Behavioural Selection Pressure Generates Hierarchical Genetic Regulatory Networks

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Introduction

The field of 'evo-devo'—evolutionary developmental biology—is making rapid inroads to biological questions that encompass phylogenetic evolution and ontogenetic development, specifically in regards to genetic regulatory networks (GRNs). However, there is relatively little understanding so far of how selection pressure shapes GRNs (Carroll 2000). We have shown that by enhancing evolutionary algorithms with genetic regulatory networks, it is possible to not only evolve simulated agents that can perform behavioural tasks, but it is also possible to analyze both evolved GRNs, and the evolutionary history of them in the evolving population (Bongard 2002). Here we show that successful evolutionary runs produce heirarchical GRNs: there is a dominant unidirectional flow in gene regulation, and relatively few cyclical gene regulation pathways. Artificial Ontogeny extends the genetic algorithm to include ontogenetic development. In the results presented below, agents are tested for how fast they can travel over an infinite horizontal plane during a pre-specified time interval. The fitness determination is a two-stage process: the agent is first grown from a GRN (the growth phase), and then evaluated in its virtual environment (the evaluation phase). See (Bongard 2002) for methodological details.

Results

Sixty independent evolutionary runs of 300 generations each were conducted, using a variable length, floating-point genetic algorithm with a population size of 300. The best fitness curve of the most success-
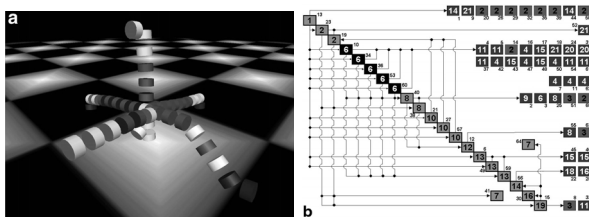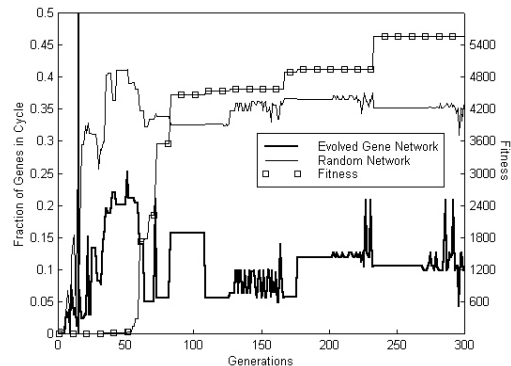

Figure 2: Evolutionary change of gene networks.

ful run is plotted in Fig. 2. The GRN of the fittest agent in each generation was transformed into a directed graph, and Warshall's algorithm was used to compute how many of the genes in each GRN were part of a cyclical genetic pathway, and scaled to the range $[0,1]$. Finally, for each of these GRNs, 10 random graphs were generated with the same number of nodes and directed edges. The proportion of nodes lying along a cyclical path was computed using the same method as for the GRNs, and divided by the total number of nodes, to determine the random graph's cyclicality. The cyclicalities were averaged for each set of 10 random graphs, and are also plotted in Fig. 2. It can be seen that after generation 15, when the agents in the population begin to move, and thus are selected based on their behaviour, the evolved GRNs begin to exhibit much lower cyclicality than the random graphs of the same size, which indicates this is an evolved response to selection pressure.

References

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Figure 1: **a:** Most successful, evolved agent. **b:** Its GRN viewed as a graph.