops ATIMCN ATSME Cloud Grid DATICS and UMAS 2012 are included **Modern Statistical Methods for Health Research** Yichuan Zhao,(Din) Ding-Geng Chen,2021-10-14 This book brings together the voices of leading experts in the frontiers of biostatistics biomedicine and the health sciences to discuss the statistical

procedures useful methods and novel applications in biostatistics research It also includes discussions of potential future directions of biomedicine and new statistical developments for health research with the intent of stimulating research and fostering the interactions of scholars across health research related disciplines Topics covered include Health data analysis and applications to EHR data Clinical trials FDR and applications in health science Big network analytics and its applications in GWAS Survival analysis and functional data analysis Graphical modelling in genomic studies The book will be valuable to data scientists and statisticians who are working in biomedicine and health other practitioners in the health sciences and graduate students and researchers in biostatistics and health   *Advances in Bioinformatics and Computational Biology* Luis Kowada,Daniel de Oliveira,2020-04-28 This book constitutes the refereed proceedings of the Brazilian Symposium on Bioinformatics BSB 2019 held in Fortaleza Brazil in October 2019 The 9 revised full papers and 3 short papers were carefully reviewed and selected from 22 submissions The papers address a broad range of current topics in computational biology and bioinformatics   **Analyzing Network Data in Biology and Medicine** Nataša Pržulj,2019-03-28 Introduces biological concepts and biotechnologies producing the data graph and network theory cluster analysis and machine learning using real world biological and medical examples   *Pattern Recognition and Artificial Intelligence* Mounîm El Yacoubi,Eric Granger,Pong Chi Yuen,Umapada Pal,Nicole Vincent,2022-05-28 This two volume set constitutes the proceedings of the Third International Conference on Pattern Recognition and Artificial Intelligence ICPRAI 2022 which took place in Paris France in June 2022 The 98 full papers presented were carefully reviewed and selected from 192 submissions The papers present new advances in the field of pattern recognition and artificial intelligence They are organized in topical sections as follows pattern recognition computer vision artificial intelligence big data   **Pattern Recognition in Bioinformatics** Tetsuo Shibuya,Hisashi Kashima,Jun Sese,Shandar Ahmad,2012-11-04 This book constitutes the refereed proceedings of the 7th International Conference on Pattern Recognition in Bioinformatics PRIB 2012 held in Tokyo Japan in November 2012 The 24 revised full papers presented were carefully reviewed and selected from 33 submissions Their topics are widely ranging from fundamental techniques sequence analysis to biological network analysis The papers are organized in topical sections on generic methods visualization image analysis and platforms applications of pattern recognition techniques protein structure and docking complex data analysis and sequence analysis   **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   Recent Advances In Artificial Life Hussein A Abbass,Terry Bossomaier,Janet Wiles,2005-11-04 Artificial life is now a recognized discipline of research with many important applications and software tools However many theoretical issues remain unresolved This book

brings together a cross section of key developments in artificial life which in turn gives us new insight into the theory of complex systems The central ideas of the book surround genetics and evolution in an artificial life framework Topics covered include maintenance of genetic diversity hierarchical structures and stability of ecosystems Underpinning these topics are key theoretical developments surrounding network complexity the development of pattern languages for complex networks and a deeper understanding of the edge of chaos where complex systems live Practical applications include optimization gene regulatory networks modeling the spread of disease and the evolution of ageing The reader will gain an insight into the mathematical techniques at the core of artificial life and encounter a sufficient diversity of applications to stimulate new directions in their own field

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