Editorial: Biologically Inspired Networking

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Editorial:

Biologically inspired networking is the emerging interdisciplinary research field that seeks the understanding of key principles, processes and mechanisms in biological systems and leverages the understanding to develop novel networking mechanisms. To highlight recent advances in biologically inspired networking, we have organized the special issue based on selected papers presented at the 10th EAI International Conference on Bio-inspired Information and Communications Technologies (March 15–16, 2017 Hoboken, New Jersey, USA). We have also solicited papers through an open call and included in the special issue after rigorous review. As a result, we have selected 6 papers for inclusion in the special issue. The brief summary of these papers is given in the following.

In the first article titled "From Blindness to Foraging to Sensing to Sociality: an Evolutionary Perspective on Cognitive Radio Networks", Wisniewska et al. introduce the new notion of evolutionary pressures in cognitive radio societies and show how it can drive the emergence of advanced sensing capabilities and sophisticated resource sharing. In particular, they consider biologically inspired evolutionary stages of cognitive radio societies: consuming, foraging, contention-sensing, and sociality, and demonstrate that, at each stage of evolution, a subpopulation performs more advanced sensing and extract greater utility from spectrum resources. Through mathematical modelling and analysis, they identify critical factors that accelerate or inhibit evolution of cognitive radio societies.

The second article, "A Chemical Reaction Algorithm to Solve the Router Node Placement in Wireless Mesh Networks" by Sayad et al., considers the router node placement in wireless mesh networks. Specifically, this paper considers the following problem: given a set of mesh clients deployed in a rectangular area, determine the best placement of mesh routers so that both client coverage and network connectivity are maximized. To solve this problem, a metaheuristic technique is inspired based on the observation that, in chemical reactions, molecules interact to reach a low stable energy state. Simulation results are provided to demonstrate that the proposed bio-inspired algorithm outperforms the existing genetic algorithm and simulated annealing.

In the third article titled "A Cognitive Routing Protocol for Bio-Inspired Networking in the Internet of Nano-Things (IoNT)", Al-Turjman proposes a framework for data delivery in nano-scale networks. The proposed framework facilitates the development of energy-efficient applications in the Internet of Nano Things (IoNT) where data is relayed via nano-routers from multifarious nanonodes towards a gateway connected to a large-scale network such as the Internet. In packet routing and data delivery in the proposed framework, the entire network energy is considered and the next hop is chosen. Simulations results are presented to confirm the effectiveness of the proposed approach in comparison to other baseline energy-aware routing protocols.

In the fourth article titled "Bio-inspired Active System Identification: a Cyber-Physical Intelligence Attack in Networked Control Systems", Sa et al. consider cyber-physical attacks on Networked Control System (NCS) and propose an Active System Identification attack where the attacker injects data on the NCS to learn about its model. This attack is implemented based on two bio-inspired metaheuristics: backtracking search optimization algorithm and particle swarm optimization. The performance of implemented attacks is analyzed and the BSA-based attacks are found more effective. Toward the end, they demonstrate the degree of accuracy that the System Identification attack may achieve, highlighting the potential impacts and encouraging the research of possible countermeasures.

The mathematical properties of high-dimensional (HD) spaces show remarkable agreement with behaviors controlled by the brain. Computing with HD vectors, referred to as "hypervectors," is a brain-inspired alternative to computing

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with numbers. In the fifth article titled "Hyperdimensional Computing for Blind and One-Shot Classification of EEG Error-Related Potentials", Rahimi et al. describe the use of HD computing to classify electroencephalography (EEG) error-related potentials for noninvasive brain–computer interfaces. Their algorithm naturally encodes neural activity recorded from 64 EEG electrodes to a single temporal–spatial hypervector without requiring any electrode selection process. Using the full set of training trials, HD computing achieves higher classification accuracy compared to a conventional machine learning method.

The last article, "Similar Feed-Forward Loop Crosstalk Patterns may Impact Robust Information Transport across *E. coli* and *S. cerevisiae* Transcriptional Networks" by Syed et al., considers that evolved biological network topologies may resist perturbation to allow for more robust information transport across larger networks. They apply machine learning based regression modeling to evaluate how feed-forward loops interlinked by crosstalk altered information transport across a network in terms of packets successfully routed over networks of noisy channels via NS-2 simulation. They then observe that feed-forward loop crosstalk patterns correlate substantially with an improved chance for successful information transmission. They also observe that both *E. coli* and Yeast subnetworks demonstrate similar FFL crosstalk patterns that could enable robust information transport in these two organisms. This finding may potentially allude to common design principles in transcriptomic networks from different organisms.

As summarized above, this special issue highlights recent results in the emerging interdisciplinary field of biologically inspired networking. Although this field of biologically inspired networking has a long history, further research is needed for its practical application and development. We hope that the special issue facilitates further advances of the field. To conclude the editorial remarks, we thank the Edit-in-Chief, Dr. Imrich Chlamtac for helping us organize the special issue. We also thank all authors and reviewers who contributed to this special issue.

Tadashi Nakano is an Associate Professor of the Institute for Datability Science, Osaka University. He is currently serving as the Chair of the Technical Committee on Molecular, Biological and Multiscale Communications in the IEEE Communications Society. He is also serving as an Associate Editor of IEEE Transactions on Molecular, Biological and Multi-scale Communications (T-MBMC), an Associate Editor of IEEE Transactions on NanoBioscience (T-NB), and an Editor of Elsevier Nano Communication Networks. He has been engaged in research at the intersection of computer science and biology, including design, implementation, and evaluation of molecular communication systems, synthetic biological systems, and biologically inspired systems.

Adriana Compagnoni is an Associate Professor in the Department of Computer Science at Stevens Institute of Technology. She received her B.A. and M.S. from Escuela Superior Latino-Americana de Informática, Argentina, in 1989, and her Ph.D. from Katolieke Universiteit Nymegen in 1995 under the supervision of Henk Barendregt and Mariangiola Dezani. She was an EuroFOCS Fellow at the Computer Laboratory at the University of Cambridge, UK during 1995–1997 and a Marie Curie Fellow at University of Edinburgh, UK during 1997–1998. She then joined the Computer Science Department at Stevens Institute of Technology. Her research interest centers on Programming Languages with applications to Computational Modeling and Security. In 2001 Adriana Compagnoni received an NSF CAREER award to study A Formally Verified Environment for the Production of Secure Software. She has authored 40+ international refereed publications. She has made contributions to the fields of programming languages, type systems, concurrent calculi, and language-based security. Most recently her group developed a computational platform for the stochastic simulation of concurrent autonomous agents in 3D space that has been applied to modeling antibacterial surfaces, intra-cellular viral traffic, and the effect of counterfeit components in safety critical systems.