

Topological Properties of Evolved Robot Brains

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Abstract

Functional networks—be they biological, social, or technological—have characteristics that distinguish them from random or non-functional networks (Barabasi and Albert, 1999; Albert and Barabasi, 2002; Alon, 2007). Most well-known among these characteristics is the (approximately) scale-free degree distribution (probability that a node has k edges) of functional networks, as opposed to the binomial distribution of Erdős-Renyi random graphs. Another feature is a short mean path length through the network (also known as the ‘small-world’ property) that implies that signals can travel to any part of the network quickly (Girvan and Newman, 2002). While these properties are shared by protein-protein networks (Albert, 2005), metabolic (Jeong et al., 2000; Wagner and Fell, 2001) and signaling (Barrios-Rodiles et al., 2005) networks, the topological and graph-properties of biological neural networks, in particular animal brains, are much less studied. Reigl et al. (2004) studied the connectivity patterns and computational modules in the nematode *C. elegans* brain, and found that it was structured into small computational modules that are over-represented with respect to an equivalent random network, yet with a degree distribution that is neither scale-free nor Poissonian.

The topological structure of animal brains is likely to be even more interesting than protein-protein interaction networks because the computational power of brains is thought to be almost entirely due to its wiring pattern and hierarchical organization (see, e.g., Hawkins, 2004). At the same time, this pattern is not at all well understood, and the information about the wiring pattern of *C. elegans* mentioned earlier is unique in the literature. A promising direction for the study of network topology in the absence of detailed biological data is the Artificial Life approach, where functional networks are evolved that determine the survival of artificial organisms in an artificial chemistry and genetics. Recently, we used this approach to understand modularity in evolved artificial metabolic networks (Hintze and Adami, 2008) and developed new tools to dissect their topological and functional characteristics. Here, we apply some of these tools to the study of the brains of robots that have evolved to behave in a simulated world. These brains are based on an artificial chemistry and genetics, and are grown from a single cell that harbors the genome that specifies the development and function of the brain. Because neither the structure nor the computational algorithms for function are predetermined, the resulting networks of neurons are unlike anything human engineers

would design, and instead resemble the connectivity patterns of the *C. elegans* brain. The robots that are controlled by these brains are simulated versions of real robots (the ATRV Jr. of the iRobot[®] Corporation) whose properties we tested in our laboratory. Both the robot and its environment are simulated in a three-dimensional world that implements realistic rigid body dynamics via the Open Dynamics Engine (ODE). As a consequence, evolved controllers could in principle be transplanted onto the simulated robots’ real-world counterparts.

Neural computational tissues (“brains”) are grown from genomes that implement neural network development and function based on a set of rules (“genes”) that are conditionally executed, that is, regulated, by a set of simulated proteins produced by the cells in the tissue. This system (“SIMNOESIS”) is based on the NORGEV platform (Astor and Adami, 2000; Hampton and Adami, 2004) but was completely rewritten in order to be able to evolve complex tissues that process many temporally varying input signals. We evolve neural tissues on two-dimensional grids (of up to 15x15 neurons) that control a simulated ATRV Jr. with 19 sensors (17 sonars, a compass, and a sensor relaying distance to goal), controlling two motors driven by two actuators for differential steering. The evolved tissues control complex robot behavior, such as wall-following, obstacle avoidance, and goal-finding, using a complex network structure reminiscent of the *C. elegans* connection graph. The fitness evaluation of a genome consists of growing the network, and evaluating the behavior of the robot in a 3D environment (Chaumont et al., 2007), akin to the fitness evaluation in the work of Sims (1994). Fitness evaluation and evolution via a Genetic Algorithm is implemented within the EVO software (Chaumont, 2007).

We analyze the properties of evolved neural networks using standard tools (such as edge-distribution, shortest-path length, and betweenness centrality), as well as new tools that reveal robustness and modularity via clustering methods and information theory. We find that the topological properties of evolved functional networks are very different from their randomized counterparts, and characterize the “rarity” of these networks with standard statistical tests. Finally, we compare the topological properties of our evolved networks to the connection graph of *C. elegans*.

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