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Evolutionary Computation in Gene Regulatory Network Research

Edited by
Hitoshi Iba • Nasimul Noman

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Evolutionary Computation in Gene Regulatory Network Research Hitoshi Iba,Nasimul Noman,2016-02-23 Introducing a handbook for gene regulatory network research using evolutionary computation with applications for computer scientists computational and system biologists This book is a step by step guideline for research in gene regulatory networks GRN using evolutionary computation EC The book is organized into four parts that deliver materials in a way equally attractive for a reader with training in computation or biology Each of these sections authored by well known researchers and experienced practitioners provides the relevant materials for the interested readers The first part of this book contains an introductory background to the field The second part presents the EC approaches for analysis and reconstruction of GRN from gene expression data The third part of this book covers the contemporary advancements in the automatic construction of gene regulatory and reaction networks and gives direction and guidelines for future research Finally the last part of this book focuses on applications of GRNs with EC in other fields such as design engineering and robotics Provides a reference for current and future research in gene regulatory networks GRN using evolutionary computation EC Covers sub domains of GRN research using EC such as expression profile analysis reverse engineering GRN evolution applications Contains useful contents for courses in gene regulatory networks systems biology computational biology and synthetic biology Delivers state of the art research in genetic algorithms genetic programming and swarm intelligence Evolutionary Computation in Gene Regulatory Network Research is a reference for researchers and professionals in computer science systems biology and bioinformatics as well as upper undergraduate graduate and postgraduate students Hitoshi Iba is a Professor in the Department of Information and Communication Engineering Graduate School of Information Science and Technology at the University of Tokyo Toyko Japan He is an Associate Editor of the IEEE Transactions on Evolutionary Computation and the journal of Genetic Programming and Evolvable Machines Nasimul Noman is a lecturer in the School of Electrical Engineering and Computer Science at the University of Newcastle NSW Australia From 2002 to 2012 he was a faculty member at the University of Dhaka Bangladesh Noman is an Editor of the BioMed Research International journal His research interests include computational biology synthetic biology and bioinformatics

Evolutionary Approach to Machine Learning and Deep Neural Networks Hitoshi Iba,2018-06-15 This book provides theoretical and practical knowledge about a methodology for evolutionary algorithm based search strategy with the integration of several machine learning and deep learning techniques These include convolutional neural networks Gr bner bases relevance vector machines transfer learning bagging and boosting methods clustering techniques affinity propagation and belief networks among others The development of such tools contributes to better optimizing methodologies Beginning with the essentials of evolutionary algorithms and covering interdisciplinary research topics the contents of this book are valuable for different classes of readers novice intermediate and also expert readers from related fields Following the chapters on introduction and basic methods Chapter 3 details a new research direction i e neuro evolution an evolutionary method for the generation of deep neural networks and also describes how evolutionary methods are extended in combination with machine learning techniques Chapter 4 includes novel methods such as particle swarm optimization based on affinity propagation PSOAP and transfer learning for differential evolution TRADE another machine learning approach for extending differential evolution The last chapter is dedicated to the state of the art in gene regulatory network GRN research as one of the most interesting and active research fields The author describes an evolving reaction network which expands the neuro evolution methodology to produce a type of genetic network suitable for biochemical systems and has succeeded in designing genetic circuits in synthetic biology The author also presents real world GRN application to several artificial intelligent tasks proposing a framework of motion generation by GRNs MONGERN which evolves GRNs to operate a real humanoid robot **Advanced Methodologies and Technologies in Artificial Intelligence, Computer Simulation, and Human-Computer Interaction** Khosrow-Pour, D.B.A., Mehdi,2018-09-28 As modern technologies continue to develop and evolve the ability of users to adapt with new systems becomes a paramount concern Research into new ways for humans to make use of advanced computers and other such technologies through artificial intelligence and computer simulation is necessary to fully realize the potential of tools in the 21st century Advanced Methodologies and Technologies in Artificial Intelligence Computer Simulation and Human Computer Interaction provides emerging research in advanced trends in robotics AI simulation and human computer interaction Readers will learn about the positive applications of artificial intelligence and human computer interaction in various disciples such as business and medicine This book is a valuable resource for IT professionals researchers computer scientists and researchers invested in assistive technologies artificial intelligence robotics and computer simulation Encyclopedia of Information Science and Technology, Fourth Edition Khosrow-Pour, D.B.A., Mehdi,2017-06-20 In recent years our world has experienced a profound shift and progression in available computing and knowledge sharing innovations These emerging advancements have developed at a rapid pace disseminating into and affecting numerous aspects of contemporary society This has created a pivotal need for an innovative compendium encompassing the latest trends concepts and issues surrounding this relevant discipline area During the past 15 years the Encyclopedia of Information Science and Technology has become recognized as one of the landmark sources of the latest knowledge and discoveries in this discipline The Encyclopedia of Information Science and Technology Fourth Edition is a 10 volume set which includes 705 original and previously unpublished research articles covering a full range of perspectives applications and techniques contributed by thousands of experts and researchers from around the globe This authoritative encyclopedia is an all encompassing well established reference source that is ideally designed to disseminate the most forward thinking and diverse research findings With critical perspectives on the impact of information science management and new technologies in modern settings including but not limited to computer science education healthcare government engineering business and natural and physical sciences it is a pivotal and relevant source of knowledge that will benefit every professional within the field of information science and technology and is an invaluable addition to every academic and corporate library **Handbook of Research on Computational Methodologies in Gene Regulatory Networks** 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 Genetic Programming Mauro Castelli,Lukas Sekanina,Mengjie Zhang,Stefano Cagnoni,Pablo García-Sánchez,2018-03-23 This book constitutes the refereed proceedings of the 21st European Conference on Genetic Programming EuroGP 2018 held in Parma Italy in April 2018 co located with the Evo 2018 events EvoCOP EvoMUSART and EvoApplications The 11 revised full papers presented together with 8 poster papers were carefully reviewed and selected from 36 submissions The wide range of topics in this volume reflects the current state of research in the field Thus we see topics and applications including analysis of feature importance for metabolomics semantic methods evolution of boolean networks generation of redundant features ensembles of GP models automatic design of grammatical representations GP and neuroevolution visual reinforcement learning evolution of deep neural networks evolution of graphs and scheduling in heterogeneous networks **Systems Biology for Signaling Networks** Sangdun Choi,2010-08-09 System Biology encompasses the knowledge from diverse fields such as Molecular Biology Immunology Genetics Computational Biology Mathematical Biology etc not only to address key questions that are not answerable by individual fields alone but also to help in our understanding of the complexities of biological systems Whole genome expression studies have provided us the means of studying the expression of thousands of genes under a particular condition and this technique had been widely used to find out the role of key macromolecules that are involved in biological signaling pathways However making sense of the underlying complexity is only possible if we interconnect various signaling pathways into human and computer readable network maps These maps can then be used to classify and study individual components involved in a particular phenomenon Apart from transcriptomics several individual gene studies have resulted in adding to our knowledge of key components that are involved in a signaling pathway It therefore becomes imperative to take into account of these studies also while constructing our network maps to highlight the interconnectedness of the entire signaling pathways and the role of that particular individual protein in the pathway This collection of articles will contain a collection of pioneering work done by scientists working in regulatory signaling networks and the use of large scale gene expression and omics data The distinctive features of this book would be Act a single source of information to understand the various components of different signaling network roadmap of biochemical pathways the nature of a molecule of interest in a particular pathway etc Serve as a platform to highlight the key findings in this highly volatile and evolving field and Provide answers to various techniques both related to microarray and cell signaling to the readers **AI 2011: Advances in Artificial Intelligence** Dianhui Wang,Mark Reynolds,2011-12-03 This book constitutes the refereed proceedings of the 24th

Australasian Joint Conference on Artificial Intelligence AI 2011 held in Perth Australia in December 2011 The 82 revised full papers presented were carefully reviewed and selected from 193 submissions The papers are organized in topical sections on data mining and knowledge discovery machine learning evolutionary computation and optimization intelligent agent systems logic and reasoning vision and graphics image processing natural language processing cognitive modeling and simulation technology and AI applications **Bio-Inspired Models of Network, Information, and Computing Systems** Junichi Suzuki,Tadashi Nakano,2012-07-25 This book constitutes the thoroughly refereed post conference proceedings of the 5th International ICST Conference on Bio Inspired Models of Network Information and Computing Systems BIONETICS 2010 which was held in Boston USA in December 2010 The 78 revised full papers were carefully reviewed and selected from numerous submissions for inclusion in the proceedings BIONETICS 2010 aimed to provide the understanding of the fundamental principles and design strategies in biological systems and leverage those understandings to build bio inspired systems **Evolving Connectionist Systems** Nikola K. Kasabov,2007-08-23 This second edition of the must read work in the field presents generic computational models and techniques that can be used for the development of evolving adaptive modeling systems as well as new trends including computational neuro genetic modeling and quantum information processing related to evolving systems New applications such as autonomous robots adaptive artificial life systems and adaptive decision support systems are also covered **Proceedings of the ... Congress on Evolutionary Computation** ,2004 **Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics, 8 Volume Set** Michael J. Dunn,Lynn B. Jorde,Peter F. R. Little,Shankar Subramaniam,2005-11-11 Available in print and online this unique reference brings together all four fields of genetics genomics proteomics and bioinformatics to meet your dynamic research requirements It brings together the latest concepts in these vibrant areas and ensures a truly multidisciplinary approach Topics include genetic variation and evolution epigenetics the human genome expression profiling proteome families structural proteomics gene finding gene structure protein function and annotation and more The work incorporates a vast amount of topical information profiles cutting edge techniques and presents the very latest findings from an international team of over five hundred contributors With articles for both students and more experienced scientists this is a key reference source for everyone Contains more than 450 articles covering all aspects of genomics proteomics bioinformatics and related technologies Includes a glossary containing over 550 clear and concise definitions I am pleased to recommend it heartily as a essential reference tool should remain the definitive work for many years to come THE CHEMICAL EDUCATOR Jorde and co editors have done a remarkable job in coordinating this information distilling it into a package that is both easy to navigate and over flowing in discovery ELECTRIC REVIEW **American Book Publishing Record** ,2005 **Evolutionary Computation in Gene Regulatory Network Research** Andy Goodwin,2017-05-23 This book is a step by step guideline for research in gene regulatory networks GRN using evolutionary computation EC The book is organized into four parts that deliver materials in a way equally attractive for a reader with training in computation or biology Each of these sections authored by well known researchers and experienced practitioners provides the relevant materials for the interested readers The first part of this book contains an introductory background to the field The second part presents the EC approaches for analysis and reconstruction of GRN from gene expression data The third part of this book covers the contemporary advancements in the automatic construction of gene regulatory and reaction networks and gives direction and guidelines for future research Finally the last part of this book focuses on applications of GRNs with EC in other fields such as design engineering and robotics **Elements of Computational Systems Biology** Huma M. Lodhi,Stephen H. Muggleton,2010-03-25 Groundbreaking long ranging research in this emergent field that enables solutions to complex biological problems Computational systems biology is an emerging discipline that is evolving quickly due to recent advances in biology such as genome sequencing high throughput technologies and the recent development of sophisticated computational methodologies Elements of Computational Systems Biology is a comprehensive reference covering the computational frameworks and techniques needed to help research scientists and professionals in computer science biology chemistry pharmaceutical science and physics solve complex biological problems Written by leading experts in the field this practical resource gives detailed descriptions of core subjects including biological network modeling analysis and inference presents a measured introduction to foundational topics like genomics and describes state of the art software tools for systems biology Offers a coordinated integrated systems view of defining and applying computational and mathematical tools and methods to solving problems in systems biology Chapters provide a multidisciplinary approach and range from analysis modeling prediction reasoning inference and exploration of biological systems to the implications of computational systems biology on drug design and medicine Helps reduce the gap between mathematics and biology by presenting chapters on mathematical models of biological systems Establishes solutions in computer science biology chemistry and physics by presenting an in depth description of computational methodologies for systems biology Elements of Computational Systems Biology is intended for academic industry researchers and scientists in computer science biology mathematics chemistry physics biotechnology and pharmaceutical science It is also accessible to undergraduate and graduate students in machine learning data mining bioinformatics computational biology and systems biology courses Genome Research ,2007

Handbook of Evolution Franz M. Wuketits,Christoph Antweiler,2004 This two volume handbook is unique in spanning the entire field of evolution from the origins of life up to the formation of social structures and science and technology The author team of world renowned experts considers the subject from a variety of disciplines with continuous cross referencing so as to retain a logical internal structure The uniformly structured contributions discuss not merely the general knowledge behind the evolution of life but also the corresponding development of language society economies morality and politics The result is an overview of the history and methods used in the study of evolution including controversial theories and discussions A must for researchers in the natural sciences sociology and philosophy as well as for those interested in an interdisciplinary view of the status of evolution today Proceedings of the National Academy of Sciences of the United States of America National Academy of Sciences (U.S.).,2006 **Bioinformatics** Andreas D. Baxevanis,B. F. Francis Ouellette,2005 Reviews of the Second Edition In this book Andy Baxevanis and Francis Ouellette have undertaken the difficult task of organizing the knowledge in this field in a logical progression and presenting it in a digestible form And they have done an excellent job This fine text will make a major impact on biological research and in turn on progress in biomedicine We are all in their debt Eric Lander from the Foreword to the Second Edition The editors and the chapter authors of this book are to be applauded for providing biologists with lucid and comprehensive descriptions of essential topics in bioinformatics This book is easy to read highly informative and certainly timely It is most highly recommended for students and for established investigators alike for anyone who needs to know how to access and use the information derived in and from genomic sequencing projects Trends in Genetics It is an excellent general bioinformatics text and reference perhaps even the best currently available Congratulations to the authors editors and publisher for producing a weighty authoritative readable and attractive book Briefings in Bioinformatics This book written by the top scientists in the field of bioinformatics is the perfect choice for every molecular biology laboratory The Quarterly Review of Biology This fully revised version of a world renowned bestseller provides readers with a practical guide covering the full scope of key concepts in bioinformatics from databases to predictive and comparative algorithms Using relevant biological examples the book provides background on and strategies for using many of the most powerful and commonly used computational approaches for biological discovery This Third Edition reinforces key concepts that have stood the test of time while making the reader aware of new and important developments in this fast moving field With a new full color and enlarged page design Bioinformatics Third Edition offers the most readable up to date and thorough introduction to the field for biologists This new edition features New chapters on genomic databases predictive methods using RNA sequences sequence polymorphisms protein structure prediction intermolecular interactions and proteomic approaches for protein identification Detailed worked examples illustrating the strategic use of the concepts presented in each chapter along with a collection of expanded more rigorous problem sets suitable for classroom use Special topic boxes and appendices highlighting experimental strategies and advanced concepts Annotated reference lists comprehensive lists of relevant Web resources and an extensive glossary of commonly used terms in bioinformatics genomics and proteomics Bioinformatics Third Edition is essential reading for researchers instructors and students of all levels in molecular biology and bioinformatics as well as for investigators involved in genomics clinical research proteomics and computational biology www wiley com bioinformatics *The British National Bibliography* Arthur James Wells,2009

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