

Modeling Major Transitions in Evolution with the Game of Life

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Abstract

Maynard Smith and Szathmáry's book, *The Major Transitions in Evolution*, describes eight major events in the evolution of life on Earth and identifies a common theme that unites these events. In each event, smaller entities came together to form larger entities, which can be described as *symbiosis* or *cooperation*. Here we present a computational simulation of evolving entities that includes symbiosis with shifting levels of selection. In the simulation, the fitness of an entity is measured by a series of one-on-one competitions in the Immigration Game, a two-player variation of Conway's Game of Life. Mutation, reproduction, and symbiosis are implemented as operations that are external to the Immigration Game. Because these operations are external to the game, we are able to freely manipulate the operations and observe the effects of the manipulations. The simulation is composed of four layers, each layer building on the previous layer. The first layer implements a simple form of asexual reproduction, the second layer introduces a more sophisticated form of asexual reproduction, the third layer adds sexual reproduction, and the fourth layer adds symbiosis. The experiments show that a small amount of symbiosis, added to the other layers, significantly increases the fitness of the population. We suggest that, in addition to providing new insights into biological and cultural evolution, this model of symbiosis may have practical applications in evolutionary computation, such as in the task of learning deep neural network models.

Keywords: Major transitions in evolution, symbiosis, cooperation, open-ended evolution, game of life, levels of selection.

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1 Introduction

Maynard Smith and Szathmáry [16] described eight major transitions in the evolution of life on Earth. These eight transitions can be seen as instances of the same general phenomenon: Replicating entities that previously reproduced independently come together as parts in a new whole and replicate as one. Turney [33] argued that the same phenomenon can be observed in the evolution of human culture. As examples, we outline one major transition in biological evolution (the transition from prokaryotes to eukaryotes) and one in cultural evolution (the transition from hunter-gatherer societies to horticultural societies).

Prokaryotes are single-celled organisms, including bacteria and archaea. *Eukaryotes* may be single-celled or multi-celled organisms, including protists, fungi, plants, and animals. Eukaryotic cells have more complex internal structures than prokaryotic cells, containing various *organelles* (little organs) that are wrapped in membranes. Every eukaryotic cell has a *nucleus*, which is the organelle that contains the main genetic material of the cell. Most eukaryotic cells contain many *mitochondria*, organelles that provide energy to the cell. Many plant cells contain *chloroplasts*, organelles that perform photosynthesis. Mitochondria and chloroplasts were once independent prokaryotes that were taken inside host prokaryotes to eventually become organelles [14, 15, 16]. The merging of prokaryotes to form eukaryotes is mutually beneficial: The mitochondria and chloroplasts provide energy to their hosts and the hosts provide key proteins in return. Some of the genes of mitochondria and chloroplasts have migrated into their host's genome, which enforces their replication as a whole, rather than as independent parts.

Horticultural societies clear land by cutting and burning wild trees and shrubs. The ash provides fertilizer for the crops that they plant. After a few seasons of farming, the ash is depleted and the land must be abandoned until the trees and shrubs grow back. People in horticultural societies work harder and have less freedom than people in hunter-gatherer societies, so it is not obvious why people would switch from hunting and gathering to horticulture. Nolan and Lenski [19] argued that three factors led to the transition: environmental change and excessive hunting altered the distribution and reduced the population of large game animals, human population growth resulted in increased demand for food and horticulture was better able to meet the demand than hunting and gathering, and improvements in domestication made horticulture increasingly effective. Many domesticated plants (for example, bananas) have evolved to be completely dependent on humans, analogous to the dependence of mitochondria and chloroplasts on their hosts.

Maynard Smith and Szathmáry were concerned with the problem of *levels of selection* [16, page 7]: “Why did not natural selection, acting on entities at the lower level (replicating molecules, free-living prokaryotes, asexual protists, single cells, individual organisms), disrupt integration at the higher level (chromosomes, eukaryotic cells, sexual species, multicellular organisms, societies)?” Their answer was *separation* and *compartmentalization*. To preserve the integrity of the whole individual, there must be some separation of the individual from its environment; there must be some compartmentalization of its parts. In the case of eukaryotes, mitochondria and chloroplasts are isolated from the external environment by the cell membrane and cell wall. In the case of horticulture, domesticated plants are separated in farms and gardens from wild plants that would compete with them and animals that would eat them.

Symbiosis can be defined as “the union of two organisms whereby they mutually benefit” [38, page 356]. Our focus in this paper is on instances of symbiosis in which there is a shift in the level of selection, from a lower level to a higher level. Taking the perspective of the field of evolutionary optimization algorithms [24], we view symbiosis as the product of a *genetic operator*, similar to crossover, selection, or mutation. Let us call this operator *fusion*. Fusion takes as input two distinct entities that experience selection separately and produces as output a merged entity that experiences selection as a whole. We seek to understand what happens to the course of evolution when fusion occurs repeatedly, in the same way that one might experiment with different forms of mutation or crossover to understand how they effect the course of evolution. Symbiosis implies mutual benefit, but the output of fusion may be an organism that is low in differential fitness, just as the crossover operator or the mutation operator may produce an organism that is low in differential fitness.

In this paper, we present experiments with a computational simulation of evolution that includes the usual operators (such as crossover, selection, and mutation) plus fusion. We call our simulation *Model-T* (Model of Transitions). The source code for Model-T is available for downloading [34].

Model-T has four layers: (1) simple asexual reproduction with genomes of constant size, (2) asexual reproduction with genomes of variable size, (3) sexual reproduction with crossover, and (4) symbiosis by fusion. The separation of the model into layers is not intended to reflect evolution in nature; the motivation for the layers is to be able to measure and compare the contributions of each layer to the evolution of a population.

Evolution by natural selection requires variation, heredity, and differential fitness (*selection*) [8, 10]. In Model-T, differential fitness is based on one-on-one competitions in the Immigration Game (invented by Don Woods and described in *Lifeline* in 1971 [35, page 14]). The Immigration Game is a two-player variation of the Game of Life (invented by John Conway and presented in *Scientific American* in 1970 [9]).

The Game of Life is played on an infinite, two-dimensional grid of square cells [20]. Each cell is either *dead* (state 0) or *alive* (state 1). The state of a cell changes with time, based on the state of its eight nearest neighbours (the *Moore neighbourhood*). Time passes in discrete intervals and the states of the cells at time t uniquely determine the states of the cells at time $t + 1$. The initial states at time $t = 0$ are chosen by the player of the game; the initial states form a *seed pattern* that determines the course of the game, analogous to the way an organism's genome determines its phenome. The rules for updating states are compactly expressed as B3/S23: A cell is *Born* (switches from state 0 to state 1) if it has exactly three living neighbours. A cell *Survives* (remains in state 1) if it has two or three living neighbours. Otherwise it dies.

The Immigration Game is almost the same as the Game of Life, except that there are two different live states (states 1 and 2) [35]. The two live states are usually represented by red and blue colours. The rules for updating remain B3/S23, but there are new rules for determining colour: (1) Live cells do not change colour unless they die. (2) When a new cell is born, it takes the colour of the majority of its neighbours. The initial states at time $t = 0$ are chosen by the two players of the game; one player makes a red seed pattern and the other player makes a blue seed pattern. The players agree on a time limit, given by a maximum value for t . When the game ends, the player with the most living cells of their colour is the winner.

If states 1 and 2 were displayed with the same colour (say, black), playing the Immigration Game would appear exactly identical to playing the Game of Life. The different colours are simply a way of keeping score, to turn the Game of Life into a competitive game.

The original rules of the Immigration Game allow the human players to intervene in the game as it progresses, but we have no use for interventions in our simulations. The original rules also use a finite toroidal grid of 25×25 cells instead of an infinite grid. The motivation for a finite grid is that the limited space for growth forces the seeds to interact with each other and also reduces the amount of computation required. We use a finite toroidal grid but we make the size of the toroid proportional to the size of the initial seeds, so that there is no fixed limit on the size of the initial seeds.

The four layers of evolution in Model-T are external to the Immigration Game. It is possible to build a replicator inside the Game of Life [1], but all current Game of Life replicators are much too slow for practical experiments with simulations of evolution. An advantage of having the mechanisms of evolution external to the Immigration Game is that it enables experimentation with a clean separation of the independent variables (the external evolutionary mechanisms) and the dependent variables (the fitness scores from the Immigration Game).

We chose the Immigration Game for our model of major transitions because, as a two-player competitive game, it provides a built-in way of calculating fitness; as a Life-like game, it is well-suited for modeling biology; and it turns out that implementing fusion in the Immigration Game is simple and elegant. Given two seeds as input to the fusion operator, we join them together side-by-side with a one-column space to serve as a buffer. They are then treated the same way as any other seed; that is, they live, die, and reproduce as a unit. Selection takes place at the level of the whole (the new, higher level).

Figure 1 shows an example of an Immigration Game. The first image shows the competing seeds at time $t = 0$ and the second image shows the states of the cells when the time limit has been reached. When they are not competing, the seeds are stored with only two states (0 and 1); they are only temporarily assigned colours (states 1 or 2) for the purpose of playing the Immigration Game to obtain a fitness score. The size and structure of the two seeds in the first image indicates that they are both composed of four 5×5 seeds that have been joined by three fusion operations (along with some *shrinkage*, which will be introduced in Section 3.3).

Insert Figure 1 here.

Open-ended evolution is defined as evolution that is [29, page 409] “capable of producing a continual stream of novel organisms rather than settling on some quasi-stable state beyond which nothing fundamentally new occurs.” The main contributions of our paper are (1) a computational simulation of symbiosis by fusion as a mechanism for evolution, (2) evidence that fusion has a significant impact on evolution when combined with mutation and reproduction, (3) support for the hypothesis that symbiosis by fusion can sustain open-ended evolution, and (4) source code [34] for replicating and extending the results presented here.

In Section 2, we discuss related work. Section 3 outlines the principles that guided the design of Model-T and describes each of the four layers of the model. Section 4 presents four sets of experiments:

(1) We add the layers one by one, to see what each layer contributes to the model. (2) We experiment with increasing the amount of fusion in the fourth layer. (3) We compare human-designed Game of Life seed patterns with evolved seed patterns from Model-T. (4) We use the method of Bedau, Packard, and Brown [6, 7] to visualize evolutionary activity in the four layers of Model-T. In Section 5, we discuss the implications of the experimental results. Section 6 considers possible applications of this work. Section 7 examines limitations and possibilities for future research. We conclude in Section 8.

2 Related Work

The significance of hierarchical, part-whole structure in biology and culture was emphasized by Simon [25] and Koestler [13] in the 1960s. Margulis [14, 15] argued for the importance of symbiosis in evolution in the 1970s. Maynard Smith and Szathmáry [16] observed the role of symbiosis in eight major transitions in the evolution of life on Earth and pointed out the problem of levels of selection. Their book is an analysis of the mechanisms by which each of the eight major transitions addressed the problem of shifting the level of selection from the parts to the whole.

McShea and Brandon [17] assert that the increase in complexity of organisms over time is largely due to heritable variation in part-whole hierarchies. However, their theory of increasing complexity is based only on the horizontal spread of the hierarchy (the number of parts at the same level), and has nothing to do with the vertical depth of the hierarchy (the number of levels). They state that their theory has no connection with Maynard Smith and Szathmáry's [16] major transitions in evolution.

Banzhaf et al. [2] define a meta-model that can be used to identify levels of structure in a system. For example, they discuss how their meta-model could be applied to the Game of Life. A level-0 meta-model would view the Game of Life at the level of individual cells and their states. A level-1 meta-model would view the game at the level of common entities that appear in the game as repeating patterns of cells and states, such as *gliders*, *spaceships*, and *oscillators* (these names are familiar to players of the Game of Life [20]). A level-2 meta-model would include larger structures that are composed of level-1 structures, and so on. Model-T is intended to be a model, not a meta-model. In future work, the meta-model of Banzhaf et al. [2] could be applied to analyze Model-T, but we do not pursue that here.

Moreno and Ofria [18] create a computational simulation in which cell-like organisms coordinate their activities in ways that increase their reproduction. As the simulation runs, larger groups of organisms cooperate, sharing resources and dividing their labour. However, their simulation is limited to two

hierarchical levels. It was not designed with a mechanism (such as fusion) for automatically adding new levels.

The work of Beer [3, 4, 5] on modeling *autopoiesis* (self-production and self-maintenance) in the Game of Life is also relevant here. We conjecture that the entities that evolve in Model-T will show increasing degrees of autopoiesis as the running time of the simulation increases, but we have not yet tested this hypothesis. Autopoiesis should enable a growing seed to maintain itself better in the presence of disruptive competition.

3 Description of the Model

Model-T uses the open-source Golly software for running the Immigration Game [30]. Golly is designed to support extensions using the scripting languages Lua and Python. Model-T was implemented as an open-source Python extension of Golly [34].

Most of this section is concerned with presenting the design of the four layers of Model-T, but we first discuss the principles behind the design. The principles should help to explain some of the design decisions that were made.

3.1 Conditions for Open-Ended Evolution

Brandon [8, pages 5-6] states the following three components are crucial to evolution by natural selection:

1. Variation: There is (significant) variation in morphological, physiological and behavioural traits among members of a species.
2. Heredity: Some traits are heritable so that individuals resemble their relations more than they resemble unrelated individuals and, in particular, offspring resemble their parents.
3. Differential Fitness: Different variants (or different types of organisms) leave different numbers of offspring in immediate or remote generations.

In the literature, *differential fitness* is often called *selection*. Godfrey-Smith [10] lists the same three components, calling them *conditions for evolution by natural selection*.

Past work in artificial life has shown that, although these conditions are sufficient for evolution, they are not sufficient for *open-ended* evolution [29]. We are particularly interested in symbiosis by fusion because we believe that it may be one of the conditions for open-ended evolution (in addition to variation, heredity, and differential fitness). However, it seems likely that there may be other conditions that are

required for open-ended evolution. Since the necessary and sufficient conditions for open-ended evolution are not yet known, we chose to use a relatively large number of additional conditions, some of which might be unnecessary for open-ended evolution:

1. Symbiosis, fusion, and cooperation: There should be a mechanism for symbiosis with a shift in the level of selection from the parts to the whole [16]. Hence Layer 4 adds fusion to Model-T.
2. Biotic selection: Selection can be based on an organism's biological environment (competitors, predators, disease, etc.) or other aspects of its environment (sunlight, water, soil, shelter, etc.). Our intuition is that competition with other organisms (*biotic selection*) is a particularly strong form of selection, likely to encourage open-ended evolution. This motivates using the Immigration Game (a competitive game) for calculating differential fitness.
3. Relative fitness: The fitness of an organism is relative to the fitness of other organisms, especially members of the same population. There is no absolute fitness. (This is related to biotic selection.)
4. Unlimited genome size: A genome with a limited size must contain a limited amount of information, which implies a finite bound on the space of possible organisms [31, 32]. (One way around this limit is cultural evolution, where information is stored outside of the genome.) Hence Layer 2 of Model-T adds variable size for seed patterns.
5. Gene transfer: There should be some method for sharing genes (such as plasmids or sexual reproduction) beyond replication (asexual reproduction). Hence Layer 3 introduces sexual reproduction.
6. Universal code: DNA and human language are both codes that allow great flexibility and generality [16]. The Game of Life is known to support universal Turing machines [22]. This suggests that perhaps the Game of Life may have sufficient flexibility and generality to support open-ended evolution.
7. Genotype and phenotype: Open-ended evolution may require a distinction between genotype and phenotype. In the Game of Life, we view the initial seed pattern as the genotype. The growth or decay of the seed over time, as the game runs, can be seen as the development of the phenotype from the genotype. (This is related to universal code: the genotype is the code and the phenotype is the product of decoding.)
8. Speciation: Possibly diversity requires reproductive boundaries (distinct species). Without sufficient diversity, organisms may be trapped in a local optimum. Layer 3 adds reproductive boundaries by requiring potential mates to have a certain degree of genetic similarity.

It will take much work to validate all of these conditions. We leave this as future work. In this paper, we have limited our scope to showing that fusion is a useful genetic operator that may contribute to achieving open-ended evolution in a simulation. Other lists of conditions for open-ended evolution have been given for biological evolution by Sterelny [27], for cultural evolution by Nolan and Lenski [19], and for natural and artificial evolutionary systems by Taylor [28].

3.2 Layer 1: Uniform Asexual Layer

Model-T has several parameters for controlling its behaviour. We will introduce the parameters as they are needed in explanations. All parameters contain an underscore symbol. A full list of the parameters and their values for the first experiment is given in Table 1 in Section 4.1.

Model-T uses a GENITOR-style algorithm [36, 37] with one-at-a-time reproduction, a constant population size, and rank-based tournament selection. An individual in the population is represented as an object (a data structure) containing a binary matrix that specifies a seed pattern and an array of real values that stores a history of the results of its competitions with all other individuals in the population. The population is an array of `pop_size` individuals.

Children are born one-at-a-time. Each new child replaces the least fit member of the population, maintaining a constant population size. When `pop_size` children have been born, we say that one generation has passed. A run of Model-T begins with generation zero and lasts until generation `num_generations`. A run ends when `pop_size` × `num_generations` children have been born.

In generation zero, Model-T starts with a population in which the binary matrices are randomly initialized. The probability of ones in these matrices is given by `seed_density`, which we set to 0.375, based on the advice of Johnston [12]. When all of the matrices are initialized, we then initialize the history of competition results by a series of Immigration Games, pairing every individual against every other individual `num_trials` times. The fitness of an individual is the fraction of games that it wins. Every win by one individual is balanced with a loss by another individual. It follows that the average fitness of the population as a whole is always 0.5. Fitness is relative to the population, not absolute.

A new child is created by first selecting a parent, using tournament selection. We randomly select `tournament_size` individuals from the population and the most fit member of this sample is chosen as a parent. The parent is copied to make a child. The child is then mutated by randomly flipping bits in the binary matrix, where the probability of flipping a bit is `mutation_rate`. We force at least one bit to flip, so that a child is not identical to its parent, in order to maintain diversity in the population. The new child

replaces the least fit member of population and the histories of competition results are updated by pairing every individual against the new child in a new series of Immigration Games. This is summarized in Figure 2.

Insert Figure 2 here.

The space and time allowed for an Immigration Game depend on the two seeds that are competing. Open-ended evolution requires the limits on space and time to increase as the sizes of the individuals increase: Fixed limits would set a bound on the possible variety of games. Given two seeds, let `max_size` be the maximum of the number of rows and columns in the seeds; that is, the largest width or height. Three parameters determine the space and time allowed for the two seeds: `width_factor`, `height_factor`, and `time_factor` (see Table 1 in Section 4.1). The width of the Golly toroid is set to `max_size` times `width_factor`. The height of the toroid is set to `max_size` times `height_factor`. The maximum time (the number of time steps in the game) is set to the sum of the width and height of the toroid, multiplied by `time_factor`.

We describe Layer 1 as the *uniform asexual layer* because reproduction is asexual (each child has only one parent) and the size of the seed pattern matrix is uniform (it remains constant throughout the run of Model-T). Layer 1 is intended as a minimalist baseline evolutionary system. The following layers are expected to improve upon Layer 1.

3.3 Layer 2: Variable Asexual Layer

Layer 2 is like Layer 1, except we now have three different kinds of mutation: (1) With probability `prob_flip`, the child will be mutated by flipping bits, according to `mutation_rate`. (2) With probability `prob_shrink`, the child will be mutated by removing an outer row or column from the binary matrix. (3) With probability `prob_grow`, the child will be mutated by adding an outer row or column to the binary matrix. These three kinds of mutation are mutually exclusive; that is, the sum of `prob_flip`, `prob_shrink`, and `prob_grow` is one. This is summarized in Figure 3.

Insert Figure 3 here.

There is a minimum size for matrices (`min_s_xspan` columns and `min_s_yspan` rows), in order to limit how much a matrix can shrink. If growth is selected, the new column or row is initialized by randomly setting bits, where the probability of ones is given by `seed_density`.

We want growth in the model, so that there is no upper bound to the amount of information that can be stored in a genome (the binary matrix of an individual). The motivation for shrinkage is to see whether any growth that is observed is a consequence of increased fitness or it is due to random drift in the space of genomes. If the growth is due to random drift, then it should eventually flatten out as it balances with shrinkage.

3.4 Layer 3: Sexual Layer

Layer 3 adds sexual reproduction to Model-T. The first parent is chosen by tournament selection, just as in Layers 1 and 2. The second parent is chosen by looking for all individuals in the population with a degree of similarity to the first parent that is between `min_similarity` and `max_similarity`. The similarity of two individuals is measured by the fraction of corresponding bits in their matrices that have the same values. The similarity of two matrices is defined as zero if the matrices have different sizes. The second parent is chosen by tournament selection from this reduced sample of potential mates. This is summarized in Figure 4.

Insert Figure 4 here.

If there are no suitable mates with the required degree of similarity, Layer 3 passes the first parent on to Layer 2, for asexual reproduction. Many organisms can reproduce either sexually or asexually, depending on the availability of mates and other circumstances.

When two parents have been selected, they produce a child by crossover. First, we choose between crossing rows or columns, with equal probability. If rows are chosen, we randomly choose a horizontal crossover point and we make a new child by combining the rows above the crossover point from one parent and the rows below the crossover point from the other parent. Likewise, if columns are chosen.

After crossover, we pass the child on to Layer 2, where it undergoes bit flipping, shrinkage, or growth. It might seem that crossover is sufficient; that Layer 2 is not needed here. However, there is a limit to the variety that can be produced by swapping rows and columns.

3.5 Layer 4: Symbiotic Layer

Layer 4 adds fusion and fission to Model-T. First, a seed is chosen by tournament selection, just as in Layers 1, 2, and 3. There are then three possibilities: (1) With probability `prob_fission`, the chosen seed will be split apart. One part will enter the population and the other part will be discarded. (2) With probability `prob_fusion`, a second seed is chosen by tournament selection and the two seeds will be fused together. (3) If neither fusion nor fission are chosen, then Layer 4 will pass control over to Layer 3. We expect that `prob_fusion` and `prob_fission` will be set to values near zero, so the most likely event is that Layer 4 will pass control on to Layer 3 for sexual reproduction, reflecting the fact that fission and fusion are relatively rare events in nature. This is summarized in Figure 5.

Insert Figure 5 here.

If fission is chosen, the next step is to find the sparsest row or column in the binary matrix. The matrix is then divided into two parts along the sparsest row or column. One part is discarded, including the sparsest row or column, and the remaining part enters the population as a new entity.

If fusion is chosen, the two seeds are randomly rotated and then joined side-by-side with one column of zeros between them. The column of zeros is intended to act as a buffer, to reduce the potential for conflict or interference between the two seeds when they are joined together. The column of zeros also acts as a marker to provide a natural splitting point for possible fission events in the future. Layer 1 will eventually flip some of the bits in this column of zeros, turning them into ones.

Fission and fusion in Layer 4 are somewhat analogous to shrinkage and growth in Layer 2. The motivation of fission is to counterbalance fusion, just as shrinkage counterbalances growth. The expectation is that, if fusion does not contribute to fitness, then any random drift towards increased size due to fusion will eventually be limited by fission.

Layers 1, 2, and 3 are forms of *reproduction*, in which a child is similar to its parent (in the case of Layers 1 and 2) or parents (in the case of Layer 3). Fusion in Layer 4 is analogous to sexual reproduction in Layer 3, in that two seeds are involved in the production of a new seed, but the size of the new genome is greater than the sum of the sizes of the two original genomes. The “child” of fusion is not similar to its “parents”. We will see in the experiments in Section 4 that Layer 4 behaves quite differently from Layer 3.

Layer 4 tends to result in a rapid increase in the size of seeds over the course of a run of Model-T. This is a positive outcome, since it confirms our expectations for a model of major transitions in evolution, but it is problematic from a practical point of view, because Model-T is designed to increase the time limit for the Immigration Game when the seeds are larger, in order to give more time for a clear win to emerge from the game; thus the simulation slows down as the seeds become larger. For this practical reason, we have designed Model-T with a linear upper bound on the size of seeds. The upper bound is set using the parameters `max_area_first` and `max_area_last`, where `max_area_first` is the maximum area of a seed in the first generation and `max_area_last` is the maximum area of a seed in the last generation. For generations between the first and last, the maximum area is determined by linear interpolation. (The area of a seed is the number of columns in the seed's binary matrix multiplied by the number of rows.)

4 Experiments with the Model

In this section, we present four sets of experiments with Model-T.

4.1 Measuring the Contributions of the Layers

In the first set of experiments, we evaluate the contributions of each of the layers of Model-T. We run Model-T twelve times with Layer 1 alone, twelve times with Layer 2, twelve times with Layer 3, and twelve times with Layer 4. We compare each layer in terms of the fitness of the seeds, their size, their density, and their diversity. Table 1 shows the parameter settings for Model-T in these experiments.

Insert Table 1 here.

All of the comparisons that we make here are based on samples of the populations taken during runs of Model-T. One run of Model-T generates 20,000 children (`num_generations` × `pop_size`). Each generation is defined as the birth of 200 children (`pop_size`). For each generation from 0 (the initial random population) to 100 (the final population), we store the top 50 (`elite_size`) fittest individuals (where fitness is relative) in a file for later analysis.

As we discussed in Section 3, fitness in Model-T is relative to the population. The fitness of an individual is the fraction of Immigration Games that it wins in competitions against the other individuals in the population. Therefore, it does not make sense to compare the fitness value of a seed in one population with the fitness value of a seed in another population. The fitness used in Model-T is *relative* and *internal*. To compare fitness across different layers and different populations, we need to define a fitness measure

that is *absolute* and *external* to Model-T. Given a seed from any population and any layer, we calculate its absolute fitness by competitions against randomly generated seeds with the same matrix size (the same number of rows and columns) and the same matrix density (the same fraction of ones in the matrix). For a given seed, we randomly generate its opponents by copying the seed and shuffling the values in the resulting matrix. Figure 6 gives the absolute, external fitness curves for each of the four layers.

Insert Figure 6 here.

Because the absolute fitness only compares seeds of the same size and density, any statistically significant difference in the absolute fitness values for two seeds must be due to the structures of the seeds (the pattern of zeros and ones) and to how their structures determine their development from genome to phenome over the course of the Immigration Game. Comparing seeds that are matched by size and density is analogous to comparing wrestlers that are matched by height and weight. Table 2 shows the statistical significance of the differences of the fitness curves in Figure 6. All of the differences are significant, except for the difference between Layers 2 and 3 (variable asexual reproduction and sexual reproduction).

Insert Table 2 here.

Figure 7 plots the growth in area for each of the four layers. Comparing Figures 6 and 7, we see the same general trends in both cases: Layer 1 has the lowest fitness and area, Layer 4 has the highest fitness and area, and Layers 2 and 3 are roughly similar to each other. Since absolute fitness is measured by competitions between seeds that have the same number of rows and columns, increasing fitness cannot be a direct consequence of increasing area. Increasing fitness must be an indirect consequence of the greater structural complexity that is permitted by increasing area.

Insert Figure 7 here.

Figure 8 shows the density of the seeds for the four layers. In Layer 1, the size of the seeds is fixed at 5×5 , since the initial number of rows and columns in the seed matrix is $s_xspan \times s_yspan$ and there is no mechanism in Layer 1 for seeds to change size. The density begins at 0.375 (seed_density) and slowly rises to a steady level of about 0.533. In the other three layers, where seeds are allowed to increase in

area up to the limit given by the parameters `max_area_first` and `max_area_last` (120 and 170), density falls over time. Layers 2 and 4 have approximately the same curves in Figure 8, but the density in Layer 3 (sexual reproduction) falls more slowly than in Layers 2 and 4. It seems that sexual reproduction slows down the rate of change in the population, but symbiosis in Layer 4 compensates for this slowing.

Insert Figure 8 here.

Figure 9 indicates the amount of diversity in the population for the four layers. We measure the diversity by the standard deviation of the fitness in the elite population sample. A low standard deviation indicates that the elite sample has little variety; all of the seeds are doing approximately the same thing. A high standard deviation indicates that the elite sample embodies a variety of different strategies. Layer 4 appears to have a more diverse population than the other three layers.

Insert Figure 9 here.

It seems that there are a number of interesting relations connecting fitness (Figure 6), area (Figure 7), density (Figure 8), and diversity (Figure 9), but it is possible that these relations are statistical artifacts. Therefore, we look at the correlations between all pairs of these four variables and test their statistical significance. The results are given in Table 3. All of the pairs have a significant relation, except for density and diversity.

Insert Table 3 here.

Summarizing Table 3, larger area implies lower density, greater diversity, and greater fitness. Lower density indicates greater fitness. Greater diversity entails greater fitness.

4.2 Increasing the Probability of Fusion

Given that our goal in this paper is to model symbiosis as a mechanism for major transitions in evolution, it is satisfying to see in Figure 6 and Table 2 that Layer 4 (symbiosis by fusion) is significantly more fit than the other layers. Note that this was achieved with `max_area_first` = 120 and `max_area_last` = 170, parameter settings that strongly cap the growth of the seeds (see Section 3.5 for discussion of these parameters). In this section, we try to see what happens when `max_area_first` and `max_area_last` are

both set to 10,000. We also increase `prob_fusion` from 0.005 to 0.01, doubling the probability that fusion will occur. We call this Layer 4XL (XL for *extra large*).

Unfortunately, Layer 4XL became much too slow around generation 50, so we ended this experiment early. Figure 10 compares the fitness of Layer 4 and Layer 4XL. The curve for Layer 4XL is flat after generation 62, which is the last generation reached before we terminated the six parallel runs of Layer 4XL. The final fitness score of Layer 4XL is about 0.953, which tells us that the final elite populations won about 95% of their battles against opponents of the same area and density.

Insert Figure 10 here.

Figure 11 compares the areas of Layer 4 and Layer 4XL. The average area in the final generation of Layer 4 is about 120, whereas the average area in the final generation of Layer 4XL is about 6,500. With `prob_fusion` = 0.01, fusion only takes place in 1 in 100 births. The remaining births are either fission (also 1 in 100 births) or sexual reproduction (98 in 100 births). This shows that a small amount of fusion can cause area to increase more than 50-fold. Fusion is a powerful genetic operator.

Insert Figure 11 here.

If we extrapolate the curve for Layer 4XL in Figure 11, it looks like the area in the final generation might have reached about 14,000. Towards the end, the execution time between each generation would have been many days.

4.3 Comparing Evolution and Design

It might be argued that our external fitness measure, based on competitions against randomly generated seeds with the same matrix size and density as the seed that is to be evaluated (see Section 4.1), is not sufficiently challenging. How would evolved seeds fare against human-engineered seeds, instead of random seeds? We address that question here.

The Golly software [30] comes with a substantial collection of human-engineered Game of Life seed patterns that can be pitted against the evolved seeds. In this section, we compare the seeds in the final generations of the experiments in Sections 4.1 and 4.2 with human-engineered seeds. Table 4 summarizes the properties of these evolved seeds.

Insert Table 4 here.

To be fair, we focus on the human-engineered seeds that are comparable to the evolved seeds in terms of their area, since we know from Table 3 that area and fitness are closely related. Since Layer 4XL has an area of 6,500 in its final generation, we set a limit of 10,000 on the areas of the human-engineered seeds. Table 5 gives the results of this contest.

Insert Table 5 here.

Looking at the bottom row of Table 5, if we rank the layers in increasing order of fitness, then we have Layer 1, Layer 3, Layer 2, Layer 4, and Layer 4XL. This is the same ranking we can see in Figures 6 and 10, where fitness is based on competition with random seeds. Although the human-engineered seeds are more challenging than the random seeds, the results are qualitatively similar.

The human-engineered seeds are at a disadvantage in this contest, since they were not designed to play the Immigration Game. An exception is the class of human-engineered seeds called *Breeders* [20]. These are seed patterns that have been engineered to fill space as quickly and densely as possible. There is only one breeder in Table 5 (spacefiller.rle), and we can see that it won against all five evolved layers. Golly has other breeders, but they all have areas greater than 10,000. If we raise the area limit from 10,000 to 50,000, there are five breeders below the area limit. These five breeders win in all competitions with the evolved seeds. Human engineering triumphs over Model-T evolution, but this may change if Model-T is given the computational resources to achieve higher seed areas.

4.4 Visualizing Evolutionary Activity

In this section, we visualize the evolutionary activity in the four layers of Model-T using a variation on the method of Bedau, Packard, and Brown [6, 7]. The intention is to focus on the individuals that have been most successful in a given run of Model-T. We pick out the 20 individuals with the highest cumulative normalized internal relative fitness in a run and we plot their careers over the course of the run. These plots give us insight into what is happening in the four layers.

Recall from Section 4.1 that we sample the top 50 (elite_size) fittest individuals in each generation (each 200 births) and store the samples for analysis. To measure cumulative normalized fitness, we

calculate the normalized fitness of every individual in every sample and then we score each individual by the sum of its normalized fitness values over all of the samples. To calculate normalized fitness, we first sort the individuals in an elite sample in order of increasing relative internal fitness and number them from 1 to 50. The normalized fitness of the i -th individual is i divided by 50, which ranges from 0.02 for the least fit member of the sample to 1.0 for the most fit member. If an individual does not appear in a given sample, its normalized fitness in the sample is defined as zero. If an individual appeared in every sample in every generation from 0 to 100 and always had the highest fitness, its cumulative normalized fitness would be 101.

After we have calculated the cumulative normalized fitness of every individual that appears in one of the 101 elite samples, we select the top 20 individuals with the highest cumulative normalized fitness values and plot their careers over the generations. An individual's career begins in the first generation in which it has a nonzero normalized fitness and it ends in the last generation in which it has a nonzero normalized fitness. The plots show the growth of each individual's cumulative normalized fitness over the course of its career.

Figure 12 shows the evolutionary activity for Layer 1. The top 20 individuals all appear early in the run and have long careers. This tells us that there is little evolutionary activity in Layer 1.

Insert Figure 12 here.

Figure 13 plots the evolutionary activity for Layer 2. We see a substantial change from Layer 1 in Figure 12. Careers are much briefer in Figure 13 and the final cumulative scores are lower. In Figure 12, the last birth was in generation 46, but Figure 13 has eight births from generation 46 onwards. The competition is clearly more intense with Layer 2 than with Layer 1.

Insert Figure 13 here.

Figure 14 presents the top careers for Layer 3. It appears that Layer 3 is somewhere between Layers 1 and 2 in terms of the degree of competition. The last birth was in generation 49. The highest cumulative score was 44.8, whereas the highest cumulative score in Layer 1 was 74.0 and the highest cumulative score in Layer 2 was 22.7.

Insert Figure 14 here.

In Figure 15 with Layer 4, the greatest concentration of evolutionary activity begins after the midway point in generation 50. Six careers begin before generation 50 and fourteen careers begin afterwards. It appears that the pace of evolution is picking up as time goes on, unlike what we see in Layers 1, 2, and 3.

Insert Figure 15 here.

The four plots in this section indicate that the fusion operator, combined with mutation by bit flipping, growth, and shrinkage, may be capable of open-ended evolution. Further work is required to explore this hypothesis.

5 Discussion of Results

Maynard Smith and Szathmáry [16] focus on the details of how each of the eight major transitions in the evolution of life managed to shift selection from the lower level to the higher level. In each case, the solution to the shifting problem was different. Our objective with Model-T was to capture this shifting operation at a level of abstraction that views all of the eight major transitions as essentially the same. The fusion operator in Model-T simply joins the two parts into a whole and then applies selection to the new whole, without going into the details of how that shift in selection happens in a specific instance.

A model must abstract away from the details of reality. The challenge is deciding which details to ignore and which details to include. Instead of viewing symbiosis as a mutually beneficial union [38], we view it as a genetic operator that fuses two (or more) individuals, for better or for worse. If they thrive and reproduce, good; if not, then try another pair. This ignores the complexity of symbiosis, the difficulty of enforcing cooperation, and the problems of shifting selection from the lower level to the higher level. Analogously, software models of crossover [24] typically ignore the complexity of crossover in real life, omitting the details of meiosis, mitosis, and cytokinesis.

In Model-T, when two seeds are joined by fusion to make a new seed, if the new seed is more fit than its components, then we have symbiosis: Both of the parts benefit from their fusion. The precise mechanism (the specific characteristics of the pattern of bits in the new seed) by which that symbiosis

succeeds is different in each case. There may be an interesting story to tell about the various mechanisms for symbiosis that arise in runs of Model-T, but that story is outside of the scope of this paper.

Section 4.1 shows that Layer 4, symbiosis by fusion, significantly increases fitness when combined with the other layers. The increase in fitness occurs despite several obstacles: (1) Fusion takes place in only 1 out of 200 births. (2) Fission is twice as likely as fusion. (3) 98.5% of the time, Layer 4 passes control to Layer 3, but Layer 3 is less fit than Layer 2 (although the difference is not significant; see Table 2); Layer 4 might perform better if it passed control to Layer 2. (4) The parameters `min_similarity` and `max_similarity` impose strong constraints on fusion.

Section 4.2 demonstrates that fusion can cause rapid increase in size. This is interesting from a biological perspective, given that the sizes of biological organisms span several orders of magnitude. However, it presents a practical problem when running Model-T, due to the increasing time required for the Immigration Game. We discuss this problem further in Section 7.

Section 4.3 supports our absolute external fitness measure, based on comparing evolved seeds with random seeds of the same size and density. The experiments show that comparison with human-engineered seeds yields the same ranking of the layers of Model-T.

Section 4.4 uses the method of Bedau, Packard, and Brown [6, 7] to visualize the evolutionary activity in the layers of Model-T. The visualization indicates that activity in Layer 4 increases as the generations pass, whereas activity declines in the other layers. It remains to be demonstrated that this trend will continue over longer periods of time.

6 Applications

The main goal of Model-T is to give insight into the major transitions in evolution and to contribute to our understanding of open-ended evolution. However, the insights we have gained here may have practical applications in machine learning. Recently there has been much progress in using evolutionary computing methods to design deep learning neural networks [11, 21, 26]. We believe it may be useful to add fusion as a genetic operator in these evolutionary algorithms. Given two neural networks as input, the fusion operator would combine the networks either in parallel or in serial, as illustrated in Figure 16.

Insert Figure 16 here.

More generally, although Model-T was designed specifically for evolving seed patterns for the Immigration Game, there may be many other applications for Model-T, with suitable modifications for each application. We leave this for future work.

7 Future Work and Limitations

A limitation of Model-T is the amount of time required to run the Immigration Game for large seeds, as discussed in Section 4.2. Addressing this problem may be a straightforward task of tuning the parameters, `width_factor`, `height_factor`, and `time_factor` (see Section 3.2), but we believe a more sophisticated method is required for determining the best toroid size and the best time limit for a given pair of competing seeds. One way to set the time limit would be to use some kind of test for *quiescence* to determine the end of a game. The idea is to end the game when the score appears to be nearly stable.

A puzzle from the results presented in Section 4 is the relatively poor performance of sexual reproduction in Layer 3. Simon [24] lists eleven different kinds of genetic crossover. It may be that one of the other forms of crossover will perform better than the simple single-point crossover used in Model-T. We also use a form of restricted mating in Model-T, controlled by the `min_similarity` and `max_similarity` parameters (see Section 3.4). We tried to tune these parameters to improve sexual reproduction, without success. Sexual reproduction has long been a topic for debate among evolutionary biologists, with many different theories about its role in evolution. Ridley [23] argues that a major reason for sexual reproduction is to provide resistance against parasites. One option would be to add simulated parasites to Model-T.

Table 1 shows that the parameter space for Model-T is relatively large. Experiments with Model-T are relatively slow, which makes it difficult to explore the parameter space thoroughly. Although we have run many experiments, we have only explored a tiny fraction of the parameter space.

For those who are interested in Lamarckian evolution, Model-T could be a suitable platform. Lamarckian evolution is based on the inheritance of acquired characteristics. We can simulate a kind of Lamarckian evolution as follows: (1) Put a seed into the Game of Life. This seed is the genotype. (2) Let the game run for N steps. The resulting pattern is the phenotype. (3) Take the resulting pattern out of the game and use it as a new seed. This new seed has acquired characteristics from its time in the Game of Life and these characteristics are heritable.

For those who are interested in tracking the heritage of individuals, it would be easy to modify Model-T by storing a family tree with each seed. The nodes in the tree could be pointers into a database of stored seeds. This would be useful for testing hypotheses about the properties of inheritance in Model-T.

8 Conclusion

In this paper, we have introduced a model of major transitions in evolution. The model has four layers of genetic operators. The first three layers include asexual and sexual reproduction, with standard genetic operators such as mutation and crossover. The fourth layer introduces two new genetic operators, fusion and fission. The main contribution of the paper is the fusion operator. We argue that this operator provides an abstract model of major transitions in evolution, when used in conjunction with the other operators.

In this model, the fitness of an organism is determined by competition in the Immigration Game, a variation on the Game of Life. A key insight is that the fusion operator is easy to implement in the Game of Life: Two organisms are fused by simply joining them side-by-side. In other artificial life simulations, fusion is not as straightforward as this.

Maynard Smith and Szathmáry [16] have produced a very thorough and influential study of the major transitions in evolution. If we consider the wealth of detail in their book, the idea of simulating major transitions in a computer seems hopelessly ambitious. This paper shows that modeling major transitions is tractable, if the model is sufficiently abstract.

Model-T is a simple simulation, but the outcomes of the experiments are often surprising. For example, the poor performance of Layer 3 (sexual reproduction) is puzzling. The experiments in Section 4 raise as many questions as they answer. We hope that these questions will inspire future research.

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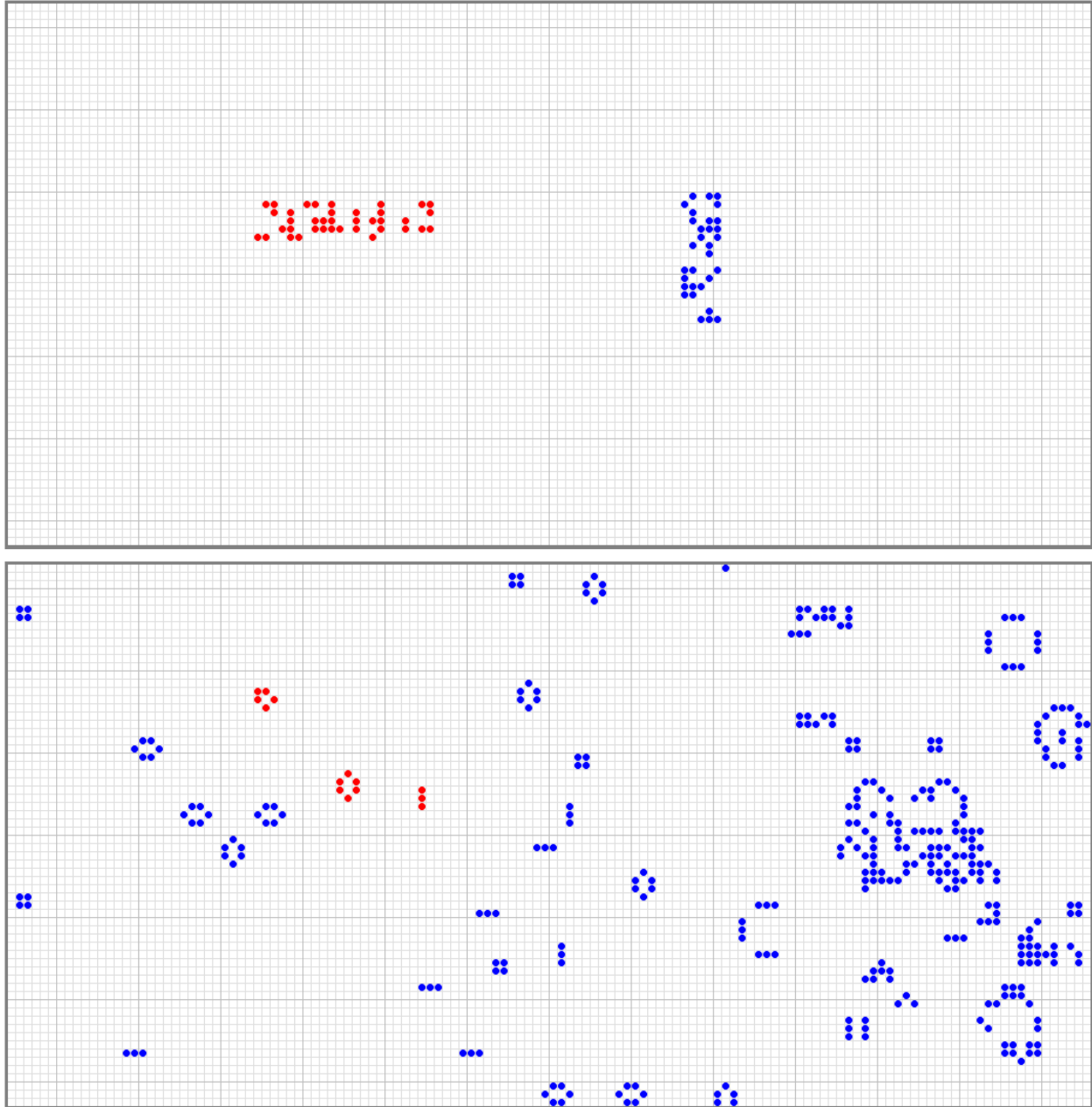


Figure 1. The first image above shows the initial state of an Immigration Game and the second image shows the final state, when the game reaches its time limit. The first image contains two competing seeds, a red seed (22×5 , 38 live cells, density 0.35) and a blue seed (20×5 , 31 live cells, density 0.31). The second image reveals that blue won the game. Both seeds were the fittest seeds in the final generations of two different runs of Model-T, in which both runs used all four layers of the model.

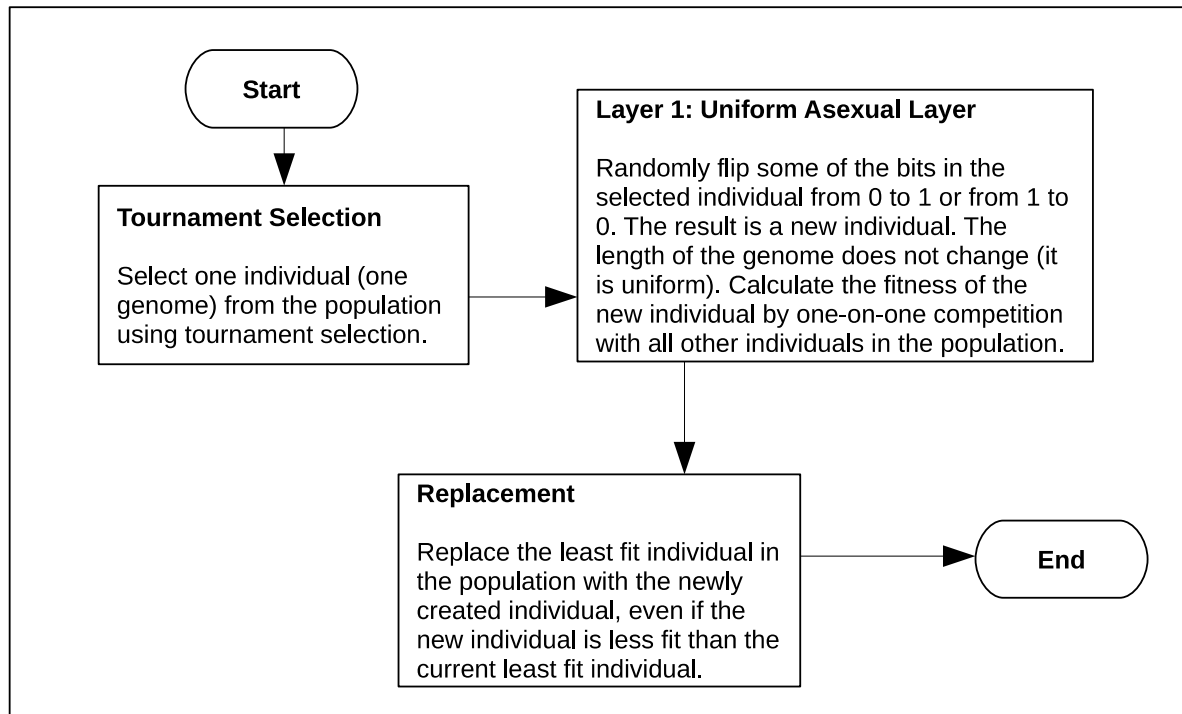


Figure 2. The flowchart above describes the process for uniform asexual reproduction. This process is a subroutine in a loop that produces a series of new individuals. For each individual that is added to the population, another is removed; hence this is a steady-state model with a constant population size. Uniform asexual reproduction takes the input individual and generates a mutated copy as the output.

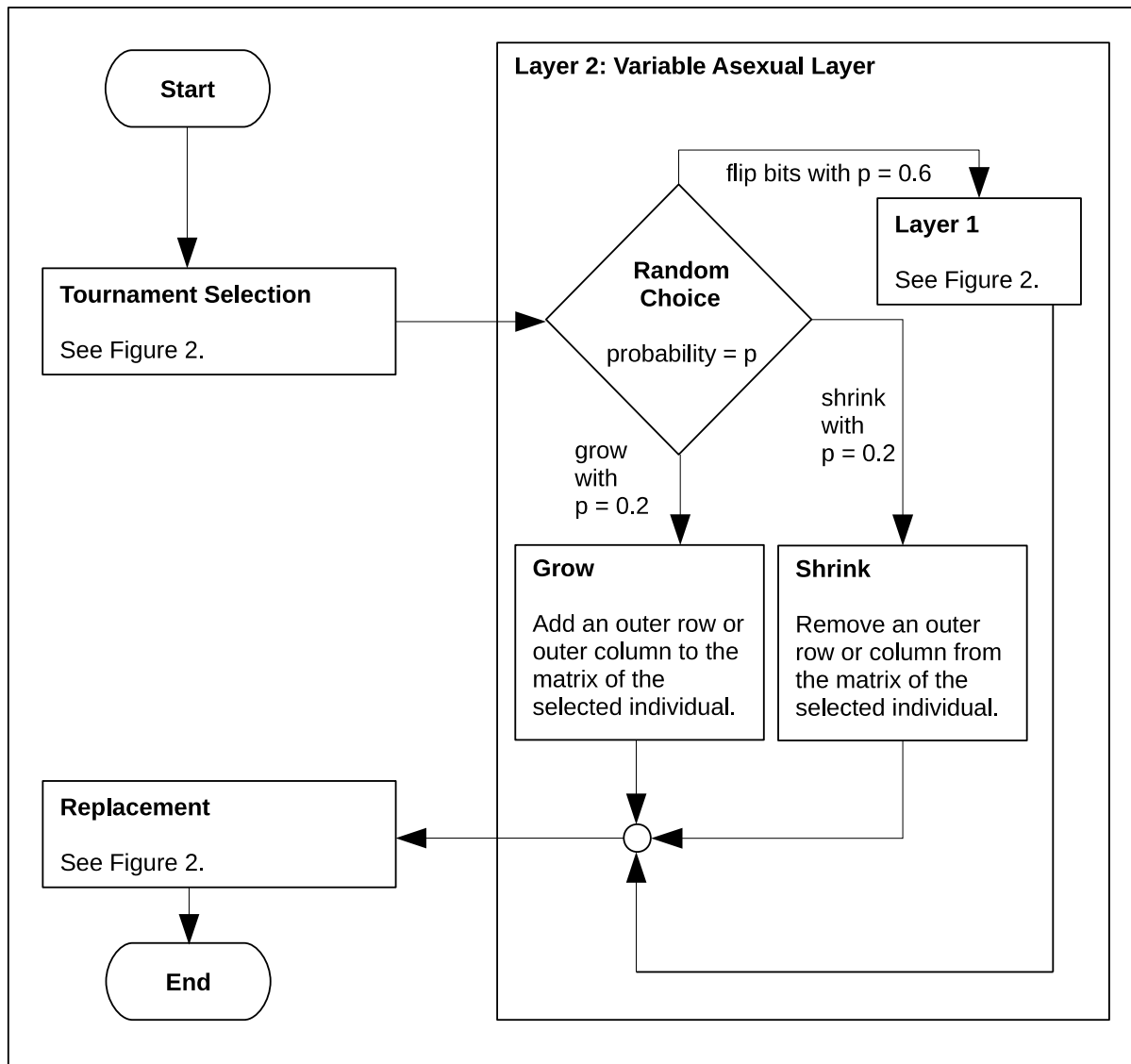


Figure 3. Layer 1 produces individuals of uniform size, whereas Layer 2 allows variable size. A random number is generated between 0 and 1. The value of the random number determines whether the individual will shrink in size, grow in size, or be passed on to Layer 1, where it will copy the size of its parent and mutate by flipping bit values.

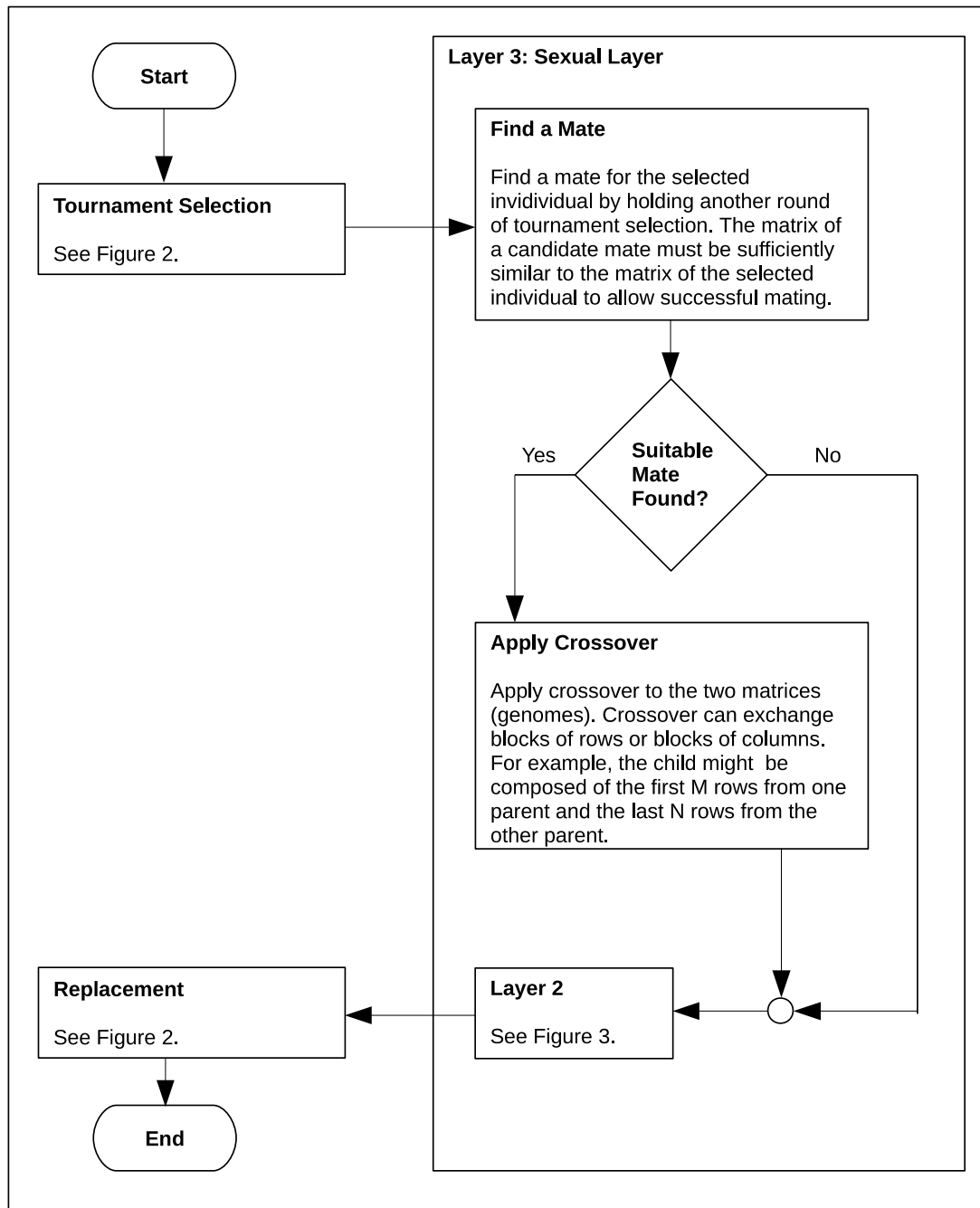


Figure 4: Layer 3 introduces sexual reproduction, where part of one individual's matrix is combined with part of another individual's matrix. The individuals are neither male nor female; any individual can mate with any other individual, so long as they are sufficiently similar. After mating, the child individual is passed on to Layer 2 where it grows, shrinks, or flips bits.

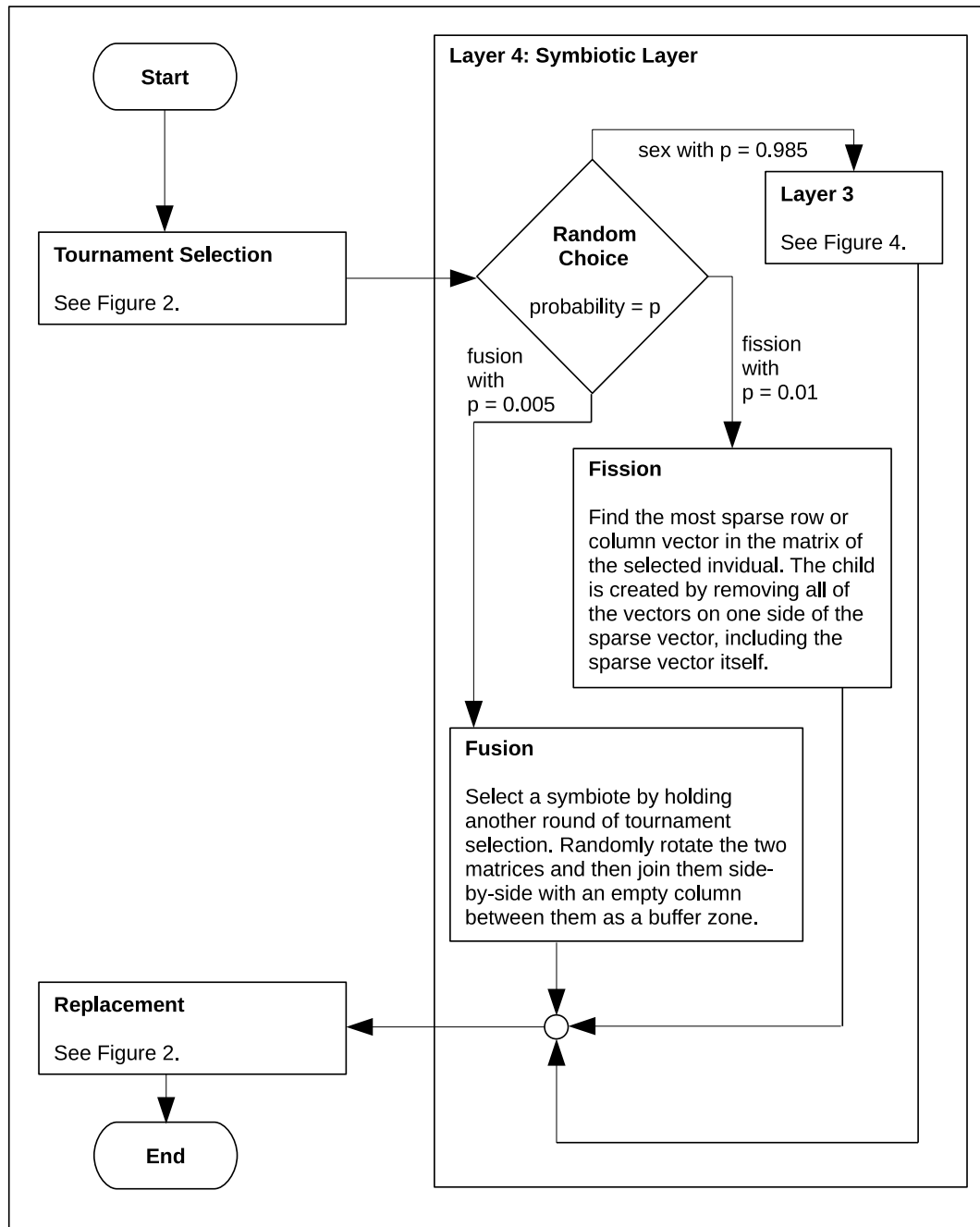


Figure 5. Unlike Layers 1, 2, and 3, Layer 4 is not a form of reproduction. With fusion, a new individual (a symbiote) is created by fusing two individuals. With fission, a new individual is created by breaking an individual into two parts. Only one of the two parts is kept. We set the probability of fission higher than the probability of fusion in order to see whether the selection for symbiotes can overcome this bias towards fission. Note that fission and fusion are much less likely than sexual reproduction.

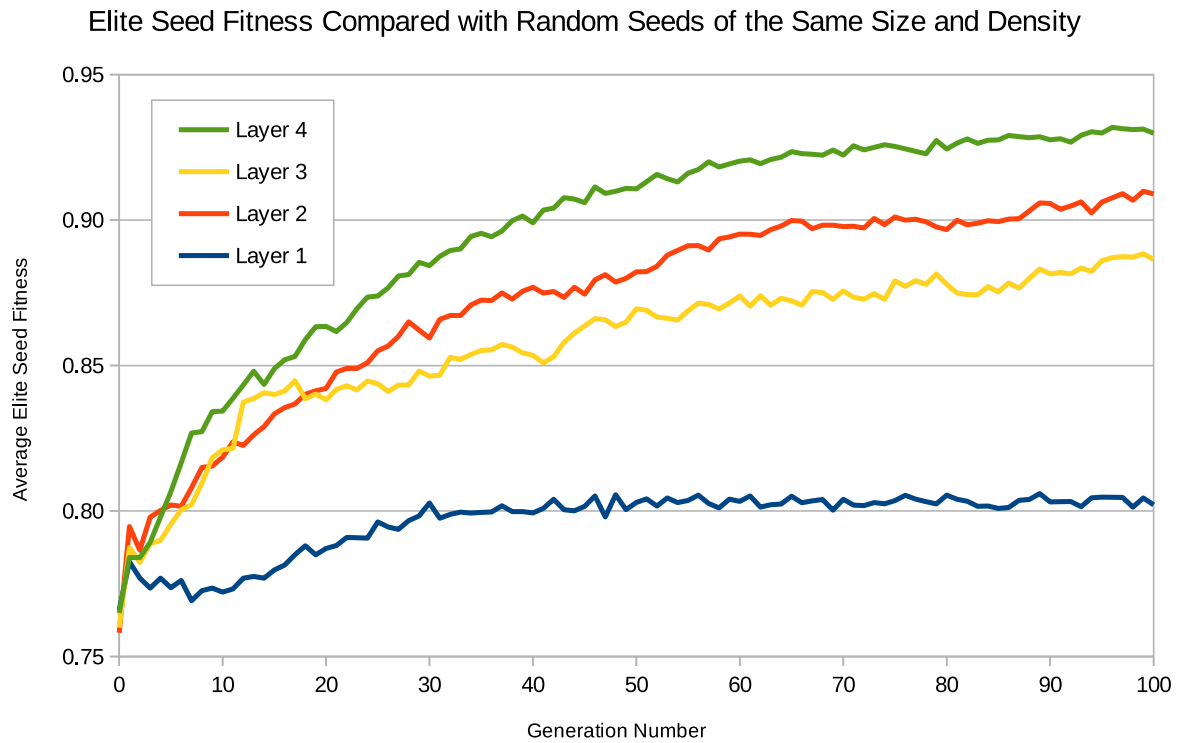


Figure 6. Each curve in this figure (that is, each layer) is the average of 12 separate runs of Model-T. The fitness of a seed is the fraction of Immigration Game contests that it wins when competing against randomly generated seeds with the same size (the same width and height) and the same density (the same number of live cells). This is an external measure of fitness that does not correspond to the internal measure used in the selection process in the four layers. The internal measure of fitness would show no progress, because it compares each individual to the population, and the population as a whole is progressing (on average) as fast as the individuals in the population are progressing.

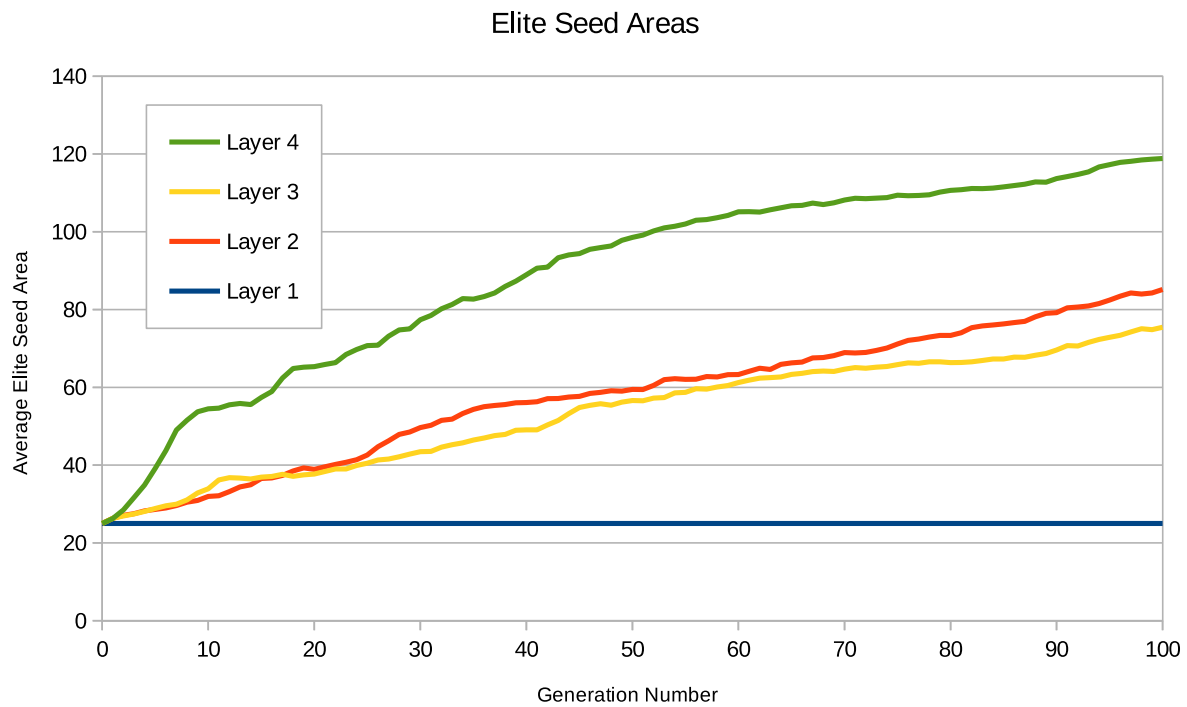


Figure 7. Each curve in this figure is the average of 12 separate runs of Model-T. Comparing this figure with Figure 6 suggests that area and fitness are positively correlated, even though the fitness in Figure 6 is based on size-matched competitions. Greater area indirectly helps fitness by allowing more information to be encoded, which permits more complex structures and actions.

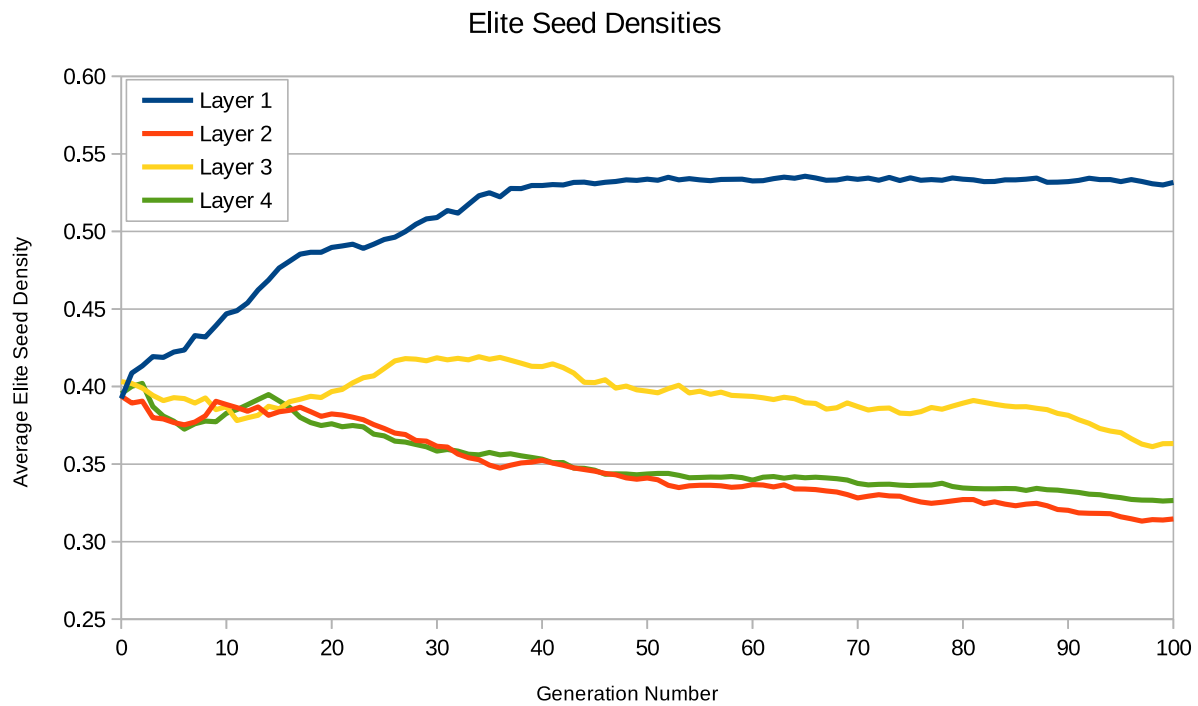


Figure 8. In Layer 1, where seed area is constant, density increases over time. In the other three layers, where seed area increases over time, density decreases. With human-designed seed patterns, we also see a negative correlation between area and density. Perhaps lower density allows information to travel longer distances, enabling greater complexity.

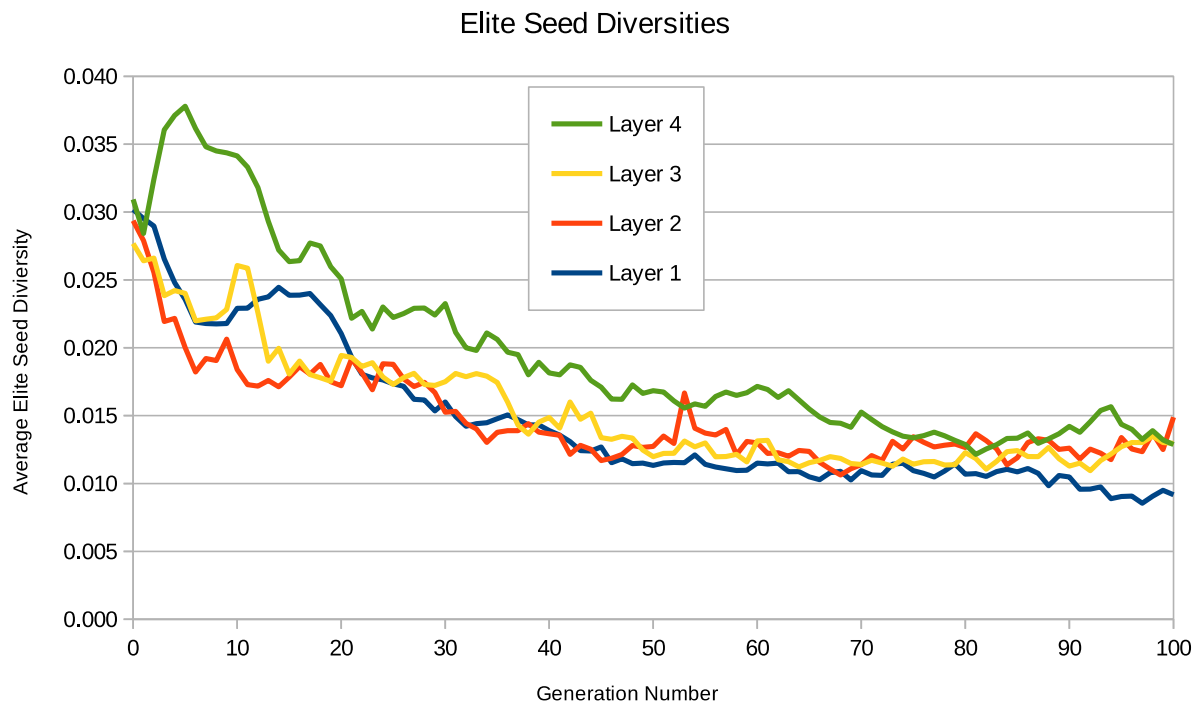


Figure 9. The diversity of the elite seed population is measured here by the standard deviation of the external measure of fitness (see Figure 6). The standard deviation is then averaged over the 12 separate runs of Model-T for each layer. Layers 1, 2, and 3 appear to have approximately the same diversities, but Layer 4 appears to be more diverse.

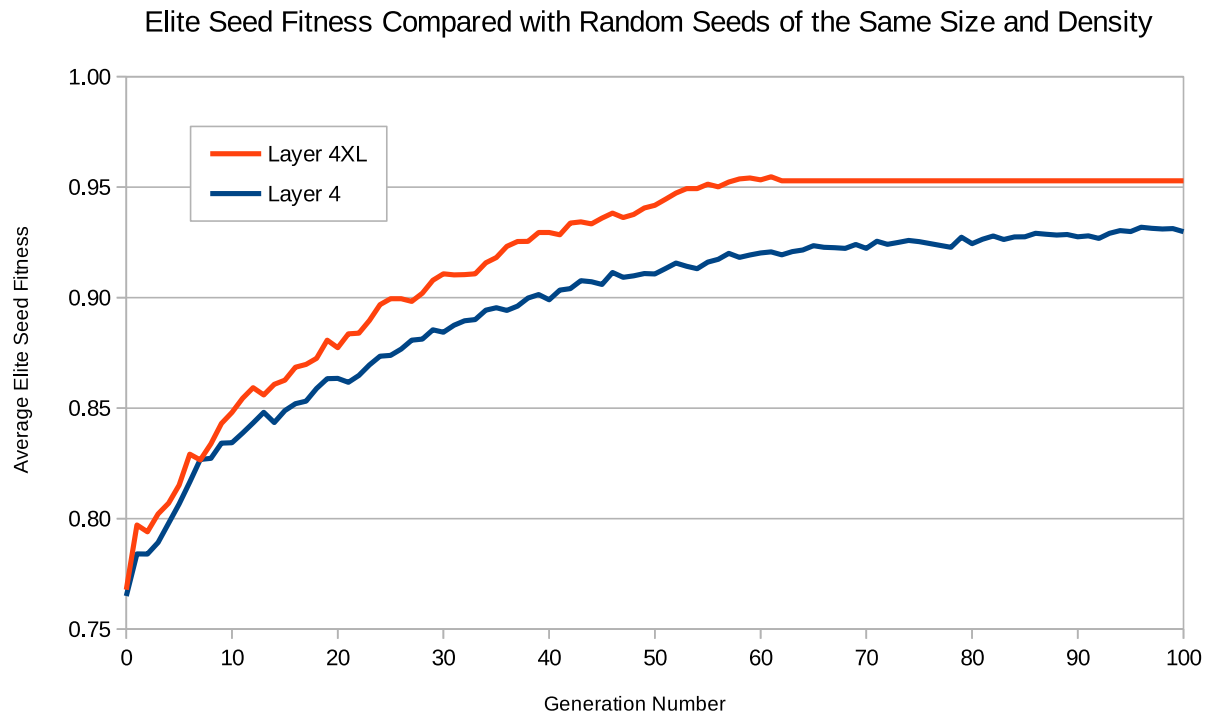


Figure 10. The curve for Layer 4 is the average of 12 separate runs of Model-T, the same as in Figure 6. The curve for Layer 4XL is the average of 6 separate runs of Model-T with `prob_fusion` set to 0.01 and both `max_area_first` and `max_area_last` set to 10,000. The experiments for Layer 4XL were terminated early because they were running too slowly. In the beginning, each generation of Layer 4XL required about 10 minutes to complete, but the final generations required more than one day to complete. When the runs were terminated, their final generations ranged from generation 39 to generation 62. To compare Layer 4XL with Layer 4, we extrapolated the fitness level of the final generations of Layer 4XL up to the 100th generation, which explains why the curve for Layer 4XL is a flat line after generation 62.

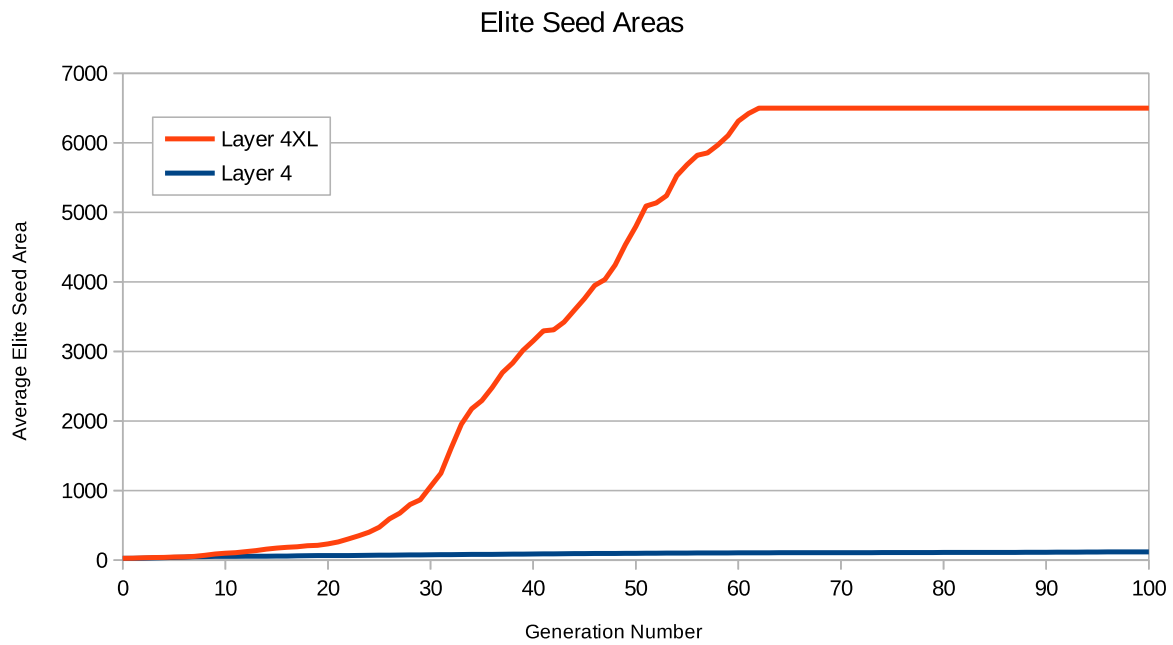


Figure 11. The curve for Layer 4 is the same curve as in Figure 7, except that here the curve is compressed by the large scale of the vertical axis. Layer 4 reaches a maximum average area of about 120, whereas Layer 4XL reaches a maximum average area of about 6,500. After generation 62, the area for Layer 4XL is extrapolated from the area in the final generation.

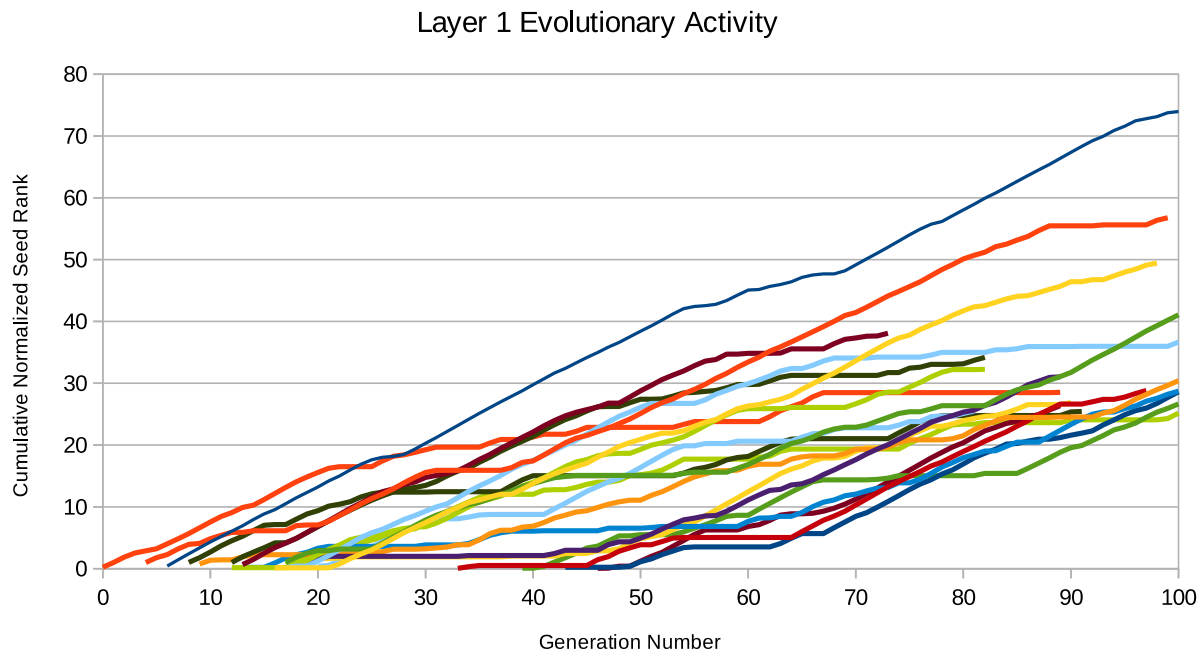


Figure 12. This figure shows the evolutionary activity in one run (randomly selected out of 12 runs) of Layer 1. Each curve plots the progress of one individual, beginning in the generation when the individual first entered the elite population and ending in the generation when the individual last appeared in the elite. There are 20 curves here, corresponding to the 20 most successful individuals. All of the successful individuals begin their careers early (before generation number 50) and many of them have very long careers. This indicates that the rate of change for Layer 1 is relatively low.

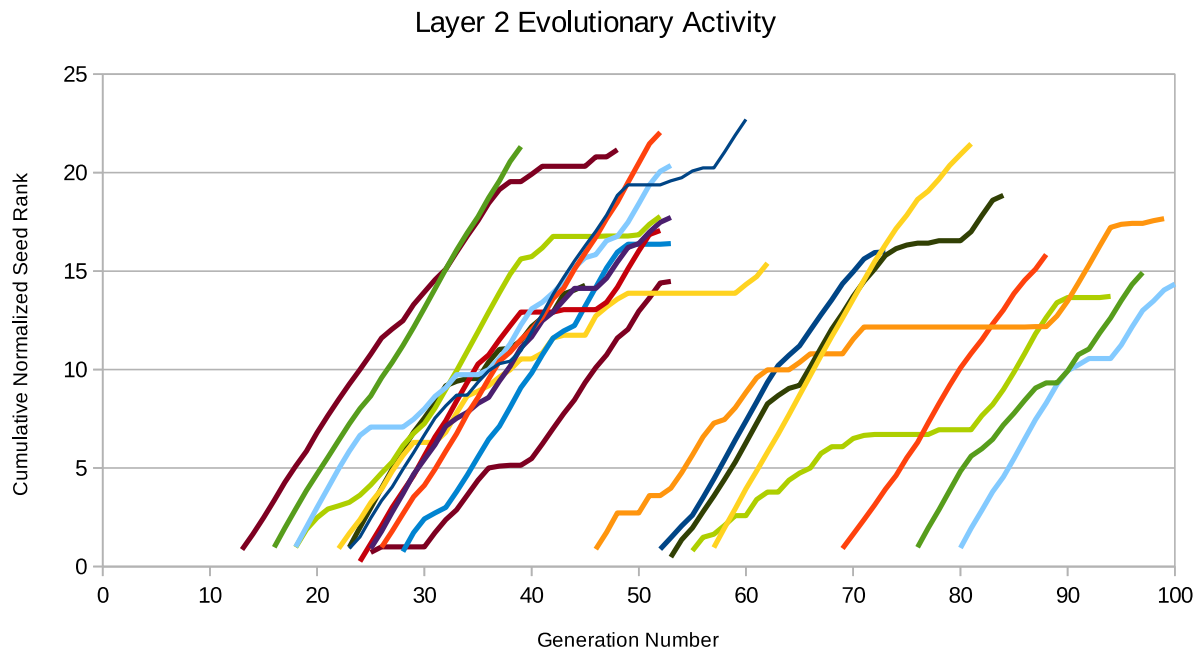


Figure 13. This figure shows the evolutionary activity in Layer 2. There is an initial burst of creativity in generations 10 to 30, but many of the successful individuals begin their careers after generation 50. The length of a career is markedly shorter in Layer 2 than in Layer 1; the competition is more severe here.

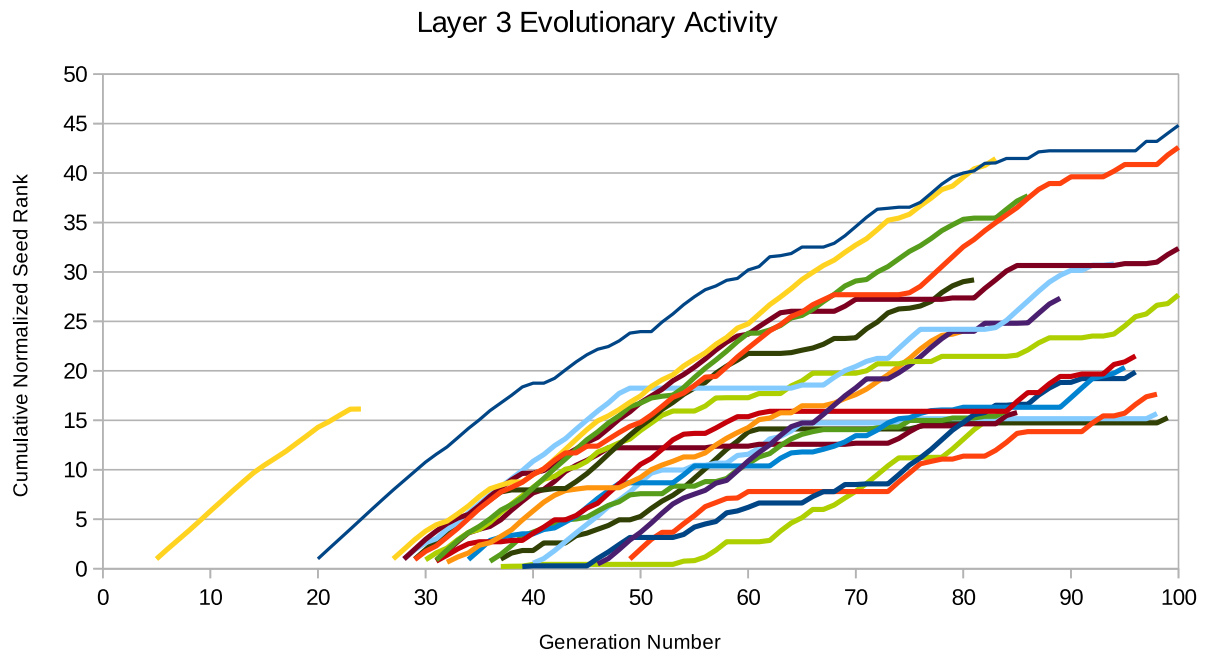


Figure 14. Layer 3 has some features that are similar to Layer 1: All of the successful individuals begin their careers early (before generation number 50) and many of them have long careers. On the other hand, it has some features that are similar to Layer 2: Much of the action is taking place here later than it did in Layer 1.

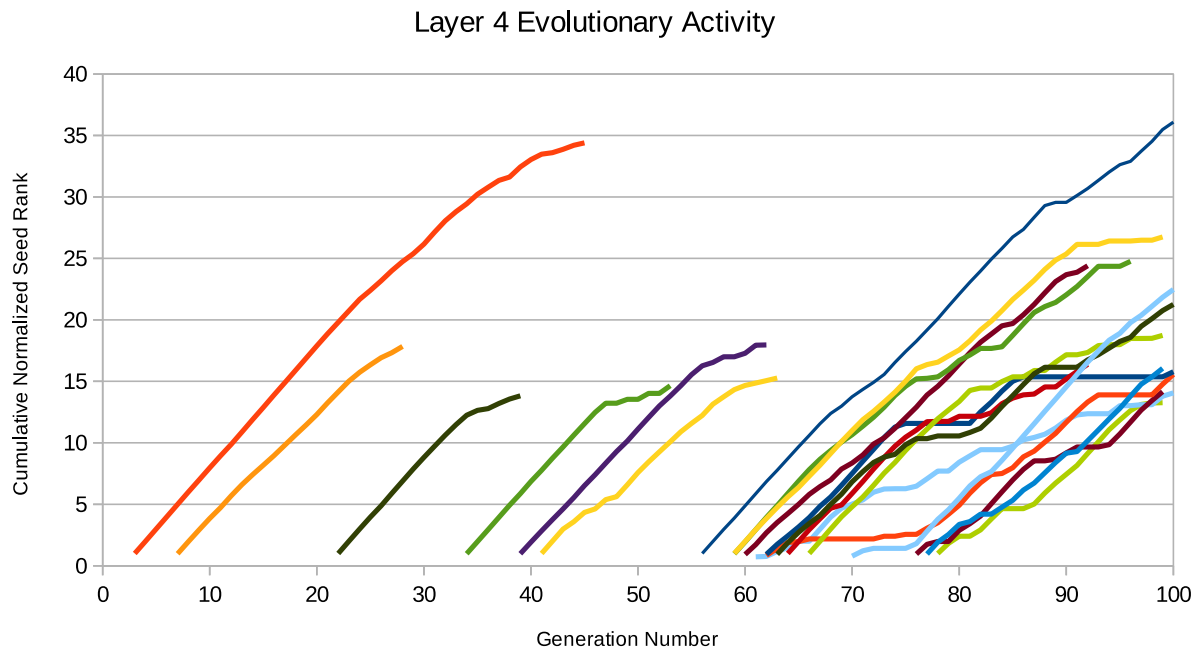


Figure 15. In Layer 4, the greatest concentration of activity begins after generation 60. In Layer 1, we saw an initial burst of activity that soon settles into stagnation. In Layer 4, we see a few early pioneers followed by increasingly dense activity.

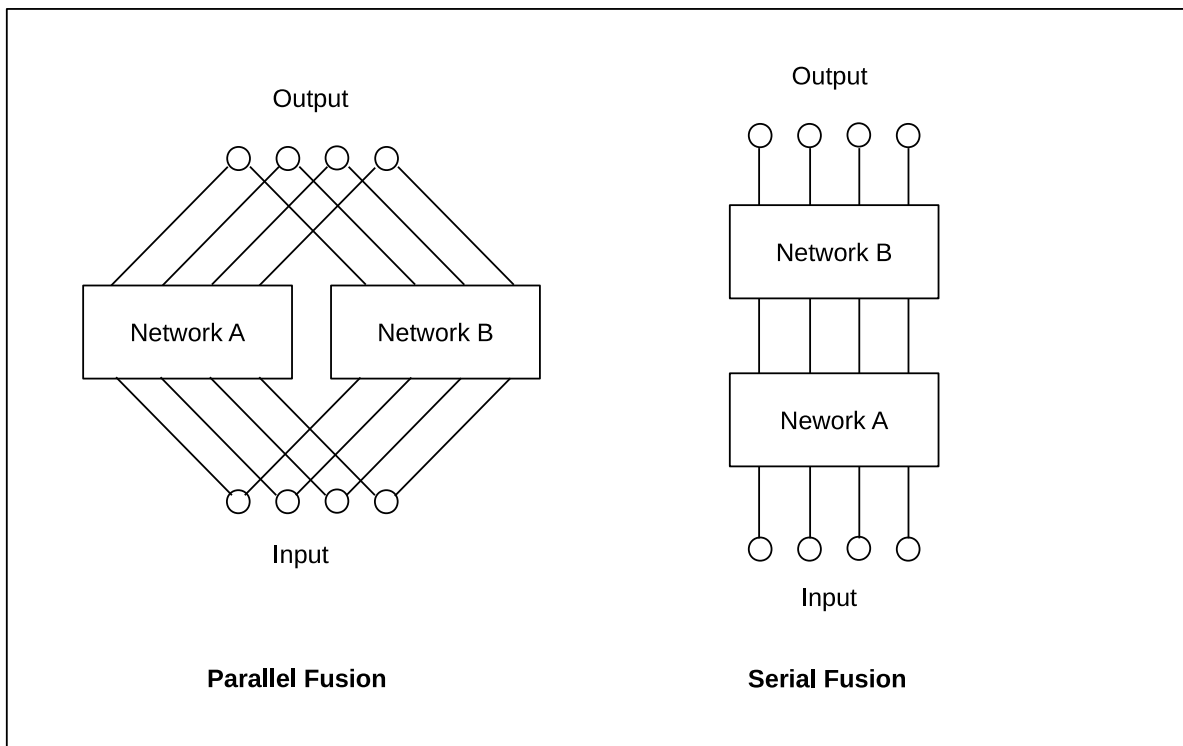


Figure 16. Fusion could be applied to neural networks by combining them in parallel or serial.

Table 1. This table lists the parameters used in Model-T and their values for the experiments presented in Section 4.1. With four layers (experiment_type_num = 1, ..., 4) and twelve runs for each layer, there are $4 \times 12 = 48$ settings for the random number seed. One generation is defined as the birth of pop_size children, therefore the number of children born in one run is pop_size \times num_generations = 20,000. The number of runs is not a parameter in the model; each run begins by starting a new instance of Golly.

Parameter Names	Parameter Values	Used in Layers
experiment_type_num	1, ..., 4	1, 2, 3, 4
random_seed	1, ..., 48	1, 2, 3, 4
pop_size	200	1, 2, 3, 4
num_trials	2	1, 2, 3, 4
num_generations	100	1, 2, 3, 4
min_s_xspan	5	1, 2, 3, 4
min_s_yspan	5	1, 2, 3, 4
s_xspan	5	1, 2, 3, 4
s_yspan	5	1, 2, 3, 4
max_area_first	120	1, 2, 3, 4
max_area_last	170	1, 2, 3, 4
seed_density	0.375	1, 2, 3, 4
width_factor	6.0	1, 2, 3, 4
height_factor	3.0	1, 2, 3, 4
time_factor	6.0	1, 2, 3, 4
tournament_size	2	1, 2, 3, 4
elite_size	50	1, 2, 3, 4
mutation_rate	0.01	1, 2, 3, 4
prob_flip	0.6	2, 3, 4
prob_grow	0.2	2, 3, 4
prob_shrink	0.2	2, 3, 4
min_similarity	0.8	3, 4
max_similarity	0.99	3, 4
prob_fission	0.01	4
prob_fusion	0.005	4

Table 2. This table tests the statistical significance of the differences in the fitness curves in Figure 6. Each layer (each curve) is summarized by the average fitness over a run, yielding a sample of twelve values, one value for each of the twelve runs of a layer. We then compare the fitness curves for all possible pairs of layers, using a two-tailed Welch t-test for samples with unequal variance (heteroscedastic variance). All of the pairs of curves in Figure 6 are significantly different, except for layers 2 and 3 (the variable asexual layer and the sexual layer).

Layers to Compare	p-value	p-value < 0.05
Layer 1 vs Layer 2	1.81E-13	Yes
Layer 1 vs Layer 3	1.35E-06	Yes
Layer 1 vs Layer 4	1.83E-15	Yes
Layer 2 vs Layer 3	7.04E-02	No
Layer 2 vs Layer 4	2.54E-04	Yes
Layer 3 vs Layer 4	2.35E-04	Yes

Table 3. This table looks at the correlations between fitness, area, density, and diversity (as displayed in Figures 6 to 9). We evaluate the statistical significance of the correlations using a two-tailed Student t-test for Pearson correlations. All of the correlations are statistically significant, except for the correlation between density and diversity. In this table, each correlation is based on comparing two samples of 48 values each (whereas Table 2 compares two samples of 12 values each).

Feature 1	Feature 2	Correlation	p-value	p-value < 0.05
area	density	-0.66	4.25E-07	Yes
area	diversity	0.73	3.31E-09	Yes
area	fitness	0.86	4.41E-15	Yes
density	diversity	-0.22	1.27E-01	No
density	fitness	-0.72	7.22E-09	Yes
diversity	fitness	0.48	5.02E-04	Yes

Table 4. This table summarizes the final generations of the layers. For Layers 1 to 4, the final generation is the 100th generation. For Layer 4XL, the final generation varies from generation 39 to 62.

Layer	Fitness	Area	Density	Diversity
1	0.802	25.0	0.532	0.0092
2	0.909	85.2	0.315	0.0149
3	0.886	75.5	0.363	0.0130
4	0.930	118.8	0.327	0.0129
4XL	0.953	6499.7	0.109	0.0790

Table 5. This table gives the scores of each of the layers when competing against human-designed patterns of comparable area. Given that Layer 4XL has an average area of about 6,500 in its final generations, we test the layers against all human-designed patterns that have an area of 10,000 or less, which is a total of 29 patterns. Each human-designed Golly pattern competes 20 times against the fittest seed in the final generation of each run of the given layer. For example, there are 12 runs for Layer 1, so 240 (12×20) Immigration Games are played with each human-designed Golly pattern. We declare that Layer 1 is the winner of the competition if it wins more than half of the games (more than 120). In the table, 1 indicates a win and 0 indicates a loss.

Golly Pattern File Name	Area	Density	Layer 1	Layer 2	Layer 3	Layer 4	Layer 4XL
agar-p3.rle	3456	0.375	0	0	0	1	1
herringbone-agar-p14.rle	2304	0.292	0	0	0	0	1
pulsars-in-tube.rle	136	0.529	0	1	0	1	1
spacefiller.rle	1274	0.157	0	0	0	0	0
vacuum-cleaner.rle	8730	0.050	0	0	0	1	1
acorn.lif	21	0.333	1	1	1	1	1
ark1.rle	928	0.017	0	0	0	0	1
ark2.rle	2332	0.008	0	0	0	0	1
blom.rle	60	0.217	1	1	1	1	1
iwona.rle	420	0.045	0	1	1	1	1
justyna.rle	374	0.053	0	1	1	1	1
lidka-predecessor.rle	135	0.096	0	1	1	1	1
natural-LWSS.rle	40	0.300	1	1	1	1	1
rabbits-relation-17423.rle	36	0.278	1	1	1	1	1
rabbits-relation-17465.rle	24	0.458	1	1	1	1	1
rabbits.lif	21	0.429	1	1	1	1	1
temp-pulsars-big-s.rle	64	0.500	1	1	1	1	1
die658.rle	400	0.288	1	1	1	1	1
line-puffer-superstable.rle	4992	0.176	0	0	0	0	0
line-puffer-unstable.rle	1683	0.251	0	0	0	0	0
pi-fuse-puffer.rle	1827	0.211	0	0	0	1	1
puffer-2c5.rle	8400	0.046	0	0	0	0	1
puffer-train.rle	90	0.244	0	1	1	1	0
heisenblinker-30.rle	5032	0.044	0	0	0	1	1
heisenburp-46-natural.rle	2346	0.052	0	1	1	1	1
eaters-misc.rle	4851	0.065	0	1	0	1	1
random.rle	9604	0.438	0	0	0	0	1
ss-eaters.rle	3026	0.050	0	1	1	1	1
stripey.rle	4290	0.467	0	0	0	0	1
Average	2307	0.223	28%	55%	48%	69%	86%