Evolutionary Computation in Gene Regulatory Network Research

Edited by

Hitoshi Iba • Nasimul Noman

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Evolutionary Computation In Gene Regulatory Network Research Wiley Series In Bioinformatics:
    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 Computation in Gene Regulatory Network Research** Hitoshi Iba,Nasimul Noman,2016-01-20 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   *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

Fuzzy Systems in Bioinformatics and Computational Biology Yaochu Jin,Lipo Wang,2008-12-28 Biological systems are inherently stochastic and uncertain Thus research in bioinformatics biomedical engineering and computational biology has to deal with a large amount of uncertainties Fuzzy logic has shown to be a powerful tool in capturing different uncertainties in engineering systems In recent years fuzzy logic based modeling and analysis approaches are also becoming popular in analyzing biological data and modeling biological systems Numerous research and application results have been reported that demonstrated the effectiveness of fuzzy logic in solving a wide range of biological problems found in bioinformatics biomedical engineering and computational biology Contributed by leading experts world wide this edited book contains 16 chapters presenting representative research results on the application of fuzzy systems to genome sequence assembly gene expression analysis promoter analysis cis regulation logic analysis and synthesis reconstruction of genetic and cellular networks as well as biomedical problems such as medical image processing electrocardiogram data classification and anesthesia monitoring and control This volume is a valuable reference for researchers practitioners as well as graduate students working in the field of bioinformatics biomedical engineering and computational biology   Computational Methods for Next Generation Sequencing Data Analysis Ion Mandoiu,Alexander Zelikovsky,2016-09-12 Introduces readers to core algorithmic techniques for next generation sequencing NGS data analysis and discusses a wide range of computational techniques and applications This book provides an in depth survey of some of the recent developments in NGS and discusses mathematical and computational challenges in various application areas of NGS technologies The 18 chapters featured in this book have been authored by bioinformatics experts and represent the latest work in leading labs actively contributing to the fast growing field of NGS The book is divided into four parts Part I focuses on computing and experimental infrastructure for NGS analysis including chapters on cloud computing modular pipelines for metabolic pathway reconstruction pooling

strategies for massive viral sequencing and high fidelity sequencing protocols Part II concentrates on analysis of DNA sequencing data covering the classic scaffolding problem detection of genomic variants including insertions and deletions and analysis of DNA methylation sequencing data Part III is devoted to analysis of RNA seq data This part discusses algorithms and compares software tools for transcriptome assembly along with methods for detection of alternative splicing and tools for transcriptome quantification and differential expression analysis Part IV explores computational tools for NGS applications in microbiomics including a discussion on error correction of NGS reads from viral populations methods for viral quasispecies reconstruction and a survey of state of the art methods and future trends in microbiome analysis Computational Methods for Next Generation Sequencing Data Analysis Reviews computational techniques such as new combinatorial optimization methods data structures high performance computing machine learning and inference algorithms Discusses the mathematical and computational challenges in NGS technologies Covers NGS error correction de novo genome transcriptome assembly variant detection from NGS reads and more This text is a reference for biomedical professionals interested in expanding their knowledge of computational techniques for NGS data analysis The book is also useful for graduate and post graduate students in bioinformatics   **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   *Multiple Biological Sequence Alignment* Ken Nguyen,Xuan Guo,Yi Pan,2016-06-10 Covers the fundamentals and techniques of multiple biological sequence alignment and analysis and shows readers how to choose the appropriate sequence analysis tools for their tasks This book describes the traditional and modern approaches in biological sequence alignment and homology search This book contains 11 chapters with Chapter 1 providing basic information on biological sequences Next Chapter 2 contains fundamentals in pair wise sequence alignment while Chapters 3 and 4 examine popular existing quantitative models and practical clustering techniques that have been used in multiple sequence alignment Chapter 5 describes characterizes and relates many multiple sequence alignment models Chapter 6 describes how traditionally phylogenetic trees have been constructed and available sequence knowledge bases can be used to improve the accuracy of reconstructing phylogeny trees Chapter 7 covers the latest methods developed to improve the run time efficiency of multiple sequence alignment Next Chapter 8 covers several popular existing multiple sequence alignment server and services and Chapter 9 examines several multiple sequence alignment techniques that have been developed to handle short sequences reads produced by the Next Generation Sequencing technique NSG Chapter 10 describes a Bioinformatics

application using multiple sequence alignment of short reads or whole genomes as input Lastly Chapter 11 provides a review of RNA and protein secondary structure prediction using the evolution information inferred from multiple sequence alignments Covers the full spectrum of the field from alignment algorithms to scoring methods practical techniques and alignment tools and their evaluations Describes theories and developments of scoring functions and scoring matrices Examines phylogeny estimation and large scale homology search Multiple Biological Sequence Alignment Scoring Functions Algorithms and Applications is a reference for researchers engineers graduate and post graduate students in bioinformatics and system biology and molecular biologists Ken Nguyen PhD is an associate professor at Clayton State University GA USA He received his PhD MSc and BSc degrees in computer science all from Georgia State University His research interests are in databases parallel and distribute computing and bioinformatics He was a Molecular Basis of Disease fellow at Georgia State and is the recipient of the highest graduate honor at Georgia State the William M Suttles Graduate Fellowship Xuan Guo PhD is a postdoctoral associate at Oak Ridge National Lab USA He received his PhD degree in computer science from Georgia State University in 2015 His research interests are in bioinformatics machine leaning and cloud computing He is an editorial assistant of International Journal of Bioinformatics Research and Applications Yi Pan PhD is a Regents Professor of Computer Science and an Interim Associate Dean and Chair of Biology at Georgia State University He received his BE and ME in computer engineering from Tsinghua University in China and his PhD in computer science from the University of Pittsburgh Dr Pan s research interests include parallel and distributed computing optical networks wireless networks and bioinformatics He has published more than 180 journal papers with about 60 papers published in various IEEE ACM journals He is co editor along with Albert Y Zomaya of the Wiley Series in Bioinformatics *Microbial Synthetic Biology* ,2013-11-06 The 40th volume of Methods in Microbiology focuses on microbial synthetic biology Synthetic biology is a rapidly growing discipline that builds on well established principles of genetic engineering and biotechnology by integrating computational and engineering approaches to the design and construction of novel biological systems This volume addresses some of the major technical challenges stand in the way of achieving a radical step change in our ability to engineer complex multi scaled biological systems These include the application of computation intelligence to the design of synthetic microbial systems design automation and constraints the impact of noise and stochasticity the engineering of biosensors the characteristic of a model bacterial chassis A key issue in Synthetic Biology is that of its social dimensions and a chapter is dedicated to the important issue Authority or expertise of contributors lLnks to websites for the design and modelling of microbes and microbial metabolism First volume to address the practical issues Discussion on responsible innovation **Multimodal Analytics for Next-Generation Big Data Technologies and Applications** Kah Phooi Seng,Li-minn Ang,Alan Wee-Chung Liew,Junbin Gao,2019-07-18 This edited book will serve as a source of reference for technologies and applications for multimodality data analytics in big data environments After an introduction the editors organize the book into four main

parts on sentiment affect and emotion analytics for big multimodal data unsupervised learning strategies for big multimodal data supervised learning strategies for big multimodal data and multimodal big data processing and applications The book will be of value to researchers professionals and students in engineering and computer science particularly those engaged with image and speech processing multimodal information processing data science and artificial intelligence *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 **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 *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 **Applications of Evolutionary Computing** Franz Rothlauf,Jürgen Branke,Stefano Cagnoni,Ernesto Costa,Carlos Cotta,Rolf Drechsler,Evelyne Lutton,Penousal Machado,Jason H. Moore,Juan Romero,George D. Smith,Giovanni Squillero,Hideyuki Takagi,2006-03-04 This book presents the refereed joint proceedings of seven workshops on evolutionary computing EvoWorkshops 2006 held in Budapest in April 2006 65 revised full papers and 13 revised short papers presented were carefully reviewed and selected from a total of 149 submissions The book is organized in topical sections including evolutionary bioinformatics evolutionary computation in communications networks and connected systems and more **Computational Intelligence in Bioinformatics** Gary B. Fogel,David W. Corne,Yi Pan,2007-12-10 Combining biology computer science mathematics and statistics the field of bioinformatics has become a hot new discipline with profound impacts on all aspects of biology and industrial application Now Computational Intelligence in Bioinformatics offers an introduction to the topic covering the most relevant and popular CI methods while also encouraging the implementation of these methods to readers research ,2019-11-23 AI Deep Neural Evolution C Java 1 AI 2 3 4 5 6 **Excel —Excel GA— **

,2016-05-25 Excel GA GP Excel Excel Excel Excel2013 2016 2 3 I 1 2 3 GA 4 GA II 5 6 7 III 8 GA GP 9   **Artificial Evolution** Pierre Collet,Nicolas Monmarché,Pierrick Legrand,Marc Schoenauer,Evelyne Lutton,2010-06-27 Annotation This book constitutes the proceedings of the 9th International Conference on Artificial Evolution held in Strasbourg France in October 2009

This book delves into Evolutionary Computation In Gene Regulatory Network Research Wiley Series In Bioinformatics. Evolutionary Computation In Gene Regulatory Network Research Wiley Series In Bioinformatics is a vital topic that needs to be grasped by everyone, ranging from students and scholars to the general public. This book will furnish comprehensive and in-depth insights into Evolutionary Computation In Gene Regulatory Network Research Wiley Series In Bioinformatics, encompassing both the fundamentals and more intricate discussions.

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