Can biological network topologies benefit engineered systems?

Preetam Ghosh, School of Computing, University of Southern Mississippi Email: preetam.ghosh@usm.edu, URL: http://orca.st.usm.edu/~pghosh/

Research Interests: Ghosh is a systems biologist primarily working on (i) reverse engineering algorithms for inferring gene regulatory networks (GRNs), (ii) analysis, modeling and visualization of GRNs, (iii) spatio-temporal simulation and modeling of biochemical networks, and (iv) understanding stochasticity and noise in biological networks. He has also been working on applying principles of genomic robustness to the design of efficient sensor and social networks and mobile computing issues in pervasive grids.

Challenges in engineered systems: While conventional schemes design systems that are optimized and engineered to perform a well-defined task, the challenge today is to design robust autonomic systems that will follow simple rules to grow and self-manage. Such designs are typically impeded by common wireless network problems characterized by scalability, heterogeneity, complexity and dynamicity that call for novel out-of-the-box approaches. The robustness features inherent in biological systems can provide insights into the solution of such networking problems. A bio-inspired mechanism should ideally possess several advantages (e.g., scalability to number of nodes, self-organizing properties, simplicity in control rules, and adaptability and robustness to changing and fluctuating environments) that are sought in engineered systems including wireless sensor networks (WSNs) and dynamic social networks.

Applying genomic robustness to WSNs: The robustness and adaptability of cellular functions to stress arises from the optimized structures of their gene regulatory networks (GRNs) among others. The transcriptional regulation of cell functions operates near target states, called "attractors" [1]. Given that genes are either expressed (ON) or not (OFF), attractors correspond to "robust" functional cellular steadystates (or phenotypes) and are indentified as the terminal states of a GRN's Boolean state-transition diagram. We hypothesize that such attractors will serve as means to (a) design novel routing strategies [2] and network topologies, (b) identify critical nodes, and (c) identify sensor-failure mitigation and packet loss strategies in WSNs. Considering individual genes as sensors and the entire GRN topology as the sensor connectivity graph, the peculiarities of the gene-gene interactions (up- and down-regulation) can determine the analogous sensor-sensor interactions [1]. Thus, the packet routing problem in WSNs is analogous to the signal transmission problem in GRNs. While such signal transmission robustness is highly sensitive to the underlying GRN topology, the equivalent packet-routing problem is also expected to benefit from the advantages of attractor based robustness (that can be defined based on the WSN topologies), wherein a solution will preserve signal transmission under selective sensor failure and a noisy wireless channel. In particular, one needs to solve the inverse WSN design problem, to identify "optimal" wiring rules that maximize the probability of successful packet transmission. The guiding principle is to follow nature's foot-steps in designing simple rules (i.e., routing algorithms) that guarantee maximum efficiency over an optimized WSN topology.

The importance of Topology: Many researchers have investigated the structure of biological networks in general and GRNs in particular and define a host of metrics to characterize them: node degree, average path length, average clustering coefficient, centrality, presence of network motifs etc. More recently, a scale-free network model has been proposed, since biological networks exhibit a power law distribution in their node degree. These networks are typically quite robust against failures generated by random removal of nodes. Thus, another important question that one needs to answer involve the identification of specific metrics in these optimized GRN topologies that are mainly responsible for their robustness (measured in terms of the number of attractors their state transition maps posses).

Acknowledgements: Thanks to M. L. Mayo, E. Perkins (US Army Labs) and S.K. Das (UT Arlington) for their contributions and NSF for providing financial support.

References

[1] P. Ghosh, M. Mayo, V. Chaitankar, T. Habib, E. Perkins, S. K. Das, *Principles of Genomic Robustness inspire Fault-tolerant WSN topologies - A Network Science based Case Study*, PerSeNS 2011.

[2] K. Leibnitz, M. Murata, Attractor selection and perturbation for robust networks in fluctuating environments, IEEE Network 24(3): 14-18 (2010).