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Evolvability, Complexity and Scalability of Cellular Evolutionary and Developmental Systems

Thesis for the degree of Philosophiae Doctor

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Abstract

Man-made systems, such as supercomputers and software, IT-infrastructures and networks of any kind, are continuously growing in size and complexity. As conventional top-down engineering techniques may have reached the limit of applicability, biological organisms have been able to evolve increasing levels of complexity. Such inherent biological complexity may be said to be open ended or unbounded. This is a result of a bottom-up emergent process which produced an astounding diversity of living organisms with remarkable abilities, such as adaptation to different environments or perturbations, and reproduction, being able to survive.

Even though a lot of work has been done towards a synthesis, it is still not completely clear how to unleash the full potential of biological properties into artificial systems. This thesis tackles the problem of better understanding the developmental process between genotype and phenotype and the evolution of complex systems made of large sets of elements interacting locally and giving rise to collective behaviour. In a traditional Evolutionary Algorithm approach, the genotype maps to a phenotype directly, i.e. direct 1-to-1 encoding. If one wants to scale-up the phenotype complexity, indirect encodings, e.g. developmental or generative mappings, are a necessity. In the experimental work, the chosen computational platform is Cellular Automata (CA). The biological metaphor can be applied to the physical structure similarities between artificial cellular systems and biological multi-cellular organisms. A CA can be considered as a developing organism, where the genome specification and the gene regulation information control the growth and differentiation of the cells. Such a dynamic developmental system can show adaptation, self-modification, plasticity, and self-replication properties.

In this thesis, four challenges of designing Evolutionary and Developmental (EvoDevo) systems are identified and studied further, each related to a specific research question:

RQ1. What kind of information must be present in the genome in order to produce computation in any of the computational classes?

RQ2. How to quantify developmental complexity, i.e. emergent phenotypic complexity?

RQ3. Do genome parameters give any information on the evolvability of the system? And if yes, can genome information be used to guide evolutionary search in favourable areas of the search space where the wanted emergent behaviour is more likely to be found?

RQ4. How can scalability of artificial EvoDevo systems be improved towards achieving systems that can fully unleash their inherent complexity, potentially at the levels of complexity found in nature?

The results in this thesis show that abstract measures of phenotypic complexity may be suited to characterize emergent cellular organisms. Genome information may be related to emergent complexity and such knowledge may be used to guide evolutionary search. For scaled-up systems, it may be possible to allow indirect encodings with genome representation growth. A framework for the evolutionary growth of genomes is proposed.

Preface

This doctoral thesis was submitted to the Norwegian University of Science and Technology (NTNU) in partial fulfilment of the requirements for the degree of philosophiae doctor (PhD). This doctoral work has been performed at the Department of Computer and Information Science, NTNU, Trondheim, under the supervision of Associate Professor Gunnar Tufte.

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I would like to thank my supervisor Associate Professor Gunnar Tufte for his invaluable support, advice and trust, but most of all for his uniqueness. Thanks for making me discover this fantastic research world when I was an exchange student, thanks for helping me as a master's student, thanks once more for having me as a PhD student. I cannot imagine a better supervisor.

I extend my gratitude to my co-supervisors Professor Helge Langseth and Adjunct Associate Professor Jørn Amundsen for valuable feedback and encouragement during the mid-term evaluation meetings. In addition, I would like to thank my colleagues in the CARD group and in the entire Department of Computer and Information Science, for having created such a stimulating and pleasant working environment.

Thanks to all my friends, those who live in Italy, those here in Norway and those all around the world. Thanks for just being who you are.

All of this would not have been possible without the love of my parents. My deepest gratitude goes to them, Ambrogina and Doriano, and my grandmother Giovanna. Finally, thanks Ann-Marie for being the most important person of my life.

Stefano Nichele
June 06, 2014

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Abbreviations

AE	Artificial Embryogeny
AI	Artificial Intelligence
AL	Artificial Life
CA	Cellular Automaton
CC	Cellular Computing
CGP	Cartesian Genetic Programming
DS	Development Step
EA	Evolutionary Algorithm
EC	Evolutionary Computation
EHW	Evolvable HardWare
EvoDevo	Evolutionary and Developmental (Systems)
FPGA	Field-Programmable Gate Array
FSM	Finite State Machine
GA	Genetic Algorithm
GP	Genetic Programming
GRN	Gene Regulatory Network
IBD	Instruction-Based Development
LUA	Last Universal Ancestor
LZ77	Lempel-Ziv 1977
NEAT	NeuroEvolution of Augmenting Topologies
RBN	Random Boolean Network
RNN	Recursive Neural Network
RQ	Research Question
SMCGP	Self-Modifying Cartesian Genetic Programming

Chapter 1

Introduction

"I must not fear. Fear is the mind-killer. Fear is the little-death that brings total obliteration. I will face my fear. I will permit it to pass over me and through me. And when it has gone past I will turn the inner eye to see its path. Where the fear has gone there will be nothing. Only I will remain."

--- Frank Herbert, Dune - Bene Gesserit Litany Against Fear

Introduction

Humans' engineering abilities are remarkable. We managed to create a large amount of artefacts and machines of increasing complexity. Yet, we did not succeed designing and engineering behaviour and properties that are as complex as they appear in nature. Biological organisms are an impressive example of very energy efficient massively-parallel decentralized computation machines that emerge out of self-organization and adaptation to different environments. Properties that we take for granted in biological systems, such as reproduction, learning, and growth, are extremely hard to engineer and design. Having those properties in man-made technology would revolutionize our way of living and computing.

That is why there is a branch of computer science studies called bio-inspired computation. Biologically-inspired techniques have been quite popular and (to some degree) successful in recent years. Nevertheless, the complexity of the tackled problems is not at the "nature level" of complexity. This is because the underlying mechanisms of natural processes such as development and evolution are difficult to synthesize [37, 38] with the same level of detail in computers.

The focus of this work is to better understand the underlying properties of artificial development and artificial evolution with the goal of reducing the gap between the natural and the artificial domain. This includes taking inspiration from nature and biology towards artificial EvoDevo systems [23] that are capable to perform computation.

The first part is devoted to the study of genome parameters, e.g. some quantification of genotype properties, and their relation to the developed phenotypes. If the emergent behaviour can be forecasted from the genotype, it may be possible to use such information at the design stage of the system. Moreover, if solutions are to be found by evolution, such information may help guiding evolution in the vast search space, where the sought behaviour is more likely to be found. This is related to the second part of the thesis, which includes studies on evolvability and complexity. The last part of this thesis tackles the problem of scalability. As in biological systems, genotype-to-phenotype mapping allows a single cell to develop into a multi-cellular organism like the human body, which consists of roughly $3.72\text{x}10^{13}$ cells. The "building instructions" included in the DNA have a much smaller representation, estimated between 22 000 and 25 000 genes [5]. For artificial systems that target the development of phenotypes made of a vast amount of components, it is not completely understood how to represent the genotype. It is also not clear which size or which mapping to use, so that evolvability is not annihilated, complexity is not bounded (open-ended evolution), and the genotype representation can automatically scale if the phenotypic resources scale-up.

The Content of the Thesis

This thesis is at the intersection of several disciplines and research fields, which may be grouped under the term "biologically-inspired computation". That means borrowing principles for biology and nature with the ultimate goal of building man-made systems that exhibit behaviour characteristic of natural living systems, e.g. self-organization, emergence, evolution, development, and ability to perform computation. Consequently, the following concepts and theories are extensively used:

- Evolutionary Design: process of generating designs (in the broader sense, e.g. evolutionary search, evolutionary optimization, evolutionary artificial life) by computers [3] by means of Darwinian evolution, i.e. evolution by natural selection;

- Morphogenetic Engineering: modelling and implementation of "self-architecturing" systems [17], inspired by biological morphogenesis and multi-cellular development [35];

- Complex Systems and Complexity Theory: emergence of collective behaviour out of the local interaction of simple parts [1] and its quantification;

- Complexification: incremental evolution of structured phenotypes, starting from simple genomes, by systematic elaboration over generations by means of gene addition [69];

- Cellular Automata: mathematical and computational models (discrete dynamical systems) for complex natural systems containing large numbers of simple components, i.e. cells, which interact locally [81];

- Artificial Life: the study of "life-as-it-could-be" [38], in contrast to biology that studies "life-as-we-know-it", based on the only kind of life available to study, i.e. carbon-chain chemistry.

Research Questions

The main research question that is addressed in this thesis is:

How to apply artificial evolution and development for the design of cellular machines that can produce complex computation and modelling?

This includes investigation of the relation between genotype and emergent phenotype in EvoDevo systems with indirect encodings and how this is related to the complexity of the mapping. In artificial life systems, a main challenge is how to specify input data, i.e. system specifications and regulation mechanisms, and how to interpret the emergent dynamics of the system, i.e. the output. In this context, cellular machines [66] are based on three main principles: simplicity, vast parallelism, and locality. One example of cellular computation machine [65] is Cellular Automata (CA).

In answering this main question, other research questions (RQs) have been addressed:

RQ1: What kind of information must be present in the genome in order to produce computation in any of the computational classes?

In this context, computational classes [81] refer to distinct universality classes which characterize CA computational behaviour. As such, this research question includes the investigation of different genome parameters and their ability to forecast the emergent developmental behaviour of cellular systems. In an EvoDevo system, the dynamics of the developing organism can be traced down to the information and representation of the genome and gene regulation. What information must be present? What information processing capability must be available in the gene regulation? What cellular actions are required to be expressed as to be able to develop a target organism? If a developmental process is considered, the amount of regulatory information available to the developmental process is crucial, e.g. number of cell types, local neighbourhoods, and cellular actions such as growth, differentiation, and death.

RQ2: How to quantify developmental complexity, i.e. emergent phenotypic complexity?

Since no universally accepted notion of complexity exists [33], many authors use it implicitly without specifying which notion of complexity they are using. Yet, without any common measure of developmental complexity, any significant claim may not be verifiable. This study focuses on phenotypic complexity measures that take into account the development process as a whole together with the phenotypic changes that occur, e.g. trajectory, transient and attractor length. Moreover, this work investigates possible measures of structural complexity, which take into account different emerging structures and morphologies, e.g. Kolmogorov-based notions of complexity [41].

RQ3: Do genome parameters give any information on the evolvability of the system? And if yes, can genome information be used to guide evolutionary search in favourable areas of the search space where the wanted emergent behaviour is more likely to be found?

Evolvability is the ability of a system, e.g. a population of individuals, not only to create genetic diversity but also to create such genetic variation that is able to adapt and evolve. This means that it can produce beneficial variants that can be inherited by natural selection. In an artificial EvoDevo system, evolvability cannot be taken for granted. It is a property that depends on the chosen genotype representation and relative genotype-to-phenotype mapping. Therefore this study investigates if genome parameters can be an indicator of evolvability and whether they can be exploited towards a balance between robustness and evolvability.

RQ4: How can scalability of artificial EvoDevo systems be improved towards achieving systems that can fully unleash their inherent complexity, potentially at the levels of complexity found in nature?

Evolutionary design targets systems of increasing complexity, built out of myriads of components. Thus, indirect encodings and some kind of generative / developmental system are often a necessity. Scaling-up the genotypes accordingly to the scaling-up of phenotypes is an open challenge. For some systems, it would not be possible to fully specify all the genotype regulations, due to the extremely high cardinality of combinations. This makes it also infeasible to have a parameterization of the genotype space for such systems. This study investigates how to fill this scalability gap, taking inspiration from nature's way of scaling, e.g. morphogenesis and gene duplication.

The described research questions are in tune with at least three points of the "Open Problems in Artificial Life" [2]:

- Explain how rules and symbols are generated from physical dynamics in living systems;
- Determine what is inevitable in the open-ended evolution in life;
- Develop a theory of information processing, information flow, and information generation for evolving systems.

Thesis Outline

This thesis contains an overview and a collection of papers. The main work and contributions are in the enclosed papers. The overview of the thesis is organized as follows:

- Chapter 2 – theoretical background and related work. This chapter gives an overview of the relevant research areas and describes the theoretical background on which this thesis is based on.

- Chapter 3 – research process with an explanation of how ideas and concepts developed and their relation to the published work. This chapter describes the logical and chronological connections to the developed ideas. Papers not included in this thesis are also described.

- Chapter 4 – research results summary. This chapter summarizes the results and reviews the included papers (for the full papers see Appendices). The core contribution of this thesis is represented by the described papers. For readability purposes, the papers are summarized in this chapter.

- Chapter 5 – concluding remarks and recommendations for further work. The last chapter concludes the thesis by reviewing the research questions and given contributions. It also describes the challenges and potential directions for future work.

- Appendices – collection of papers.

Chapter 2

Background

"I see no good reason why the views given in this volume should shock the religious feelings of any one."
--- Charles Darwin, On the Origin of Species

Artificial Development

Artificial development is inspired by biological development, which is the complex process that “builds” a multi-cellular organism starting from the “instructions” encoded in the genome, the DNA. Since the sequencing of the human genome in 2001 [79], considerable steps have been taken towards a better understanding of biological morphogenesis. Development has many interesting features that may be convenient in the artificial domain, such as the ability to shrink the representation of an adult organism in a genetic plan which consists of a number of genes several orders of magnitude smaller than the total number of cells in the developed organism [5]. Artificial development uses indirect encoding [68], in contrast to direct encodings where there is a one-to-one mapping between the genotype and the phenotype. The different genotype-to-phenotype encodings are explained in the remainder of this chapter.

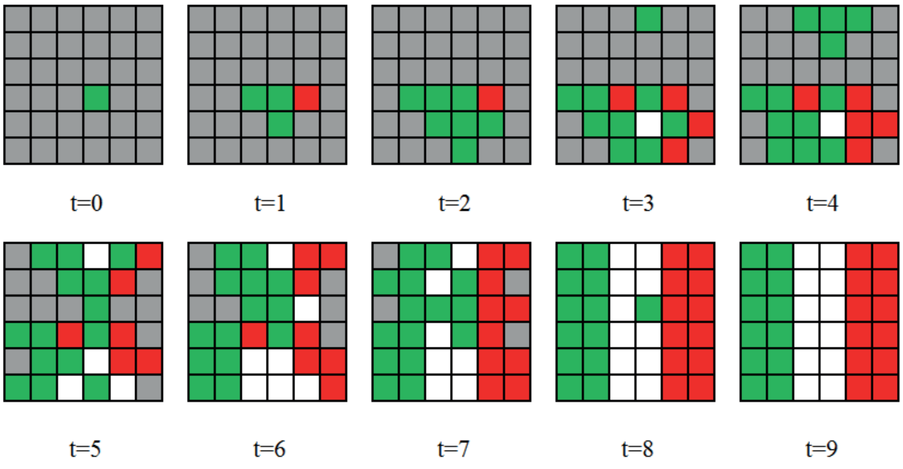

Figure 1: Example of development of an Italian Flag organism.

Figure 1 gives an example of the development of an Italian Flag multi-cellular organism. At time-step 1, only a single green cell, i.e. zygote, is placed in the centre of a 6 by 6 grid with cyclic boundary conditions. At each time-step the cellular world is updated synchronously by following the developmental plan, i.e. transition table based on neighbourhood (5 neighbours, von Neumann neighbourhood), which is present in every cell. At time-step 9 the Italian Flag pattern has emerged out of local interactions between cells and the structure remains stable afterwards, i.e. point attractor. In such a system, each cell has no knowledge of the overall state of the system, i.e. there is no central controller. The computation is purely based on local interactions between cells based on each cell's state and the neighbouring cell's state. Several types of artificial development exist. These are based on developmental rules [48, 65], generative grammars [44, 31], or other morphogenetic mechanisms [17]. The actual computation process is implemented in development steps, where cells can grow, differentiate and die. More information on the developmental model in Figure 1 is given in [55].

Artificial developmental systems may be considered to be discrete dynamic systems [32, 85] and the developmental process can be represented as series of discrete events, each representing a point in time on the developmental path from zygote to the multi-cellular organism. As such, a developmental trajectory represents all the discrete states that are traversed. This is visualized in Figure 2, where from node A there is a transition to node B, representing the state of the system at the following time step, i.e. developmental step. A trajectory starts with the initial state and ends when a state that was encountered before is traversed a second time. As such, a loop is created, i.e. attractor. An attractor can consist of a single node, a point attractor, or several states, a cyclic attractor. A transient phase can be identified as the part of trajectory from the initial state until an attractor begins.

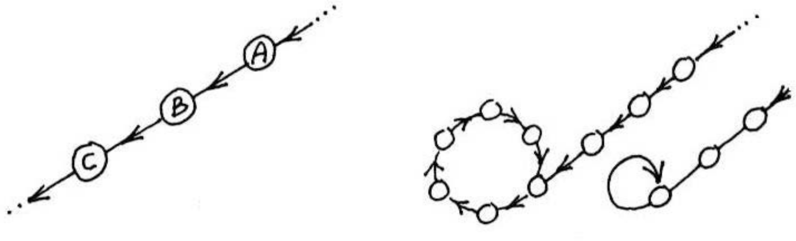

Figure 2: Trajectory and attractors of developmental systems (adapted from [84]).

Artificial Evolution

In 1859, Charles Darwin published his theories on the origin of species by means of natural selection. He summarized evolution as "...one general law, leading to the advancement of all organic beings, namely, multiply, vary, let the strongest live and the weakest die." [12]. The details of natural evolution are still under investigation by evolutionary biologists as the time-scale of evolution (millions of years) is still a challenge for direct experimentation. In computer experiments, evolution can be carried out in a realistic time and the main ideas have been applied successfully in several disciplines, such as the evolution of robot controllers [58], design of antennas [29], and many more [47, 20, 25]. In the computer context, evolution is referred to as Evolutionary Algorithms (EAs) [28]. These are population-based algorithms inspired by biological evolution. Genetic Algorithms (GAs) [22] are a branch of EAs that use genetic operators, e.g. mutation, crossover, selection to optimize solutions to different problems. Figure 3 shows a graphical representation of a standard GA. Since every individual in the population, i.e. genotype, represents a possible solution directly, i.e. phenotype, the evaluation can be executed directly and fitness is calculated for each individual. The selection process implements some sort of proportionate selection mechanism and reproduction recombinates the genes of the parents with crossover and random mutations. The offspring is then placed in the population again and the loop is repeated until some ending criteria is satisfied.

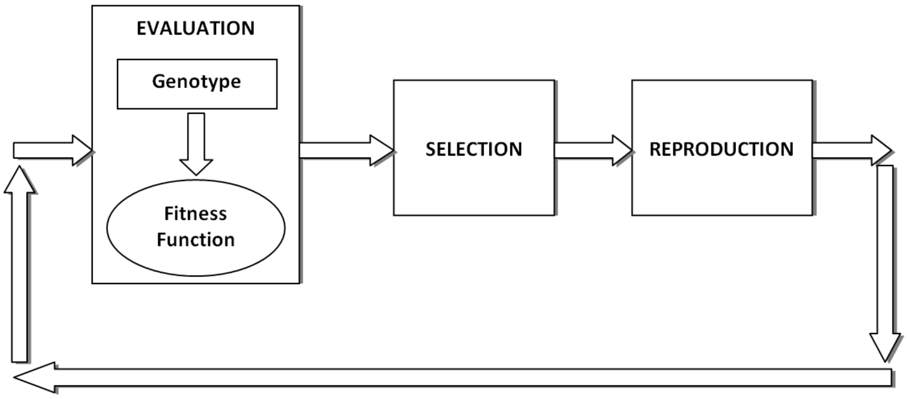

Figure 3: Graphical representation of a standard Genetic Algorithm.

EvoDevo

In Evolutionary and Developmental systems [23], solutions are produced by means of artificial development. As such, the fitness function cannot be calculated directly on the genotypes. The development process has to be executed as phenotypes are subject to fitness evaluation. A GA with artificial development is shown in Figure 4. The main difference lies in the evaluation step. The development process maps elements from the genotype space into elements in the phenotype space. Phenotypes are evaluated by the fitness function and selected accordingly. What go through the generations are not phenotypes but their genetic materials, i.e. genotypes. Standard GAs do not scale well when the problem size is increased, as due to the direct mapping between genotype and phenotype, the search space grows. Nature tells us that scalability in evolution is achieved with development, where genotypes are usually very small relative to the size and complexity of the resulting phenotype organisms [5].

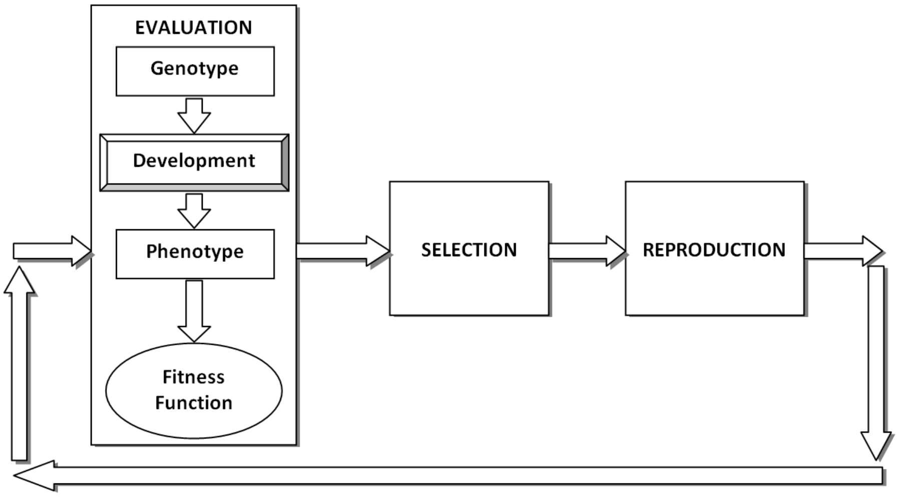

Figure 4: Graphical representation of a Genetic Algorithm with Development.

Cellular Automata

For the past 50 years computers have been based on the so-called von Neumann architecture, where one complex processor sequentially performs a single task at each time-step. Meanwhile, new computational paradigms have been explored and investigated. These new systems are based on a myriad of small and unreliable components called cells. Even if a single cell itself can do very little, the emergent behaviour of the system as a whole is capable of complex dynamics. In cellular computing [66] each cell can only communicate with a few other cells, most or all of which are physically close by, i.e. neighbours. One implication of this principle is that none of the cells has a global view of the entire system, thus there is no central controller. Such systems can be modelled using specific computational machines called Cellular Automata (CA) [48].

CAs are idealized versions of parallel and decentralized computing systems. Formally, a cellular automaton consists of a countable array of discrete sites or cells *i* and a discrete-time update rule Φ operating in parallel on local neighbourhoods of a given radius *r*. At each time the cells take on values in a finite alphabet *A* of primitive symbols: $\sigma^i_t \in \{0, 1,..., k-1\} \equiv A$. The local site-update function is shown in Equation 1.

$$\sigma^i_{t+1} = \Phi(\sigma^{i-r}_t, ..., \sigma^{i+r}_t) \qquad (1)$$

The state s_t of the CA at time *t* is the configuration of the finite or infinite spatial array: $s_t \in A^N$, where A^N is the set of all possible cell value configurations on a lattice of *N* cells. The "extended state space", denoted A^*, is the union of all states of any *N*. This is shown in Equation 2.

$$A^* = \mathrm{U}_{N \geq 0} A^N \quad \text{with} \quad A^0 = \emptyset \tag{2}$$

The CA global update rule Φ: $A^N \rightarrow A^N$ applies Φ in parallel to all sites in the lattice: $s_t = \Phi\, s_{t-1}$. For finite N it is also necessary to specify a boundary condition. The boundary cells are dealt with by having the whole lattice wrap around into a torus, thus boundary cells are connected to “adjacent" cells on the opposite boundary. The metaphor with biology can be exploited on CAs because the physical structure is similar to biological multi-cellular organisms. For this reason, CA can also be used to abstract and simulate a biological developmental process [18, 61].

John von Neumann [80] studied the first cellular automaton in the 1940s, as an abstract model of self-reproduction of machines inspired by biology [82]. With the contribution of Stanislaw Ulam [78], he defined a 29 state 2D CA that was able to self-replicate. In the 1960s, research on cellular automata was conducted through analysis of variations produced by a single automaton. For example, between 1960 and 1970, John Conway’s Game of Life automaton [4] was introduced and studied extensively to understand the behaviour of specific CA rules capable of complex dynamics. Later in 1980s, Stephen Wolfram demonstrated that one-dimensional cellular automata could be sufficient to investigate the totality of behaviour of CA rules. Instead of studying single CA rules, he grouped rules producing similar behaviour and studied different classes depending on the emergent patterns [81]. Wolfram identified four different computational classes:

- **Class 1 - fixed**: CA development leads to a homogeneous state. Almost all initial configurations relax after a transient period to the same fixed configuration. In this class, the outcome of development is determined with probability 1, independently on the initial state. The process is not reversible because all previous information is lost.
- **Class 2 - cyclic**: CA development leads to a set of stable and periodic structures. Almost all initial configurations relax after a transient period to a fixed point or a temporarily periodic cycle of configurations, which is dependent on the initial configuration. Some parts of the initial configuration are filtered out and others are propagated forever. The process is not reversible because information is partially lost during development.
- **Class 3 - chaotic**: CA development leads to a chaotic pattern. Almost all initial configurations relax after a transient period to chaotic behaviour. The development process is completely reversible since the previous state can be predicted from the current state, i.e. chaotic behaviour is not random.
- **Class 4 - complex**: CA development leads to complex localized structures, sometimes long-lived. Information is propagated by the automaton at variable speed. The process is non-reversible as the current site values could have arisen from more than one previous configuration. This is the only class that contains non-trivial automata.

All different cellular automata can be associated with one of the previous classes. In practice, with finite lattices, there is only a finite number of possible configurations and all rules lead to periodic behaviour. However, in theory the lattice is supposed to be infinite. The number of possible CA configurations grows exponentially with the increase of CA size and number of cell types. For example, whilst a 1D CA of size 16 and 2 cell types has 2^{16} (=65536) possible states, a 2 dimensional CA of size 16 by 16 and 3 cell types has 3^{256} (~$1.39\text{x}10^{122}$) possible states.

Wolfram proposed that the automata in the class 4 are capable of universal computation [81]. Figure 5 shows a CA rule-space set, with examples of space-time behaviours of CA in different classes [40].

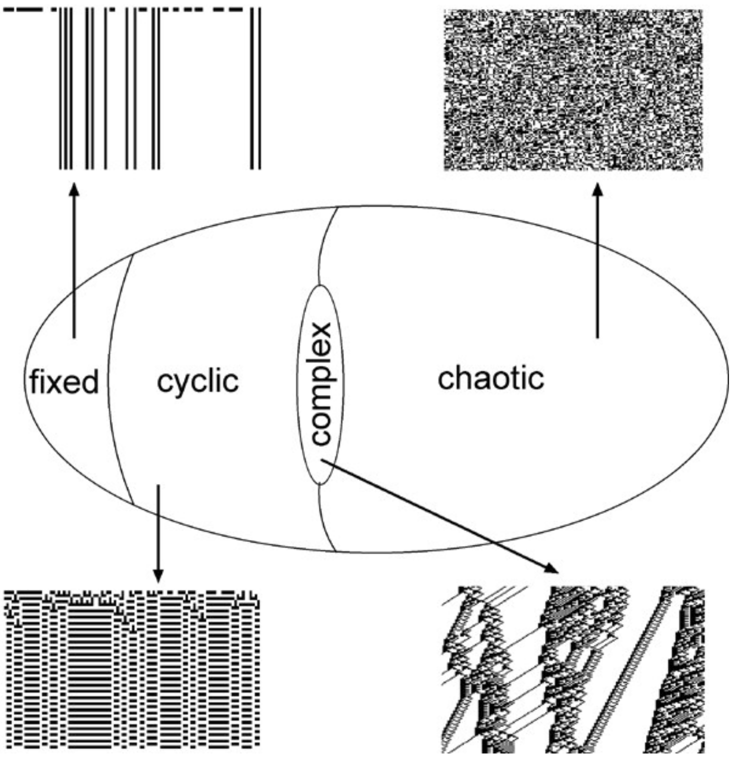

Figure 5: Chris Langton's schematic of rule space structure, with example space-time behaviours (adapted from [40]).

Edge of Chaos and Genome Parameters

The Edge of Chaos refers to a region in the CA rule space where there is a phase transition between ordered and chaotic behavioural regimes. Langton [39] hypothesized that it is more likely to find rules capable of complex computation in a region where the value of a parameter (λ) is critical. λ (Lambda) is defined as follows in Equation 3.

$$\lambda = 1 - \frac{q}{tot} \qquad (3)$$

A quiescent state *q* has to be chosen, which is usually the state representing the empty or dead state. In Equation 3, the ratio *(q/tot)* represents the fraction of "non-quiescent" states in the rule-table used for CA development. When λ is equal to zero, all the rules lead to a quiescent state and when λ is equal to Equation 4, the rule-table is the most heterogeneous (*k* represents the number of different possible states of a cell).

$$\lambda = 1 - \frac{1}{k} \qquad (4)$$

Traversing λ from 0 to *1-1/k*, it is possible to observe all the CA behaviour described by the Wolfram classes, from ordered behaviour to chaotic behaviour. For certain λ critical values, the CA tend to show complex and long-lived patterns as in Wolfram's class 4. Langton [39] hypothesized that Wolfram's class 4, the only one with CA capable of universal computation, is located somewhere around this critical value of λ, at the Edge of Chaos. It may be said that in such a region the basic conditions to support computation, i.e. information transmission, storage and modification, are most likely present [39]. Langton studied entropy as a measure of the information carried by each cell during the CA development and mutual information between a cell and itself at the next time step. His research supports the hypothesis that for λ values in the proximity of phase transitions, it is more likely to have well balanced conditions to support computation [39]. For example, information storage involves low entropy. On the other hand, information transmission requires increasing entropy. If a system needs to have both in order to perform computation, there must be a trade-off as it may happen in the proximity of phase transitions. Figure 6 shows a schematic plot of possible location of Wolfram classes in Langton's Lambda space [36].

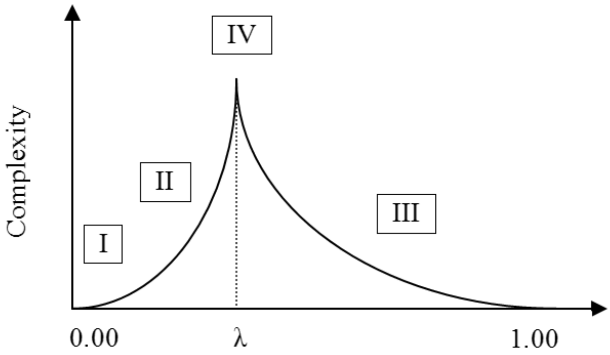

Figure 6: Location of the Wolfram classes in λ space (adapted from [36]). Class 4 is at a phase transition between ordered and disordered dynamics.

Besides Lambda, other genome parameters have been previously proposed. A neighbourhood dependent parameter was presented by De Oliveira [14] under the name Absolute Activity. Li [42] introduced Mean Field Parameters which monitor if the majority of the regulatory actions follow the "mean" configuration. De Oliveira [14] presented a very similar parameter called Neighbourhood Dominance. Binder [8, 9] introduced the Sensitivity parameter which measures the number of changes in the output of the transition table based on a change in the neighbourhood, one cell at a time, over all the possible neighbourhoods of the rule being considered. This has also been studied by De Oliveira [13, 14] under the name of Context Dependence. Wuensche [83] defined the Z parameter, derived from a pre-image calculation algorithm in the state-space. Different genome parameters have been shown to have specific abilities to characterize the CA rule space. However, most of the literature deals with 1-dimensional two-state CA.

Genotype-to-Phenotype Encodings

In the field of Evolutionary Computation (EC), each problem is represented as a genotype and a specific fitness function is designed to evaluate qualities of the wanted solutions. Evolutionary Algorithms (EAs) often use a one-to-one genotype-to-phenotype mapping, which means that a candidate solution generated by the EA can be directly mapped to the medium the solution was designed for. As such, each property and characteristic of the phenotype needs to be encoded in the genotype. Figure 7 depicts an example of direct mapping where each phenotypic property (network connection) is represented by a gene in the genome. If the desired phenotype requires more connections, the genotype would need more genes and consequently the EA search space would grow. Typical examples of EAs with direct mappings are evolved artificial neural networks for robot controllers [58]. Here the size of the network is predefined and thus the available number of genes to represent connections among them and/or connection weights are also predefined. The more complex the phenotype, the more complex the genotype.

Another possibility is to open for a redundant genotype-phenotype mapping [62] where the cardinality of the genotype space is larger than the cardinality of the phenotype space, i.e. many-to-one mapping. The nature of the mapping allows neutral genotype mutations [63] that do not alter the phenotypic characteristics but enable moving through the search space more easily and reduce chances of getting trapped in local optima [64]. Redundant representations are less efficient encodings that rely on additional genes that do not encode relevant information [60]. In nature, ontogeny allows shrinking complex organisms into compact genomes. EAs are very resource demanding and, if one-to-one direct mapping is used (or redundant mapping), they suffer from an inherent scalability problem. In general, a solution or an algorithm is said to be scalable if it is able to provide acceptable performances when the instance of the problem increases in size. Acceptable or tolerable performances may be referred to be non-exponential resources demand for a linear increase in the problem size. This is not the case for EAs, where an increase of the problem size does not reflect a proportional increase in the search space.

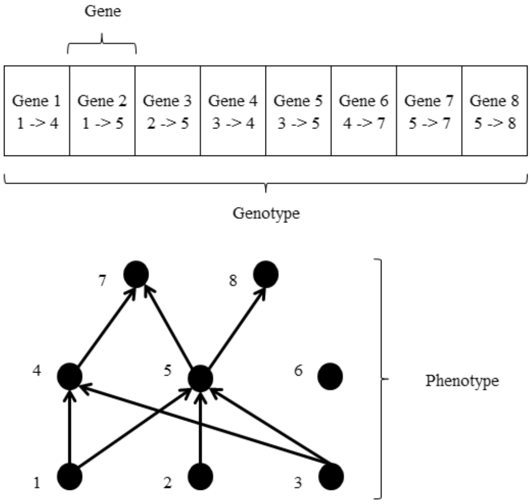

Figure 7: Example of direct mapping between genotype and phenotype. Each connection between two nodes in the network is represented by a specific gene.

One solution for the resource-demanding nature of EAs is to take inspiration from nature and somehow shrink the genotype, i.e. indirect mapping. This reduces the overall complexity of the genotype (and the search space magnitude) while adding more complexity to the genotype-to-phenotype mapping and the underlying development process. Thus the challenges are finding an efficient developmental mechanism and a suitable indirect representation that is able to exploit such a development process.

Even though developmental systems are widely used [75, 16, 47, 30, 68], the genotype representation scalability challenge still exists. For several developmental systems it would not be feasible to represent all the possible regulatory combinations in the genotype, e.g. complete regulatory information for Tufte's CA based model [74] would require the specification of 54^5 regulatory possibilities, Miller and Banzhaf's cellular developmental Cartesian Genetic Programming (CGP) model [47] a total of 768^9, von Neumann's universal constructor [48] 29^5 combinations. For many systems, using fixed-length genotypes, i.e. a subset of all the possible regulatory combinations, is a necessity. In cellular models the total possible number of regulatory combinations is N^K, where N is the number of possible states each cell can hold and K is the neighbourhood. Bidlo [7] had an instruction-based cellular model with 4 possible cell states and neighbourhood of size 5 which used a restricted transition function of only 10 entries, Tufte [73] had a model with 13 possible cell states and 5 neighbours whether the available regulatory rule-set was restricted to 64. Tufte and Thomassen [77] investigated scaling of genomes with fixed-length representation and allowed 4, 5, 6 and 32 regulation rules out of the possible regulatory information based on 3 cell types and 5 neighbours (13 cell types for genome of size 32). In all such cases, the maximum representation was pre-defined and could not change during evolution. The available regulatory information was designed a priori by trial and error or by estimation and did not guarantee that a possible solution could be found at all or that the same solutions could be achieved with a smaller genotype representation. Moreover, the maximum complexity of the system was predetermined, in the sense that the reachable search space was shrunk by the chosen representation. If one wanted to scale-up the system by allowing a larger neighbourhood or more available cell states, the chosen representation may not be large enough to accommodate solutions anymore.

Complexification

Biological organisms are the best example of scalability, ranging from simple unicellular to multi-cellular organisms, where trillions of cells develop from a single cell which holds the complete genome. Roughly 3Gb of information is required to encode the necessary base pairs for a fully sequenced human genome [79]. Obviously, the optimization of the genetic plan is the result of evolution by natural selection. The means of genome optimization are genetic operators, e.g. mutation, crossover. However, genomes of different species have different lengths. There is scientific evidence that all species have evolved and diverged from a common ancestor [72] [70], i.e. last universal ancestor (LUA), which was most likely a unicellular organism that has lived some 3.5 to 3.8 billion years ago [15] [21]. The mechanism of gene duplication [71] played an important role in genome expansion through evolution. This process allowed the addition of new genes to offspring genomes. In fact, some parental genes are not only copied but duplicated more than once. This leads to an offspring with larger genome than the parents, which allows genetic novelty and potential evolutionary innovation [59]. When a gene is duplicated, it creates a redundant gene with less selection pressure. This means that the duplicated gene can undergo mutations without having deleterious effects and eventually lead to a new functionality which produces an increase in fitness. The natural and biological process of incremental genome growth and elaboration [46] is known as complexification. Complexification through gene duplication is a plausible explanation of how compact, efficient and robust genomes have evolved and solved an inherent scalability issue, such as the representation of a complex multi-cellular organism in a simpler and shorter genetic plan, which allows morphogenesis.

Martin [46] investigated the impact of gene duplication in the origin of vertebrates. He claimed that such a duplication process produced an increased genome complexity before the origin of fish. Such duplication events happened at relatively high rates. Moreover, not only beneficial duplications become fixed in the genome but also neutral duplications with respect to fitness. In some cases, when the original gene faces negative mutations, the duplicated gene becomes also fixed. Key factors for gene expansion by gene duplication and optimization are then mutation and fixation. Zhang [86] studied the process of acquisition of new functions in duplicated genes. He argued that gene duplication is an extremely important factor for evolution, providing new genetic material for evolution to exploit by mutation, drift and selection, which leads to new gene functions or specialization of existing ones. In fact, in the three domains of life, i.e. bacteria, archaea and eukarya, there is strong evidence that large portions of genes appeared by gene duplication (data from sequenced genomes). As an example, around 38% of the Homo Sapiens genome is the result of gene duplication [43] and around 1800 duplication events took place since humans diverged from chimpanzees in roughly 6 million years. This produces evidence that such a mechanism contributes to plasticity / adaptation to changing environments and speciation, as well as the emergence of complex regulatory mechanisms in gene regulatory networks.

Yet, the same degree of scalability, evolvability and complexity is not achieved in evolved artificial developmental systems, partly because of the intricate genotype-to-phenotype mapping and relative encoding (direct encoding or fixed-length encoding), that leads to an extremely high dimensionality of the search space. Moreover, with direct encodings this incremental approach is difficult to achieve because each gene maps to a specific phenotypic functionality/structure and duplicating it would result in significant alterations of the phenotype [67]. It may be argued that in order to retain the advantages of biological complexification, it is necessary to exploit indirect encodings, where duplication would not have a disruptive effect. Newly added genes, once incorporated in the genome, would have time to be gradually modified without too severe consequences on development and eventually being optimized.

An alternative that can scale both genotype and phenotype information is to allow a variable length genome. If a mechanism of adding genes through gene duplication is allowed, it is possible to grow the genome size incrementally. This complexification strategy may help to solve the genotype representation scalability problem. Previous work done towards achieving genome size expansion includes [11], [27], [34], [45]. Federici and Downing [19] investigated neutral gene duplication in a cellular model with environmental chemicals. They studied genome scalability with direct encoding and embryonal stages, using a gene regulatory model based on recursive neural networks (RNN). Stanley and Miikkulainen [69] introduced NeuroEvolution of Augmenting topologies (NEAT), a complexification method for the incremental evolution of neural network architectures. Their main goal was to evolve robot controllers with direct encodings through gene duplication. They argued that incremental evolution of complex neural network genomes relies on three main technical components: meaningful crossover by means of historical markings for gene alignment, innovation through speciation which enables optimization, start from minimal genomes and allow incremental increase is size. Research on complexification of developmental systems with direct encodings may not be conclusive, but the basic idea regarding incremental evolution of genome representations have the potential for exploration with indirect encodings [67], where nature-like levels of complexity are targeted. This would allow starting from simple potential solutions in a low dimensional space and incrementally increasing the genotype complexity, disregarding how large a genotype would be to encode a solution.

Chapter 3

Research Summary

"It was the best of times, it was the worst of times."
--- Charles Dickens, A Tale of Two Cities

This chapter describes the research process and how the papers in this thesis were produced. It connects the theoretical background presented in Chapter 2 to the results presented in Chapter 4. To simplify the discussion, the papers are grouped into five categories according to the main contribution of each paper. The categories are summarized in Table 1. In Figure 8, a chronological representation of the work categories and different papers is presented. Figure 9 represents the same categories from a logical perspective, how the concepts are connected and how the work is related. A detailed description of both chronological and logical connections is discussed in the remainder of this chapter.

Research Process

The research work described in this thesis was part of a four-year PhD programme conducted at the Department of Computer and Information Science, Faculty of Information Technology, Mathematics and Electrical Engineering, NTNU. As agreed with the Department, 25% of the time was devoted to teaching duties. Only the research-related part of the PhD is included in the thesis.

Table 1: Paper Categories

Category	*Topic*	*#papers*
A	Genome composition and emergent behaviour: genome parameters, Lambda, forecast emergent developmental behaviour	2
B	Complexity: structural complexity, Kolmogorov approximations	1
C	Evolvability: parameters to guide evolution, incremental evolution	2
D	Scalability: evolutionary growth of genomes	2
E	Papers not included in the thesis	3

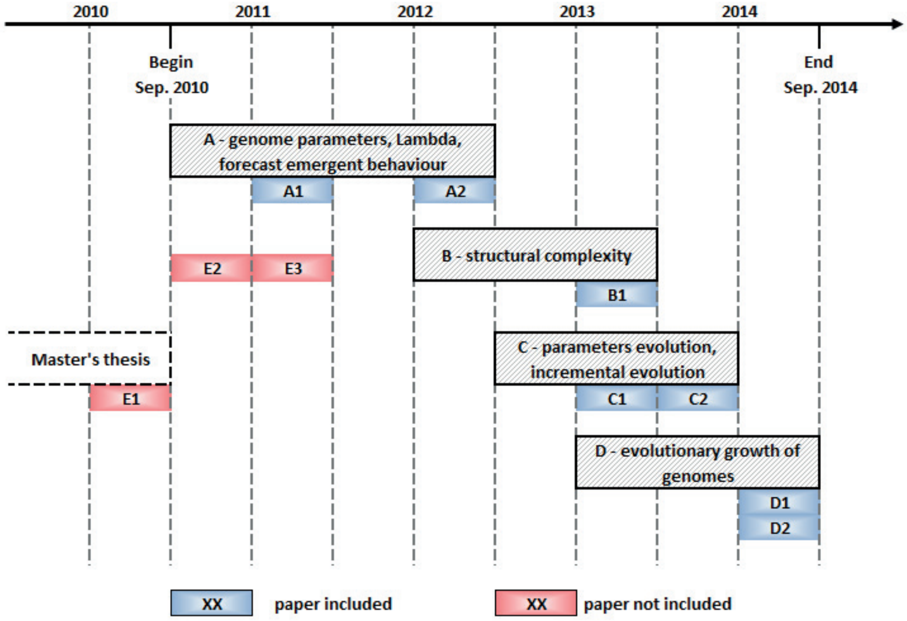

Figure 8: Chronological Structure of Papers and Concepts

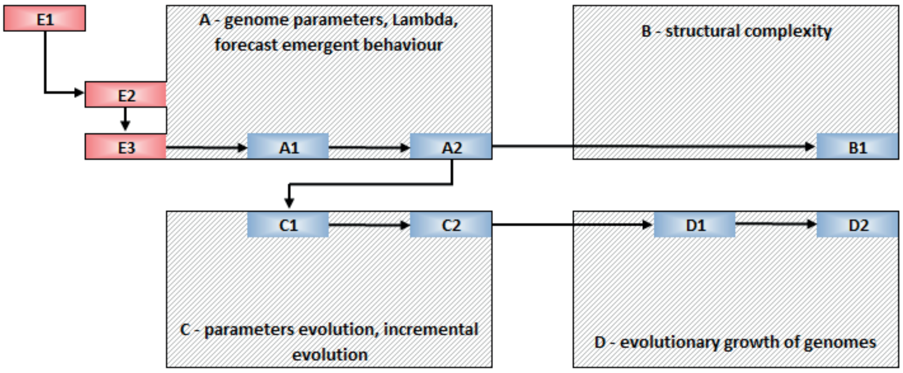
E1
A - genome parameters, Lambda, forecast emergent behaviour
B - structural complexity
E2
E3
A1
A2
B1
C1
C2
D1
D2
C - parameters evolution, incremental evolution
D - evolutionary growth of genomes

Figure 9: Logical Structure of Papers and Concepts

How the Ideas Developed

The initial idea was inspired by my master's thesis work, from which a paper was published as a summary [52], E1 in Figure 8 and Figure 9 (referred to as chronological representation and logical representation respectively). This work gave me a detailed insight into uniform and non-uniform cellular automata, the concepts of trajectories and attractors as measures of emergent behaviour, and a clear understanding of the genotype-to-phenotype mapping concept. As such, this was a valid starting point for further investigation.

Category A

As shown in the chronological representation, the PhD work started in September 2010. The first research topic is represented in Category A and relates to the first research question (RQ1). In general, the initial idea included investigation of genome information and the ability to forecast the emergent developmental behaviour. The initial choice of genome parameter was Langton's Lambda, in relation to trajectory and attractor length, cells' growth and change rate. This is investigated in Paper A.1. Other parameters have been also studied and compared in Paper A.2. The papers included in Category A are summarized and referenced in Table 2.

Table 2: Paper Category A

ID	*Title*	*Ref.*
A.1	On the Correlations Between Developmental Diversity and Genomic Composition	[76]
A.2	Genome Parameters as Information to Forecast Emergent Developmental Behaviors	[53]

Category B

During the investigation of the ideas in Category A, the second research question (RQ2) started to be addressed. This was analysed in more detail in Paper B.1, which is clearly connected to Category A, as shown in the logical representation. Previously studied complexity measures, such as trajectory and attractor length are investigated in relation to a more specific measure of structural complexity based on approximations of Kolmogorov complexity [41] by means of Lempel-Ziv compression. The paper in Category B is summarized and referenced in Table 3.

Table 3: Paper Category B

ID	*Title*	*Ref.*
B.1	Measuring Phenotypic Structural Complexity of Artificial Cellular Organisms	[56]

Category C

Almost in parallel with Category B, the ideas in Category C started to develop as a clear continuation of the work carried out in Category A. Since it was shown that genome parameters could give useful information about the emergent phenotypic behaviour, Category C investigated plausible applications of genome information to guide evolution and to give information on the evolvability of the system. This addressed the third research question (RQ3). The papers included in Category C are summarized and referenced in Table 4.

Table 4: Paper Category C

ID	*Title*	*Ref.*
C.1	Evolution of Incremental Complex Behavior on Cellular Machines	[54]
C.2	Investigation of Genome Parameters and Sub-Transitions to Guide Evolution of Artificial Cellular Organisms	[57]

Category D

During the development of the ideas in Category C, some concerns arose particularly about how to achieve scalability in EvoDevo systems. Genotype information may not be fully specified for systems where some characteristics are scaled-up, or it may be impossible to extrapolate genome parameters as to be able to guide evolution or forecast the system behaviour. As such, in order to address the fourth research question (RQ4), an evolutionary growth of genomes was investigated in Category D. The papers included in this category are summarized and referenced in Table 5.

Table 5: Paper Category D

ID	*Title*	*Ref.*
D.1	Evolutionary Growth of Genome Representations on Artificial Cellular Organisms with Indirect Encodings	[51]
D.2	Evolutionary Growth of Genomes for the Development and Replication of Multicellular Organisms with Indirect Encodings	[55]

Category E

Category E groups papers that were produced by the author but not included in this PhD thesis. In particular, Paper E.1 is more concerned with the author's master's thesis, which gave the initial ideas of what to investigate in this PhD research. Paper E.2 and E.3 are related to the first research question (RQ1) and Category A, but do not provide any concrete results, as they were written in the very first months of research. State-of-the-art and preliminary results were included. The papers included in Category E are summarized and referenced in Table 6.

Table 6: Paper Category E

ID	*Title*	*Ref.*
E.1	Trajectories and Attractors as Specification for the Evolution of Behavior in Cellular Automata	[52]
E.2	Discrete Dynamics of Cellular Machines: Specification and Interpretation	[49]
E.3	On the Edge of Chaos and Possible Correlations Between Behavior and Cellular Regulative Properties	[50]

Chapter 4

Research Results Summary

"Second star to the right, and then straight on 'til morning."
--- J. M. Barrie, Peter Pan

This chapter provides an overview of the papers included in this thesis, where and when they were published. The included papers are discussed in Sections A.1 through E.3. Each section contains the abstract of the paper and a description of the main contribution of the different co-authors. When relevant, the sections also include a discussion about how the work is seen in retrospective. The new papers D.1 and D.2 are very recent and do not include a real retrospective view. As such, a paper description with a state-of-the-art analysis is given. Finally, Section E lists the papers that are not included in this thesis.

Paper A.1

On the Correlations Between Developmental Diversity and Genomic Composition
G. Tufte and S. Nichele
13th Annual Genetic and Evolutionary Computation Conference, GECCO
ACM 2011

Abstract

In this work we target to measure genomic properties in EvoDevo systems so as to predict phenotypic properties related to the emergence of artificial organisms. We propose a measurement, λd, based on the composition of the genome, which can give prediction of how the emerging organism will develop. The experimental approach uses a minimalistic developmental model. The results show that the parameter λd can predict phenotypic properties. The aim of introducing a parameter like λd is to get more knowledge on the relation between genomic properties and phenotypic properties of developing organisms.

Roles of the Authors

I contributed to the formulation of the initial idea proposed by Tufte. I also ran all the simulations and proposed the experimental setup, tested the results, and analysed the data. Tufte contributed through supervision and wrote most of the paper. I wrote parts of the paper, provided feedback and corrections.

Retrospective View

This paper continued the preliminary work started in [49] on CA of size 3x3 cells. Here the considered grids are of 4x4 cells and 5x5 cells. Moreover, λd genome parameter is investigated not only in relation to trajectory and attractor length but also in relation to internal qualities of the developmental process, i.e. growth and change rate. At this stage of research, the promising results obtained with Lambda opened several research directions, which I addressed in the following papers.

Paper A.2

Genome Parameters as Information to Forecast Emergent Developmental Behaviors

S. Nichele and G. Tufte

11th International Conference on Unconventional Computation and Natural Computation, UCNC

Springer 2012

Abstract

In this paper we measure genomic properties in EvoDevo systems, to predict emergent phenotypic characteristic of artificial organisms. We describe and compare three parameters calculated out of the composition of the genome, to forecast the emergent behavior and structural properties of the developed organisms. The parameters are each calculated by including different genomic information. The genotypic information explored are: purely regulatory output, regulatory input and relative output considered independently and an overall parameter calculated out of genetic dependency properties. The goal of this work is to gain more knowledge on the relation between genotypes and the behavior of emergent phenotypes. Such knowledge will give information on genetic composition in relation to artificial developmental organisms, providing guidelines for construction of EvoDevo systems. A minimalistic developmental system based on Cellular Automata is chosen in the experimental work.

Roles of the Authors

I had the main idea, ran all the simulations, tested the results, analysed the data and wrote the paper. Tufte contributed through discussions and corrections of the paper.

Retrospective View

This paper studied different genome parameters and their ability to capture developmental properties. The identified parameters were different in the way they used genome information. It would have been advantageous to investigate Cellular Automata with a larger number of cells. This would have been challenging as very long attractors may have been found, but it would have been realistic for cells' growth rate and change rate. Moreover, at this stage it was not clear how to address situations where the number of available cell types was scaled-up and thus the CA developmental table would increase exponentially, making it unrealistic to list all the regulatory combinations. This would have affected the way parameters are calculated, e.g. with incomplete genotype information.

Paper B.1

Measuring Phonotypic Structural Complexity of Artificial Cellular Organisms. Approximation of Kolmogorov Complexity with Lempel-Ziv Compression

S. Nichele and G. Tufte

4th International Conference on Innovations in Bio-Inspired Computing and Applications, IBICA

Springer 2013

Abstract

Artificial multi-cellular organisms develop from a single zygote to different structures and shapes, some simple, some complex. Such phenotypic structural complexity is the result of morphogenesis, where cells grow and differentiate according to the information encoded in the genome. In this paper we investigate the structural complexity of artificial cellular organisms at phenotypic level, in order to understand if genome information could be used to predict the emergent structural complexity. Our measure of structural complexity is based on the theory of Kolmogorov complexity and approximations. We relate the Lambda parameter, with its ability to detect different behavioral regimes, to the calculated structural complexity. It is shown that the easily computable Lempel-Ziv complexity approximation has a good ability to discriminate emergent structural complexity, thus providing a measurement that can be related to a genome parameter for estimation of the developed organism's phenotypic complexity. The experimental model used herein is based on 1D, 2D and 3D Cellular Automata.

Roles of the Authors

I had the main idea, supervised the running of all the simulations, tested the results, analysed the data and wrote the paper. Tufte contributed through discussions and corrections of the paper. A master's student carried out part of the experimental work under my supervision.

Retrospective View

The approach of using a compression algorithm as an approximation of Kolmogorov complexity has been found to be promising. One of most interesting features is the dimensionality independence, i.e. can be applied to 1D, 2D or 3D CA. One aspect that has not been covered is the actual complexity of specific developed morphologies or shapes. Moreover, how to relate such a complexity measure with the development or self-replication of different structures and complexities, such as those used in Paper D2, e.g. French Flag or Norwegian Flag.

Paper C.1

Evolution of Incremental Complex Behavior on Cellular Machines

S. Nichele and G. Tufte

12th European Conference on the Synthesis and Simulation of Living Systems, ECAL

MIT Press 2013

Abstract

Complex multi-cellular organisms are the result of evolution over billions of years. Their ability to reproduce and survive through adaptation to selection pressure did not happen suddenly; it required gradual genome evolution that eventually led to an increased emergent complexity. In this paper we investigate the emergence of complexity in cellular machines, using two different evolutionary strategies. The first approach is a conventional genetic algorithm, where the target is the maximum complexity. This is compared to an incremental approach, where complexity is gradually evolved. We show that an incremental methodology could be better suited to help evolution to discover complex emergent behaviors. We also propose the usage of a genome parameter to detect the behavioral regime. The parameter may indicate if the evolving genomes are likely to be able to achieve more complex behaviors, giving information on the evolvability of the system. The experimental model used herein is based on 2-dimensional cellular automata. We show that the incremental approach is promising when evolution targets an increase of complexity.

Roles of the Authors

I had the main idea, ran all the simulations, tested the results, analysed the data and wrote the paper. Tufte contributed through discussions and corrections of the paper.

Retrospective View

This paper was our first approach to evolving genomes incrementally and use genome parameters as a measurement of the evolvability of the system. At this stage, it was still not clear how to evolve variable length genomes, but this work laid the foundation for further research in Paper D.1. In Paper C.1, the incremental evolution approach was shown to be better than a traditional GA for the evolution of cellular organisms with trajectories and attractors of different lengths. It would have been interesting to investigate the robustness of the evolved solutions. For example, how fragile they are to external perturbations, both at genotype level, i.e. mutations in the rule table, and at phenotype level, i.e. perturbation of the system state during development.

Paper C.2

Investigation of Genome Parameters and Sub-Transitions to Guide Evolution of Artificial Cellular Organisms

S. Nichele, H. Wold and G. Tufte

16th European Conference on the Applications of Evolutionary Computation, EvoApplications

Springer 2014

Abstract

Artificial multi-cellular organisms develop from a single zygote to complex morphologies, following the instructions encoded in their genomes. Small genome mutations can result in very different developed phenotypes. In this paper we investigate how to exploit genotype information in order to guide evolution towards favorable areas of the phenotype solution space, where the sought emergent behavior is more likely to be found. Lambda genome parameter, with its ability to discriminate different developmental behaviors, is incorporated into the fitness function and used as a discriminating factor for genetic distance, to keep resulting phenotype's developmental behavior close by and encourage beneficial mutations that yield adaptive evolution. Genome activation patterns are detected and grouped into genome parameter sub-transitions. Different sub-transitions are investigated as simple genome parameters, or composed to integrate several genome properties into a more exhaustive composite parameter. The experimental model used herein is based on 2-dimensional cellular automata.

Roles of the Authors

I had the main idea, supervised the development and simulation, checked the data results, and wrote the paper. Wold carried out most of the experimental work under my supervision, as part of his master's thesis. Tufte contributed through discussions and corrections of the paper.

Retrospective View

This paper tackled the problem of using genome information to guide evolution. The chosen genome parameter was Lambda, as it was the one studied in more details in the previous papers. The chosen measurement of developmental complexity was trajectory length, as it contained information on both the transient and attractor length. It may have been more interesting and intuitive to use attractor length as a measure of developed organisms, as it is more often used in the literature and it was suggested by some anonymous reviewers of the paper. Moreover, genome parameter sub-transitions have been shown to be promising in forecasting the emergent behaviour, showing similar potential to Lambda. In order to have more definitive results on the point, it would have been interesting if the paper had included a study on the usage of sub-transitions during evolution, as done in the first part of the paper with Lambda.

Paper D.1

Evolutionary Growth of Genome Representations on Artificial Cellular Organisms with Indirect Encodings

S. Nichele, A. Giskeødegård and G. Tufte

Artificial Life – Official Journal of the International Society of Artificial Life

MIT Press 2014 – SUBMITTED

Abstract

Evolutionary design targets systems of continuously increasing complexity and size. Thus, developmental or generative mappings, i.e. indirect encodings, are often a necessity. “Scaling-up” the complexity of a developed phenotype, and thus the relative solution space, does not explicitly affect the genotype search space, since each genotype does not represent a specific phenotype object directly. Phenotype solutions are the result of an incremental building process. As the phenotype information is not encoded directly into a low-level genotype, the high-level developing information relies on an efficient mapping. Varying the amount of genotype information changes the cardinality of the mapping which, in turn, affects the development process. As such, open questions are: how much information must be present in the genotype? How to find genotype size and representation in which a developmental solution of given complexity would fit? Using the whole set of possible regulatory combinations may be intractable or hardly evolvable due to the cardinality of the search space. On the other hand, a restricted pool of genes may not be big enough to encode a solution, i.e. potential solutions may be excluded due to a reduced solution space, or may need complex heuristics to find out a realistic size. In nature, the genomes of biological organisms are not fixed in size; they slowly evolved and acquired new genes by random gene duplications. Newly added genes that potentially produced an increased fitness were kept and integrated in their genomes. Such incremental growth of genome information can be beneficial also in the artificial domain. For an Evolutionary and Developmental (EvoDevo) system with indirect encoding, we investigate an incremental evolutionary growth of genotype,

without any a priori knowledge on the necessary genotype size. An incremental increase in the dimensionality of the search space allows evolving increasingly complex solutions, providing scalability of the state and solution space. The key aspect of evolutionary genotype growth is the ability to solve difficult problems by starting with simple solutions in a low dimensional space and incrementally increasing the genotype complexity, by means of gene duplication. The experiments presented in this paper show that such an approach evolves scalable genomes, able to adapt genetic information content whilst compactness and efficiency are retained. The results are consistent when the target phenotypic complexity, the geometry size and the number of states per site are scaled-up. An artificial cellular developmental system based on cellular automata (CAs) is used as a test bed.

Roles of the Authors

I had the main idea, supervised the development and simulation, checked the data results, and wrote the paper. Giskeødegård carried out most of the experimental work under my supervision, as part of his master's thesis. Tufte contributed through discussions and corrections to the paper.

Analysis Summary

The idea of incremental evolution was tested before but still on fixed genome representations. This paper introduced a novel complexification method for cellular systems with indirect encodings. Other complexification methods presented in the literature have been shown to be promising with direct encodings. The idea of combining indirect encodings with incremental evolution of genome size provided a solution to the problem of scaling-up resources in artificial systems. In such case, it would not be realistic to calculate genome parameters because of the cardinality of the genotype space or because of incomplete genotype information.

Paper D.2

Evolutionary Growth of Genomes for the Development and Replication of Multicellular Organisms with Indirect Encodings

S. Nichele and G. Tufte

International Conference on Evolvable Systems, ICES SSCI (Symposium Series on Computational Intelligence)

IEEE 2014

Abstract

The genomes of biological organisms are not fixed in size. They evolved and diverged into different species acquiring new genes and thus having different lengths. In a way, biological genomes are the result of a self-assembly process where more complex phenotypes required more intricate and larger genomes to survive. In the artificial domain, evolutionary and developmental systems have often static size genomes, e.g. chosen beforehand by the system designer by trial and error or estimated a priori with complicated heuristics. As such, the maximum evolvable complexity is predetermined, in contrast to open-ended evolution in nature. In this paper, we argue that artificial genomes may also grow in size during evolution to produce high-dimensional solutions incrementally. We propose an evolutionary growth of genome representations for artificial cellular organisms with indirect encodings that, starting from a single gene, adds new genes when necessary, thus increasing the number of degrees of freedom and expanding the available search-space. Cellular automata (CA) are used as test bed for two different problems: replication and morphogenesis. The chosen CA encodings are a standard developmental table and an instruction based development. Results show that the proposed evolutionary growth of genomes' method is able to produce compact and effective genomes, without the need of specifying the full set of regulatory configurations.

Roles of the Authors

I had the main idea, ran all the simulations, tested the results, analysed the data and wrote the paper. Tufte contributed through discussions and corrections of the paper.

Analysis Summary

This paper provided a practical application of the evolutionary growth of genomes proposed in Paper D.1. The same methodology was tested with a different indirect mapping, i.e. instruction-based development. The identified problems were the development of structures from a single cells and the self-replication. The proposed approach has been shown to produce solutions to both problems. The evolved solutions are more compact and optimized than a standard genetic algorithm with fixed size genomes. Moreover, such a method does not require any a priori knowledge on the problem complexity. As such, it can be considered a valid alternative to any traditional fixed size genomes evolutionary algorithm, where there is an indirect mapping between the genotype and the phenotype.

Other Publications

In addition to the above publications, I have also produced the following contributions, which are not included in the thesis:

Paper E.1

Trajectories and Attractors as Specification for the Evolution of Behavior in Cellular Automata
S. Nichele and G. Tufte
Congress on Evolutionary Computation, CEC WCCI (World Congress on Computational Intelligence)
IEEE 2010

Paper E.2

Discrete Dynamics of Cellular Machines: Specification and Interpretation
S. Nichele
13th Annual Genetic and Evolutionary Computation Conference, GECCO
ACM 2011 (Doctoral Consortium Paper + Poster)

Paper E.3

On the Edge of Chaos and Possible Correlations Between Behavior and Cellular Regulative Properties
S. Nichele
IDI Doctoral Consortium
NTNU 2011

Chapter 5

Concluding Remarks and Further Work

"Omnis cum in tenebris praesertim vita laboret."
"Life is one long struggle in the dark."
--- Lucretius, De Rerum Natura (On the Nature of Things)

In this last chapter, the thesis contributions are summarized and the research questions raised in the beginning of this research are reviewed, together with some suggestions for future research directions.

Conclusion

In this thesis, novel bio-inspired techniques have been studied in order to design and exploit artificial EvoDevo systems. In particular, some of the main challenges have been identified and investigated with the goal of achieving artificial systems that can show evolvabilty, emergent complexity and scalability. The chosen test bed platform was Cellular Automata. CAs have similar properties to biological organisms, where a single cell, a zygote, develops into a multi-cellular organism by following the instructions encoded in the genome. Due to indirect genotype-to-phenotype mapping, the first part of the thesis was devoted to the investigation of genome parameters that could forecast the emergent developmental phenotypes (Paper A.1. and Paper A.2). As such, Lambda and other genome parameters were investigated in relation to emergent trajectory length, attractor length, cells' growth rate, and cell's change rate. Interesting genome parameter properties were found, in particular the potential for exploration of genome parameters during evolution.

In a parallel task, emergent complexity was studied, both as an abstract measure of phenotypic complexity, e.g. attractors or trajectories (Paper A.1 and Paper A.2), and as a measure of structural complexity by means of approximations derived from Kolmogorov complexity [41] (Paper B.1). Both measures have been found to be suitable for cellular systems, especially in relation to a genome parameter such as Lambda.

As genome parameters were shown to be able to characterize the phenotype space based on genome information, it was decided to use such knowledge to evaluate the overall evolvabilty (Paper C.1) and, as a step forward, to guide evolution towards favourable areas of the parameter space where the sought solution was more likely to be found (Paper C.2). This method has been suitable when trajectories of different lengths were to be evolved. Moreover, parameter sub-transitions were identified for such cases where it would not be possible to use Lambda (or other parameters) because of missing genome information, i.e. only a set of all the regulatory combination was present, or it would not be realistic to specify the complete genotype due to the high number of neighbourhood configurations. Such sub-transitions could be used as simple parameters or composed together to create custom parameters. In particular, the ratio between death and growth sub-transitions has been shown to have potential to characterize the development of cellular organism with trajectories and attractors of different complexities.

Finally, a strategy to achieve scalability has been investigated for such systems where it would not be feasible (or it would be not realistic) to exploit genome information due to scaling-up in the state space (set of all possible combinations of states the system can show), in the rule space (set of all the permutations of neighbourhood configurations) or in the search space (set of all genotypes targeted by evolution). The proposed complexification method for systems with indirect encodings, named evolutionary growth of genomes has been found to produce compact and effective genomes when cellular organisms with attractors of different lengths ought to be evolved (Paper D.1). Such a method has been successfully used in relation with another indirect mapping, i.e. instruction-based development, for evolving solutions to the replication problem (self-replication of given structures) and the development problem (development of a given structure from a zygote). The proposed method was able to evolve solutions starting from a genome made only of a single gene and incrementally increasing the genome size by means of gene duplication, followed by genome optimizations (Paper D.2).

As this thesis investigates several aspects of EvoDevo systems such as evolvability, complexity, and scalability, it can be considered as a pool of ideas and suggestions for further investigation rather than providing a conclusive final answer. In the next section the main contributions are described in relation to the initial research questions. The last section is devoted to further work.

Contributions

Looking back at the main research question in the thesis:

> *How to apply artificial evolution and development for the design of cellular machines that can produce complex computation and modelling?*

the question was approached through four sub-questions. In this section, the latter are reviewed and linked together with the main results and contributions presented in the thesis.

RQ1. What kind of information must be present in the genome in order to produce computation in any of the computational classes?

- Genome parameters can give a plausible indication of what kind of information must be present in the genome in order to achieve certain developmental properties, such as attractor and trajectory length, cells' growth and change rate.

- Genome parameters do not guarantee that a specific genome would develop a target phenotype with a sought behaviour (even though it is more likely); on the other hand, they may guarantee that a specific genome would not end up in a specific computational class if the parameter value is not within the wanted range. For example, if a genome's Lambda value for a 2D CA with three cell types is 0.66, the emergent behaviour is more likely to be in the "edge of chaos" but it may end up in the "frozen" region. However, if the Lambda would be 0.25, it is guaranteed that the emergent behaviour will not be in class IV (of the Wolfram CA classes).

- Genome parameters, such as Lambda, have been shown not to be a specific case for certain CA settings; they can be generalized for cellular systems of different dimensionalities, CA grid size and the number of available cell types.

- Genome sub-transitions of different groups can be identified, e.g. growth, differentiation, death and no-change. As such, sub-transitions could be used as a single-transition parameter or composed together into a multiple-transition parameter. In particular, the composite death minus growth transitions difference has been revealed to be well suited to identify cellular organisms that develop long trajectories.

RQ2. How to quantify developmental complexity, i.e. emergent phenotypic complexity?

- Even though complexity can be considered at several levels, e.g. genotype complexity, phenotype complexity, genotype-to-phenotype mapping complexity, in an EvoDevo system the emergent complexity is a measurement of phenotypic and developmental properties. As such, the considered measurements have to quantify cell organization and/or functions that the organism is able to perform, the developing organism as a whole, and occurring phenotypic changes in terms of stability and structure.

- For a given organism, an initial cell, i.e. zygote, follows a developmental trajectory and after a transient phase reaches an attractor, i.e. a final stable state (point attractor) or a self-reorganizing cycle (cyclic attractor). As such, trajectory length and attractor length have been found to be plausible abstract measures of complexity, i.e. they do not code for any specific problem or computational task.

- Approximations of Kolmogorov complexity based on compression algorithms, e.g. Lempel-Ziv, may be used to quantify and estimate the emergent structural complexity. Such measurements have been shown to be consistent with other complexity measures such as attractor and trajectory length. Moreover, they could be related to the information present in the genome, i.e. genome parameters such as Lambda, and have been shown to be dimensionality independent.

RQ3. *Do genome parameters give any information on the evolvability of the system? And if yes, can genome information be used to guide evolutionary search in favourable areas of the search space where the wanted emergent behaviour is more likely to be found?*

- Genomes with a given parameter value are likely to evolve to genomes with similar developmental behaviour, as long as mutation results in an offspring with similar parameter value. This may give information on the evolvability and adaptivity of the system. Such ability of adaptive evolution is necessary for a system to be able to evolve.
- Genome parameters, such as Lambda and parameter sub-transitions, may be used to guide evolution in favourable areas of the search space where the sought emergent behaviour is more likely to be found. The search space would be explored in a smoother way, reducing the amount of potentially uninteresting search space available to evolution.

RQ4. *How can scalability of artificial EvoDevo systems be improved towards achieving systems that can fully unleash their inherent complexity, potentially at the levels of complexity found in nature?*

- Complexification in nature provides a scalability strategy for open ended evolution. A similar strategy has been proposed and tested successfully for artificial EvoDevo systems. Evolutionary growth of genomes has been shown to produce compact and effective genomes without the need for fully specifying all the regulatory combinations or estimating a priori the necessary genome pool with complex heuristics. Solutions are evolved starting from a low dimensional search space, e.g. single gene, and incrementally increasing the genotype complexity when necessary.
- Indirect encodings are a necessity when highly complex systems are targeted, e.g. potentially at levels of complexity found in nature.
- Gene duplication is a plausible mechanism for genotype expansion, which increases the dimensionality of the search space incrementally and allows genetic novelty and potential evolutionary innovation.
- Evolutionary growth of genomes may be applied for different genotype-to-phenotype mappings. In particular, it has been found to be suitable with traditional CA transition functions based on neighbourhood configurations and more intricate encodings, e.g. instruction-based development, for the evolution of organisms with different attractor lengths and the development and self-replication of given structures.

Further Work

While this research work was conducted, several research opportunities for possible fruitful extensions have been encountered. New questions have emerged and still remain open for investigation. As such it may be said that this thesis partially answers the initial theme of applying artificial evolution and development for the design and modelling of cellular machines that can produce complex computation.

The proposed methods, e.g. genome parameters to guide evolution, and evolutionary growth of genomes, may not be considered definitive as more investigation is required, particularly towards systems' robustness. Evolved solutions may be compared in terms of how fragile they are to external perturbations, both at genotype level, i.e. mutations in the rule table, and at phenotype level, i.e. perturbation of the system state during development.

Another interesting aspect that is worth investigating is the usage of other genome parameters to guide evolutionary search. These include: Sensitivity [8], Mean field parameters [42], Z [83], or other sub-transitions (either single transitions or multiple transitions). The Lambda parameter [39] was used extensively in this thesis but other parameters were only investigated partially.

The used methods and principles from complex systems theory may be applied to other domains, such as evolution in materio [24, 10], to investigate materials for favourable computational properties, i.e. explore measurable local properties such as neighbourhood information exchange between nano-devices. As a result, that localized information may be related to global behavioural properties.

On the scalability theme, evolutionary growth of genomes may be expanded further, not only in terms of increased search space but also in the state space. Essentially let the growth happen both in terms of genotype size, i.e. number of genes, and states that each cell can hold, i.e. number of possible states per site. This may help to achieve true complexification, meaning that the boundaries would not be fixed by the state space, which is more or less fixed in every artificial system. This may allow systems to evolve for arbitrary complexity levels and find solutions to arbitrary complex problems [67].

In addition, the employment of evolutionary growth of genomes with instruction-based development [6] has potential for future investigation. Here, the chosen instruction set may be optimized and reduced in order to minimize the cardinality of the instruction space. Another research path would be to test this approach on other interesting computational tasks besides development and replication, e.g. rotation or mirroring of given structures.

One of the most exciting yet speculative future directions may be to introduce instructions that can modify the program itself, as investigated in Self-Modifying Cartesian Genetic Programming (SMCGP) [26]. This may allow artificial cellular systems with diversification of cells' programs, enabling potentially hierarchical organization and aggregation of cells, similar to biological cells, tissues, organs, and organisms.

To conclude with a metaphor, the beauty of this research field and the work conducted in this thesis is exactly its open-endedness: potentially infinite new ideas and open questions for future work, which is just as open-ended as evolution and complexity in nature.

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Appendices

Paper A.1

On the Correlations Between Developmental Diversity and Genomic Composition

G. Tufte and S. Nichele

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On the Correlations Between Developmental Diversity and Genomic Composition

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ABSTRACT

In this work we target to measure genomic properties in EvoDevo systems as to predict phenotypic properties related to the emergence of artificial organisms. We propose a measurement, λd, based on the composition of the genome, that can give prediction on how the emerging organism will develop. The experimental approach uses a minimalistic developmental model. The result show that the parameter λd can predict phenotypic properties. The aim of introducing a parameter like λd is to get more knowledge on the relation between genomic properties and phenotypic properties of developing organisms.

Categories and Subject Descriptors

I.2.2 [**Artificial Intelligence**]: [Cellular arrays]

General Terms

Design, Experimentation

Keywords

Development, Cellular Computation, Emergence

1. INTRODUCTION

Evolved artificial developmental systems are systems that share and hold favourable features and there by also some of the inherent complexity of natural biological systems [34]. Favourable features of such artificial Evolutionary Developmental (EvoDevo [12]) systems may include adaptation [29], robustness [18] or scalability [16]. The biological inspiration to achieve such goals may be based on selected biological processes, e.g. adaptation by phenotypic plasticity [29], robustness by self-repair [23] or scalability of phenotypic size by growth [2].

Many artificial developmental systems are based on a cellular developmental model [7, 19, 3, 23, 30, 28], as in the biological counterpart the key element of cellular models is a cell. The cell is an autonomous unit that serve as construct and constructor of the emerging organism. Another key element in many of these models is an evolved gene regulatory network that is in control of cellular action, e.g. growth, differentiation and apoptosis. A consequence of such a cellular approach is a model that depends on autonomous cellular processes influencing on the developmental path and the behaviour/form of the resulting artificial organism. However, developmental models do not need to follow a cellular approach, many models depend on other principles then an autonomous cell, e.g. generative systems [15, 9], self modifying systems [14] or cellular encoding [11].

The topic of this work falls within EvoDevo systems with a developmental cellular model. As such, other models with their potential pros and cons are not covered any further.

The characteristics leading from the inherent autonomous properties place developmental systems within dynamical systems. Further, the cellular nature and lack of global control can result in nonlinear phenomena. These characteristics define several properties that may be favourable and necessary qualities to reach the target sought, but at the same time inherent property of such non-linear dynamic system also bring problematic issues. For instance a developmental system may show robustness to external perturbation [24], however the underlying model of the developmental process, i.e. a Cellular Automata (CA), is sensitive to initial information [33].

The dynamics of developing organisms can be traced to the information and representation of the genome and gene regulation; what information must be present? And what information processing capability must be available in the gene regulation network? These questions are highly connected to what kind of organisms an EvoDevo system can produce by evolution. ”Kind of organisms” includes dynamical properties related to self-organisation of structure and behaviour. If the developmental process is considered, the amount of regulatory information available to the developmental process is crucial. What amount of information must be available to the gene regulation? What cellular actions are required to be expressed as to be able to develop a target organism? e.g. von Neumann’s self-replicating automata [31] was originally defined with cells capable of expressing 29 states, later reduced by Codd to 8 [4]. For developmental systems we would like to be able to define what a cell needs to express, e.g. number of cell types, and what cellular reg-

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ulatory information that is needed to develop an artificial organism.

When an opinion on the above issues exists there is a need to define a genome representation for the evolutionary process. An important factor here is evolvability, we need a genome and a gene regulation process that is evolvable, i.e. can be included in an evolutionary search that stand a good chance of finding a possible candidate that fulfils the targeted goal.

By taking inspiration from earlier work of Langton [21] we try to explore possible connections between a measurement of how the genome is composite and phenotypic properties related to the developmental path of the emerging organism. The measurement proposed is similar to Langton's λ parameter. However, the definition of λ is modified to replace the CA with a simple minimalistic developmental system.

The experimental approach taken tries to reveal such possible connection between genetic information and developmental properties.

The article is laid out as follows: background information and motivation for the work is presented in Section 2. In Section 3 the development model used in the experiments is presented together with thoughts on genome representation and phenotypic properties. Section 4 discusses possible measurements of genetic and phenotypic properties. Results of the experiments are given in Section 5. A discussion of the ideas and the results are presented in Section 6. Finally Section 7 concludes the work.

2. BACKGROUND AND MOTIVATION

Developmental systems are closely connected to several complex systems. The lack of global control in developmental artificial organisms place such systems in the emergent computation [8] regime. Even though many developmental systems deal with structure as phenotypic target property [6, 23, 5, 28] instead of organisms that execute a computational property emerging from the development of a machine structure [10, 30]. The computations executed in every cell process the local information available to the cell and regulate cellular actions that are expressed in the phenotype, either as a change in structure and/or as a change in the developing computational machine. As such, the process of development itself is a dynamic system that interacts with its environment on a cellular and organism level [1].

2.1 A Developmental λ

The work of Langton and follow up findings on edge of chaos and possibility of a measurement for plausibility of computation [21, 27] may not be conclusive [26], but the basic idea regarding behaviour, i.e. number of states and transient length, linked to cellular regulative properties have a potential for exploration as to get an extended understanding of developmental systems.

2.2 Cellular Properties and EvoDevo Paths

A cellular developmental system may share properties with CAs and other sparsely connected networks. However, the processes of growth and differentiation in developmental systems part such system from other cellular systems. A developmental system is not static, the structure of the phenotype change according to cellular changes. Changes may materialise as an alteration in phenotypic shape directly influencing on phenotypic properties if structure is a goal in itself [5], or the cellular change may influence on computational behaviour by modifying the composition of a developing machine [29].

The dynamic machine and computational behaviour can be governed by two set of state variables and corresponding different dynamic laws. There exists a state space for the dynamic machine where each machine state (configuration) may produce a state space for computational behaviour.

3. EVOLUTION AND DEVELOPMENT

3.1 A Development Model

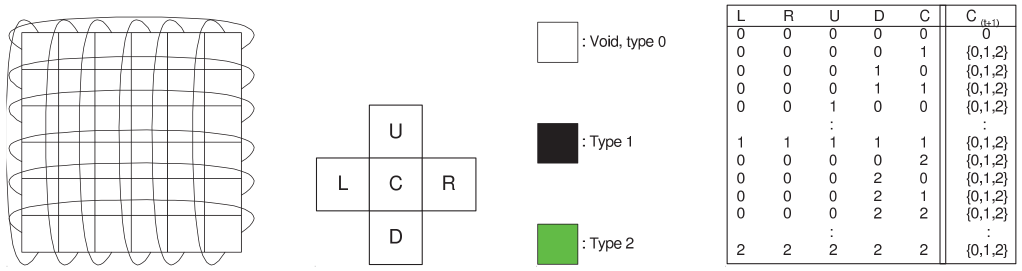
The developmental model used herein is similar to other models based on cellular automata, e.g. [23, 18, 29], including a synchronized cellular cycle, parallel operation and discrete cell states. To be able to have a complete regulatory network for all possible regulatory states the model needs to be minimalistic. However, two features are not taken to the minimal. The number of cell types is set to three instead of two. This was done to keep within multicellular development, i.e. two types of cells in addition to cells that are defined to be dead (void). To be able to keep the principle of a growing (expanding) organism there is a constraint on how a cell can come "alive". This constrain is to only allow cells that have at least one neighbour expressing a cell type different from void to be able to come alive. We also choose to use a two dimensional world as to make the phenotype closer to a developing organism.

In Figure 1 the minimalistic developmental model is shown. The organisms develop in a two dimensional grid world as illustrated in Figure 1(a). Development starts from a single cell placed in the grid. The placement of the first cell is of no importance as the grid uses cyclic boundary conditions.

The extracellular communications only include cell types. In Figure 1(b) possible communication for a cell is shown. The centre cell's (C) developmental process have information concerning the cell's own state and cell type of the four neighbouring cells.

To be able to conduct the experiments a developmental model with a limited number of regulatory possibilities was needed. Therefore the model was restricted to include three possible cell types, void (or dead) counts as a cell type since all possible states in the cellular neighbourhood must have an unique representation. With three cell types multicellularity is possible and at the same time the number of all possible cellular states in the defined neighbourhood is not terrifying large, i.e. max 243 (or 3^5). A developing organism will consist of different construct of these three cells. Figure 1(c) show a graphical representation where each cell is given a distinguishable colour.

The result is a minimalistic model were all input combinations to the development processes consist of only 3^5 possibilities. As such, all possible regulatory input combinations and resulting cellular actions can be represented as a table. The table in Figure 1(d) is a scaled down illustration. For the first entry in the table, i.e. all regulatory inputs set to 0, the output of the development process is fixed at 0. This is done to fulfil the stated constraint related to growth. All other regulatory inputs have a possibility of regulating the cell to be at any of the available cell types, indicated by the triplet $\{0, 1, 2\}$. Note that a cell can be regulated to "no change" if the regulatory output is the same as the centre cell of the regulatory input, i.e. $Ctype(t + 1) = Ctype(t)$.



L	R	U	D	C	$C_{(t+1)}$
0	0	0	0	0	0
0	0	0	0	1	{0,1,2}
0	0	0	1	0	{0,1,2}
0	0	0	1	1	{0,1,2}
0	0	1	0	0	{0,1,2}
		:			:
1	1	1	1	1	{0,1,2}
0	0	0	0	2	{0,1,2}
0	0	0	2	0	{0,1,2}
0	0	0	2	1	{0,1,2}
0	0	0	2	2	{0,1,2}
		:			:
2	2	2	2	2	{0,1,2}

(a) A 2D-grid defining the organism size.

(b) Cellular neighbourhood.

(c) Cell types.

(d) Genetic information. Regulatory input and cellular actions.

Figure 1: A minimalistic cellular developmental model.

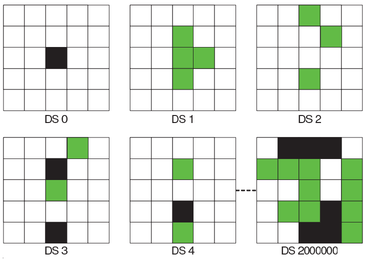


Figure 2: An example of a developing organism.

Figure 2 shows a developing organism using the minimalistic developmental model. Here the grid size is set to $5x5$ cells, the colours used to indicate cell types are taken from Figure 1(c). At Development Step (DS) 0 the organism consists of only a single cell of type 1 (the zygote), at DS 1 the first cell has divided and differentiated into three cells of type 2. At DS 2 – DS 4 the change in phenotypic structure along the developmental path can be observed. The last shown organism is at DS 2000000.

3.2 Representation and Evolvable Information

In the model described in Section 3.1 the local information is the cell state (type) of the five cells in a von Neumann neighbourhood. The developmental model's possible cellular actions are given by the defined next states $t + 1$ in the transition table in Figure 1(d). The genome, or evolvable information, may not necessarily cover all regulatory possibilities. That is, there may be that the size of the genome constrains the number of possible regulatory conditions and corresponding actions. For most developmental models this is an inevitable necessity, e.g. complete regulatory information for Tufte's model [29] would require a specification of 54^5 regulatory possibilities or for Miller and Banzhaf's model [25] a total of 768^9. A complete coverage of all possible regulatory conditions would require a development process with an undesirable amount of logic (or any signal processing resources). Artificial EvoDevo-system often consists of a predefined developmental model with defined developmental processes. Further, the evolvable information is similar to a genome consisting of genes that together with possible intracellular and extracellular information regulates actions of the developmental processes.

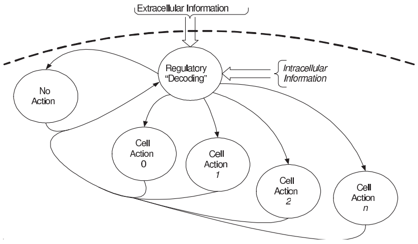


Figure 3: The inner working of a simple developmental process.

Figure 3 illustrates the relation between regulatory information and development as a quasi Finite State Machine (FSM). The state *Regulatory "Decoding"* take regulatory information from a local cellular neighbourhood (*Extracellular Information*) and information from the cell itself (*Intracellular Information*) as input to a gene regulation process defined by the genome. Cellular action, indicated by state *Cell Action* $0 - n$, is promoted out of the outcome of the gene regulation process. In this example the cell can express a change, e.g. in intracellular state, or no change if the regulatory information codes for a jump to the *No Change* state.

The state *no change* is also the state the cell will be in for all input regulatory information that not explicit regulates to a cellular action, e.g. input information may be the total of *Extracellular* and *IntraCellular*. This implies that all regulatory input combinations not covered in the genome will indirectly regulate the cell into the *No Change* state. As such, a genome of a size that do not cover all regulatory possibilities will in a way have a given part that indirectly code for the developmental process of *No Change* in Figure 3.

3.3 EvoDevo

The relation between evolution, development and the evolution of development in biological systems is still a relative unexplored area. Even though a lot of work is done toward a synthesis [12] there is a lack of possibilities to obtain experimental proof due to the time scale of evolution. As such work is often based in philosophy of biology. In the artificial domain there is no lack of possibilities to monitor all processes. It is possible to see cause and effect on all levels from evolutionary changes to detailed influence on developmental trajectories. However, there is a lack of knowledge of what properties that make a developmental process successful. Further, the issue of genetic information and representation lack an understanding on the level of how should a developmental genome be designed for a successful result.

To add some knowledge to the puzzles we try to explore the relation between a simple developmental model and the information in the developmental genome. That is, we want to investigate how the compositions of information in the genome with regards to gene regulation influence on the developmental trajectory.

3.4 Genome information, Developmental Processes and Phenotypic Variation

We address the above problems by using a developmental model where the total of regulative input can be coded completely in the genome. Such a genome will not include any implicit DCs in its gene regulation specification and developmental actions. This does not imply that all of the genome information is expressed in the phenotype, i.e. no redundant information, rather that such a genome open for a possibility to specify all regulatory input combinations without a need to replace genetic information.

If the genome codes for developmental actions explicitly for all possible input combinations evolution can actually exploit all of the combinations. In contrast the model of Tufte [29] uses a genome that have a fixed length far smaller then all possible regulatory combinations. In Tufte's model genome size varies from experiment to experiment, e.g. 64 rules opens for 64 different regulation possibilities out of the total of 54^5. This implies that if a regulatory combination (rule) is to be added an existing rule must be dropped.

A similar approach as Langton's is taken, monitoring and comparing the behaviours of the system. Here Langton's emergent CA behaviour is replaced by what may be characterised as "developmental behaviour". Developmental behaviour is an attempt to monitor and classify properties of expressed change in developing phenotypes, i.e. change in phenotypic structure over the lifetime of organisms, in relation to what and how information are present in the genome. As for Langton, our hypothesis is that there is a connection between regulatory information describing behaviour on a cellular level and the emerging behaviour of the system as a whole. In Langton's work this connection was between CA transition rules and the behaviour of the CA. Herein a connection between regulative information in a developmental genome and structural properties of a developing organism is investigated.

4. QUANTIFICATION OF GENOMES AND DEVELOPING ORGANISMS

As stated, Langton's use of λ as a prediction of behaviour in CAs is similar to the experimental investigation taken. A kind of developmental λ (λd), that can be extracted from the genome (regulatory information) and linked to properties of the developing organism is sought.

4.1 λd Extracted from Genetic Information

The developmental model with its total of 3^5 regulatory combinations makes it possible to specify genetic information that can explicitly code for all possible regulatory input combinations and corresponding developmental actions. Since all regulatory inputs are to be covered, the developmental model's genetic information only need to code for the regulative outcome. That is, the genetic information only specifies the developmental action (growth, differentiation or no action) for each input combination. This enables genomes in the form of strings of 3^5 symbols, where a symbol can code for each of the defined cell types (see Figure 1(c)). This string of symbols composes the column $C(t+1)$ in Figure 1(d).

The genetic string can be any 3^5 length string of 3 symbols (as long it complies with the given constraint) of the total of the 3^{243} possible strings. Following Langtons definition of λ a quiescent state must be chosen. The void (type 0) is taken as the quiescent state. The number of symbols representing void in the symbol string is used in the calculation of λd together with the number of non quiescent states, here all entries specifying growth or differentiation to cells of type 1 and 2.

$$\lambda d = \frac{K^N - n}{K^N} \tag{1}$$

A developmental λ can then be calculated according to Equation 1. n denotes the number of transitions to the quiescent state, for the developmental genome. Here, n gives the number of transitions to the void cell type (type 0). K defines the number of cell states, for the described developmental model. That is, $K = 3$, cell can be of type: void, 1 or 2. The cellular neighbourhood, or regulatory inputs, is given by N. Here $N = 5$, the von Neumann neighbourhood.

By using the composition of the transition table it is possible to calculate a λd that gives a numerical representation of the local cells developmental behaviour. This value is only based on the local cellular properties of neighbourhood, possible cell types and the composition of the genome that is present in every cell.

4.2 Trajectories and Attractors as a Classification Criteria

Having defined genetic information as the local cellular parameter λd, a measurable quantity must be identified for the developmental organism. Properties that can be used need to be of a type that can provide information on the developing organism as a whole and the phenotypic change in the organism. Changes here denote a phenotypic alteration in developmental time, e.g. change in phenotypic form from development step n to $n+1$. Such measurement of change may also be viewed as dynamic behaviour of developing organisms. However, here behaviour is the same as the emergence of structure as a result of development.

In developmental mappings there are several possible outcomes when emergence of phenotypic structure is considered. It may be argued that a stable final structure is important [25], i.e. development reaches a structure (or state) that is stable by self-regulation. On the other hand it may be argued that a dynamic phenotypic structure with self-reorganizing possibilities may be an important part for computation and/or adaptation for developmental machines [29].

Anyhow, dynamic behaviour of a developing organism is defined by its state space, i.e. the emergence of a developing organism given by its initial conditions and the genome. For a given organism a trajectory in the state space starts from an initial cell (zygote) and follows the developmental path, i.e. trajectory. The state information can include morphology, size, behaviour etc. The trajectory describing the developmental path can end up in a final stable organism; a point attractor or as a self-reorganising organism; a cyclic attractor. As such, the developmental trajectory with its transient part and attractor can represent a possible quantifiable measurement of the development of an artificial organism.

Applying trajectory information to quantify developmental properties gives information regarding stability of the organism, does development create a stable organism or does the organism end with a structure that change form in a cyclic manner. Both alternatives provide interesting knowledge that would be favourable if it can be predicted already at the design point of developmental models, genome representation and/or genetic operators.

4.3 Possible Interpretations of λd

Measurements of attractor and trajectory length together with their ratio may indicate information about structural and adaptive properties of the organism. If the transient phase of the trajectory is considered, the length indicates the number of phenotypic changes involved in the developmental path. Such knowledge can be used to tune the system toward a hypothesis of expected need for developmental steps as to develop an organism of a given structural complexity. For example, if there exist knowledge of the range of steps (or substructures) required to reach a phenotype structure with desired properties. Knowledge related to attractor length may be used the same way. There may be knowledge of what range an attractor length may have in order to meet a goal, e.g. for self-replication: number of required steps based on number of possible cell types and cell neighbourhood [20].

A more speculative use of the trajectory/attractor information may be to try to predict phenotypic plasticity [32] as an indication of adaptivity. The argumentation regarding using λd toward indication of adaptivity relates to a hypothesis connecting long attractors to the ability to change, i.e change in phenotypic structure during development.

The model described in Section 3.1 do not include any external information except the state of the initial cell. Any developmental path of the model will be deterministic starting from two of the three possible initial configurations (an initial cell of type one or two). An initial cell of type 0 (void) will not develop as the model requires a minimum of one cell alive for any phenotypic change. As the model in our investigation do not include environmental influence in the gene regulation, i.e. no possibility to deviate from the trajectory given by the initial configuration and genome, there is no direct access to measeur effects on development caused by dynamic attractor landscapes and environmental perturbations.

5. EXPERIMENTS

The experiments are divided in two main categories. First, an investigation of the relation between the defined λd and the trajectory length and the length of the attractor cycle. This set of experiments targeted to investigate if λd could be used as a measurement to predict developmental properties. Experimental results regarding trajectory and attractor length as a function of λd is presented in Section 5.2.

In the second set of experiments the goal was to find correlations between internal qualities of the developmental processes (growth, cell death and differentiation) and the λd value. Growth and differentiation is herein taken as indication of the activity of the developmental processes and there by thought of as a measure of different developmental phases. Two phases of interest are defined. First, a growth phase where the organism expand in size toward an "adult" form. Second, change in the adult organism. We introduce two measurements; growth and change rate that can be a related to the λd parameter. Details of the experiments regarding growth and change rate and their relation to λd are given in Section 5.3.

5.1 Experimental Setup

In the experiments herein the main idea is to generate genomes with a given property. As such, there is no evolution, instead genomes are generated with predefined λd values. The generated genomes are developed and the developing phenotypes are investigated as to quantify properties as to see if there exists a correlation with the genomic λd value.

The minimalistic developmental model presented in Section 3.1 is the test case for the experiments. The genome is a string describing the result of every cellular action (given in column $C_{(t+1)}$ in Figure 1(d)).

In order to generate genomes with different λd value a similar method to Langton's [21] random table method is used. λd was given by Equation 1. The void cell type was defined as the quiescent state. The λd span from 0 to 1 and was investigated by generating test sets of genomes with λd at intervals of 0.01. The test genomes were generated in the following manner as to produce genomes with a correct λd; for every entry in the table:

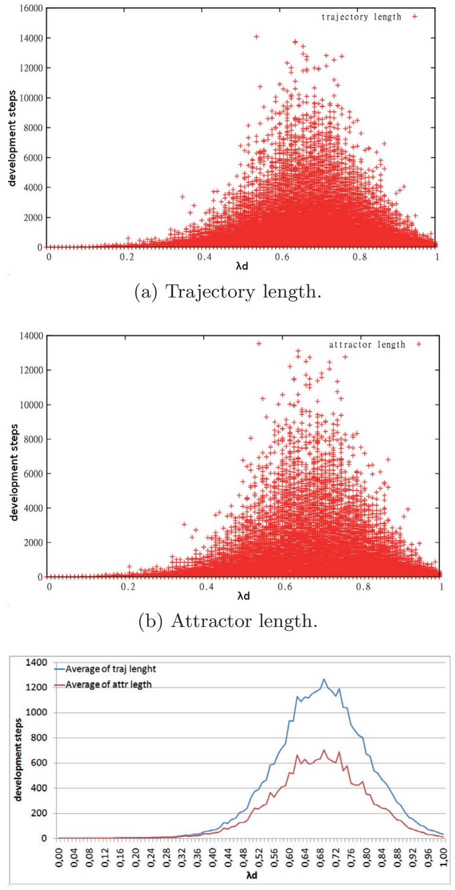
- With probability $1 - \lambda d$, the cell type at the next developmental step is quiescent (type 0);
- With probability λd, the cell type at the next developmental step is a generated by a uniform random distribution among the other cell types (type 1 or 2).

In the experiments an organism size of maximum 4x4 cells and 5x5 cells were used. The set up of cellular array size and number of tests for each λd are covered in the description of the experiments.

5.2 Experiment I

In these experiments the genomes were generated according to the λd parameter in Section 5.1. The trajectory length and attractor was recorded and plotted as a function of λd. As much work in developmental systems deals with the problem of scalability and other issues related to the size of the phenotype the experiment is repeated for two differently sized cellular arrays.

The arrays size was set to 4x4 and 5x5. The size of the arrays was chosen as to be able to carry out experiments in reasonable computational time. Organisms of 4x4 and 5x5 cells may be considered rather small, however, the theoretical maximum attractor length is 3^{16} for the 4x4 array and



(a) Trajectory length.

(b) Attractor length.

(c) Average trajectory and attractor length.

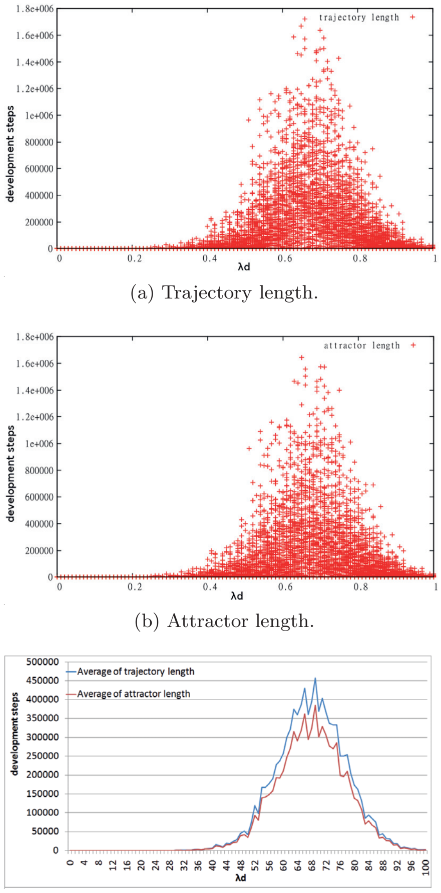
Figure 4: Experiment I. Results for 4x4 organisms plotted as function of λd. 1000 tests for each λd.

3^{25} for the 5x5 array. As such, even at the chosen array sizes, the variation in trajectory and attractor length can show a huge deviation.

For the 4x4 array a 1000 test was carried out for each λd value. The complete data output of the experiment is presented in Figure 4(a). Each data point shows the trajectory length, i.e. the length of the sequence of unique configurations of cells during development.

To be able to discriminate between organism with a long developmental path with many unique developmental steps and organism with a long cyclic attractor, i.e. the length of the cyclic attractor after the transient phase, the attractor length is presented in Figure 4(b) a point attractor is here given the length of one.

To further illustrate the results, Figure 4(c) shows the average trajectory and attractor length. The plot is created out of the raw data presented in Figure 4(a) and Figure 4(b).



(a) Trajectory length.

(b) Attractor length.

(c) Average trajectory and attractor length.

Figure 5: Experiment I. Results for 5x5 organisms plotted as function of λd. 100 tests for each λd.

When the organism size was scaled up from 4x4 to 5x5 the computational demand required that the number of tests for each λd was reduced to 100. Figure 5(a) shows the complete set of data results regarding trajectory lengths for 5x5 cell organisms. As for the 4x4 experiment, Figure 5(b) present attractor length and Figure 5(c) shows the average of trajectory and attractor length.

5.3 Experiment II

Experiments in section 5.2 deal directly with phenotypic properties, i.e. the emergent form of the organism along the developmental path. As to further investigate if a genomic measurement such as λd can be taken into account as to predict developmental properties the focus was changed to investigate developmental processes. In the model two main processes can be identified; growth and differentiation. Growth increases the number of cells "alive" and differentiation changes the cell type. As such, we want to define a way to quantify growth and differentiation during development according to λd.

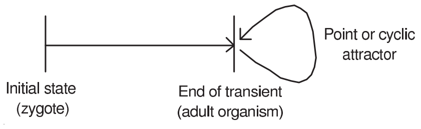


Figure 6: Growth and change rate illustrated as phases in the life time of a developing organism.

Two measurements are defined; growth rate and change rate these measurements can be quantified in relation to λd. Growth is defined (not exactly biological correct) as the transient phase of a trajectory. The measurement of growth chosen is the size of the organism, i.e. all cells of type non-void. Change is defined as the number of cells that change cell type from development step to development step along the attractor. Figure 6 illustrates the measurements of growth and change. Growth rate is defined as the size of the organism at the end of the transient phase, indicated by the arrow going from zygote to adult organism in the figure. Change is a measurement of the number of cells changing type from development n to development step $n+1$. Change rate is the average of change for all development steps in the attractor. In Figure 6 this measurement is the cycle that indicates the attractor. The change rate can then be seen as a measurement of the adult life of the organism.

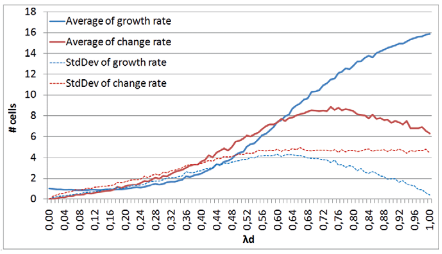


Figure 7: Experiment II. Average growth and change rate in correlation to λd on a 4x4 organism. Average over a 1000 tests for each λd value.

In the experiment a 4x4 organism applying a 1000 tests at each λd value was used. The average growth and change rate was measured and plotted according to the λd value. The result of the experiment can be seen in Figure 7.

6. DISCUSSION

The experiments presented have some common results with Langtons work, i.e. the sudden increase in the length of trajectories, attractors and transient phase of a developing organism. In Figure 4(c) and 5(c) this phenomenon can clearly be observed as the length of the trajectory, attractor and difference between trajectory and attractor length increase around $\lambda d = 0.67$. However, the goal was to investigate if it is possible to measure properties of the genome composition as an indicator of how the resulting organism will develop instead of Langton's work on potential computational properties of the system related to phase transitions.

The plots in Figure 4(a), 4(b), 5(a) and 5(b) show a very similar trend of how the data points are distributed according to the λd value. This result is in itself encouraging as it indicate that the observed correlation between λd and the state space properties measured is not a special case related to the development model and a given size constraint.

The plots in Figure 4(a) and 5(a) show that the length of the trajectories depend strongly on λd. As such, the result show that a calculation based on genome composition can reflect a predictable developmental behaviour. As stated in Section 4.3 knowledge of probable developmental path properties, such as length, may help evolution if there exist knowledge of what developmental path length that is likely to be needed to reach a phenotype with certain structural properties.

The plots regarding attractor length in Figure 4(b) and 5(b) show that if plasticity can be taken as a measurement toward adaptivity, the λd can be used as to guide toward part of the search space where genomes with long attractors are more likely to be found. It is important to note, as stated in Section 4.3, that such an interpretation is a little speculative. However, when it comes to adaptivity and evolution the results are also interesting. The plots regarding trajectories and attractors show that genomes with a given λd value will most likely mutate to genomes with similar developmental behaviour as long as the mutation result in an offspring with similar λd. Even though the variance of the plots showing all data points is high, specially for long trajectories/attractors, the trend shown in Figure 4(c) and 5(c) is easy to spot.

The results in experiment II further emphases a relation between the measurement of genomic composition and developmental behaviour. In Figure 7 the growth rate shows that for low values of λd the transient phase of the developmental path is rather short. Further, the standard deviation is low. Genomes with this property have a rather high probability of short developmental time with a point or short attractor. This knowledge is useful if a requirement is to develop stable organisms.

The change rate shares a common path with the growth rate. However, it shows that the organisms developed in the upper middle of λd change their form at a rather high rate from development step to development step. The decrease in change rate for high λd values may relates to a move to a less chaotic regime. As for the results in experiment I the results of experiment II should be helpful if knowledge exist of sought properties of the emerging developmental organism. An example can be that a fast growing organism will probably be rather stable and include few changes in form.

The measurement used herein is close to complexity measurements of phenotypic properties [17]. Kolmogorov inspired complexity measurements [22, 13] is related and can be used in the same way as the chosen state space measurement. This is part of ongoing work.

7. CONCLUSION

The presented λd used as a measurement of genomic composition has shown to be rather well suited to predict developmental behaviour. The results clearly show a correlation between genomic composition and developmental properties.

The distribution of developmental behaviour according to λd found can be exploited as to be able to design EvoDevo systems with smoother search space. Further, if there exist knowledge of developmental properties related to the development of form, parameters like λd can be exploited to point evolution toward parts of the search space where the existence of sought behaviour is more likely. Another important use of parameters, such as λd, is in the design phase of EvoDevo systems. If the system is not able to exhibit behaviour in the different regimes resulting from different λd values, it is given that the system can not be applied to problems that most likely require such developmental behaviour.

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Paper A.2

Genome Parameters as Information to Forecast Emergent Developmental Behaviors

S. Nichele and G. Tufte

11th International Conference on Unconventional Computation and Natural Computation, UCNC 2012

September 3 - 7, 2012
Orleans, France

Paper B.1

Measuring Phenotypic Structural Complexity of Artificial Cellular Organisms

Approximation of Kolmogorov Complexity with Lempel-Ziv Compression

S. Nichele and G. Tufte

4th International Conference on Innovations in Bio-Inspired Computing and Applications, IBICA 2013

August 22 - 24, 2013
Ostrava, Czech Republic

Paper C.1

Evolution of Incremental Complex Behavior on Cellular Machines

S. Nichele and G. Tufte

12th European Conference on the Synthesis and Simulation of Living Systems, ECAL 2013

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Evolution of Incremental Complex Behavior on Cellular Machines

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Abstract

Complex multi-cellular organisms are the result of evolution over billions of years. Their ability to reproduce and survive through adaptation to selection pressure did not happen suddenly; it required gradual genome evolution that eventually led to an increased emergent complexity. In this paper we investigate the emergence of complexity in cellular machines, using two different evolutionary strategies. The first approach is a conventional genetic algorithm, where the target is the maximum complexity. This is compared to an incremental approach, where complexity is gradually evolved. We show that an incremental methodology could be better suited to help evolution to discover complex emergent behaviors. We also propose the usage of a genome parameter to detect the behavioral regime. The parameter may indicate if the evolving genomes are likely to be able to achieve more complex behaviors, giving information on the evolvability of the system. The experimental model used herein is based on 2-dimensional cellular automata. We show that the incremental approach is promising when evolution targets an increase of complexity.

Introduction

Evolved artificial developmental systems' remarkable range of products, i.e. biological organisms, with variety in form, function and "complexity", all tailored to fill their niche, is an alluring design concept. Such bio-inspired design methodology can be used for any kind of system to create a variety of artifacts that can handle different problems.

However, knowledge and methods to be able to exploit similar core processes [14] for the design of artificial organisms are still subjects of exploration and research.

Evolved artificial developmental systems have shown many favorable features that are borrowed from natural biological systems, such as the main subject here, the ability to evolve inherent complexity as a response to evolutionary pressure [27]. Evolvable, or in particular EvoDevo systems are products of bottom-up processes, in contrast to typical top-down engineering design approaches. A system emerging as a product of a bottom-up process can target system properties out-of-bounds for traditional top-down designed artifacts. Self-organization, self-construction, adaptivity, scalability and robustness are all example of such hard to reach properties.

In contrast to the open ended evolution in nature, evolution of artificial EvoDevo systems often includes an expressed goal; fitness is a kind of usability [15] measurement. The target functionality is defined and thus placed within some complexity measure. Such complexity can be defined at several levels. The complexity of the machine's composition, i.e. the number of components and connections can be quantified. Another complexity measurement may be functionality in terms of information processing. Quantification of complexity in artifacts and biological organism has no common defined unit of measurement or ratio of comparability. However, intuitively there are differences. Such differences can be related to the composition of artifacts/organisms or as a measure of their functionality. If complexity, for an organism, is a measurement of functional properties within its environmental niche, different levels of behavioral complexity can be said to exist. In this context, high complexity is not a goal in itself; it is merely a product of the species adaptation to be able to reproduce. The genetic information included in the genotype and the developmental processes for any particular specie has evolved and diverged through adaptation from the primordial soup. As such, the behavioral complexity of organisms is a product of the evolved interplay between genetic information and developmental processes.

As a step toward more knowledge of underlying processes and finding design methodologies for the exploitation of EvoDevo for artificial systems, we investigate how a gradual change in the complexity requirements, in evolutionary time, influence on EvoDevo system's ability to evolve complexity. Further, a variation of Langton's Lambda parameter [16] is used as an indicator of evolutionary genome adaptation to resulting phenotypic complexity. The taken experimental approach uses a kind of incremental complexity evolution to simulate the process of species adaptation to a changing environment requiring growth of complexity. A 2D cellular developmental model based on Cellular Automata (CA) is used in the experiments, so as to be able to visualize artificial organisms' development in 2 dimensions.

In our incremental evolutionary approach, the evolution process tackles the problem of targeting complexity incrementally. Instead of seeking for maximum complexity in the early generations, the problem is divided in sub-problems. Generations are divided in intervals and in every interval the target complexity demand is increased, keeping the target functionality unvaried, i.e. the class of problems is the same. In such way, it may be possible to evolve favorable genes for intermediate complexity levels, which may be beneficial in order to achieve higher complexity in the long term.

Since no universally accepted definition of complexity exists, many authors use it implicitly without specifying which notion of complexity they are using. Yet, without any common measure of genotype or phenotype complexity, any significant claim is not verifiable. Genome complexity measures may sometimes be unfitting, since the amount of information encoded in the genome is not directly proportional to the complexity of the emergent organisms. Even in nature, some unicellular eukaryotic organisms have much larger genomes than humans. In addition, there are other factors that impact on the organisms' complexity during their growth, e.g. the environment.

One may argue that complexity of an EvoDevo system may be measured in terms of information contained in a genome, by ranking through a Turing machine, by quantifying the capacity for a genome to exploit a provided area of growth, using approximations of Kolmogorov complexity [5, 6, 9]. The used complexity measure is based on compression of CA behavior in terms of trajectory and attractor lengths, a kind of adaptation of principles from Kolmogorov complexity.

The article is laid out as follows: background information and motivation on incremental evolution is presented in Section 2. In Section 3 Lambda genome parameter is introduced and in Section 4 the developmental model used in the experiments is described. Section 5 explains the genetic algorithms used herein. The experimental setup is illustrated in Section 6 and in Section 7 the results of the experiments are presented together with a discussion of the ideas and the results. Finally Section 8 concludes the work.

Incremental Evolution

A general evolutionary strategy may be too difficult for the evolution system to discover possible solutions directly. Instead, it is possible to learn complex behaviors incrementally, starting from a simple behavior and gradually making the task more challenging [1]. Incremental evolutionary approaches have been used successfully to evolve complex behaviors step by step. Many studies investigated the training of artificial neural networks with Genetic Algorithms (GAs), in order to evolve robots controller able to perform complex action sequences, e.g. complex light switching behavior [2] or robot duels controllers [3]. This approach has shown interesting results, being able to evolve converged populations to the new task. On the other hand, conventional evolutionary methods may have too high selective pressure in the early stages of the evolution, getting the GA blocked in an unfruitful area of the search space. If the population is first evolved to an easier behavior, it may be possible to discover and access a region of the solution space where even more complex behaviors are more likely to be found. As such, the ultimate complex behavior may be reached incrementally by evolving a sequence of intermediate behaviors with growing complexity:

$$\text{Behavior 1} \xrightarrow{\Delta} \text{B 2} \xrightarrow{\Delta} \ldots. \xrightarrow{\Delta} \text{B n-1} \xrightarrow{\Delta} \text{B n}$$

In this way, genotypes are evolved gradually and the search is driven on solutions that are likely to benefit and retain existing capabilities. Conventional evolution tends to fluctuate between idiosyncratic but still not interesting solutions [12]. Incremental evolution may foster continuing innovation by elaborating on available solutions.

Genome Parameter: λ

In our cellular developmental model, we are aiming to target complex phenotypic properties. Attractor length, i.e. development reaches a structure or state that is stable by self-regulation (point attractor) or a dynamic phenotypic structure that is self-reorganizing (cyclic attractor), is the chosen metric. The strategy is therefore to evolve intermediate genotypes that develop and express specific attractor lengths. Every fixed number of generations, we increase the sought attractor length value to increment the complexity demand.

In terms of evolvability, since we want to investigate if the evolving genotypes are able to evolve and develop more complex phenotypes, we attempt to measure the behavioral regime using a genome parameter. Parameters obtained from the genome information can be used to estimate the dynamic behavior of the system. In this work, the genotypes are represented as a transition rule table, where developmental actions are defined as a function of the neighborhood configuration (see next chapter for details). In this way, it is possible to analyze the different developmental actions and calculate parameters obtained from the genome table.

Several genome parameters have been previously proposed in order to measure genotype properties. Langton [16] studied a parameter λ as a measure of the activity level of the system and its disorder. A similar parameter, neighborhood dependent, is Absolute Activity presented by de Oliveira [20]. Li [21] introduced Mean Field Parameters to monitor if the majority of the regulatory actions follow the "mean" configuration. de Oliveira [20] presented a very similar parameter called Neighborhood Dominance. Binder [22, 23] introduced the Sensitivity parameter which measures the number of changes in the output of the transition table based on a change in the neighborhood, one cell at a time, over all the possible neighborhoods of the rule being considered. This has also being studied by de Oliveira [24, 20] as Context Dependence. Different properties of genome parameters have been investigated in details in [11]. In particular, the λ parameter has shown interesting abilities to discriminate genotypes in different behavioral classes, e.g. fixed, chaotic, random [13]. As such, we monitor the λ value along the evolutionary process. λ is calculated according to Equation 1.

$$\lambda = \frac{K^N - n}{K^N} \qquad (1)$$

n represents the number of transitions to the quiescent state (i.e. inactive or dead state), *K* is the number of cells types and *N* is the neighborhood size (see following section for details).

Cellular Developmental Model

The developmental model used in this work is a minimalistic cellular developmental model based on cellular automata, similar to cellular models used in [25, 26, 19]. The system herein is close to the field of Morphogenetic Engineering [7], where the goal is "self-architecturing" systems. In embryomorphic systems [8], the approach is based on embryogenesis: the self-assembly of myriads of cells starting from a single zygote which holds the complete genotype information.

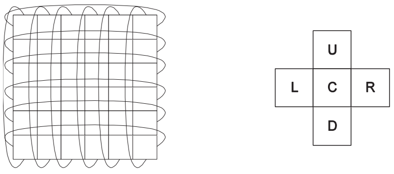


Fig. 1: Developmental model with cyclic boundary conditions and von Neumann neighborhood configuration.

A CA can be considered as a developing organism, where the genome specifications and the gene regulation information control the cells' growth and differentiation. The behavior of the CA is then represented by the emerging phenotype, which is subject to size and shape modifications, according to the cellular changes along the developmental process. Such dynamic developmental system can show adaptation, self-modification, plasticity [18] or self-replication properties [17].

L	R	U	D	C	$C_{(t+1)}$
0	0	0	0	0	0
0	0	0	0	1	{0,1,2}
0	0	0	1	0	{0,1,2}
0	0	0	1	1	{0,1,2}
0	0	1	0	0	{0,1,2}
		:			:
1	1	1	1	1	{0,1,2}
0	0	0	0	2	{0,1,2}
0	0	0	2	0	{0,1,2}
0	0	0	2	1	{0,1,2}
0	0	0	2	2	{0,1,2}
		:			:
2	2	2	2	2	{0,1,2}

Fig. 2: Developmental table with neighborhood configurations and relative developmental actions.

The model is based on a two-dimensional cellular automaton with cyclic boundary conditions, as shown in Figure 1. The number of cell types is set to three (type 1 and 2 plus the quiescent or dead cell type 0) in order to keep the property of multicellularity. A single cell (zygote) is placed in the centre of the development grid and develops according to a developmental table based on von Neumann's neighborhood (five neighbors). All the possible regulatory input combinations are explicitly represented in the development table, i.e. 243 (3^5) neighborhood configurations.

To ensure that cells will not materialize where there are no other cells around, a restriction has been set: if all the neighbors of an empty cell are empty, the cell will be empty also in the following development step. This is represented in the first entry of the developmental table in Figure 2. A more detailed description of the development model is given in [10, 11].

Genetic Algorithm

The Genetic Algorithm used in the experiments is tested with two different fitness functions: a classical fitness approach that targets the maximum complexity and an incremental growth of fitness. An incrementally growing fitness denotes a changing environment that requires more complex behaviors to survive. It must be underlined that the two different fitness functions could in theory perform the same way. The same genotypes could be discovered through evolution since there are no restrictions in the areas of the search space that are being explored. Anyway, this is very unlikely to happen, since the environment is interpreted differently on the evolutionary time scale. The GA consists of a population of ten individuals and uses a roulette wheel technique for proportionate selection of two potentially useful individuals. The worst three elements are replaced by two new individuals that are copies of the two selected ones with mutation rate 0.02 for each of the entries in the developmental table. The third new element is generated by uniform one-point crossover of the two selected individuals.

As we mentioned, the main difference between the two evolutionary strategies lies in the fitness function. In the classical scenario, the fittest individual is the one with longest attractor length. In the incremental approach the fittest is the individual with smallest difference between the actual length and the target length in that specific generation, i.e. environmental requirements at specific moments in evolutionary time.

The target length is defined as follows: in the first generation it is set as 1, i.e. point attractor. In this phase, the GA searches for phenotypes that end up with a single point attractor. Every fixed number of generations, the target value is incremented by a constant value. It is expected that in the following interval of generations, the population will be able to evolve and adapt towards the new target, i.e. an increasing complexity demand for longer attractor length along the evolutionary timeline.

Details on the development process, number of generations, length of the intervals and initial conditions of the genotypes are given in the next section, which describes the experimental setup. Source code is available upon request.

Experimental Setup

In the experiments herein, the main idea is to generate an initial population of ten genotypes, develop the corresponding phenotypes (starting from a single cell placed in the centre of the grid) until an attractor is found, evaluate the phenotypes with a fitness function and evolve the chosen genomes throughout the generations. This process is repeated for GA with standard fitness function and GA with incremental fitness function. The performances of the different algorithms are evaluated, measuring the ability to achieve sought complexity in terms of attractor length, i.e. number of development steps between two repetitions of the same state. This experimental setup is represented graphically in Figure 3.

Two different strategies of generating the initial population are investigated:

- From "dead genomes": all the transitions in the developmental table lead to the dead state and the value of λ is uniform. In this scenario, the GA has to evolve "dead" genomes, i.e. the developed phenotype results in a dead

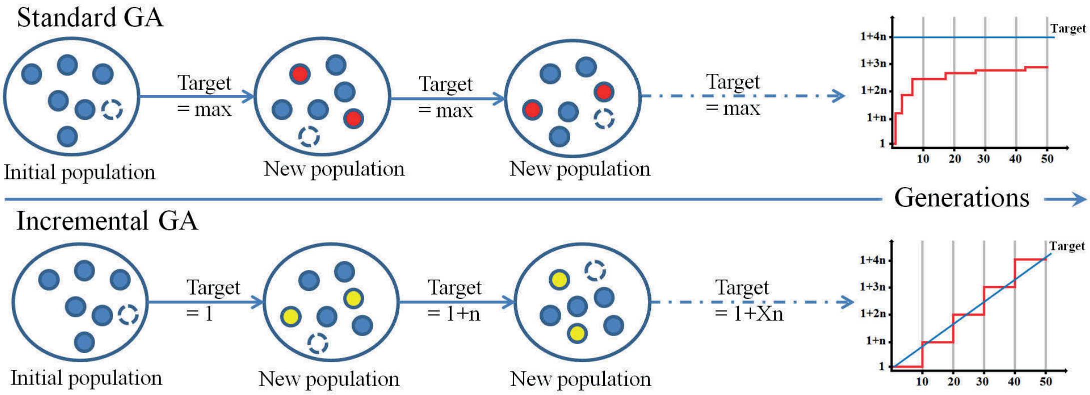


Fig. 3: Experimental Setup: GA with standard fitness on top (targeting maximum complexity), GA with incremental fitness on bottom (target fitness increased gradually)

organism after the first development step, towards "alive" genomes. This approach could be interesting since favorable genes are evolved from scratch, especially when random initialization is not possible or feasible.

- From random genomes: the initial population of genomes is initialized randomly[1]. In this way, it is possible to have extremely fit genomes, or very unfit, from the first generations. In both cases, it may be particularly difficult to evolve towards genomes with favorable characteristics to reach the defined goal. The parameter λ has a distributed value.

The way genomes are generated has a strong impact on how the resulting phenotypes will behave. Trying to understand the relation between genotypes and possible resulting phenotypes means understanding which kind of information is present in the genome and which behavioral properties may emerge. Since in our model all the possible regulatory combinations are fully specified together with the corresponding developmental actions, it is possible to calculate the Lambda genome parameter for each individual in the population. λ is calculated out of the regulative outcome in the developmental table, i.e. column C(t+1) in Figure 2. Following Langton's definition [16], a quiescent state must be chosen. We choose the void cell type (type 0) as the quiescent state. Lambda is then calculated by 1 – the ratio between transitions to the quiescent state and the total number of transitions in the developmental table. It is implicit that if the population is initialized with dead genomes, all the transitions in the developmental table will lead to the quiescent state. Thus, λ will be 0, which means genotypes with low behavioral activity. On the other hand, when the population is initialized with random genomes, λ is more likely in the vicinity of a critical behavioral regime, near the Edge of Chaos [16]. In this area of the solution space, it is more likely to find complex behaviors.

Monitoring Lambda along all the evolutionary process will give information on the ability of the population to evolve and adapt to the target complexity level. λ, as an indication of computation, has been discussed in [28]. However, from previous work [16, 11], we know that the attractor length of a certain organism is strongly related to its λ value, which can be calculated from the genome composition. As such, Lambda could be used to drive evolution in desired parts of the search space where the desired behavior is more likely to be found. This is part of ongoing experimentation. λ here is measured to gain information of the evolution of genome composition and interpreted as an indicator of the evolvability of the system, which may confirm our hypothesis that an increase in complexity is more likely to happen if evolutionary search leads towards the desired behavioral regime.

Results and Discussion

In the experiments herein, the array size of the CA was set to 4x4. The size of the arrays was chosen as to be able to carry out experiments in reasonable computational time.

Organisms of 4x4 cells may be considered rather small; however, the theoretical maximum attractor length is 3^{16}. As such, even at the chosen array size, the number of development steps to reach an attractor could be rather big.

Experiment 1: Dead Genomes

The first set of experiments consists in comparing the behavior of standard GA and incremental GA, staring from dead genomes. In both cases, the GAs run for 30000 generations. The standard approach targets the maximum attractor length for all the 30000 generations whether the incremental approach increments the target attractor length by 10 development steps every 20 generations. It is noticeable that there are clear advantages with an incremental approach for the evolution of complexity.

In Figure 4 (a) the results of a canonical GA are presented. Here the target was the maximum complexity. It is clear that a standard approach could discover in some early generations

[1] Marsenne twister is used for initialization of randomized genotypes and genetic operators (mutation and crossover).

good candidates but often the algorithm gets trapped in some unfruitful regions of the search space and for several generations there are no improvements. All the single samples are represented by the thin lines. The dashed line is the average over all the tests and after 30000 generations the attractor length has a value around 4000 development steps. Here the deviation is quite big, since in some cases the maximum length is far from the average. For example, in one case it is close to 12000 development steps while in many other cases is lower than 2000. In Figure 4 (b) the results for the incremental approach are plotted. The straight line represents the target complexity value for each generation, measured as number of development steps inside the attractor. The thin lines here follow quite accurately the target line. The dashed line represents again the average. It is possible to see that average and target are overlapping for the first 15000 generations, whether in the last 15000 generations the average is slightly lower than the target. Overall, the average attractor length after 30000 generations is around 13000 development steps. Here the deviation, represented by the dotted line, is quite small. This means that the incremental approach is able to minimize the distance from the target in each generation. Figure 4 (c) is a comparison of the two different strategies. It is evident that the incremental approach overcomes the standard approach since the first 2500 generations. After that, the canonical GA struggles to find good solutions on average and has difficulties to evolve and jump up in complexity. On the other hand, the incremental approach shows very promising results even if in the last generations there is a small degradation of the performances. Overall, the difference between the averages is significant (p<.0001, Student's t-test).

Finally, Figure 4 (d) represents a comparison of the measured Lambda parameter in each generation. The standard GA evolves to genotypes with a maximum parameter value of 0.4. The incremental GA discovers genotypes with Lambda between 0.6 and 0.7. This means that those genotypes are in a completely different behavioral regime. Earlier work from Langton [16] identified a critical value of Lambda where the behavioral regime of the system encounters a phase transition between ordered and chaotic dynamics. In such area of the search space it is more likely to find the primitive functions to support computation: transmission, storage and modification of information. Further support to this hypothesis is given by previous work on the investigation of probable relationship between attractor length and Lambda [10]. In the experiments herein, λ is used as a measurement and its increase is not a

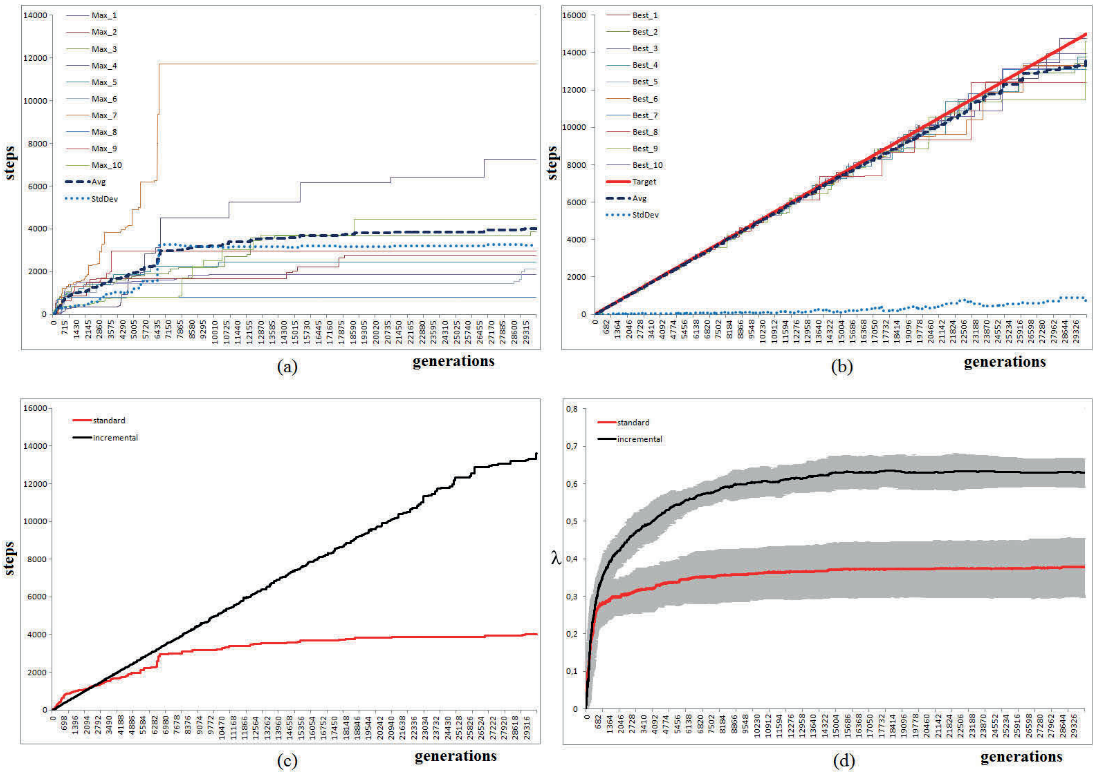


Fig. 4: Results for Experiment 1, developmental tables initialized with "dead genomes". Avg. and std. dev. over 10 runs. (a) standard GA approach: generations vs. attractor length (thin lines represent single runs); (b) incremental GA approach: generations vs. attractor length (thin lines represent single runs); (c) comparison of averages: standard GA approach vs. incremental GA approach; (d) comparison of Lambda parameter: λ for standard GA approach vs. λ for incremental GA approach.

goal in itself. Figure 5 shows a plot over the λ space where genotypes were generated according to a specific parameter value and the resulting attractor length was measured.

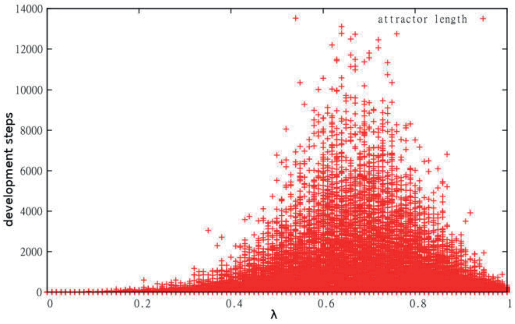


Fig. 5: attractor length as function of λ. Results for 4x4 organisms and 1000 tests for each λ value. Adapted from [10].

In those experiments, the cellular automata configuration was the same as in the experiments herein: 2-dimensional grid with neighborhood of size 5 and 3 possible cell types. With such configuration, the most heterogeneous genotypes are generated when λ is 0.66. In fact, in the scattered plot, it is more likely to find long attractors in that area of the solution space. On the other hand, when λ is around 0.4, the behavioral regime is in an intermediate region where organisms show ordered dynamics. As such, it may be more challenging to evolve towards longer attractor lengths. Relating this results with those in Figure 4 (d), it is possible to conclude that the standard GA gets trapped in an area of the search space where the sought behavior (maximum complexity) is less likely to be found. Moreover, it may be difficult for the GA to escape from such region of the search space. The incremental approach is able to evolve genotypes with parameter value around 0,65, which may be beneficial to find longer attractors. Even if not so good solutions are found in that area of the search space, it may be still more probable for the GA to be able to discover better solutions, since the sought behavior is more likely to appear.

Extended Evolutionary Time

Subsequently, the incremental GA is executed again for 500.000 generations and the target is incremented by 10 development steps every 500 generations. This is done to check the behavior of the GA when the algorithm has more generations to evolve and adapt the population towards the new complexity value.

In Figure 6 (a) the target line and the actual line (average) are completely overlapping. This means that, given enough time to the population to evolve to the sought complexity level, it is possible to keep increase the complexity with minimum deviation from the target. In each generation interval, the genetic algorithm is able to discover favorable genes and use it as a starting point for the next intervals. Evolution is based on already present capabilities, developed incrementally.

Figure 6 (b) and Figure 6 (c) respectively represent the average distance from the target and the percent average distance from the target. It is possible to observe that such span predictably increases along the 500000 generations. Even that, the average distance from the target level suddenly decreases below 1% since the first generations. In conclusion, it may be possible to tune the generation intervals in a way that evolution has enough time to evolve the whole population and prepare it to the following complexity improvements.

Experiment 2: Randomized Genomes

In the second set of experiments, the behavior of standard GA and incremental GA is tested again for 50000 generations, starting from random genomes, i.e. genomes initialized with a uniform random distribution among the three cell types. By doing that, the standard GA proceeds to select the individual in the population with longest attractor length, targeting maximum complexity. As such, in Figure 7 (a) the average attractor length does not start from the origin. During the first few generations there are several jumps in complexity but after this fruitful stage the average line stabilizes and tends to become flat. Figure 7 (b) summarizes the results for the incremental approach. In this case, since complexity is evolved gradually, individuals with long attractor lengths are left aside in favor of individuals that are closer to the sought initial behavior, i.e. point attractor.

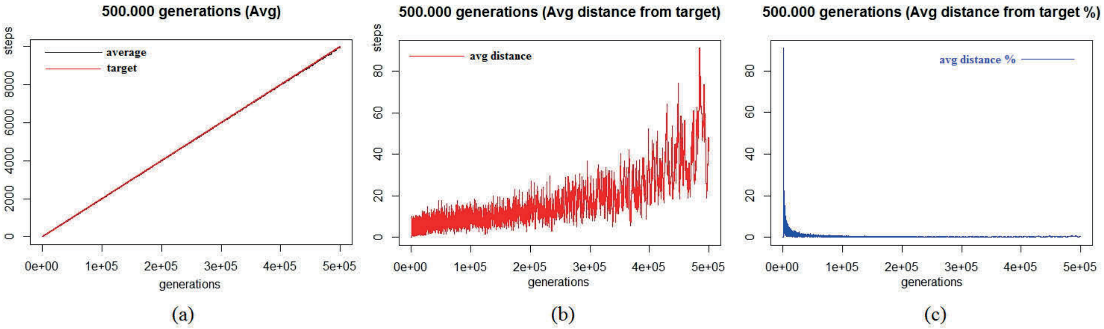
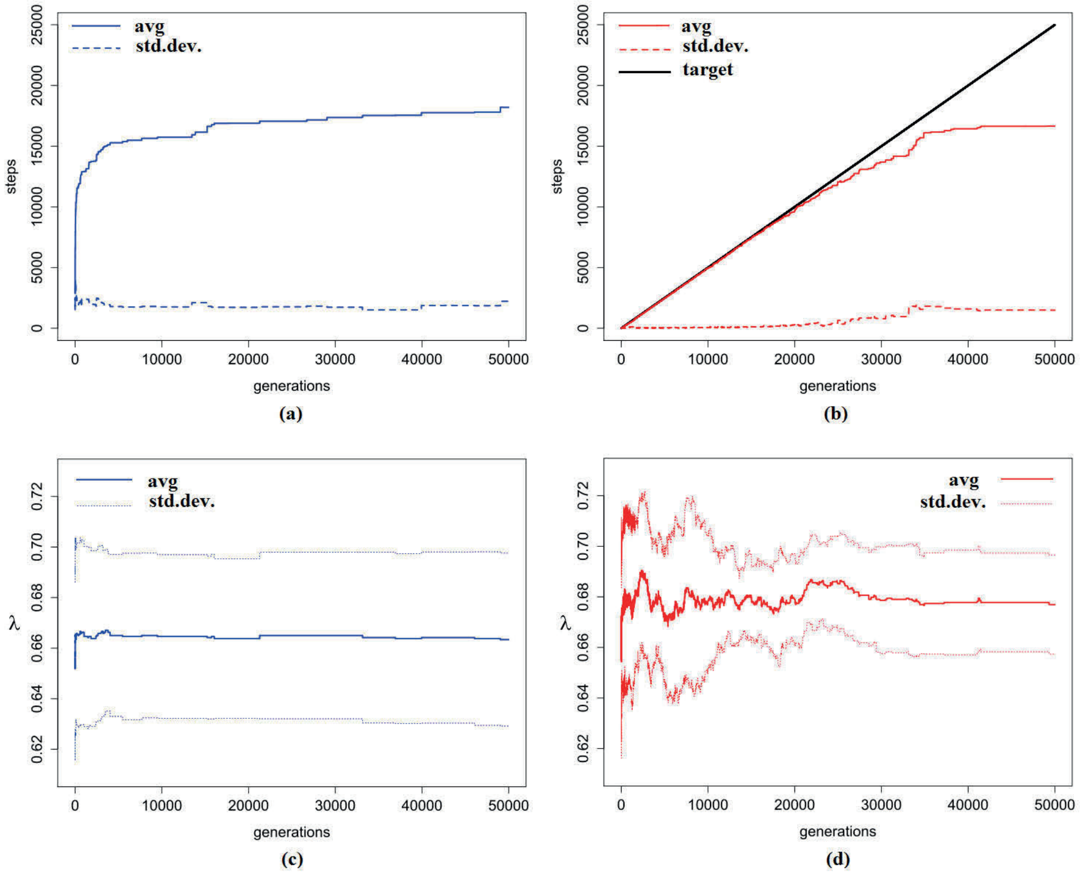


Fig. 6: Incremental GA approach with extended evolutionary time (500000 generations), developmental tables initialized with "dead genomes", average over 6 runs. (a) Target attractor length and actual attractor length (overlapping); (b) Average distance from target in development steps; (c) Average distance from target %

Implicitly, in the beginning the algorithm is forcing organisms to exhibit low complexity to survive, since only in the subsequent generations the environment will become more demanding and will require evolving in complexity. During the first 25000 generations the target line and the actual line are very close. In the last 25000 generations the reached complexity level is very similar to the GA with standard fitness, both in terms of average attractor length and standard deviation. The difference between the averages is not significant (p=.0850, Student's t-test).

Figure 7 (c) and 7 (d) show the average λ along the generations. Since genotypes were initialized randomly, it is more likely that the developmental tables are the most heterogeneous [16].

As a result, λ is positioned already in an area of the solution space where highly complex individual are likely to appear. For the standard GA, the average λ is smoother and does not show high activity of the GA. Once the algorithm finds good solutions, it is more probable that will hardly improve with better solutions. This could be a drawback for evolvability, especially if one would like to evolve intermediate complexity levels. On the other hand, for the incremental approach, λ fluctuates more within the behavioral region, exhibiting high activity of the GA that continues to explore the solution space. Moreover, the incremental strategy would fit better if the system would need to reach intermediate complexity levels.



(a)

(b)

(c)

(d)

Fig. 7: Results for Experiment 2, developmental tables initialized with random genomes. Average and standard deviation over 10 runs. (a) standard GA approach: generations vs. attractor length (avg. and dev.); (b) incremental GA approach: generations vs. attractor length (avg. and dev.); (c) Lambda parameter for standard GA approach (avg. and dev.); (d) Lambda parameter for incremental GA approach (avg. and dev.).

Conclusion

The presented experiments investigated the emergence of complexity in cellular machines, using two different evolutionary strategies: a standard approach, where the target was the maximum complexity and an incremental approach, where complexity was gradually evolved.

We showed that the incremental approach has clear advantages when evolution targets an increase of complexity, especially when the population's genome parameter is towards uniform, i.e. intermediate complexity levels in equilibrium with the environmental pressure. Such knowledge is important at the design stage of EvoDevo systems, where developmental actions are not manually programmed but discovered through evolutionary processes.

We also proposed the usage of Lambda genome parameter to detect the behavioral regime. This may be useful to indicate if the evolving genomes are likely to be able to achieve more complex behaviors, giving information on the evolvability of the system. Such ability of adaptive evolution is necessary for a system to be able to evolve complexity.

Moreover, when it comes to adaptivity, the results herein show that genomes with a given parameter value will most likely mutate to genomes with similar developmental behavior, as long as the mutation results in an offspring with similar parameter value. Our current work is focused on the usage of genome parameters to guide evolution towards favorable areas of the solution space. Furthermore, genome parameters may help to keep the population closer to the desired developmental behavior and supervising its genetic distance. This is in tune with at least two points of the current challenges in the field of artificial life [4]: "explain how rules and symbols are generated from physical dynamics" and "develop a theory of information processing, information flow and information generation for evolving systems".

As a future work, it may be possible to compare the robustness of solutions evolved incrementally versus solutions evolved with a standard approach. In particular, how fragile they are to external perturbation, both at genotype level, i.e. mutations in the rule table, and at phenotype level, i.e. perturbation of the system state during development.

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Paper C.2

Investigation of Genome Parameters and Sub-Transitions to Guide Evolution of Artificial Cellular Organisms

S. Nichele, H. Wold and G. Tufte

16th European Conference on the Applications of Evolutionary Computation,
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Granada, Spain

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Paper D.1

Evolutionary Growth of Genome Representations on Artificial Cellular Organisms with Indirect Encodings

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Evolutionary Growth of Genome Representations on Artificial Cellular Organisms with Indirect Encodings

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Abstract—**Evolutionary design targets systems of continuously increasing complexity and size. Thus, developmental or generative mappings, i.e. indirect encodings, are often a necessity. "Scaling-up" the complexity of a developed phenotype, and thus the relative solution space, does not explicitly affect the genotype search space, since each genotype does not represent a specific phenotype object directly. Phenotype solutions are the result of an incremental building process. As the phenotype information is not encoded directly into a low-level genotype, the high-level developing information relies on efficient mapping. Varying the amount of genotype information changes the cardinality of the mapping which, in turn, affects the development process. This raises several open questions: How much information must be present in the genotype? How to find the genotype size and representation in which a developmental solution of given complexity would fit? Using the whole set of possible regulatory combinations may be intractable or hardly evolvable due to the cardinality of the search space. On the other hand, a restricted pool of genes may not be large enough to encode a solution, i.e. potential solutions may be excluded due to a reduced solution space, or may need complex heuristics to find a realistic size. In nature, the genomes of biological organisms are not fixed in size; they slowly evolve and acquire new genes by random gene duplications. Newly added genes that potentially produce an increased fitness are kept and integrated in their genomes. Such incremental growth of genome information can be beneficial also in the artificial domain. For an Evolutionary and Developmental (EvoDevo) system with indirect encoding, we investigate an incremental evolutionary growth of genotype without any a priori knowledge on the necessary genotype size. An incremental increase in the dimensionality of the search space allows increasingly complex solutions to evolve, providing scalability of the state and solution space. The key aspect of evolutionary genotype growth is the ability to solve difficult problems by starting with simple solutions in a low dimensional space and incrementally increasing the genotype complexity by means of gene duplication. The experiments presented in this paper show that such an approach evolves scalable genomes that are able to adapt genetic information content whilst compactness and efficiency are retained. The results are consistent when the target phenotypic complexity, the geometry size, and the number of cell states are scaled-up. An artificial cellular developmental system based on cellular automata (CAs) is used as a test-bed.**

Keywords—Artificial Development, Evolution, Emergence, Cellular Automata, Complexification.

I. Introduction

Evolutionary developmental biology (EvoDevo) looks into the interplay between evolution, development, and embryonic. EvoDevo links together evolutionary processes, e.g. mutation and selection, and the processes leading from genotype to phenotype [12]. Artificial Evolutionary and Developmental systems share many principles with their natural counterpart, e.g. embryogenesis, self-organization, plasticity, genotype-to-phenotype mapping, and range from systems that aim to be true to biology [22] to computer models that borrow principles at a high abstraction level [15, 16, 18]. However, there are differences between natural and artificial domain, such as the definition and choice of the right genotype encoding, e.g. size / number of genes, to represent a developing phenotype solution of increasing complexity. One of the means that allowed nature to overcome this scalability problem was the possibility to acquire new genes by random gene additions during evolution [33, 45]. In other words, the genome of biological organisms is not fixed in size; it has evolved in a way that genes that potentially produce an increased fitness, e.g. by interacting with other genes, are more likely to be kept and integrated in the genome; however those that result in decreased fitness are less likely to be inherited by natural selection. In the artificial domain, evolutionary systems often rely on fixed genotypes in terms of representation, size or encoding, thus lack the necessary scalability to unleash their inherent complexity.

In this paper, we argue that an incremental growth of genome size can be beneficial also for artificial systems, providing a strategy to avoid speculating on the proper genotype size beforehand by the system designer. Evolution can be initialized by very simple genomes, e.g. containing only a single gene. Evolution would then be allowed cloning genes and systematically elaborate based on the newly added degrees of freedom. Each genome addition would result in an increased dimensionality of the search space, thus opening the possibility of finding new potential solutions. Evolution would search and optimize candidates in a simple search space and increase it when needed, therefore providing the necessary system scalability.

Natural development exploits compact representations of phenotypes by encoding regulatory information in genomes that, starting from a single cell, i.e. zygote, will develop the desired organism through morphogenesis. For example, an organism like the human body, which consists of roughly 3.72 x 10^{13} cells, has a genome with an estimate of 22000 to 25000 genes [3]. An open question for artificial systems is how to find genotype size and representation in which a potential solution would fit. One possibility is to use a one-to-one mapping between genotype and phenotype, i.e. direct encoding. Unfortunately this does not scale well, especially considering the extremely large amount of entities composing the phenotype. Another possibility is to fix the genome size a priori thus reducing the available search space. The system designer would then make assumptions on the necessary genome pool or use heuristics to estimate it. In such case, evolvability would be predetermined and constrained to the space available to encode solutions. For several artificial systems, such as cellular automata or neural networks, many solutions to the same problem may exist. Thus, it is not trivial to estimate the exact number of necessary genes. One may then decide to use a very large genotype to represent what is likely to be a large enough search space so that a possible solution may be available. Again scalability is an issue here. With a fixed genotype representation, the maximum evolvable complexity is fixed and it does not comply well with open ended evolution problems. Moreover, even if the defined genotype encoding allows possible solutions in the resulting search space, those may be not easily accessible if neutrality is not guaranteed by the chosen genotype-to-phenotype mapping. Neutrality makes it possible to have a many-to-one mapping, where neutral genome mutations have no observable phenotype effects. However, they allow moving in advantageous areas of the search space and reduce the chances of getting trapped in local optima, thus favoring diversity. Neutrality can be achieved by having redundant representations, at a price of less efficient encoding, where the additional genes do not increase the relevant information represented [35].

In the present work, an artificial cellular system based on Cellular Automata (CAs) is used as a test-bed. This model may be placed within abstract computational models of development. Therefore, we do not aim at a truly biological model of development. EvoDevo in our model should be considered as the interplay between genotype and developing organism, and the developmental effects on evolution. CAs share many principles with natural biological systems, where the key element is a cell. The cell is an autonomous unit that serves as construct and constructor for the emerging organism. Every cell contains an evolved transition table that acts as a regulation mechanism and is in charge of controlling cellular actions, e.g. growth, differentiation and apoptosis. Such cellular model depends on autonomous cellular processes influencing the developmental path and the behavior/form of the resulting artificial organism. The dynamics of the developing organism can be traced down to the information and representation of the genome and gene regulation. What information must be present? And what size is required to encode the desired emergent organism? For the described developmental system we would like to be able to incrementally evolve and optimize the regulatory information, i.e. transition table, making it compact and effective. A better knowledge of what creates scalable solutions and scalable systems within the field of cellular EvoDevo will be beneficial for the understanding of large and complex artificial cellular systems with indirect encodings.

The article is structured as follows: Section 2 provides background information and Section 3 gives a motivation for this work. In Section 4 an abstract framework is proposed and in Section 5 scalability issues are investigated. Section 6 presents the cellular developmental model and Section 7 introduces the evolutionary growth of genomes. Section 8 describes the experimental setup and Section 9 presents the experimental results. A discussion and future work is given in Section 10 and Section 11 concludes the paper.

II. Background

To be able to restrict and address scalability issues, the principles of natural biological systems are reviewed in the perspective of achieving a framework towards scalability in the artificial counterpart. We begin by reviewing how nature solves scalability issues by development and by making genomes incrementally more complex. Then we present how scalability is addressed for artificial developmental systems (with direct encodings, fixed length encodings and indirect encodings).

A. Scalability and Complexity in Biological Organisms

Biological organisms are the best example of scalability, ranging from simple unicellular to multi-cellular organisms, where trillions of cells develop from a single cell which holds the complete genome, roughly 3 Gb of information to encode the necessary base pairs for a fully sequenced human genome [52]. Obviously, the optimization of the genetic plan is the result of evolution by natural selection. The means of genome optimization are genetic operators, e.g. mutation, crossover. However, genomes of different species have different lengths. There is scientific evidence that all species have evolved and diverged from a common ancestor [46] [44], i.e. the last universal ancestor (LUA), which was most likely a unicellular organism that lived some 3.5 to 3.8 billion years ago [6] [11]. The mechanism of gene duplication [45] played an important role in genome expansion through evolution. This process allowed the addition of new genes to offspring genomes. In fact, some parental genes are not only copied but duplicated more than once. This leads to an offspring with larger genome than the parents, which allows genetic novelty and potential evolutionary innovation [33]. When a gene is duplicated, it creates a redundant gene with less selection pressure. This means that the duplicated gene can undergo mutations without having deleterious effects and eventually lead to a new functionality which produces a fitness increase. The natural and biological process of incremental genome growth and elaboration [26] is known as complexification. Complexification through gene duplication is a plausible explanation of how compact, efficient and robust genomes have evolved incrementally.

Martin [26] investigated the impact of gene duplication in the origin of vertebrates. He claimed that such a duplication process produced an increased genome complexity before the origin of fishes. Such duplication events happened at relatively high rates. Moreover, not only beneficial duplications become fixed in the genome but also neutral duplications in respect to fitness. In some cases, also when the original gene faces negative mutations, the duplicated gene becomes fixed. Key factors for gene expansion by gene duplication and optimization are then mutation and fixation. Zhang [54] studied the process of acquisition of new functions in duplicated genes. He argued that gene duplication is an extremely important factor for evolution, providing new genetic material for evolution to exploit with mutation, drift and selection, which leads to new gene functions or specialization of existing ones. In fact, in the three domains of life, i.e. bacteria, archaea and eukarya, there is strong evidence that large portions of genes appeared by gene duplication (data from sequenced genomes). As an example, around 38% of the Homo Sapiens genome is the result of gene duplication [24] and around 1800 duplication events took place since humans diverged from chimpanzees in roughly 6 million years. This produces evidence that such a mechanism contributes to plasticity / adaptation to changing environments and speciation, as well as the emergence of complex regulatory mechanisms in gene regulatory networks.

However, the same degree of scalability, complexity and evolvability is not achieved in evolved artificial developmental systems, partly because of the complex genotype-to-phenotype mapping and relative encoding (direct encoding or fixed-length encoding), that leads to an extremely high dimensionality of the search space. With direct encodings this incremental approach is difficult to achieve because each gene maps to a specific phenotypic functionality/structure and duplicating it would result in significant alterations of the phenotype [41]. In this paper, we argue that in order to retain the advantages of biological complexification, it is necessary to exploit indirect encodings, where duplication would not have a disruptive effect. Newly added genes, once incorporated in the genome, would have time to be gradually modified without too severe consequences on development and eventually being optimized.

B. Scalability within context

Scalability within the boundaries of cellular evolutionary and developmental systems, e.g. cellular automata, strongly relate to some definition of spaces. These spaces are interconnected, which makes the scalability aspect also interconnected.

- State Space: each entity composing the system, e.g. cell / node, can hold a finite number of states. The state space is the set of all the possible combinations of states the system, i.e. a developing organism, can show. Allowing for more states would scale-up not only the state space but also the genotype-to-phenotype mapping and their related spaces.
- Rule Space: interactions of system components occur on a local basis among neighboring entities. The rule space is the set containing the permutations of the states of the entities in a neighborhood. Scaling the

state space would affect the rule space exponentially. Allowing for more neighboring interactions, e.g. changing the neighborhood size, would scale-up the rule space.

- Search Space: the set of all possible genotypes that can be composed with the chosen encoding and discovered by evolutionary search. It is strongly affected by the state space and rule space. The search space or genotype space is a key factor for the success of evolutionary search and depends on the defined encoding, genotype size and number of genes allowed (for a fixed genotype encoding).
- Solution Space: the set of all possible phenotypes. The solution space is different from the search space due to the genotype-to-phenotype mapping. It is strongly influenced by the available phenotypic resources, e.g. the geometry in a cellular system or the topology in a neural network. Scaling-up the phenotypic resources would increase the solution space exponentially.

This means that a system designer faces a challenge when deciding upon issues such as the right genotype encoding, size, and states, since a small change in one of the above-mentioned spaces has a cascade effect on the other spaces, which will be scaled accordingly. The cardinality of those spaces changes with the complexity of the problem.

C. Scalability in EvoDevo Systems

In the field of Evolutionary Computation, each problem is represented as a genotype and a specific fitness function is designed to evaluate qualities of the wanted solutions. Evolutionary Algorithms (EAs) often use a one-to-one genotype-to-phenotype mapping, which means that a candidate solution generated by the EA can be directly mapped to the medium the solution was designed for. Thus, each property and characteristic of the phenotype needs to be encoded in the genotype. Figure 1 presents a direct mapping where each phenotypic property (network connection) is represented by a gene in the genome. If the phenotype was allowed to have more connections, the genotype would become more complex and consequently enlarge the EA search space. Typical examples of EAs with direct mappings are evolved artificial neural networks for robot controllers [32]. Here the size of the network is predefined and thus the available number of genes (to represent connections among them and connection weights) is also predefined. The more complex the phenotype is, the more complex the genotype becomes.

Another possibility is to open for a redundant genotype-phenotype mapping [38] where the cardinality of the genotype space is larger than the cardinality of the phenotype space, i.e. many-to-one mapping. The nature of the mapping allows neutral genotype mutations [39] that do not alter the phenotypic characteristics but enable moving through the search space more easily and reducing chances of getting trapped in local optima [40]. Redundant representations are less efficient encodings that rely on additional genes that do not encode relevant information [35]. In nature, ontogeny allows “shrinking” complex organisms into compact genomes.

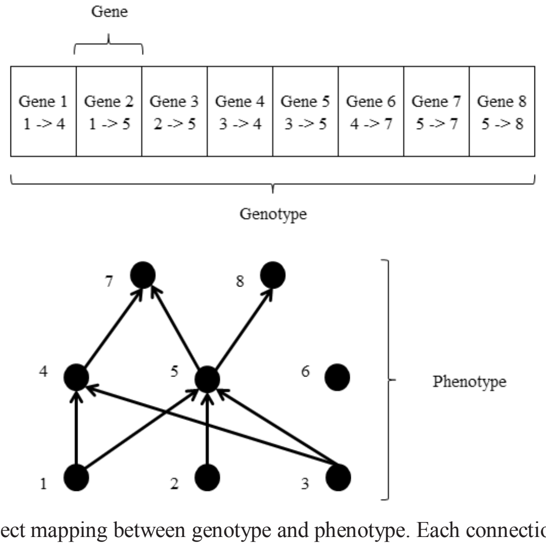


Figure 1: Example of direct mapping between genotype and phenotype. Each connection between two nodes in the network is represented by a specific gene.

EAs are very resource demanding and, if one-to-one direct mapping is used (or redundant mapping), they suffer from an inherent scalability problem. In general, a solution or an algorithm is said to be scalable if it is able to provide acceptable performances when the instance of the problem increases in size. Acceptable or tolerable performances may be referred to be non-exponential resources demand for a linear increase in the problem size.

This is not the case for EAs, where an increase of the problem size does not reflect a proportional increase in the search space. One solution for the resource-demanding trait of EAs is to take inspiration from nature and somehow shrink the genotype, i.e. indirect mapping. This reduces the overall complexity of the genotype (and the search space magnitude) while adding more complexity to the genotype-to-phenotype mapping and the underlying development process. Thus the challenges are finding an efficient developmental mechanism and a suitable indirect representation that is able to exploit such development process.

Even though developmental systems are widely used [49, 7, 27, 14, 42], the genotype representation scalability challenge still exists. For several developmental systems it would not be feasible to fully specify all the possible regulatory combinations in the genotype, e.g. complete regulatory information for Tufte's CA-based model [48] would require the specification of 54^5 regulatory possibilities, Miller and Banzhaf's cellular developmental Cartesian Genetic Programming (CGP) model [27] a total of 768^9, von Neumann's universal constructor [28] 29^5 combinations. For many systems, using fixed-length genotypes containing only a subset of all the possible regulatory combinations is a necessity. In cellular models the total possible number of regulatory combinations is N^K, where N is the number of possible states each cell can hold and K is the neighborhood. Bidlo [4] for his instruction-based cellular model with four possible cell states and neighborhood of size 5 used a restricted transition function of only 10 entries, Tufte [47] had a model with 13 possible cell states and five neighbors whether the available regulatory rule-set was restricted to 64. Tufte and Thomassen [51] investigated scaling of genomes with fixed-length representation and allowed 4, 5, 6 and 32 regulation rules out of the possible regulatory information based on three cell types and five neighbors (13 cell types for genome of size 32). In all such cases, the maximum representation was pre-defined and could not change during evolution. The available regulatory information was designed a priori by trial and error or by estimation and did not guarantee that a possible solution could be found at all or that the same solutions could be achieved with a smaller genotype representation. Nonetheless, the maximum complexity of the system was predetermined, in the sense that the reachable search space was shrunk by the chosen representation. If one wanted to scale up the system by allowing a larger neighborhood or more available cell states, the chosen genotypes may not have been large enough to represent a candidate solution, as the cardinality of the mapping would be changed.

An alternative that can scale both genotype and phenotype information is to open for a variable length genome. An example of variable-length general encoding that can be applied for indirect construction of phenotypes [36] is Genetic Programming [21]. If a mechanism of adding genes through gene duplication is allowed, it is possible to incrementally grow the genome size. This complexification strategy may help to solve the genotype representation scalability problem. Previous work was done towards achieving genome size expansion, for example [5], [13], [20], [25]. Federici and Downing [9] investigated neutral gene duplication in a cellular model with environmental chemicals. They studied genome scalability with direct encoding and embryonal stages, using a gene regulatory model based on recursive neural networks (RNN). Stanley and Miikkulainen [43] introduced NeuroEvolution of Augmenting topologies (NEAT), a complexification method for the incremental evolution of neural network architectures. Their main goal was to evolve robot controllers with direct encodings through gene duplication. They argued that incremental evolution of complex neural network genomes relies on three main technical components: meaningful crossover by means of historical markings for gene alignment, innovation through speciation which enables optimization, start from minimal genomes and allow incremental size increase. Taking inspiration from the presented research on complexification of developmental systems with direct encodings, we investigate the basic idea using indirect encodings [41]. An incremental evolution of genome representations may have the potential for exploration on developmental systems with an indirect genotype-to-phenotype mapping.

III. Framework for Incremental Evolution of Genome Representations

This section presents a possible framework for incremental evolution of genome representations on artificial cellular organisms with indirect encodings. Using indirect encodings is a necessity, since for highly complex systems (potentially at biological complexity levels), the search in the space of final solutions would be intractable [41].

Conventional genetic algorithms consist of few steps, which can be summarized as follows:

1. Initialize random population;
2. Compute fitness;
3. Proportionate selection;
4. Crossover and mutation;
5. Generate new population;
6. Jump to step 2 and repeat until the convergence criteria is satisfied.

For embryomorphic systems, the fitness evaluation cannot be performed directly on the individuals in the population, due to the indirect mapping between genotype and phenotype. As such, each genotype is developed starting from a single cell, i.e. zygote, to a multi-cellular organism (phenotype) which is subject to fitness evaluation. Altenberg [1] presented a theoretical method for selective genome growth where new degrees of freedom in the genome representation are added incrementally. When a new gene is incorporated into the existing genome, it does not only produce immediate phenotypic effects but it carries with it new kinds of variants that can give rise to in the future. In Altenberg's methodology, the growth of genotype size is not kept in the generations by means of natural selection but it is brute-forced to produce an increase of fitness or rejected otherwise. The gene addition is based on a repetitive structure which tries to add a gene until it successfully increases the fitness of the individual. In contrast, we argue that exaptation is a key component of evolution, where the phenotypic response to a genetic operator, e.g. mutation or gene addition, is not obvious and not necessarily instantaneous. It may need some generations before some genetic traits are expressed in the phenotype, development may not be able yet to exploit it, but when such genetic information becomes optimized and integrated in the genome it could finally produce larger phenotypic improvements than a single gene could do. Exaptation is the ability to let evolution shift the function of a genetic trait, which was previously evolved to serve another function, to provide a new function. We propose the following framework, which allows gene addition by gene duplication and exaptation is promoted by natural selection.

A. *Genome Growth Regulation Mechanisms*

A conventional genetic algorithm is modified with the introduction of four regulation mechanisms to control genome growth:

1. There is an upper bound on the maximum number of genes that can be added, which coincides with the size of the maximum rule space for the considered neighborhood and possible cell states, i.e. maximum number of combinations that can be generated by permutation of all the neighborhood configurations with the available number of cell states;
2. There is a duplication rate which guarantees that a new gene is added with a certain probability to each individual in the population (duplication is not deterministic but stochastic);
3. Added genes are guaranteed time for optimization, before a new addition can occur. In other words, there is a counter and a threshold which specifies that growth can occur only after x generations without an increase in the overall best fitness in the population. This means that as soon as an increase in the fitness occurs the counter resets, ensuring that duplication happens when there is no room for further genotype optimization.
4. There is an elitism mechanism. This is done to guarantee that genotypes with compact and effective genomes will be kept in the population no matter what. This enables speciation and survival of species with smaller genomes.

B. *Gene Addition*

Gene addition is a simple operation per se. If the four above-mentioned regulation properties hold for a given genotype (1. upper bound not reached, 2. genotype selected for gene addition, 3. no overall fitness increase during the last x generations, 4. genotype not in elite), a gene addition occurs. As depicted in Figure 2, a genotype that consisted of n genes at a given generation, acquires a new gene which is an exact copy of a randomly selected gene already present in the genome. The selected gene is copied and appended; the genotype consists now of n+1 genes.

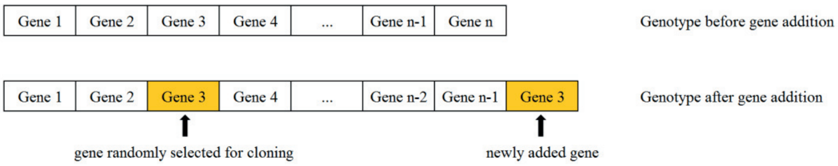


Figure 2: genotype before and after gene addition. A random gene is cloned and appended.

C. *Crossover and Mutation*

Since the population will consist of genotypes with a different number of genes, crossover has to support the crossing of different sized genotypes. This is done by choosing a crossover point from the smaller genome. Then a swap is performed between the chosen genotypes. This is shown in Figure 3 (c). If the genotypes have equal size as in Figure 3 (a), single-point crossover is performed which produces the result shown in Figure 3 (b).

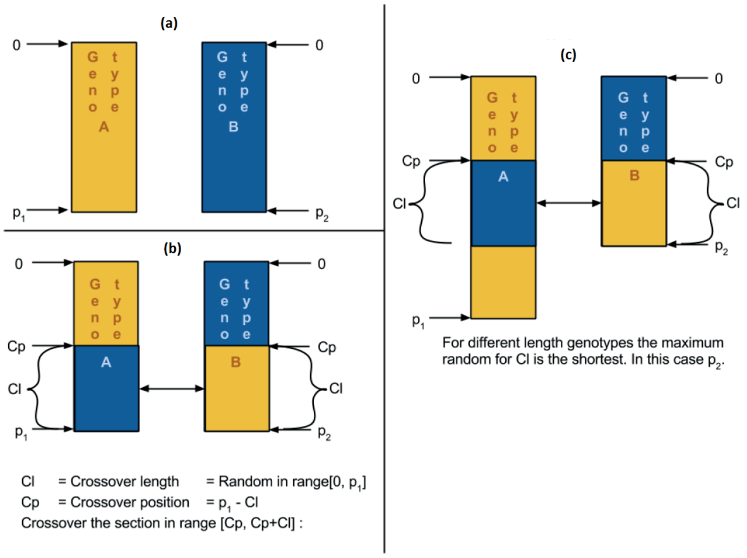

(a)
0
0
Genotype A
Genotype B
p1
p2
(b)
0
0
Genotype A
Genotype B
Cp
Cp
Cl
Cl
p1
p2
Cl = Crossover length = Random in range[0, p1]
Cp = Crossover position = p1 - Cl
Crossover the section in range [Cp, Cp+Cl] :
(c)
0
0
Genotype A
Genotype B
Cp
Cp
Cl
Cl
p2
p1
For different length genotypes the maximum random for Cl is the shortest. In this case p2.

Figure 3: crossover scheme. Left: parents of equal size before crossover (a) and after crossover (b), Right: parents of different size (c).

Each gene in a genotype is represented within a bit sting and every bit has an equal chance of mutating, i.e. bit flipping. Since the genotype is growing in size, the mutation rate is calculated for each genotype, keeping an equal mutation rate relative to the size of the genotype. The mutation rate is linearly adaptive, meaning it decreases with increased fitness on a genotype, ranging from 100% to 5% of the defined mutation probability. This gives fewer mutations for fit individuals (typically with larger genomes), which avoids large jumps in fitness landscape and encourages location of fitness peaks.

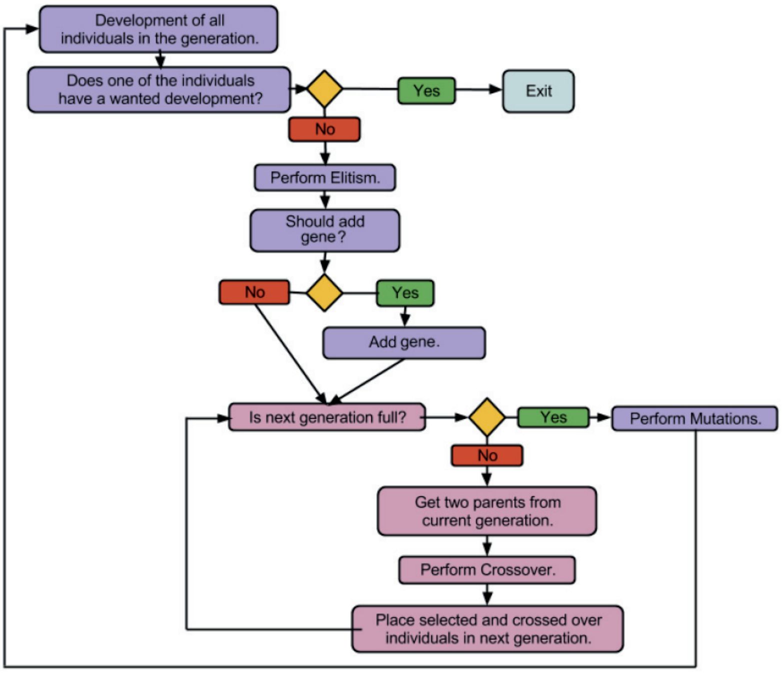
D. Selection

In the process of selecting individuals either for offspring generation or for gene addition, a weighted selection is implemented, which consists of the sum of the three following weighting contributions:

1. The actual fitness of the phenotype, which is a standard objective measure of individual's fitness;
2. The genotype exploitation parameter, which consists of the number of gene regulatory combinations actually triggered during phenotype development, i.e. the ratio between used genes and total genes in the considered genotype. This promotes the emergence of effective and efficient genomes, by rewarding individuals that exploit a large number of the available genes;
3. The innovation parameter, which rewards genotypes with larger genomes. This is done to promote innovation by genome growth and it is tightly coupled with the inherent regulation on active genes. This parameter is needed because gene duplication does not guarantee an immediate innovation and fitness increase but most likely a neutral or negative effect, thus being discarded too often. To calculate it, for each individual we find the percentage of the population's collective genotype size that an individual genotype size covers. Further, we scale this percentage to a selected ratio to achieve a suitable impact on the fitness. Elitism guarantees that fit individuals with smaller genomes will survive and genomes with newly added genes, but not yet optimized, will still be allowed to evolve.

E. Summary

The regulation mechanisms, crossover of different size genotypes, weighted selection and gene addition are incorporated in the GA, as shown in the flow chart presented in Figure 4. The initial population is initialized with genotypes with a single gene, thus the available search space is minimal. This implicit process is not included in the flow chart to improve readability. The first step is development of genotypes due to the nature of EvoDevo with indirect encodings. Phenotype fitness is then evaluated in the second step and if a solution is found the algorithm ends. If the fitness condition is not satisfied, elitism is performed. Note that the fitness calculation includes the above-mentioned mechanisms and weightings and, in particular, it checks if there has been a fitness improvement compared to the best fitness recorded so far. This is in charge of resetting the counter that determines the theoretical minimum optimization time for each previously added gene and controls whether a stochastic gene addition may be performed. If this is the case, the "Add Gene" block clones a random gene and resets the optimization counter. Then crossovers and mutations occur until the population is restored to the required size.



Development of all individuals in the generation.
Does one of the individuals have a wanted development?
Yes
Exit
No
Perform Elitism.
Should add gene?
No
Yes
Add gene.
Is next generation full?
Yes
Perform Mutations.
No
Get two parents from current generation.
Perform Crossover.
Place selected and crossed over individuals in next generation.

Figure 4: flow chart of the proposed framework for incremental evolution of genome representations.

The gradual increase in search space provided by the presented framework could theoretically reduce the likelihood of evolution getting stuck in local optima, since when a new degree of freedom is added, the previous local optima are replaced by a new set of a higher dimension [10]. Such gradual evolution and exploration would allow a gradual increase in complexity, which is not limited by a fixed-representation.

IV. MOTIVATION

The main motivation behind this work is not achieving a speed-up in evolutionary search. Rather, we propose a framework for cellular EvoDevo systems with indirect encodings that is scalable and independent from the chosen fitness metric. We investigate if it is possible to find solutions without any specification on the genotype size and let evolution find the necessary representation and genome length for the target solution. Our work is designed to obtain compact and effective genotypes for: (a) systems where it would not be possible to estimate a priori the necessary genome length to contain a candidate solution; (b) systems where it would not be possible to specify all the regulatory combinations. This may provide the necessary system scalability, leading to increasingly complex solution. To test the hypothesis, we propose a cellular developmental model based on cellular automata. Artificial cellular systems share some common properties with biological cellular systems, where the key component is a cell. Cells interact on a very local level without any knowledge on the overall state of the system. The only information available on each cell is its own state and the state of a few neighbors that are physically close. Computation is executed in parallel on all the cells in the systems and it is regulated by a genotype that specifies cellular regulatory inputs and relative cellular actions, e.g. cell growth, differentiation, and apoptosis. The available regulatory information is the same for every cell. For a simple developmental system, the number of regulatory input combinations is not extremely large and can be fully specified in the genome. This is important since we want to compare evolution with a static fully-specified genotype and evolution with a growing genotype.

In this work we look closer at the correlations between the genome length/genome exploitation and evolutionary results. We evolve different cellular behavior/structures using a large genome (fully specified, i.e. all the possible regulatory input combinations), a growing genotype and a small genome (a restricted genome pool out of all the possible regulatory input combinations). By comparing these methods to each other, we can get an understanding of how restrains affect the evolved organism. We consider the genome usage for the evolved solutions on different complexities. Further, we pose some answers to questions such as: Are we going to find that growing a genotype produces compact and effective genotypes? Or will the results be similar to those of an organism evolved with a large genotype? How will this type of evolution scale? Could a cellular EvoDevo-system which evolves organisms with a growing genotype exhibit emergent or implicit behavior not found in organisms evolved with a static large genotype? Will this kind of evolution actually be able to produce results at all?

Once the proposed framework is found to be able to evolve a solution with a minimalistic developmental system, we scale-up the system complexity and available resources. A simple way of making Cellular Systems capable of very complex behavior is to increase the amount of cell states, which in turn increases the regulatory rule space, the evolutionary search space, and the system state space exponentially. If the proposed framework is able to achieve results while changing the number of cell states, it would mean that the framework could support growing evolution in both search and state space, which means it would ideally allow to tackle problems of increasing complexity. The presented experiments are mainly to investigate if the growth evolution function is able to create solutions with more cell states. We also investigate if the growing evolution function is able to find solutions in cellular spaces with different size geometries. By increasing the geometry, the solution space expands considerably, i.e. the number of states the system can exhibit.

V. Scalability

In today's society, we often use computers to solve very large problems. For instance, extensive problems with a vast amount of variable parameters can be tackled with an EA, but even so it requires much computational power / time and often produces large solutions (solution here refers to the specification of a candidate solution in the genotype). Having a good understanding of scalability can help both the usage of computational power, the size of the solutions, and might even be able to shrink the size of the problem. To increase EA scalability to large problems, development has been widely used, which creates small solutions to problems that normally require larger solutions. This again makes the solutions manageable, making scaling a valuable tool. EvoDevo systems are often applied within the field of cellular development, e.g. CA, which makes cellular systems already a method that scales well [37]. One way in which scalability can be increased is by reducing the state or search space for a wanted solution, which essentially reduces the size of the fitness landscape, making systems scale to solve larger problems. Knowing what makes algorithms create solutions that are scalable in geometry (or resources) can reduce the problem, making the resource consumption manageable. Having a good understanding of scalability gives a better utilization of resources, and makes it possible to create solutions to problems which one normally does not have enough resources to solve, or makes runtimes of currently solvable problems faster. There are of course many other ways to reduce the real runtime of an EA, for instance massively distributed or parallelized algorithms. But these will also benefit from a smaller search space and state space, which can be achieved by scaling in efficiency. By understanding how solutions scale in geometry, it can become possible to evolve small solutions that scale-up to larger geometries with linear increase, or without the loss of functionality.

At the design stage of a cellular EvoDevo system, the choices of the genotype size/encoding, the number of system states and the available resources have an impact on the search space, state space and solution space [2]. In the next sections, all these three relevant scalability aspects are addressed.

A. Scalability in effectiveness (search space)

Effectiveness with regards to an EA is the measure of the amount of genes used in an evolved solution compared to the minimum amount of genes needed for the solution to work. Also, the amount of genes used in an evolved solution compared to the amount of genes available for each individual in a population during evolutionary search. With regards to a cellular system, effectiveness is the measure of used regulatory input combinations, i.e. neighborhood configurations, compared to theoretical maximum regulatory information. This is a key factor for scalability since reducing the genotype size greatly decreases the search space.

In the first set of experiments we fix the target phenotypic complexity/behavior and the CA geometry and evolve solutions with a full genotype, i.e. all the possible regulatory information are fully specified (maximum genome length for the chosen cellular model). The results are compared to solutions obtained with a restricted gene pool where only a limited amount of regulatory combinations can be specified. Finally we evolve solutions with our proposed framework on incremental growth of genome representations, which automatically increases the size of the genotypes. We evaluate the genotypes of the found solutions in terms of compactness, i.e. the size of the whole genotype, and effectiveness, i.e. number of triggered genes during development in contrast to the total available genes in the genotype solutions.

B. Scalability of states (state space)

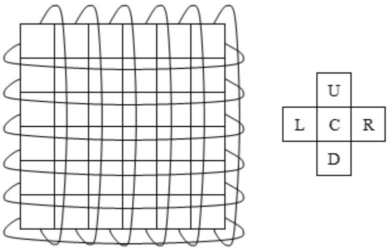
In the second set of experiments we investigate if the proposed framework is able to evolve solutions when the state space increases. For a cellular system, this means scaling-up the number of available states each cell can hold. This exponentially increases the total number of regulatory input combinations (rule space). The number of necessary genes to encode a solution is not known in advance and thus the choice of an incremental growth of genome size seems realistic.

C. Scalability in geometry (solution space)

In the last set of experiments we scale-up the available phenotypic resources, i.e. increase the cellular geometry size. Having a larger world to develop solutions increases the solution space exponentially and changes the genotype to phenotype indirect mapping. This intuitively makes it harder to estimate a priori the necessary genome representation. Again, an incremental genome growth could bypass the issue.

VI. Cellular Developmental Model

Our test-bed model is a cellular developmental system based on cellular automata, i.e. synchronized cellular cycle, parallel operation and discrete cell states, similar to cellular models used in [19], [27], [48]. The system here is close to the field of Morphogenetic Engineering [8], where the goal is “self-architecturing” systems. In embryomorphic systems, the approach is based on embryogenesis: the self-assembly of myriads of cells starting from a single zygote which holds the complete genotype information.



L	R	U	D	C	$C_{(t+1)}$
0	0	0	0	0	0
0	0	0	0	1	{0,1,2, ..., n-1}
0	0	0	1	0	{0,1,2, ..., n-1}
0	0	0	1	1	{0,1,2, ..., n-1}
0	0	1	0	0	{0,1,2, ..., n-1}
:	:	:	:	:	:
1	1	1	1	1	{0,1,2, ..., n-1}
0	0	0	0	2	{0,1,2, ..., n-1}
0	0	0	2	0	{0,1,2, ..., n-1}
0	0	0	2	1	{0,1,2, ..., n-1}
0	0	0	2	2	{0,1,2, ..., n-1}
:	:	:	:	:	:
n-2	n-2	n-2	n-2	n-2	{0,1,2, ..., n-1}
0	0	0	0	n-1	{0,1,2, ..., n-1}
0	0	0	n-1	0	{0,1,2, ..., n-1}
0	0	0	n-1	1	{0,1,2, ..., n-1}
0	0	0	n-1	2	{0,1,2, ..., n-1}
:	:	:	:	:	:
n-1	n-1	n-1	n-1	n-1	{0,1,2, ..., n-1}

Figure 5: geometry, neighborhood and genome developmental table of the cellular developmental model.

A CA can be considered as a developing organism, where the genome specifications and the gene regulation information control growth and differentiation of the cells. The behavior of the CA is then represented by the emerging phenotype, which is subject to size and shape modifications, according to the cellular changes along the developmental process. Such a dynamic developmental system can show adaptation, self-modification, plasticity [53] or self-replication properties [23]. The model is based on a two-dimensional cellular automaton with cyclic boundary conditions, as illustrated in Figure 5. As such, the totality of regulative inputs can be coded completely in the genome. This does not imply that all of the genome information is expressed in the phenotype. To ensure that cells will not materialize where there are no other cells around, a restriction has been set: if all the neighbors of an empty cell are empty, the cell will also be empty in the following development step. The organisms develop starting from a single cell placed in the grid, i.e. zygote. The placement of the first cell is of no importance as the grid is wrapped around as a torus. The local cellular communication is based on the von Neumann neighborhood (5 neighbors) and includes only cell types, both intracellular, i.e. the cell’s own state and extracellular, i.e. the neighboring cells’ state. Intracellular and extracellular information regulates actions of the developmental processes. Figure 6 illustrates the relation between regulatory information and development as a quasi Finite State Machine (FSM). The state Regulatory ”Decoding” takes regulatory information from a local cellular neighborhood (Extracellular Information) and information from the cell itself (Intracellular Information) as input to a gene regulation process defined by the genome. Cellular action, indicated by state Cell Action 0/n-1, is promoted out of the outcome of the gene regulation process. In this example the cell can express a change, e.g. in intracellular state, or no change if the regulatory information codes for a jump to the No Action state. The state No Action is also the state the cell will be in for all input regulatory information that does not explicitly regulate a cellular action, e.g. input information may be the total of Extracellular and Intracellular. This implies that all regulatory input combinations not covered in the genome will indirectly regulate the cell into the No Action state. As such, a genome of a size that does not cover all regulatory possibilities will have a given part that indirectly codes the developmental process of No Action in Figure 6. As the model under investigation does not include environmental influence in the gene regulation, i.e. no possibility to deviate from the trajectory given by the initial configuration and genome information, there are no effects on development caused by dynamic attractor landscapes and environmental perturbation.

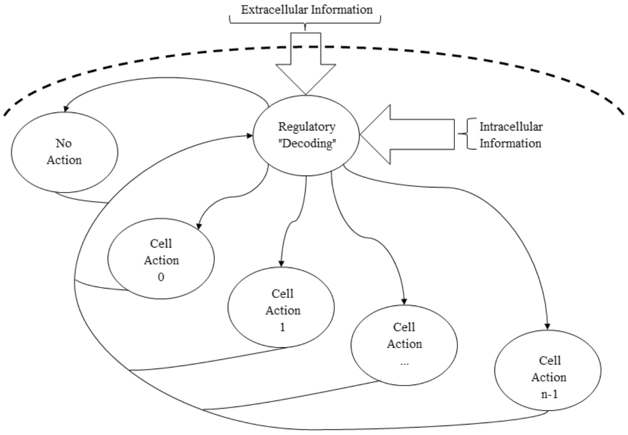


Figure 6: Intracellular and extracellular regulation.

The presented developmental model allows for an arbitrary number of possible cell states and cellular actions. If a minimalistic setting where only three cell states is considered, i.e. a quiescent cell type plus two other cell types to guarantee cell differentiation and the concept of multi-cellular organism, the gene regulatory information which covers all the possible cellular actions will consist of $3^5 = 243$ combinations. As such, a developing organism will consist of different constructs of the three cell types. In general, n^n^k possible transition functions are available, where n is the number of cell states and k is the neighborhood size. Figure 7 shows an example of a developing organism using the described minimalistic setting. Here the grid size is set to 5X5 cells and different colors indicate the different cell types. The change in phenotypic structure can be observed along the developmental path.

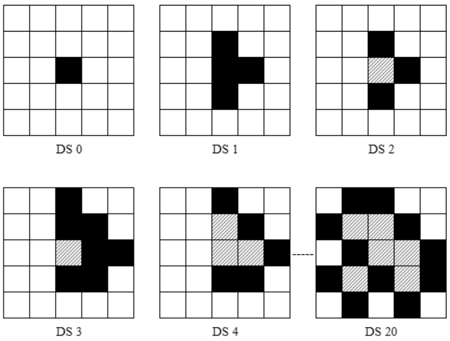


Figure 7: Example of developing cellular organism.

Having defined genetic information for the cellular model, a quantifiable measure has to be defined for the developed organisms. Properties that can be used need to provide information on the developing organism as a whole and the occurring phenotypic changes [17]. For a given organism, the initial cell (zygote) follows a developmental trajectory and after a transient phase reaches an attractor, i.e. a final stable state (point attractor) or a self-reorganizing cycle (cyclic attractor). Previous work investigated the relation between developmental genomes and resulting attractors [30] [31]. As such, the attractor length is the chosen metric of phenotypic complexity.

VII. Evolutionary Growth of Genomes

The genotype information is composed of a set of genes that represent the regulatory information (neighborhood L, R, U, D and C in Figure 5) and relative cellular action (C_{t+1} in Figure 5). This is specified as a developmental table, as shown in Figure 5. In our model each developmental rule (a gene) is a 32 bit field where n-bits of each field are reserved for a neighbor site (based on the number of cell states). For example two states will require 1 bit, three states require 2 bits, four states also require 2 bits etc. As such, not all the bits in the field are necessarily used; this depends on the chosen number of available cell states. In the growing genome function there is no restriction on duplicate genes and copies can appear through gene duplication, mutation or crossover. As a regulation mechanism for redundant genes (equal neighborhood configuration) that may be active at the same time if the conditions in the regulatory decoding hold, modulo is used for unambiguous cellular actions and rules firing. This means that all the possible actions for a given neighborhood are summed and moduloed against the maximum number of cell states. Such a genetic regulation mechanism ensures a deterministic outcome.

There are three different ways of representing and evolving the GA population, i.e. genomes:

- Full evolution function: the initial population consists of full genotypes, i.e. a number of genes equal to the possible regulatory input combinations, where the neighborhood configurations are fully specified and the next value of the central cell in the neighborhood is initialized as the quiescent state;
- Restricted evolution function: here the size of the genotypes is reduced and only a small set out of all the regulatory combinations is specified. The genotype cannot change size for the whole evolutionary run. The next value of the central cell in the neighborhood (for the available genes) is initialized as the quiescent state;
- Growing evolution function: the population is uniform and composed of single-gene genotypes. The only neighborhood configuration that is specified consists of all quiescent states and the next value of the central cell in the neighborhood is also initialized as the quiescent state. The genotype builds-up according to the growing mechanism described earlier.

VIII. Experimental Setup

The initial population for all the experiments is set to 100 individuals and each configuration is averaged over 20 evolutionary runs. Each individual is developed for 2000 development steps. The GAs have the following settings: mutation rate of 2.6 mutations per individual (adaptive), elitism of one individual, crossover rate 0.02, add gene rate 0.02 with threshold of 10 generations without increase in overall best fitness. Three different sets of experiments are presented.

In the first set of experiments we investigate how the growing evolution function performs compared to the full or restricted evolution. In order to be able to fully specify the regulatory input combinations, the number of available cell states is set to three. With von Neumann neighborhood of radius five, a full genotype would consist of $3^5 = 243$ regulatory combinations. If a different configuration would have been chosen, e.g. with hundreds of cell types, the full genotype size would become so large that it would be unreasonable to define the entire rule space. The first experimental set-up is designed to compare full, restricted and growing evolution function with a setting where the whole genome can be explicitly specified. The chosen array size is 4X4 = 16 cells, which leads to a theoretical maximum attractor length of 3^{16} development steps. Different attractor targets are considered, as given in Table 1, together with the maximum number of generations the GA is allowed run in order to find the wanted attractor. The attractor length is measured as the number of development steps that occurred between two repetitions of the same state, i.e. the same state is encountered twice. Previous work has shown that attractor length is a plausible measure of phenotypic complexity [50, 30, 31, 29, 17]. The chosen metric of complexity, i.e. attractor length, is an abstract measure that does not code for any specific problem or computational task, e.g. majority, synchronization or a specific phenotypic structure. For the scope of this research, no specific computational task is implied, since we want to capture general properties on the developing organism as a whole and the phenotypic changes that occur during development.

Attractors	7	10	20	40	80	160	200	400
Generations	4000	4000	4000	6000	6000	8000	8000	10000

Table 1: Attractor length targets and relative generations allowed.

First the full evolution function and the growing evolution function are executed for all the wanted attractors. Statistics on effectiveness of the resulting genomes are collected: total number of genes and used number of genes. The total number of genes for the growing evolution function is used to determine plausible genotype sizes for the restricted evolution function. The used fitness weightings are 0.6 for the actual fitness, 0.2 for the genotype exploitation parameter and 0.2 for the innovation parameter. The resulting fitness *F* is calculated as in Equation 1.

$$F = 0.6 f + 0.2\, e + 0.2\, i \qquad (1)$$

In Equation 1, *f* represents the normalized actual fitness, i.e. how close the individual is to the wanted attractor length, *e* is the exploitation parameter, i.e. normalized ratio of genes triggered during development and total number of genes in the considered genotype, *i* is the innovation parameter, i.e. normalized value of genotype size.

In the second set of experiments, we evolve different attractor lengths (7, 10, 20 and 40 development steps) with more available cell states. For each of the chosen attractors, the state space is scaled-up to allow 5, 6 or 7 cell types. The number of available generations is the same as the first set of experiments. Using a setting with 7 available cell types and 5 neighbors would not be practical for a full evolution function. Such genotype would need to specify 7^5 regulatory combinations and the search space size would be 7^{16807}. Again, statistics on effectiveness of the resulting genomes are collected: total number of genes and used number of genes.

The third set of experiments consists of evolving different attractors with the growing evolution function, when the cellular world geometry scales up. By increasing the geometry, the solution space expands considerably. The tested CA geometries are 4X4 = 16 cells, 6X6 = 36 cells, 8X8 = 64 cells and 16X16 = 256 cells. Three cell states are allowed and the target attractors considered are 5, 7 and 10 development steps. The maximum number of generations the GA is allowed to run is 8000. The used fitness weightings are 0.8 for the actual fitness, 0.05 for the genotype exploitation parameter and 0.15 for the innovation parameter. A new negative weighting is also introduced, namely the border condition parameter, which could weigh up to -0.25. The border condition parameter measures how much the development of the organism relies on border conditions, i.e. ratio of border cells exploited and total number of border cells. This was done to promote organisms that exploited border conditions as little as possible, developing self-organizing attractors based on genome regulations rather than collisions.

IX. Results

A. *Scalability in effectiveness – genome comparison*

Three evolutionary strategies are tested and compared: full evolution function, restricted evolution function and growing evolution function. Each of the strategies is executed 20 times and the results are averaged over the runs, for each of the target attractor lengths. The main aspect is to evaluate how well genome utilization is achieved by the growing strategy compared to the full and restricted strategies. Having a good utilization with a growing evolution would mean that such a strategy is able to find solutions of arbitrary complexity using a reduced search space and making the process of deciding the genotype representation size unnecessary.

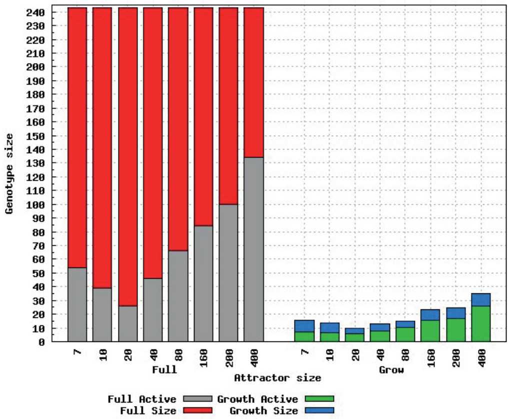


Figure 8: genotype size and # activated genes (measured as genes number) during development of organisms with different attractor lengths. Full evolution function on the left and growing evolution function on the right. Averages are calculated over successful evolutions of 20 runs.

Figure 8 depicts the average gene usage and genome size for successful runs targeting different attractor lengths, comparing full and growing evolution function. It is clearly observable that evolutionary growth of genotype representation gives both a smaller genotype size and a better utilization of the available genes. The full evolution function has a genotype size of 243 genes (all the possible regulatory input combinations = 3^5) while the growing evolution starts with a genotype consisting of a single gene. For example, if the results for attractor target 10 are analyzed in Figure 8, the full evolution function evolves fixed size genomes of 243 genes (red bar). The number of genes triggered during development is 38.8 on average (gray bar). On the other hand, the growing evolution function produces genomes of 13.6 genes (blue bar) with 6.3 genes triggered on average (green bar). The results of average genotype size for growing evolution are used to find appropriate values for the restricted evolution genotype size. Three sizes are chosen: one equal genotype size to that achieved by the growing evolution function, one slightly smaller and one slightly larger (differences for low and high restriction are relative to the size). Genome sizes for the restricted genotype pool are summarized in Table 2.

Attractor	Low Restriction	Mid Restriction	High Restriction
7	12	16	20
10	11	13	15
20	8	10	12
40	10	13	16
80	12	15	18
160	20	24	28
200	21	25	29
400	30	35	40

Table 2: genome sizes for the restricted genotype pool, measured as # genes.

Figure 9 compares the growing evolution function and restricted evolution function with the defined fixed representations. The mid restriction has similar results to those obtained by the growing evolution function, in terms of the total number of genes (this was fixed a priori for the restricted evolution, based on the average results obtained by the growing evolution function) and in terms of number of used genes during development.

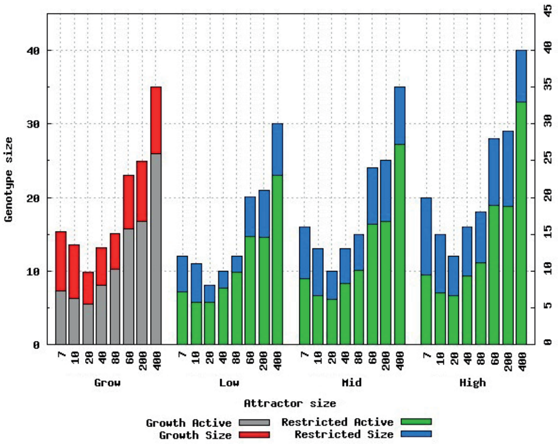


Figure 9: comparison of growing evolution function and restricted evolution function with the defined fixed representations (Low, Mid and High).

The overall results over the successful runs are summarized in Table 3. For each different attractor length, the average genotype size and average genes usage are calculated, together with the standard deviation. The growing evolution function performs better for all the tested attractor lengths in terms of genome effectiveness (total genome usage highlighted in yellow).

Attractor	Full				Grow				Restricted (mid)			
	Used		Total		Used		Total		Used		Total	
	Avg	StdDev	Avg	StdDev	Avg	StdDev	Avg	StdDev	Avg	StdDev	Avg	StdDev
7	59.9	23.6	243	-	7.3	1.3	15.4	4.8	8.9	1.2	16	-
10	38.8	19.1	243	-	6.3	1.4	13.6	3.5	6.7	1.2	13	-
20	26.0	10.5	243	-	5.6	0.7	9.9	1.9	6.6	1.5	12	-
40	46.1	10.9	243	-	8.0	1.7	13.2	2.9	8.3	1.4	13	-
80	66.4	17.1	243	-	10.3	1.3	15.1	2.9	10.1	1.6	15	-
160	84.1	17.5	243	-	15.7	3.5	24.1	7.5	16.3	2.1	24	-
200	100.0	13.3	243	-	16.2	4.0	23.8	7.5	17.9	2.9	25	-
400	134.2	16.5	243	-	26	-	35	-	27.3	4.6	35	-

Table 3: comparison of the three different evolution functions (Full, Growing and Restricted), average and standard deviation over successful evolutions of 20 runs (- means 0 or n.a.)

The success rate was predicted to be higher for the full evolution function than for the restricted and growing evolution function, since a full genotype representation does not need to simultaneously grow the genotype and increase the fitness. Looking at the success rate summarized in Table 4, it is observable that the prediction was reasonably accurate. The success rate is very dependent on the number of generations available to discover solutions and the number of given development steps, which are not the main goal here. The number of available generations was predefined and it is intuitive that growing evolution relies on the number of available generations to incrementally build up the genotype.

Attractor	Grow	Full	Rest(Low)	Rest(Mid)	Rest(High)
7	18/20	15/20	18/20	19/20	18/20
10	20/20	20/20	19/20	20/20	20/20
20	20/20	20/20	20/20	20/20	20/20
40	20/20	20/20	19/20	20/20	20/20
80	15/20	20/20	10/20	14/20	14/20
160	14/20	20/20	9/20	9/20	14/20
200	16/20	20/20	13/20	10/20	12/20
400	1/20	20/20	1/20	4/20	3/20

Table 4: comparison of success rates for different attractor lengths.

Figure 10 (left) presents a comparison of the different evolutionary functions for attractor length of 20 development steps. The growing evolution function climbs incrementally towards the wanted attractor, which is because it needs to build up the genotype iteratively. It is important to highlight once more that the goal here was not analyzing the convergence speed but the effectiveness of the obtained genotypes. Having a closer look at the growing evolution function in Figure 10 (right), which shows the genotype growing (green line) while evolving attractor length (blue line), it is possible to see that such a strategy has an inherent growing regulation mechanism. In the first phase the genotype grows more, whether once the achieved fitness is close to the wanted attractor the algorithm optimizes more the available genes without the need of extra adding.

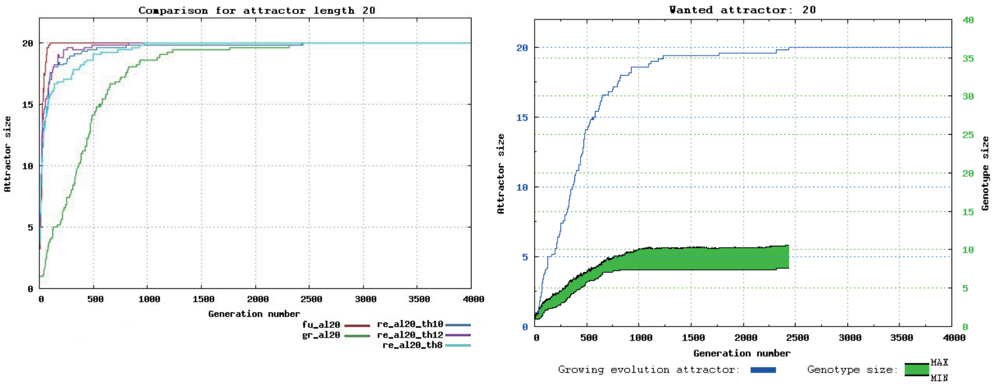


Figure 10: comparison of the different evolutionary functions for attractor length of 20 development steps on the left [1]; growing evolution function and relative genome size on the right; average over 20 runs.

In Figure 11 the wanted attractor is 200 development steps. While for organisms with shorter attractor lengths (10, 20, 40 development steps) the given generation span was enough to discover solutions in all the runs, with longer attractors (80, 160, 200, 400 development steps) more generations are needed. However, in all the runs, the genotype is growing as the relative phenotype complexity grows. In all the experiments it is possible to notice a faster growth in the early generations and slower growth later when genotypes get optimized.

Note that solutions were found for all target attractor lengths. The success rates are shown in Table 4. Figures 10 and 11 represent averages over 20 runs.

[1] See Appendix 1 for a description of Figures Labeling

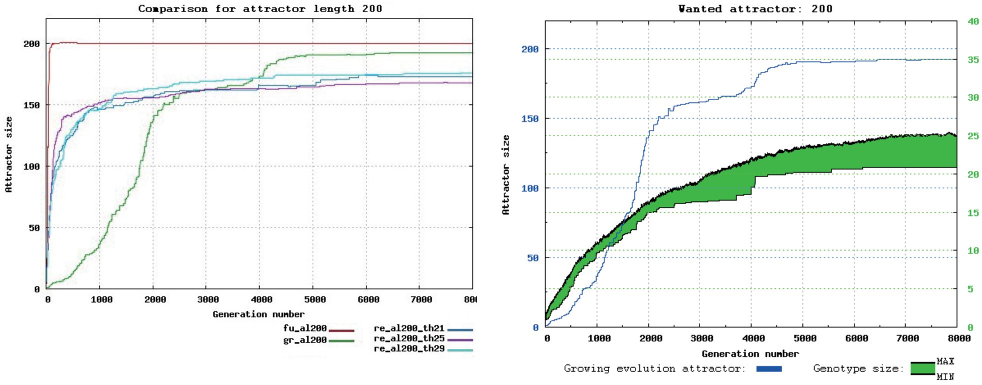


Figure 11: comparison of the different evolutionary functions for attractor length of 200 development steps on the left; growing evolution function and relative genome size on the right; average over 20 runs.

Table 5 summarizes the statistical significance of the comparisons using Student T-Test between obtained genotype sizes and between average genes usage. For all the wanted attractor lengths, the differences between growing evolution function and full evolution function is significant (p<0.001), both in terms of genotype size and genes activated during development). This means that growing evolution function is able to evolve better genotype representations, with more compact and effective genomes.

If the growing evolution function and restricted evolution function are compared (fixed representation with the same genotype size as the one produced by growing evolution function), no statistical significance between the averages was found. The only difference was a higher success rate for the growing evolution function on average, compared to the restricted evolution function. Obviously, if a restricted pool of genes is considered, there is the problem of estimating the exact amount of genes that are most likely enough to represent a wanted solution. There is no such problem with an incremental growth of genome, where the necessary size is evolved.

Attractor	Used (Grow VS Full)	Total (Grow VS Full)	Used (Grow VS Rest)	Total (Grow VS Rest)
7	p<0.0001	p<0.0001	p=0.0004	p=0.5805
10	p<0.0001	p<0.0001	p=0.3370	p=0.4867
20	p<0.0001	p<0.0001	p=0.0061	p<0.0001
40	p<0.0001	p<0.0001	p=0.4629	p=0.7633
80	p<0.0001	p<0.0001	p=0.8198	p=0.8625
160	p<0.0001	p<0.0001	p=0.06426	p=0.9776
200	p<0.0001	p<0.0001	p=0.9731	p=0.9793
400	p<0.0001*	p<0.0001	p=0.2652*	p=0.1778*

Table 5: statistical significance, 2-tail Student T-Test (*not enough successful runs, closest result to the wanted attractor length is also considered).

Overall, the growing evolution function was able to outperform the full evolution function and the restricted evolution function in the aspect of genotype efficiency, which was the main goal here. An example of evolved solution is shown in Figure 12, which produced a compact genotype composed by only 6 genes (a fully-specified genotype would consist of 243 genes). The evolved solution is particularly efficient as all the 6 genotype rules are actively used during development.

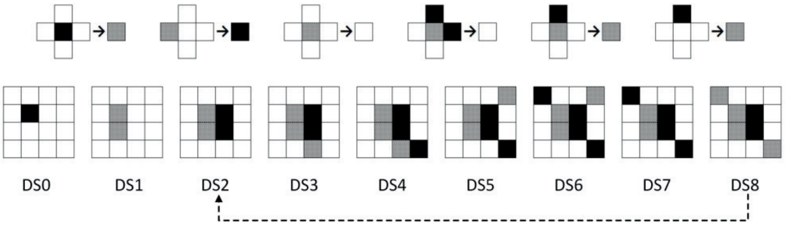


Figure 12: Example of developed solution for geometry 4X4 cells, 3 cell states, target attractor = 7 dev. steps (DS), evolved with growing evolution function. Top row shows the evolved transition table composed by 6 genes (initialized with a single gene), obtained after 308 generations. All 6 genes are triggered during development.

B. *Scalability – state space*

Increasing the state space, i.e. the system allows more cell types, gives rise to a genotype scalability problem. The more cell states are available for the system to exploit, the more regulatory combinations become possible and thus representing all the neighboring configurations in the genotype may not be feasible. Moreover, the search space the GA has to explore grows exponentially. Using a growing evolution function seems a good solution to overcome such problem. In this set of experiments 5, 6 and 7 cell states are available. When more states are available, evolution needs more generation to allow optimization of existing genes, since it is more likely to have gene additions and mutations that are fitness-neutral. The main goals here are to achieve an incremental growth of complexity while genotypes grow in size, i.e. growth evolution function still works for increased state space, and the found genotypes (matching the solution or close-by, where the genotype is already of a suitable size but needs more optimization time) are compact and effective.

Figure 13 compares the growing complexity for different attractor lengths. In all the four cases, having 7 states makes evolution require more generations than having 6 or 5. Nevertheless, the system is still evolvable.

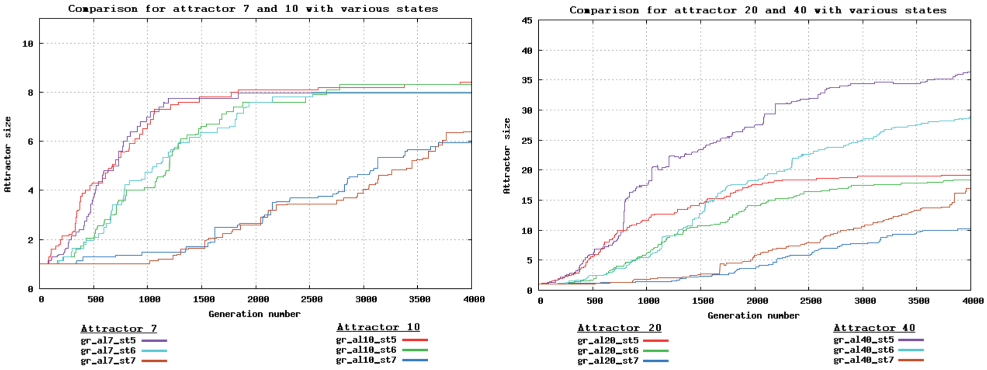


Figure 13: comparison of evolution of various attractor lengths when increasing the number of possible states per cell. Average of successful evolutions over 20 runs.

The compactness and effectiveness of the resulting genotypes is shown in Figure 14. It is possible to see that increasing the state space does not reflect in an increase of genotype size. If all the regulatory combinations were explicitly expressed in a full genotype, there would be an exponential increase of genome length for a linear increase of the available states.

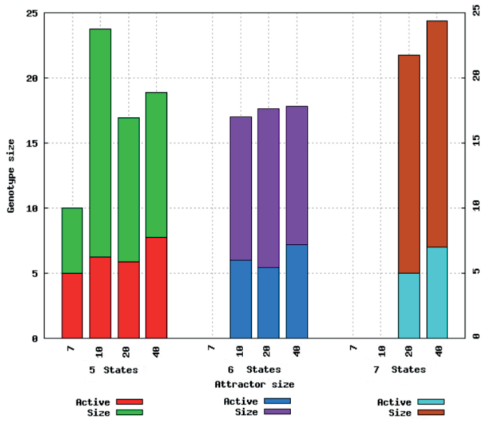


Figure 14: comparison of genotype size and genes activated during development, growing evolution function when the number of possible states per cell increases. Average of successful evolutions over 20 runs. No exact solution was found with 6 cell types for attractor 7 and with 7 cell types for attractors 7 and 10.

Further studying the genotype growth shows that gene duplication is regulated by having a higher growth rate in the early generations. Figure 15 presents an example where the considered organism's attractor length is 40 development steps. As hypothesized, the more cell states available, the more generations are needed. It is clearly visible that more gene additions happen in the beginning in all the three cases. This is not reflected in the same sudden fitness increase and, the more states available, the longer the transient before a fitness increase is noticeable. With 7 available states, several genes are added at the beginning, producing lower impact on the overall fitness. While the duplication rate slows down and genotypes get optimized, fitness starts to improve.

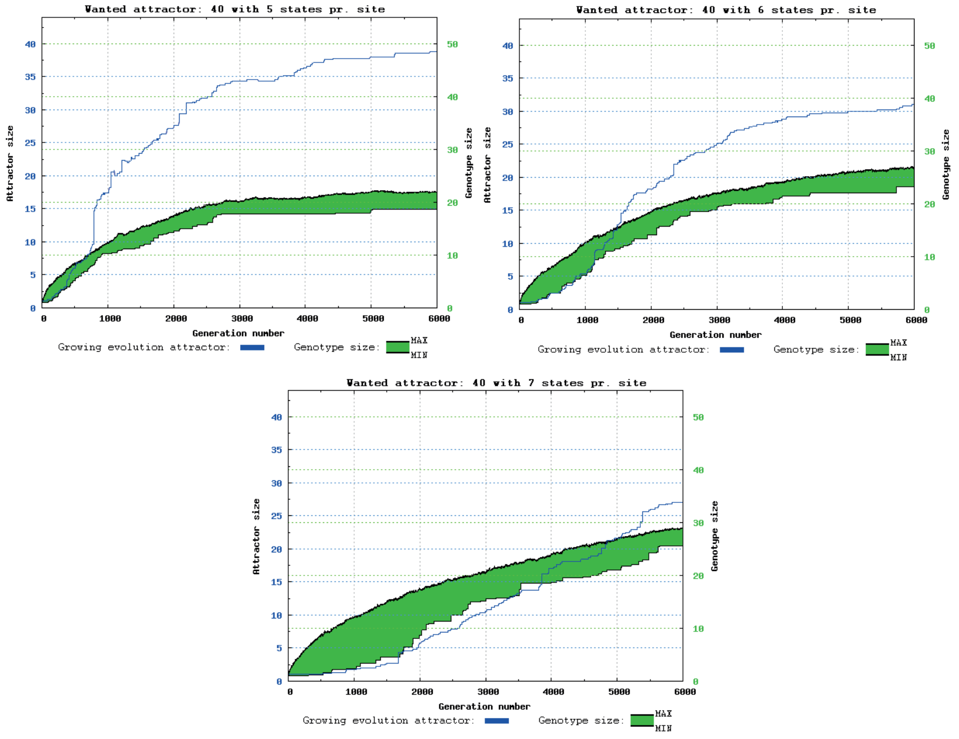


Figure 15: growing evolution function for attractor length of 40 development steps; 5, 6 and 7 cell types. Average of successful evolutions over 20 runs.

The presented experiments reveal that growing evolution function scales well when the state space scales-up. Overall, the growing evolution function produces compact and effective genomes that would not be achievable by specifying all the gene regulatory combinations.

C. Scalability – geometry

Scaling of the phenotype resources, i.e. the available number of cells in the grid world, changes the genotype-to-phenotype mapping. This means that for the same genotype representation, the possible number of emergent phenotypes would grow exponentially. Having a large geometry size gives a higher offset for the average evolved attractor length from the wanted attractor. Developing attractors which are relatively shorter than the geometry length makes an attractor that regulates based on boundary conditions difficult to evolve. It would also need some structural set-up in the form of a complex transient phase. Table 6 displays the success rate for the different grid sizes. As hypothesized, the geometry with 16X16 cells has a lower success rate. Nevertheless, successful solutions are evolved for all the attractor lengths on all geometries.

	4X4	6X6	8X8	16X16
Attractor 5	20/20	20/20	14/20	5/20
Attractor 7	20/20	20/20	20/20	8/20
Attractor 10	20/20	20/20	19/20	9/20

Table 6: success rate for increased geometry size.

Figure 16 compares the evolved genome size and number of genes used during development for the genotypes evolved with growing evolution function. Since the organisms use a regulation that exploits border conditions, there is a dependency between attractor length and geometry. That is why it is not possible to identify a specific trend. As an example, an organism that develops an attractor of 5 development steps requires fewer genes on an 8X8 geometry than on a 6X6 geometry. For that reason, it would be extremely difficult to estimate the necessary genome representation size when the phenotype space increases.

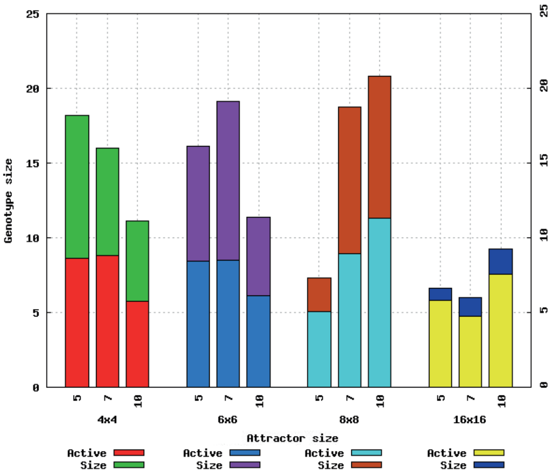


Figure 16: comparison of genotype size and number of activated genes during development when the size of the geometry increases. Average of successful evolutions over 20 runs.

The average of the evolutionary runs is plotted in Figure 17, for the target attractor lengths of 5, 7 and 10 development steps. Each line represents a different geometry. It is possible to see that for some specific combinations of geometry size and wanted attractor, evolution approaches the target value incrementing the attractor length by adding and optimizing. In some other cases, the number of available genes is enough to develop organisms with longer attractors than the wanted length. In such cases, evolution would have to optimize the available genes to obtain a shorter attractor. This happens because none of the attractor lengths is a multiple of the geometry side and because the simplest way to regulate an attractor is taking advantage of the boundary conditions. It is extremely important that in such case, growth does not get out of control.

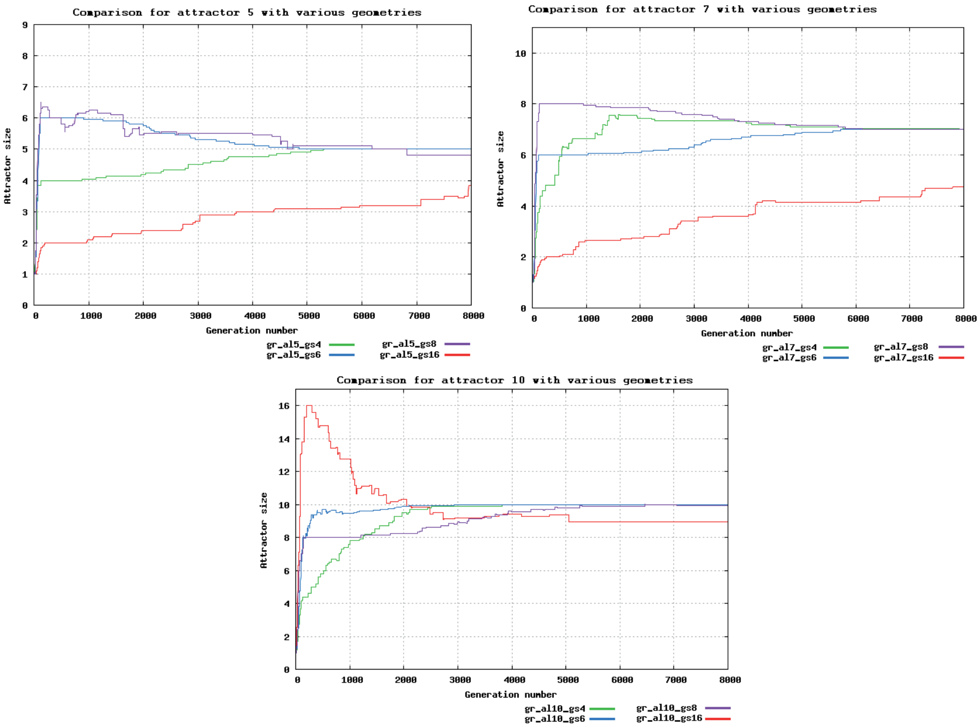


Figure 17: comparison of growing evolution, different attractors with increased geometry. Average over 20 runs.

Figure 18 illustrates an example of evolved attractor of size 10 development steps on the four different geometries (average over 20 runs). Growing evolution function is able to find compact and effective genotypes when the geometry size is scaled-up. Moreover, the growth rate tends to slow down along evolution and the number of available genes does not keep growing.

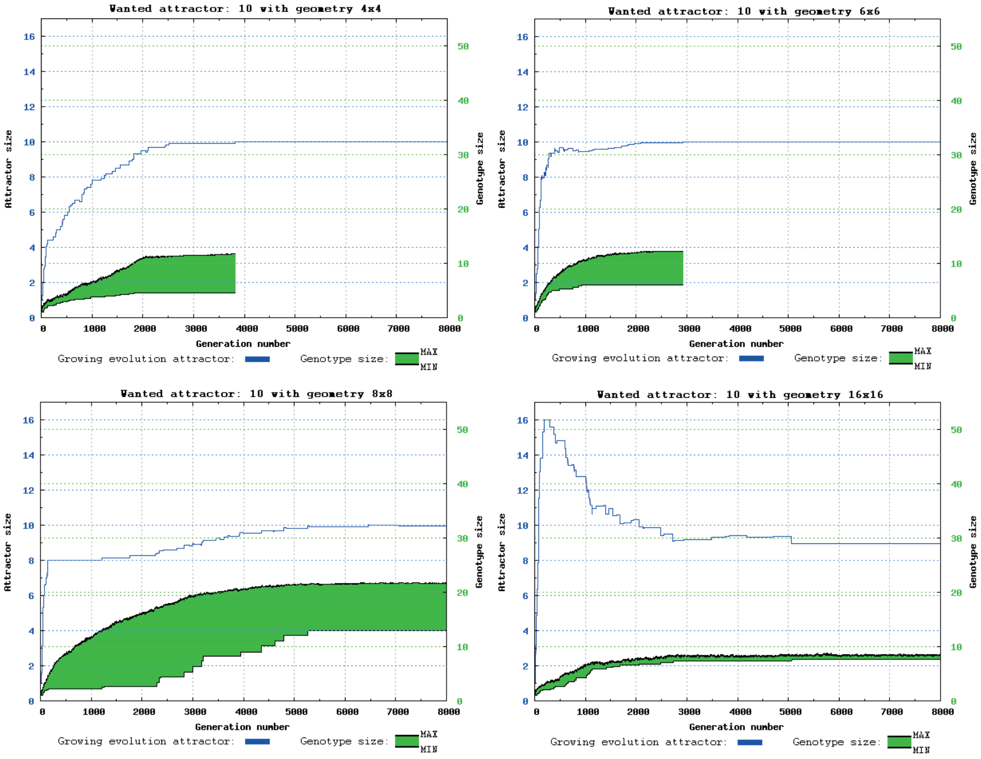


Figure 18: evolved attractors and genotypes size for different geometries of size 4X4, 6X6, 8X8 and 16X16. Average over 20 runs.

X. Discussion and Future Work

The main idea behind this work is that a growing genotype evolution function would essentially create genotypes which did not explore an unnecessary area of the search space. As such, it can be a valid alternative to the process of deciding upon a static representation which is large enough to contain a solution to the desired problem. A static representation is often bloated compared to the needed representation, because finding a size that is large enough to contain a solution but small enough not to be bloated is difficult. Analyzing the results, the idea of growing an effective genotype is plausible. The growing evolution starts with a population of small and simple genotypes and grows their size incrementally. This is done by increasing the search space with gene duplications and further optimizing them with mutations and crossovers. Each iteration of the process changes the fitness landscape since new possible genes may emerge, making previous local optima disappear and creating new optima. Getting a growing genotype evolution function to work was not trivial as full genotype evolution or restricted evolution function. There are many parameters and the tuning involved in the configuration can lead to different results. The optimization of parameters was outside the scope of this report and the same configuration was used for all the experiments (except a few exceptions, described in the previous sections). Nevertheless, most of the experiments performed well, which tells us that the set-up was most likely enough for the scope of this research. The used set-up and configuration is by no means optimal, but adequate for the purpose of proving a point. The presented results are persistent throughout changes in complexity, geometry size and number of cell states, indicating that growing evolution function is able to achieve effective solutions with automatically created representations.

Another key point to discuss is elitism, which is often used with fixed-size genotypes. With a growing evolution function, it could have some drawbacks for evolvability. Elitism works like an “anchor” fastening a generation to the currently best individual, which for the growing evolution function anchors also the amount of genes in the genotype. Elitism makes the fitness landscape exploration have a limit on how far from the current fitness and genotype size it can go. Elitism may be removed (or reduced, as in this work with only one elite) and rather another genotype size regulation may be implemented. For example, in [43] speciation is used to allow mating only between individuals in the same group and newly added genes have a better ability to not get rooted out by natural selection.

The solutions found in all the different sets of experiments are successful and the resulting genotypes are more compact and effective. Growing a genotype is a valid alternative to defining a static representation or using a full representation with all the possible regulatory combinations. Comparing the result of the growing evolution function to the restricted evolution function shows that the performances are similar. This means that the growing genomes are reasonably optimized.

An inherent result of the growing evolution function to target organisms that develop an attractor of a specific number of development steps is a rather small transient. This is consistent with other work [34], [4] where there is no instruction sequence or construction arm and the construction of structures is a fission-like process with high parallel processing.

The goal in this work was to evolve organisms which produced attractors of different lengths, instead of simply achieving a given structure. This means that the resulting solutions take advantage of geometry regulation, i.e. actively use the geometry to build structures that achieve the required attractor size. These structures have directional movement, but because of periodic boundary conditions, they cycle around the grid and return to sites that have previously occupied. This way, structures can either move at a certain speed which combined with the geometry results in an appropriate attractor or move and leave behind structures with which it can interact when cycling around the boundary, essentially creating an environment for itself to evolve within. As such, repeating patterns within an attractor may emerge. For larger geometries, having attractors that do not rely on boundary conditions would mean having a larger set of genes regulating a developing mechanism and a stopping mechanism. A kind of location fixed attractor which stays within a fixed geometric space even if the total geometry is limitless is very difficult to achieve. That is why most of the solutions take advantage of geometry regulations.

Evolutionary and Developmental Systems and Artificial Intelligence rely on efficient search of optimized structures, most likely very large structures that suffer from an inherent scalability issue. Evolutionary growth of genome representations is the tool that allows such scaling-up, starting from the very simple and incrementally elaborating. As a consequence, it may be advantageous to explore it in such domains where scalability is a goal.

As future work, it may be interesting to investigate evolutionary growth of genome representations not only in terms of search space but also in the state space. Essentially let the growth happen both in terms of genotype size, i.e. number of genes, and states that each cell can hold, i.e. number of possible cell states. This would achieve true complexification, meaning that the boundaries are not fixed by the state space (which is more or less fixed in every artificial system). This would allow systems to evolve for arbitrary complexity levels and find solutions to arbitrary complex problems.

XI. Conclusion

The experiments presented in this paper show that the evolutionary growth of genotype representations for EvoDevo systems with indirect encodings produces compact and effective genomes. This is without the need of fully specifying all the regulatory combinations or estimating a priori the necessary genetic pool with complex heuristics. Three types of scalability issues are discussed. (1) The scalability of the search space: the growing evolution function outperforms restricted evolution and full evolution in terms of genome size and genome exploitation by complexification of simple genotypes with the incremental addition and optimization of new genes. The result is that complexity of achieved solutions grows while evolution progresses. (2) The scalability of the state space: growing evolution function is effective when the number of available cell states is scaled-up and a fully specified genome would not be possible. (3) The scalability of phenotypic resources: developmental systems take advantage of an indirect genotype-to-phenotype mapping and scaling-up the phenotype resources increases the complexity of the mapping. The growing evolution function provides the necessary genotype scalability to elaborate solutions with compact and effective genomes when the grid world where organisms develop is increased in size.

Overall, the key aspect of evolutionary growth of genotype representations is the ability to solve difficult problems by starting with simple solutions in a low dimensional space and incrementally increasing the genotype complexity, disregarding how large a genotype would be to encode a solution. As such, it is a powerful strategy in the field of evolutionary and developmental systems with indirect encodings, where nature-like levels of complexity are targeted.

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APPENDIX 1 – FIGURES LABELING

This paragraph describes the labeling template and abbreviations used for the following figures: 10, 11, 13, 15, and 17.

fu = full evolution function;
gr = growing evolution function;
re = restricted evolution function (th = threshold, number of available genes in the fixed restricted representation).

al = target attractor length
st = number of cell states
gs = geometry size (the size of the CA grid world where organisms are developed, x by x cells)

Example 1:
fu_al200 = Full evolution function, target attractor length of 200 development steps.

Example 2:
re_al20_th10 = Restricted evolution function with maximum 10 genes, target attractor of 20 dev. steps.

Example 3:
Gr_al7_st6 = growing evolution function, target attractor length of 7 dev. steps, 6 possible states per cell.

Example 4:
Gr_al10_gs16 = growing evolution function, target attractor length of 10 dev. steps, cellular automaton geometry of 16 by 16 cells.

Paper D.2

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