

Special issue on the frontiers of natural computing

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Published online: 20 October 2013
© Springer Science+Business Media Dordrecht 2013

Keywords Natural computing · Biochemical networks · Neural networks · Evolutionary algorithms · Synthetic biology · Self-assembly · Development

1 Preface

Natural computing is the study of computational processes that occur in biological and other naturally-occurring systems, whether these processes occur in silico, in vivo, or in vitro. Many of the ideas underlying natural computing can be traced back to the early days of modern computer science, and the work by visionaries such as Turing and Von Neumann. Since these early days, the field has continued to grow and generate new ideas, leading to the development of distinct research communities in areas such as neural computing, evolutionary algorithms, synthetic biology, and artificial life, to name but a few.

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The aim of the Frontiers of Natural Computing workshop, held at the University of York, UK from 10th to 12th September 2012, was to bring people together from the different strands of natural computing, and provide a venue to collectively talk about the future development of the field. With this in mind, we invited speakers and solicited contributions from across the field of natural computing. The resulting programme of talks and poster presentations covered many diverse but related areas of research, including: synthetic biology, systems biology, artificial life, discrete dynamical systems, evolutionary algorithms, neural computing, artificial development, membrane computing, artificial immune systems, information theoretic approaches, hardware architectures and methods for complex systems modeling and analysis.

This special issue contains six articles contributed by delegates who presented at the event. All articles were fully peer reviewed, and we would like to thank the people involved in this process. We would also like to take this opportunity to thank all those who attended and helped to organise the event, and we would especially like to acknowledge the generous financial support of the EPSRC (under the grant “Artificial Biochemical Networks: Computational Models and Architectures,” ref. EP/F060041/1), which enabled us to offer free attendance to delegates, and provide bursaries to student attendees.

A prominent issue addressed by the workshop was the question of how much we still have to learn from biological and natural systems. The first article, “*Consideration of Mobile DNA: New Forms of Artificial Genetic Regulatory Networks*,” by Larry Bull, is very much within this vein of investigation. Recently it has become apparent that transposable elements (or “jumping genes”) in DNA have had a profound influence upon the evolution of modern-day species. In this paper, the author extends the classic random

Boolean network model of gene regulation with a mechanism inspired by mobile DNA, showing how the resulting structural dynamism is favoured by evolution when exploring complex fitness landscapes.

In addition to their role in understanding biological systems, computational models of gene regulatory and other biochemical networks can be used as computational techniques in their own right. Our contribution to this special issue, “*Biochemical Connectionism*,” explores this theme, and in particular focuses upon how our understanding of the structure and organisation of biochemical networks can complement and inform conventional neural connectionist models. We demonstrate these ideas through a number of examples, showing how connectionist models of biochemical networks have been used to solve a range of hard control and signal processing tasks.

Despite the proliferation of natural computing paradigms, there remain deep theoretical relationships between different nature-inspired algorithms. This idea is explored in a contribution by Boris Mitavskiy, Elio Tuci, Chris Cannings, Jonathan Rowe and Jun He, entitled “*Geiringer Theorems: From Population Genetics to Computational Intelligence, Memory Evolutive Systems and Hebbian Learning*”, in which the authors outline a mathematical theory that takes in learning across a range of natural computing paradigms, including evolutionary computing and neural computing.

Arguably one of the most exciting emerging trends in natural computing is synthetic biology, which can be regarded as the implementation of computation in vivo. The first article in this vein, “*Expanding the landscape of Biological Computation with Synthetic Multicellular Consortia*,” by Ricard Solé and Javier Macia, discusses the advantages of breaking away from conventional engineering principles and taking motivation from the spatial organisation of biological molecular circuits. In particular, the authors introduce the idea of cellular consortia, describing how these provide a natural mechanism for solving the wiring problems that occur in large synthetic molecular circuits.

Another potential mechanism for achieving complexity in synthetic biology is to leverage self-assembling biochemical processes. In their article, “*Exploring Programmable Self-Assembly in Non-DNA Based Molecular Computing*,” Germán Terrazas, Hector Zenil and Natalio Krasnogor simulate and explore the interactions between a group of conjugating compounds called polyphyrins, noting how their ability to form highly dynamic patterns might be used as the basis for molecular computing. The authors also speculate about how polyphyrin-based molecular computing may complement, and in some circumstances have advantages over, more widely used DNA-based molecular computing.

Concepts of self-assembly and self-organisation have become popular in a number of fields of natural computing. In their article “*A Review of Morphogenetic Engineering*,” René Doursat, Hiroki Sayama and Olivier Michel consider systems in which complex architectures come about through processes of this kind, providing a taxonomy of the various natural, synthetic and computational systems that fall within the area that they refer to as ‘morphogenetic engineering.’ Central to their taxonomy are the various ways in which these systems come about, for instance through constructive processes, coalescence, development, and generational grammars.

An important theme explored in all these papers, and at the workshop more generally, is the idea of doing natural computing in a way that is *natural* to biological systems, rather than conventional computer systems. Biology is a very active research area, and our understanding of how biological systems compute is continuing to be refined, and in many cases redefined, by new research results. This is both a blessing and a curse to natural computing: a blessing since the pool of inspiration is forever growing, but sometimes a curse because this knowledge is always incomplete, and occasionally even wrong. Nevertheless, natural computing continues to be an exciting and stimulating field to work in, and we hope you enjoy reading this special issue as much as we enjoyed putting it together.