

ABSTRACT

COMPUTER EVOLUTION OF GENE CIRCUITS FOR CELL- EMBEDDED COMPUTATION, BIOTECHNOLOGY AND AS A MODEL FOR EVOLUTIONARY COMPUTATION

by

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This dissertation describes how to improve automated design and evolution in computers using the structuring of genetic programs in biological systems. It also shows how to 'reprogram' cells to perform useful tasks by embedding computer-evolved code in biological organisms. This reprogramming makes it possible to exploit in new contexts the cell's ability to self-repair, replicate, and generate chemicals, light, or motion at microscopic scales.

Biological systems evolve to create clever designs for solving problems, using mechanisms that do not explicitly involve knowledge or intelligence. The designs that result are often superior to the best human designs. The mechanisms involved reuse and recombine previously discovered structures -building blocks- to generate more complex designs. Such processes reduce problems that grow exponentially in difficulty with size to simpler problems with a hierarchical structure.

AI search techniques like Genetic Algorithms attempt to emulate this mechanism and harness it for automated programming and problem solving and have been

successfully applied in a vast number of areas as a powerful black-box design and optimization tool.

However, current implementations still require significant human input in the initial problem formulation (whereas real evolution does not), which also results in different customizations for each problem, making it difficult to determine what characteristics are most useful for their performance. In contrast, biological evolution uses the same structures and mechanisms (DNA) to solve problems as different as flying or optimizing metabolic reactions.

I address these problems by identifying and testing key mechanisms and features responsible for the success of evolution from a computational perspective, and use them to explain previous results and build a single all-purpose implementation that, much like electronic circuits, avoids unwanted human overhead and customization by using the same sub-symbolic building blocks (gates and circuit patterns like loops, counters) for each problem.

I demonstrate its biological soundness by comparing simulation results to human-designed gene circuits and by developing a step-by-step mapping and fabrication of corresponding DNA sequences for a few examples (using genetic engineering to manipulate cellular aging, chemotaxis) which I then insert and test in cells.

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TABLE OF CONTENTS

ACKNOWLEDGMENTS	ii
LIST OF FIGURES	vi
LIST OF TABLES	x
PART I Introduction	1
CHAPTER 1 Overview:.....	4
PART II Foundations	11
CHAPTER 2 Genetic Engineering and Artificial Life.	13
2.1 Artificial Life Research.....	15
2.2 Biological computation.....	18
2.3 Problems with human design of Gene Circuits and the need for moving toward automatic computer design.....	20
2.4 Computer Design and Evolution of Blueprints for Gene Circuits and Genetic Modifications.....	26
CHAPTER 3 Artificial Intelligence and Biologically Inspired Computer Algorithms	28
3.1 Levels of Organization in Science, Engineering and Artificial Intelligence:.....	30
3.2 Research Directions in Artificial Intelligence.....	30
3.3 Cognitive and Logic-Based Systems	31
3.4 Search Algorithms and Combinatorial Explosion	33
CHAPTER 4 Building Blocks in Problem Solving and Design	36
4.1 The Importance of Representation and Encoding in Evolving Systems.....	38
4.2 Choosing the proper level of representation	41
4.3 Finding the Elusive Building Blocks in Computer Evolution	43
PART III Addressing unresolved issues in Computer Evolution Theory	48
CHAPTER 5 Revising Computer Evolution through Molecular Genetics and Sub-symbolic Building Blocks	51
5.1 The Larger Role of Molecular Genetics in Evolution	51
5.2 Descriptive vs. Algorithmic Representation	52
5.3 A common problem with previous work reintroducing molecular concepts in GA.....	57

5.4	Bit rearrangement and position-independent representations.....	58
5.5	Symbolic vs. sub-symbolic representation and gene expression.....	62
PART IV Modeling Biological Programs, evolution, and reuse mechanisms		
IN computers		65
CHAPTER 6 Revisiting GA and Learning Classifier Systems		67
6.1	Escaping GA's No Free Lunch Theorems.....	71
CHAPTER 7 The living cell as an operating system for evolution and integration of biological nanomachines		74
7.1	Two main types of cells: Eukaryotes and Prokaryotes	77
7.2	Designing devices from assembly of not fully understood biological nanomachines.....	80
7.3	Biological Hardware vs. Abstract Problem Solving.....	81
CHAPTER 8 Modifications in the Three Aspects of Biological Programs: Execution, Encoding, and Evolutionary Operators:		84
8.1	Execution	85
8.1.1	Protein-protein interactions.....	85
8.1.2	Fast Reversible and Enzymatic Interactions	86
8.1.3	Signal Degradation and Accumulation	88
8.1.4	Multiple Message lists and compartments	90
8.1.5	Metabolic and Environmental Simulations.....	92
8.2	Encoding	97
8.2.1	Markers and Floating Redundant Representation.....	98
8.2.2	Modifiers	101
8.2.3	Multiple regulatory elements and protein domains	102
8.3	Evolution and Genetic Operators.....	104
8.3.1	Homologous Recombination	104
8.3.2	Transpositions, insertions, deletions and duplications.....	105
8.3.3	Mutations	106
CHAPTER 9 Summary: Properties of the Ideal Computer Evolution Algorithm.....		107
9.1	Sub-symbolic building blocks.....	108
9.2	Supporting and Assembling Mechanisms in Execution:	109
9.2.1	Voting mechanisms and Parallel Execution	110
9.2.2	Variable scoping	110
9.2.3	Developmental assembly of faster decision systems, self- assembly and fractal encoding.....	111
9.3	Supporting and Assembling Mechanisms in Evolution and design.....	112
9.3.1	Exploitation vs. exploration by replicate and diverge mechanisms	112
9.3.2	Resistance to damage	113
9.3.3	Fine-tuning and gradation	113
9.3.4	Program reuse by call by reference mechanisms	114
9.3.5	Preserving potentially useful genetic material	114

PART V Experimental Simulations and Comparisons of Search Performance	117
CHAPTER 10 Test problem: repression-only gene circuits	120
10.1 Shorthand notation and encoding.....	121
10.2 Experiment Set 1: Impact of position independence on recombination and crossover effectiveness.....	124
10.3 Experiment Set 2: Recombination of provided building blocks in variable-length list representation.....	127
10.3.1 Negative Effect of List Duplicate node removal	130
10.4 Experiment Set 3: Parallel Graph vs. Sequential Tree Structure	131
10.5 Experiment Set 4: Evolution vs. Standard Search (Hill Climbers).....	134
10.6 Simple thought experiment on the advantages of fractal representation	138
PART VI Converting Computer representation of circuits into a Practical Genetic Engineering Implementation	141
CHAPTER 11 Controlling cell-immortalization and aging.....	143
CHAPTER 12 Simple computer encoded programs for controlling cell-immortalization and aging	152
CHAPTER 13 Genetic Engineering implementation and construction steps.....	156
13.1 Retrieving full-length gene sequences.....	156
13.2 Concatenating DNA sequences.....	158
13.3 Extracting and copying DNA sequences from organisms and vectors.....	160
13.4 Verifying constructs by DNA sequencing	165
CHAPTER 14 Experimental results in living cells.....	167
PART VII Environment Simulations of Re-programmed Swimming Bacteria	173
CHAPTER 15 Bacterial Chemotactic Swimming: Environment simulation of complex behavior and time dynamics from simple circuits	175
15.1 Experimental Setup.....	176
15.2 Environment Simulation	177
15.3 Simplified Gene Circuit Representation	178
PART VIII CONCLUSIONS AND FUTURE DIRECTIONS	186
CHAPTER 16 Concluding Remarks.....	187
16.1 Contributions.....	187
CHAPTER 17 Future Directions - Toward Larger and More Complex Programs and Implementations.....	190
BIBLIOGRAPHY	194