Keynote Abstract I

Bio-inspired Computing: Small-Scale and Large-Scale Systems

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Abstract:
Bio-inspired computing can be a fragmented area of research for the uninitiated. In this talk, I will present a critical survey of the whole field, as it has been defined by the BIC-TA conference series. I will consider four types of systems. Firstly, abstract computational models such as cellular automata.

Then, small-scale systems such as DNA. Thirdly, medium-scale systems including computer vision, and finally large-scale systems such as swarms. I will consider where all these systems fit into the framework of biology, and how optimal they compute. The talk will be illustrated with examples from neurobiology. In neurobiology, the abstract computational models include artificial neural networks. The small-scale systems are spiking neuron models and the medium scale systems are bio-inspired classifiers. The large-scale neural systems are the crowds and social networks of our modern world.

Biography:
Prof. Philippe De Wilde obtained his PhD degree in Mathematical Physics and the MSc degree in Computer Science in 1985. He was a Lecturer and Senior Lecturer in the Department of Electrical Engineering, Imperial College London, between 1989 and 2005. He is currently a Professor in the Intelligent Systems Lab of the Department of Computer Science, School of Mathematical and Computer Sciences, Heriot-Watt University, Edinburgh, United Kingdom. He is also Head of the School of Mathematical and Computer Sciences.

He has published 44 journal papers, 48 conference papers and book chapters. He has published four books, including "Neural Network Models" (Springer, 1997), and "Convergence and Knowledge Processing in Multi-agent Systems" (Springer, 2009).

He develops biological and sociological principles that improve the design and decision making of networks. His research interests include decision making under uncertainty, networked populations, coordination mechanisms for populations, neural networks, neuro-economics and multi-agent systems.

Prof. De Wilde is a senior member of IEEE, member of the IEEE Computational Intelligence Society and Systems, Man and Cybernetics Society, and the British Computer Society.
Keynote Abstract II

Bio-molecular Computing of Finite-State Automata

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Abstract:
We overview a series of our research on implementing finite automata in vitro and in vivo in the framework of DNA-based computing.

First, we employ the length-encoding technique proposed and presented in to implement finite automata in test tube. In the length-encoding method, the states and state transition functions of a target finite automaton are effectively encoded into DNA sequences, a computation (accepting) process of finite automata is accomplished by self-assembly of encoded complementary DNA strands, and the acceptance of an input string is determined by the detection of a completely hybridized double-strand DNA.

Second, we report our intensive in vitro experiments in which we have implemented and executed several finite-state automata in test tube. We have designed and developed practical laboratory protocols which combine several in vitro operations such as annealing, ligation, PCR, and streptavidin-biotin bonding to execute in vitro finite automata based on the length-encoding technique. We have carried laboratory experiments on various finite automata of from 2 states to 6 states for several input strings.

Third, we present a novel framework to develop a programmable and autonomous in vivo computer using Escherichia coli (E. coli), and implement in vivo finite-state automata based on the framework by employing the protein-synthesis mechanism of E. coli. Our fundamental idea to develop a programmable and autonomous finite-state automaton on E. coli is that we first encode an input string into one plasmid, encode state-transition functions into the other plasmid, and introduce those two plasmids into an E. coli cell by electroporation.

Fourth, we execute a protein-synthesis process in E. coli combined with four-base codon techniques to simulate a computation (accepting) process of finite automata. This approach enables us to develop a programmable in vivo computer by simply replacing a plasmid encoding a state-transition function with others. Further, our in vivo finite automata are autonomous because the protein-synthesis process
is autonomously executed in the living E. coli cell. We show some successful experiments to run an in vivo finite-state automaton on E. coli.

**Biography:**

Prof. Yasubumi Sakakibara is a Professor at the Department of Biosciences and Informatics, Keio University, Japan. He received his degree of Doctor of Science from Tokyo Institute of Technology in 1991. He spent one year as postdoc at UC Santa Cruz and collaborated with Prof. David Haussler on the project of stochastic context-free grammars for modeling RNAs. He also worked for Fujitsu Laboratory.

His research interests are Bioinformatics including Comparative genomics, RNA sequence analysis, and DNA computers, and Computer Science.

He was the PC Chairman of the 17th International Conference on Genome Informatics (GIW2006), the Organizing Chairman of the 20th International Conference on Genome Informatics (GIW2009), and the PC Chairman of the 16th International Conference on DNA Computing and Molecular Programming (DNA16). He is an editor of Natural Computing: an International Journal, and a member of associate editorial board of Frontiers in Non-Coding RNA. He is also a member of Japanese Society of Bioinformatics, and International Society for Computational Biology.
Abstract:
Membrane Computing originates from the observation that eukaryotic cells have an internal organisation defined by membranes. In the framework provided by Membrane Computing several biological processes and phenomena occurring in eukaryotic cells have been studied from a computational point of view or have been used to develop algorithms for solving computationally hard problems.

Some of the questions that this fascinating field of research tries to answer are:
1. How could we use living cells to perform computation?
2. Would our definition of computation change as a consequence of this?
3. Could such a cell-computer outperform digital computers?

In this talk I will give an overview on Membrane Computing and an answer to the questions above.

Biography:
Dr. Pierluigi Frisco is a lecturer in the School of Mathematical and Computer Sciences, Heriot-Watt University, UK. After completing his PhD at the Leiden University, The Netherlands (September 2004), Dr. Frisco was appointed as a lecturer in the Department of Computer Science at the University of Exeter from where he moved to his present post in 2006.

Dr. Frisco's research has always been at the interface of Computer Science, Mathematics and Biology. His research interests are system biology, theoretical computer science and natural computing.

Recently, Dr. Frisco wrote a monograph "Computing with Cells: Advances in Membrane Computing" (Oxford University Press). He is a member of the Conference on Membrane Computing steering committee. He is also the editor of the International Journal of Natural Computing Research.