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

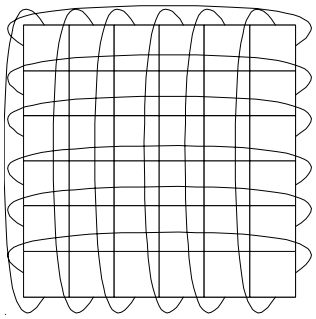
The developmental model used herein is similar to other models based on cellular automata, e.g. [23, 18, 29], including a synchronized cellular cycle, parallel operation and discrete cell states. To be able to have a complete regulatory network for all possible regulatory states the model needs to be 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.

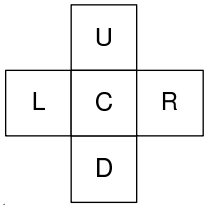
The extracellular communications only include cell types. In Figure 1(b) possible communication for a cell is shown. The centre cell's (C) developmental process have information concerning the cell's own state and cell type of the four neighbouring cells.

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.

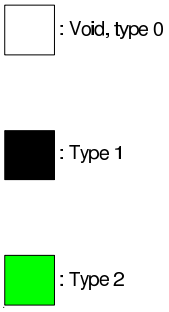
The result is a minimalistic model were all input combinations to the development processes consist of only 3^5 possibilities. As such, all possible regulatory input combinations and resulting cellular actions can be represented as a table. The table in Figure 1(d) is a scaled down illustration. For 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. $Ctype(t+1) = Ctype(t)$.



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



(b) Cellular neighbourhood.



(c) Cell types.

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}

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

Figure 1: A minimalistic cellular developmental model.

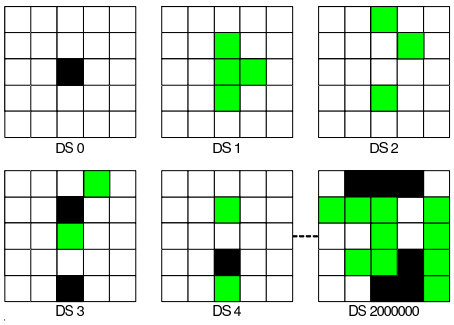


Figure 2: An example of a developing organism.

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.

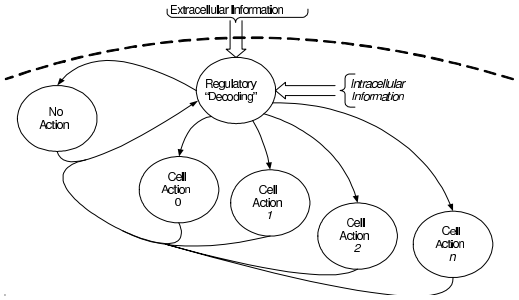


Figure 3: The inner working of a simple developmental process.

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:

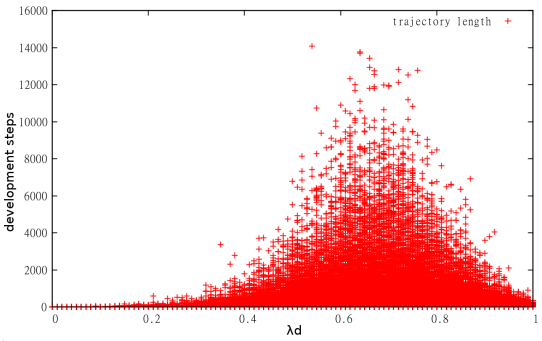
- With probability $1 - \lambda d$, the cell type at the next developmental step is quiescent (type 0);
- With probability λd, the cell type at the next developmental step is a generated by a uniform random distribution among the other cell types (type 1 or 2).

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.

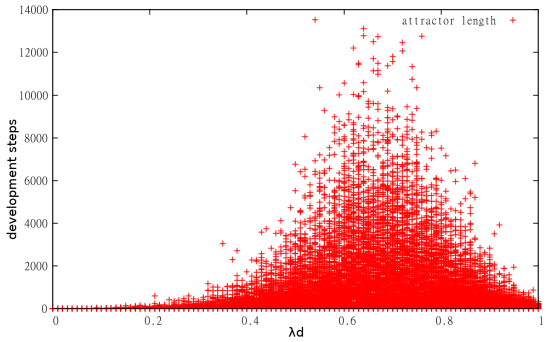
5.2 Experiment I

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.

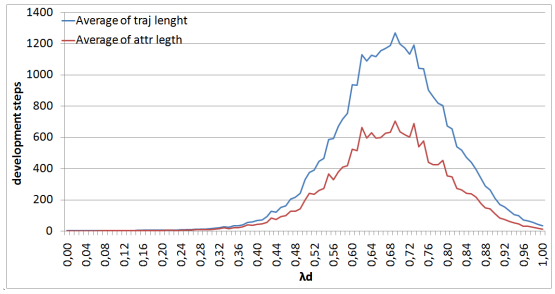
The arrays size was set to 4x4 and 5x5. The size of the arrays was chosen as to be able to carry out experiments in reasonable computational time. Organisms of 4x4 and 5x5 cells may be considered rather small, however, the theoretical maximum attractor length is 3^{16} for the 4x4 array and



(a) Trajectory length.

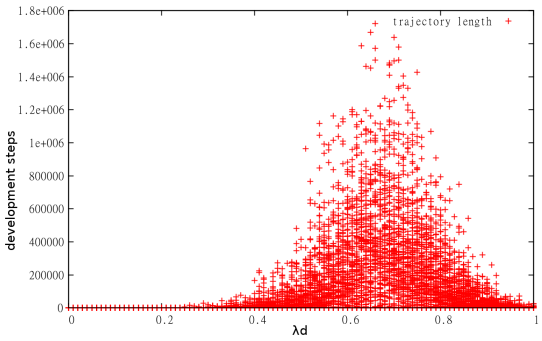


(b) Attractor length.

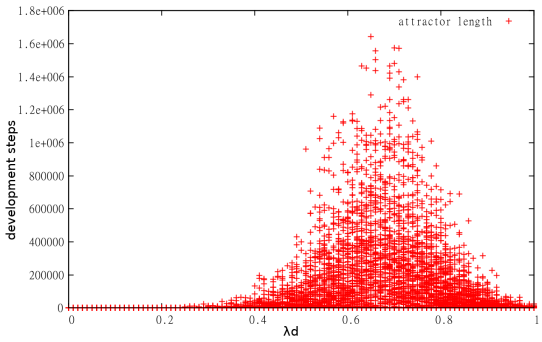


(c) Average trajectory and attractor length.

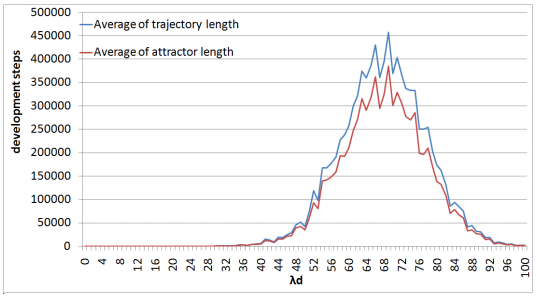
Figure 4: Experiment I. Results for 4x4 organisms plotted as function of λd. 1000 tests for each λd.



(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.

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).

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 differentia-

tion changes the cell type. As such, we want to define a way to quantify growth and differentiation during development according to λd.

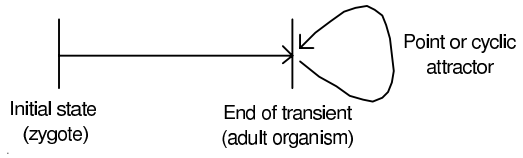


Figure 6: Growth and change rate illustrated as phases in the life time of a developing organism.

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.

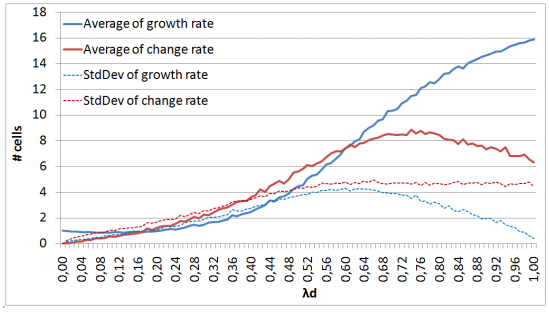


Figure 7: Experiment II. Average growth and change rate in correlation to λd on a 4x4 organism. Average over a 1000 tests for each λd value.

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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