

Tomasz G. Smolinski, Mariofanna G. Milanova and Aboul-Ella Hassanien (Eds.)
Applications of Computational Intelligence in Biology

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Applications of Computational Intelligence in Biology

Current Trends and Open Problems

With 107 Figures and 43 Tables



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To my mother

Aleksandra Smolińska

Tomasz G. Smolinski

To

my family

Mariofanna G. Milanova

To

my family

Aboul-Ella Hassanien

Preface

Computational Intelligence (CI) has been a tremendously active area of research for the past decade or so. There are many successful applications of CI in many subfields of biology, including bioinformatics, computational genomics, protein structure prediction, or neuronal systems modeling and analysis. However, there still are many open problems in biology that are in desperate need of advanced and efficient computational methodologies to deal with tremendous amounts of data that those problems are plagued by. Unfortunately, biology researchers are very often unaware of the abundance of computational techniques that they could put to use to help them analyze and understand the data underlying their research inquiries. On the other hand, computational intelligence practitioners are often unfamiliar with the particular problems that their new, state-of-the-art algorithms could be successfully applied for. The separation between the two worlds is partially caused by the use of *different languages* in these two spheres of science, but also by the relatively small number of publications devoted solely to the purpose of facilitating the exchange of new computational algorithms and methodologies on one hand, and the needs of the biology realm on the other.

The purpose of this book is to provide a medium for such an exchange of expertise and concerns. In order to achieve the goal, we have solicited contributions from both computational intelligence as well as biology researchers. We have collected contributions from the CI community describing powerful new methodologies that could, or currently are, utilized for biology-oriented applications. On the other hand, the book also contains chapters devoted to open problems in biology that are in need of strong computational techniques, so the CI community can find a brand new and potentially intriguing spectrum of applications.

We have divided the book into four major parts. Part I, *Techniques and Methodologies*, contains a selection of contributions that provide a detailed description of several theories and methods that could be (or to some extent

already are) of great benefit to biologists dealing with problems of data analysis (including large-volume, imprecise, and incomplete data), search-space exploration, optimization, etc.

In Chapter 1, by *Andrew Hamilton-Wright and Daniel W. Stashuk*, present a statistically based pattern discovery tool that produces a rule-based description of complex data through the set of its statistically significant associations. Although many biologists are familiar with statistical data analysis methods and use them quite extensively to quantify and summarize their data, they relatively rarely employ more complex statistically motivated techniques to thoroughly mine their databases in search of concise patterns and/or classification rules. This chapter provides an introduction to such types of analysis, supported by a discussion of the performance of the presented technique on a series of biologically relevant data distributions.

Chapter 2, by *Lech Polkowski and Piotr Artiemjew*, describes another very powerful methodology designed to deal with analysis of inexact and/or incomplete data. By utilizing the presented theory of Rough Sets (RS), biologists would be able to cope with uncertainty due to ambiguity of classification caused by incompleteness of knowledge, so prevalent in many real-life databases.

Chapters 3, by *Thomas McTavish and Diego Restrepo*, and 4, by *Antonio López Jaimes and Carlos A. Coello Coello*, treat on selected aspects of the field of Evolutionary Computation (EC). EC, itself being biologically-inspired (by the principles of evolution, natural selection, etc.), is by no means being used exclusively in biological problems and has found many applications across many disciplines. Very potent and flexible approaches based on Genetic Algorithms (GAs), Evolution Strategies (ESs), Multi-Objective Evolutionary Algorithms (MOEAs), have been very successfully applied to many problems of function optimization, parameter space exploration, etc. The first of the two chapters presents an introduction to Evolutionary Algorithms (EAs) in general and their applicability to various biological problems, focusing on EAs' use as an optimization technique for fitting parameters to a biological model. The second chapters concentrates on MOEAs (as applied to problems where multi-criteria optimization is necessary) and discusses some of their potential uses in biology.

Part II of the book, *Current Trends*, presents a selection of chapters describing specific existing and on-going applications of Computational Intelligence in biology.

In Chapter 5, *Wit Jakuczun*, introduces a technique based on a hybridization of wavelets and Support Vector Machines (SVMs), called Local Classifiers, for analysis and classification of signals. The author also presents an

application of the method to a real-life problem of analysis of local field potentials recorded within barrel cortex of an awake rat.

Ryszard Tadeusiewicz, in Chapter 6, presents a systematic study of an application of Artificial Neural Networks (ANNs) for evaluation of biological activity of chemical compounds. Even though ANNs are quite commonly utilized for such prediction tasks, little is known about the specific parameters of a network that should be employed for a given dataset. In this chapter, the author compares several different ANN architectures and provides a detailed discussion of benefits and weaknesses of each one of them.

In the study described in Chapter 7, by *Bai-Tao Zhou and Joong-Hwan Baek*, the authors use machine vision to detect distinctive behavioral phenotypes of thread-shape microscopic organism, such as *Caenorhabditis elegans* (*C.elegans*). The first part of this chapter introduces an animal auto-tracking and imaging system capable of following an individual animal for extended periods of time by saving a time-indexed image sequences representing its locomotion and body postures. Then the authors present a series of image processing procedures for gradually shrinking the thread-shape representation into a Bend Angle Series expression (BASe), which later is the foundation of n-order-difference calculation for static and locomotion pattern extraction. Finally, for mining distinctive behaviors, the Hierarchical Density Shaving (HDS) clustering method is applied for compacting, ranking and identifying unique static and locomotion patterns, which combined represent distinctive behavioral phenotypes for a specific species.

In Chapter 8, *Dah-Jye Lee et al.* introduce a simple and accurate real-time contour matching technique specifically for applications involving fish species recognition and migration monitoring. The authors describe FishID, a prototype vision system that employs a software implementation of their newly developed contour matching algorithms. They also discuss the challenges involved in the design of this system, both hardware and software, and present results from a field test of the system at Prosser Dam in Prosser, Washington, USA.

Chapter 9, by *Dawn R. Magness, Falk Huettmann, and John M. Morton*, propose to utilize the technique called Random Forests to predicted species distribution maps that would serve as a metric for ecological inventory and monitoring programs. The authors use Random Forests a highly accurate bagging classification algorithm to build multi-species avian distribution models using data collected as part of the Kenai National Wildlife Refuge Long-term Ecological Monitoring Program (LTEMP). The chapter provides some background on the application of this method to real-life data and a discussion of its value for evaluating climate change impacts on species distributions.

Concluding Part II is Chapter 10, by *John T. Langton, Elizabeth A. Gifford, and Timothy J. Hickey*, in which the authors present a number of visualization methods and tools for investigating large, multidimensional data sets, which are very common in virtually every biology lab nowadays. The chapter focuses on approaches that have been used to analyze a model neuron simulation database but could be applied to other domains.

Part III, *Open Problems*, contains a collection of chapters describing biological problems, for which, although some computational methods have been utilized to deal with them, there is still a need for efficient CI techniques to be applied.

Chapter 11, by *Laila A. Nahum and Sergio L. Pereira*, calls for an integrated approach between molecular evolution and Computational Intelligence to be applied to analysis of molecular sequences to determine gene function and phylogenetic relationships of organisms. The authors point out areas in the field of phylogenomics (*phylogenetics* and *genomics*) that require further development, such as computational tools and methods to manipulate large and diverse data sets, which may ultimately lead to a better system-based understanding of biological processes in different environments.

In Chapter 12, *Vladik Kreinovich and Max Shpak*, discuss the computational aspects of aggregability for linear and non-linear systems, which directly relate to aggregability in biological systems such as population genetic systems and multi-species (multi-variable) systems in ecology. More specifically, the authors investigate the problem of conditional aggregability (i.e., aggregability restricted to modular states) and aggregation of variables in biologically relevant quadratic dynamical systems.

In the study described in Chapter 13, by *Ying Xie et al.*, the authors designed and implemented a prototype of a conceptual biology research support platform that consists of a set of interrelated information extraction, mining, reasoning, and visualizing technologies to automatically generate several types of biomedical hypotheses and to facilitate researchers in validating generated hypotheses. Such a platform could utilize vast amounts of published biomedical data, via interacting with certain search engines such as PubMed, to enhance and speed up biomedical research. The chapter presents a detailed description of the proposed approach as well as a discussion of future research and development directions and needs.

Chapter 14, by *Cengiz Günay et al.*, concludes this part of the book. This chapter constitutes mini-proceedings of the Workshop on Physiology Databases and Analysis Software that was a part of the Annual Computational Neuroscience Meeting CNS*2007 that took place in Toronto, Canada

in July of 2007 and comprises of several selected contributions provided by the participants. In Section 14.2, Thomas M. Morse discusses the current uses and potential applications of CI for electrophysiological databases (EPDBs). Sections 14.3 by Pdraig Gleeson et al., 14.4 by Horatiu Voicu, 14.5 by Cengiz Günay, and 14.6 by Peter Andrews et al., describe some currently available data-exchange and analysis platforms and implementations. Finally, Sections 14.7 by Gloster Aaron and 14.8 by Jean-Marc Fellous present some interesting open problems in electrophysiology with examples of analysis techniques, including CI-motivated approaches.

We have decided to devote the last section of the book, Part IV, entirely to *Cognitive Biology*, as it symbolizes a perfect common ground for the intersection of Computational Intelligence and biology. On one hand, the CI community has already tremendously benefited from the insights derived from research in this sub-field of biology (e.g., development of multi-agent systems has been an extensively pursued area of CI for several years now), but on the other, there is a seemingly endless sea of opportunities for applications of CI methodologies to further study cognition.

In Chapter 15, *Stan Franklin and Michael H. Ferkin* advocate studying animal cognition by means of computational control architectures based on biologically and psychologically inspired, broad, integrative, hybrid models of cognition. The authors introduce the LIDA (Learning Intelligent Distribution Agent) model. By using this model, animal experiments can be replicated in artificial environments by means of virtual software agents controlled by such architectures. The study described in this chapter explores the possibility of such experiments using a virtual or a robotic vole to replicate, and to predict, the behavior of live voles, thus applying computational intelligence to cognitive ethology.

Chapter 16, by *David Windridge and Josef Kittler*, is a survey of the fundamental constraints upon self-updating representation in cognitive agents of natural and artificial origin. The authors argue that perception-action frameworks provide an appropriate basis for the development of an empirically meaningful criterion for validating perceptual categories. In this scenario, hypotheses about the agent's world are defined in terms of environmental affordances (characterized in terms of the agent's active capabilities). Accordingly, the grounding of such a priori 'bootstrap' representational hypotheses is ensured via the process of natural selection in biological agents capable of autonomous cognitive-updating.

The editors are very grateful to the authors of the contributions included in this volume and to the referees for their tremendous service by critically reviewing the chapters. We would especially like to thank Prof. Janusz Kacprzyk, Editor-in-chief of the series "*Studies in Computational*

Intelligence,” and Dr. Thomas Ditzinger, Senior In-house Editor of Springer Verlag, Germany, for their help, editorial assistance, and excellent cooperation to produce this important scientific work. We sincerely hope that this collection of contributions from biologists and CI practitioners alike will prove useful to researchers in both those fields and that it will facilitate a productive dialog between the two spheres of science and result in fruitful collaborations and scientific advancements on both sides.

Atlanta, Georgia, USA
Little Rock, Arkansas, USA
Cairo, Egypt
December, 2007

Tomasz G. Smolinski
Mariofanna G. Milanova
Aboul-Ella Hassanien
(editors)

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