On location independent representations and self-organization

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1. INTRODUCTION

We study the self-organization of genomic symbols on a genetic algorithm with a location independent representation—the Proportional Genetic Algorithm (PGA) [2]. Self-organization of genomic symbols is possible because location independent representations ensure the absence of selective pressure for a particular order. We hypothesize that self-similarity emerges because self-similar genomes are more robust with respect to crossover and mutation and because it favors positive correlations between the form and quality of candidate solutions.

The PGA is a Genetic Algorithm (GA) with a representation based on protein concentrations rather than on the usual gene ordering. A PGA translates strings of genes into multisets of proteins prior to fitness evaluation. As a result, there is no fitness pressure for any particular gene ordering and the order of the genes is free to evolve along with the candidate solutions that they encode. Previous studies have shown that genomic symbols under these circumstances are evenly distributed throughout the genome and that they appear to form building blocks of a peculiar type: coarse grained versions of the entire genome. We ask the fundamental questions: *what is the emergent genomic ordering when there is no selective pressure for any particular ordering? and why?*. We use two very different methods to analyse the emergent genomic structure: standard equal-symbol correlation analysis, and an experimental method of our own making to analyse the self-similarity of genomic segments with repect to fitness. Our results can be summarized as follows:

1. The equal-symbol correlation on completely location independent genomes, as implemented by the PGA, resembles white noise behavior and the emergent genomic structure is self-similar with respect to fitness.

2. Emergent genomic self-similarity seems to produce the following effect: it favors positive correlations between form and quality of candidate solutions, a key property needed for stochastic search algorithms such as evolutionary algorithms; and it reduces schemata disruption caused by crossover.

2. CONCLUSION

When genomic order is free to evolve, the genome self-organizes in response to the dynamics of the evolutionary system. In the PGA case, it self-organizes into a fractal-like structure in which genomic segments have approximately the same fitness as the entire genome. These fractal-like genomic structures appear to favor a key property for stochastic search: the positive correlation between form and quality of candidate solutions.

For the full experimental analysis and results, we refer the reader to [1].

3. REFERENCES

[1] I. Garibay, A. S. Wu, and O. Garibay. On favoring positive correlations between form and quality of candidate solutions via the emergence of genomic self-similarity. In *Proceedings of the 2005 Genetic and Evolutionary Computation Conference*, Washington, D.C., 2005. ACM.

[2] A. S. Wu and I. Garibay. The proportional genetic algorithm: gene expression in a genetic algorithm. *Genetic Programming and Evolvable Hardware*, 3(2):157–192, June 2002.