P. Musilek, M. Reformat, L. Kurgan (Eds.), Editorial: Biologically Inspired Computing and Computers in Biology, Special Issue of *Neural Network World*, 15(3), 2005, p. 187

This special issue of Neural Network World takes the reader on a round trip from biology to computers and back. The growing interplay between the two areas has brought numerous contributions and innovations to biologically inspired computing and applications of computers in biology. Works presented in this volume sample the broad territory from different perspectives by bringing together theoretical, applied and survey papers.

The issue opens with paper by Gecow presenting an abstract model for adaptive evolution of complex systems. The author presents the results of computer simulations of the model and draws interesting conclusions regarding the problem of recapitulation of phylogeny in ontogeny. Remaining in the realm of biology, paper by Lee describes an attempt to model two important components of an axiomatic model of consciousness. In particular, the paper sets forth models of planning and emotion through digital neuromodelling. Neural models have been also used by Graham and Dawson to analyze data related to face-sensitive event-related potentials. Alongside artificial neural networks, statistical methods have been applied to data analysis. The results presented in the paper suggest sensitivity of the studied phenomena to long-term memory.

The second group of contributions takes inspiration from swarm systems. The paper by Cervantes et al. applies binary particle swarm optimization algorithm to discover classification rules. The authors show that the algorithm can improve the results of other machine learning methods in the resolution of discrete classification problems. Mirzayans et al. apply swarm intelligence to computer vision. Their system evolves a swarm of feature-detecting agents and then characterizes objects in an image based on the properties of the converged population.

The third theme of this collection concerns biological applications of computing. Pizzi proposes a novel approach of selecting features for classification of high-dimensional biomedical spectra. Finally, Mukherjee and Mitra provide a general survey of fuzzy measures in Hidden Markov Models and their application to broad range of areas including bioinformatics and computational biology.

Last, but not least, we thank the authors who submitted and contributed their work to this special issue working on a tight schedule. We also extend our thanks to referees who spent their valuable time reviewing the manuscripts. We greatly appreciate the promptness of their responses, which allowed us to publish the special issue in a timely manner.

Petr Musilek, Marek Reformat, Lukasz Kurgan
University of Alberta

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