LEVELS OF COMPARTMENTALIZATION IN ARTIFICIAL EVOLUTION

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Abstract. This paper addresses the use of particular encoding schemes in evolutionary systems. We define three paradigms of DNA encodings: *non-compartmentalized DNA*, *partially compartmentalized* DNA, and *fully compartmentalized* DNA. We demonstrate that there is a significant and increasing advantage to the use of *partially* and *fully compartmentalized* models as the complexity of a structure increases. Implications for the design of evolutionary systems including biological systems are discussed.

keywords: compartmentalization, transposons, artificial evolution, natural evolution

1. Introduction

Transposons (MacPhee, 1991; Finnegan, 1994) are fascinating pieces of DNA which have the surprising ability to move around, create duplicate copies, and excise themselves over successive generations and during duplication. They are units of DNA which encode complete functions not dependent on other pieces of DNA for their expression. Transposons are nearly ubiquitous in Nature and are thought to make up over 90% of the DNA found in human beings. Their general capability to provide functions, generate new functions of a cell, create genetic defects, and correct them is a rich set of effects that has yet to be generated by the artificial life community.

Their power comes from the fact that DNA that can encode whole functions can be reconnected to produce novel systems of fundamental importance with great efficiency. They are a subject of intense study in the genetic algorithm and evolutionary computation communities and should become important in the artificial life community beyond the scope of the building block hypothesis and related issues.

How transposons arose is also intellectually interesting. Perhaps the simplest question centers around the nature of the origin of these structures. Transposons certainly appear in natural systems and their analogs appear in some evolutionary systems. However, how much of the structure of transposons depends on the nature of the replicating system, and how much depends on the requirement to build efficient evolutionary systems? If transposons are simply a result of the way in which life historically arose on earth, then they have no natural place in artificial systems. However, if they are a result of an evolutionary requirement, then it would seem to be advantageous to understand that requirement and to build them into our evolutionary models.

Many evolutionary models exist in the recent literature, each one with its own general structure. Of these, genetic algorithms are the most common and they have been used to do a variety of things including designing hardware and optimizing functions. Genetic algorithms are powerful due to their ability to share information that is beneficial. This is the basis of the *building block hypothesis* and forms the basis for a great deal of genetic algorithm literature (Forrest and Mitchell, 1993). One important problem that has been recently addressed is the identification of *linkages* between parts of the genome and identifications of recodings of the search space in such a way that these linkages are minimized (Kazadi 1997; Kazadi 1998; Munetomo and Goldberg, 1999).

A particularly exciting application of genetic algorithms has recently been undertaken by Adrian Thompson (Thompson 1999a(b,c), 1998a(b)) in studying hardware evolution of field programmable gate arrays (FPGA), and is becoming more popular as a practical means of generating useful hardware designs. In these studies, a genetic algorithm is used to generate circuits in the FPGA. However, this work does not seem to deal with the use of advanced genetic operators nor take advantage (or even seem to be aware) of techniques of compartmentalization.

Tierra (Ray 1992; Ray 1994; Adami 1995a) and Avida (Adami 1994; Adami 1995b; Ofria and Adami 1999) are examples of artificial ecosystems in which no explicit fitness function has been designed. The evolving agents are self-replicating strings of DNA modelled to function in a virtual environment using an analog of the 80x86 processor. The main difference between these two systems is that Tierra is built on a single completely connected soup, while Avida is designed on a two-dimensional spatially separated toroidal lattice. Each agent may replicate itself to a neighboring cell during its processor time, may compete with agents currently occupying the cell for the space, and has a nonzero probability of a number of addition and alteration mutations at every replication. While these systems exhibit fascinating dynamics, they evolve at a rate which has a power law distribution of epochs in time, a somewhat slower evolution rate than one might wish to be restricted to.

Genetic programming (Koza 1992; Koza 1994) contains no explicit limitation in the length of the genome. Functional trees are built up which serve to solve a practical design problem. The ability of the trees to be used in a modular way allows subfunctions to be built up and to be incrementally added to a functional tree system. This is an example of a *partially compartmentalized* model, which has advantages we clarify in this study.

The rest of the paper is organized as follows. Section 2 discusses compartmentalization and the expected time of construction of differing paradigms. Section 3 presents the theoretical distribution of epochs in time, providing motivation for application of this theory to existing models of evolutionary systems. Finally, Section 4 offers some concluding remarks.

2. A Mathematical Model of Compartmentalization

In this section, we introduce the concept of DNA compartmentalization and discuss a mathematical justification for its requirement in evolutionary systems. We focus on evolutionary systems which are built up incrementally, weighing both the addition of new elements and the modification of connections between elements. We assume that DNA is a string made up of *building blocks*, which are units of DNA that may take on one of several possible settings. On top of these building blocks are connections which must be properly configured between independent blocks or groups of building blocks. We assume that the length of the DNA is not constant and that new building blocks may be added to the structure with some probability.

2.1. **The nature of compartmentalization.**

Definition 2.1. A **compartment** is a subset of a DNA string consisting of elements which code for the structures which carry out a specific function, group of functions, or no function at all. Such a grouping must exclude elements which in whole or in part define other functions. An **elemental compartment** is a compartment which is not capable of being broken up into smaller compartment, with retention of all functions initially encoded.

Note that an elemental compartment can have multiple functions.

Definition 2.2. A **non-compartmentalized encoding** is an encoding in which there exists no natural structure within the DNA which codes a given device. Any specific element of DNA is equally probable of being a part of a given substructure in the evolving system.

This includes, among others, infinite length genetic algorithms. Unless explicitly introduced in the system, there are no self-contained functional units within such implementations.

Definition 2.3. A **partially compartmentalized encoding** is an encoding in which there exist natural substructures which may be completely duplicated without alteration of function.

Genetic programming algorithms are also examples of partially compartmentalized encodings.

Definition 2.4. A **completely compartmentalized encoding** is an encoding in which connectivity and functionality may at once be specified by the DNA or be a natural consequence of some "natural" laws governing the behavior of the structures built by the encoding.

Each change in the design of a system is of one of two fundamental types. One changes the fitness of the design, while the other does not. This is an important distinction, and we formally define these.

Definition 2.5. We define an ***evolutionary step*** to be to be a change in a design that also changes its fitness. We define a ***null step*** to be a change in a design that produces no change in fitness.

The aftermath of an evolutionary step is an *epoch*, in which the new, more functional structure takes over a population of less functional structures. By successfully competing against the others, the fitter organism can create multiple copies of the new structure. New designs are then based on this model and will then have a lower improvement time. A null step, on the other hand, produces no such epoch and so all alterations must be *built on top of* the change in question thereby further increasing the improvement time.

2.2. **Rates of evolution.** Let us assume that we are working with linear DNA made up of building blocks of some kind and a method of encoding the connection between the building blocks. These building blocks may generally encode a physical entity or a computational entity.

Let us assume that we have N possible assignments for each building block. First, note that the probability of adding a specific building block is typically of $O\left(\frac{1}{N}\right)$. This, of course, assumes that the addition of each possible building block is equally likely. The probability of connecting any two building blocks correctly is $O\left(\frac{1}{m(m-1)}\right)$ where m represents the number of elements currently in the genome. So, the probability of correctly adding and connecting a building block to a device with $m-1$ elements is

$$p_a = O\left(\frac{1}{Nm\left(m-1\right)}\right) . \tag{2.1}$$

Thus, the probability of a particular design containing M elements is

$$p_d = O\left(\frac{1}{N}\prod_{i=2}^{M}\left(\frac{1}{Ni\left(i-1\right)}\right)\right) = O\left(\frac{1}{N^M M!\left(M-1\right)!}\right) \tag{2.2}$$

yielding an expected time to completion of the algorithm of

$$\tau \propto O\left(N^M M!\left(M-1\right)!\right) . \tag{2.3}$$

If one does not require a particular order to the nodes being designed, then the probability of success is conditioned by the number of possible identical solutions. In this case

$$p_d \propto O\left(\frac{M!}{N^M M!\left(M-1\right)!}\right) \tag{2.4}$$

giving the expected time to completion

$$\tau_n \propto O\left(N^M\left(M-1\right)!\right) . \tag{2.5}$$

Now let us work out the analogous evolution time for the compartmentalized approach. We assume that we have k compartments, each of length L of the same building blocks. In general, we assume that each compartment, as shown above, has a probability of being formed as given in (2.4). The probability of connecting each of these compartments correctly is typically of order

$$p_{pc} \propto O\left(\frac{1}{k(k-1)L^{2k}}\right) \tag{2.6}$$

making the total probability

$$p_p \propto O\left(\frac{1}{L^{2k}k\left(k-1\right)N^L\left(L-1\right)!}\right) \tag{2.7}$$

The expected time of construction in the partially compartmentalized model is

$$\tau_p \propto O\left(k^2 N^L\left(L-1\right)!L^{2k}\left(k-1\right)\right) . \tag{2.8}$$

Removing the time due to the connection of compartments yields the expected time to build in the compartmental model. Thus,

$$\tau_c \propto O\left(kN^L\left(L-1\right)!\right) . \tag{2.9}$$

This means that the ratio of the times is

$$\frac{\tau_p}{\tau_n} = \frac{N^L\left(L-1\right)!L^{2k}k^2\left(k-1\right)}{N^M\left(M-1\right)!}. \tag{2.10}$$

If we then let $M = kL$, we have

$$\frac{\tau_p}{\tau_n} = \frac{N^L\left(L-1\right)!L^{2k}k^2\left(k-1\right)!}{N^{kL}\left(kL-1\right)!}. \tag{2.11}$$

The corresponding ratio for the compartmental model is

$$\frac{\tau_c}{\tau_n} = \frac{kN^L\left(L-1\right)!}{N^{kL}\left(kL-1\right)!}. \tag{2.12}$$

Example 2.6. Suppose that we have $k = 2$ and $L = 4$. Then equation (2.11) is

$$\frac{\tau_p}{\tau_n} = \frac{2N^4 3!4^4}{N^8 7!} = \frac{6N^4 256}{1260N^8} = \frac{1536}{420N^4} \approx 3.66N^{-4}. \tag{2.13}$$

If we let $N = 10$, a reasonable choice for many evolutionary algorithms, the ratio is

$$\frac{\tau_p}{\tau_n} \simeq 3.66 \times 10^{-4}. \tag{2.14}$$

Clearly, this is a significant advantage with a very small level of compartmentalization. The corresponding calculation for the compartmentalization model is

$$\frac{\tau_c}{\tau_n} = \frac{N^4 3!}{N^8 7!} = \frac{1}{24N^4} \approx 4.2 \times 10^{-6} \tag{2.15}$$

an even more significant advantage.

2.3. **Types of compartmentalization.** The use of compartmentalization in generating more efficient evolution algorithms is of paramount interest in this work, and we now turn to implications of this formalism.

The ability of a device to be built up incrementally from discrete modules allows one to evolve the modules individually. This greatly reduces the expected time of completion from factorial in the number of building blocks to factorial in the number of building blocks per node multiplied by a linear term in the number of compartments. This also increases the time of completion by a factor that is factorial in the number of building compartments, but quadratic in the number of building blocks per compartment. Thus, as long as the number of building blocks is significantly larger than the number of compartments, the development time will improve greatly. We also note that this represents a *worst case scenario*; the situation is significantly easier if several of the building blocks are similar and may be duplicated.

These mathematical definitions lead us back to our previous definitions. We can see that there are three fundamental types of DNA encodings, coupled strongly to the physical system in which they live. Non-compartmentalized encoding is characterized by equation (2.5). These types of systems make use of absolutely no structural information and have no well-defined functional groups. Often times the data concerning functional groupings is scattered and must be dealt with across the genome. Infinite dimensional or incremental genetic algorithms, in which the number of elements in a vector is unbounded, are such algorithms. Algorithms which are not include genetic programming, and the Avida and Tierra systems by Adami et. al. and T. S. Ray, respectively.

The second class of structures which are partially compartmentalized include those previously mentioned: Tierra, Avida, and genetic programming. These models have implicit structure, and have elements evolving which are partially compartmental. In Tierra and Avida these might be evolving subroutines whose combinations produce the functional creature. In genetic programming these are the subtrees, which may be moved about intact and combined with other trees. These algorithms quickly create good behaviors, but have a hard time creating a large number of functional subgroups. Rather, these paradigms should generate progressively larger subgroups as the genome increases in length in order to keep the connection term of equation (2.8) small. As the length of the compartments rises, the probability of finding a useful compartment decreases factorially leading to a convergence in the compartmentalization and size of compartment. This leaves the algorithm to develop compartments of high quality and may lead to stagnation of the paradigm. These types of algorithms, while providing a great advantage over the completely non-compartmentalized model, can converge due to the second term of equation (2.8). If the number of compartments increases, so too does the difficulty in generating the design, owing only to the correct interaction between compartments.

For some algorithms, though, it might be possible to build which remove this term. These algorithms would have the interactions built as part of their structure, so that a particular compartment in the design would only be able to interact with a handful of other compartments in the design. This would allow the number of interactions to be severely curtailed, yielding a nearly linear computation time in the number of compartments. This is what biological life is capable of accomplishing through the use of proteins and embedding of this level in the physics of the universe. Such fully compartmentalized models represent a great advantage to any type of evolution.

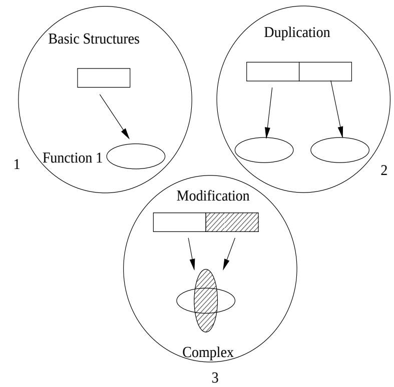


Figure 1: The fully compartmentalized model.

As one can see, Figure 1 illustrates this model. Compartmentalization in the evolutionary process organizes the DNA string based on functionality. By doing this, the number of interactions between compartments and the time for completion are reduced to a minimum while the DNA string's full capabilities for adaptability and survival are exploited. The product of the new DNA element is automatically incorporated properly with the previous one, without the need for evolution of this compatibility. The way in which this is done is model specific and embedded in the system.

Thus, we provide this table of paradigms and computation times.

Paradigm	Computation Time
Non-compartmentalized	$\tau_n \propto O\left(N^{kL}\,(kL-1)!\right)$
Partially Compartmentalized	$\tau_p \propto O\left(k^2 N^L\,(L-1)! L^{2k}\,(k-1)\right)$
Fully Compartmentalized	$\tau_c \propto O\left(kN^L\,(L-1)!\right)$

Table 2.1: Table of computational design expressions for different paradigns

3. Compartmentalization in the Generation of Epochs

An evolutionary system represents a balance between two competing requirements, the ability to shield existing systems from mutation and the need to adapt to the environment. Evolutionary systems have a tendency to leave existing designs unchanged, as the set of useful designs for a particular task are typically sparse in the space of all possible designs. Recklessly changing a design would be unlikely to produce a feasible design, resulting in the extinction of the species in question. The competing tendency, of modifying existing designs, also exists in order to produce more capable offspring. This tendency to change things requires a method of changing DNA without significantly negatively altering the functionality of it. Thus, the problem for an evolutionary design system is to preserve the function of evolving agents while still improving.

If we again assume that DNA is essentially a string of building blocks, we may estimate the probability that an improvement will occur. Let us also assume that we have some method for copying segments of DNA into new additional segments of DNA. This copying mechanism must then depend on the choice of the beginning and ending segments of DNA. We begin by investigating the non-compartmental model.

First, we assume that we have a length-independent mutation rate $0 < r < 1$ which gives the likelihood that at each iteration a given building block will mutate. Then, if we have a sequence of L building block elements and N ways to mutate each one, the probability of choosing and correctly mutating S of them, given that each mutation is independent, is

$$p_{n_M} \propto O\left(\left(\frac{r}{N}\right)^S (1-r)^{L-S}\right) \quad .$$

Now, the probability of correctly copying any given DNA sequence

$$p_{n_c} \propto O\left(\frac{1}{M\,(M-1)}\right) \tag{3.1}$$

for each pair of cutting/copying points. So, the total probability of correctly copying the chosen DNA set and correctly mutating it (creating a new functional piece of DNA) is

$$p_{n_{cr}} \propto O\left(\frac{1}{M(M-1)}\sum_{i=0}^{M-S-1}(M-S-i)\left(\frac{r}{N}\right)^S(1-r)^i\right) \tag{3.2}$$

$$= \frac{1}{M(M-1)S^2}\left(\frac{r}{N}\right)^S \frac{(1-r)\left[(1-r)^{M-S}-1\right]+r(M-S)}{r^2} \tag{3.3}$$

Once the correct changes have been made, it is necessary to incorporate these changes into the genome. This involves both correctly removing and adding the linkages between the existing and new structures respectively. In non-compartmentalized models, these are done independently so that in general, the probabilities are of order

$$p_{n_{inc}} \propto O\left(\left(\frac{1}{M\langle L\rangle}\right)^S\right) \tag{3.4}$$

where $\langle L\rangle$ is the expected length of the advantageous mutation. The product of these probabilities gives us the total probability of an epoch-generating event. Thus, the total probability is of order

$$p_n = O\left(\frac{r^{S-2}(1-r)\left[(1-r)^{M-S}-1\right]+r^{-1}(M-S)}{M(M-1)S(S-1)(MN\langle L\rangle)^S}\right) \tag{3.5}$$

yielding a time of order

$$\tau_n \propto O\left(\frac{M(M-1)S(S-1)(MN\langle L\rangle)^S}{r^{S-2}(1-r)\left[(1-r)^{M-S}-1\right]+r^{-1}(M-S)}\right) \tag{3.6}$$

If $r \ll 1$ then

$$\tau_n \propto O\left(\frac{rM(M-1)S(S-1)(MN\langle L\rangle)^S}{r^{S-1}(M-S)r+(M-S)}\right) \tag{3.7}$$

In compartmentalized models, creating copies of DNA pieces can be done simply by choosing the compartment of interest and directly copying it. This means that the probability of choosing the correct compartment is

$$p_{c_c} = O\left(\frac{1}{k}\right) \tag{3.8}$$

where k is again the number of compartments. The probability of modifying the copy correctly is given as

$$p_{c_m} \propto O\left(\frac{r^S(1-r)^{L-S}}{N^S}\right) \tag{3.9}$$

giving the expected time to correct modification as

$$\tau_{c_m} \propto O\left(\frac{N^S k}{r^S(1-r)^{L-S}}\right) \tag{3.10}$$

which becomes, if $r \ll 1$,

$$\tau_{c_m} \propto O\left(\frac{N^S k}{r^S(1-(L-S)r)}\right) \tag{3.11}$$

A partially compartmentalized model requires that the compartment of interest be correctly connected, and the previous connection be correctly disconnected. Thus, the probability of disconnecting and reconnecting the appropriate compartments is given by

$$p_{p_c} \propto O\left(\left(\frac{1}{kL}\right)^S\right) \tag{3.12}$$

making the time

$$\tau_c \propto O\left((kL)^S\right) . \tag{3.13}$$

Thus, the total time is

$$\tau_p \propto O\left(\frac{N^S k\,(kL)^S}{r^S\,(1-r)^{L-S}}\right) \tag{3.14}$$

Finally, a completely compartmentalized model has the connection taken care of by the underlying structure. Thus, the expression (3.15) is altered, becoming

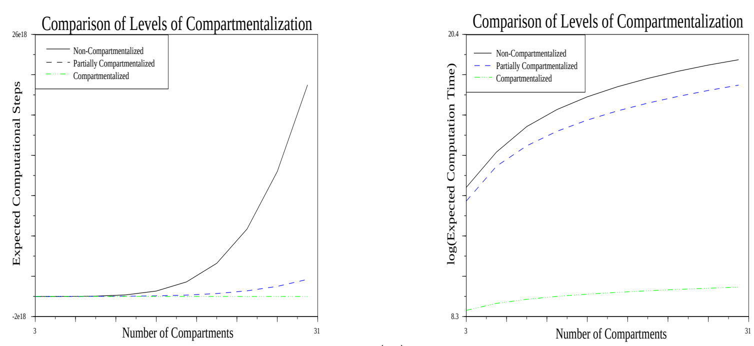
$$\tau_c \propto O\left(\frac{N^S k}{r^S\,(1-r)^{L-S}}\right) \tag{3.15}$$

If we again take $kL = M$, we may form another comparative table of the three evolutionary models.

Paradigm	Improvement Time
Non-Compartmental	$\tau \propto O\left(\frac{r(kL)((kL)-1)S(S-1)((kL)N\langle L\rangle)^S}{r^{S-1}((kL)-S)r+((kL)-S)}\right)$
Partially Compartmental	$\tau_{cm} \propto O\left(\frac{N^S k^{S+1} L^S}{r^S(1-r)^{L-S}}\right)$
Fully Compartmental	$\tau_{cm} \propto O\left(\frac{N^S k}{r^S(1-r)^{L-S}}\right)$

Table 3.1: A summarizing table of the different expected computation times for improvements in the different models.

Typical performances of the three models are as given in Figure 2.



(a) (b)

Figure 2: This gives the typical expected performance of the three compartmental models in linear (a) and log (b) format. The advantages of the partially and fully compartmentalized models are clearly visible.

Table 3.1 and Figure 2, illustrate the advantage of a compartmental model in generating *epochs,* or sweeping displacements of the current dominant species in an artificial evolutionary system. Evolutionary time is measured in epochs, rather than years, as these are the only important time measures. Because of the existence of epochs, the time required for a design or adaptation is *additive* rather than multiplicative. Any evolutionary system which is capable of generating evolutionary change which results in an epoch will come to be the dominant system in use. Clearly compartmentalization exhibits a significant and increasing advantage in the generation of any given improvement in any particular trait. Thus, it would seem that compartmentalization is a significantly advantageous design paradigm for evolutionary systems, both natural and artificial.

4. Conclusion

In this paper, we've motivated the existence of compartments in the DNA of evolutionary systems by examining the probability that a given structure may be built, given that it is composed of a specific number of building blocks of a finite number of types and equal probabilities. Three general types of evolutionary paradigms have been formulated based on their use of compartmentalization. These are *non-compartmentalized*, *partially compartmentalized*, and *fully compartmentalized* models. The main difference in the models derives from the creation of linkages between building blocks which model the system. The gains in using full compartmentalization in the design of complex structures are large when compared to the use of standard non-compartmentalized DNA.

Though no known natural or artificial system completely satisfies the assumptions of this model in that building blocks are normally not independent in their impact on the design of a piece of hardware or a biological system, the model is general enough that its main implications may be viewed as representative of other systems. Thus, we believe that these results are generally applicable to current paradigms, and may be used as a motivation for the alterations of these paradigms.

More importantly, we have understood that the removal of the difficulty in producing correct linkages is of fundamental importance when considering building complex structures. The single most difficult part of designing an improvement to an existing structure resides in this term. Models that partially or completely remove this term may be expected to perform many orders of magnitude better than those that do not. The design of new paradigms that incorporate this "physical" term into the design of the system rather than the structure may be expected to be useful tools in the design of new and interesting structures.

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