Evolution of a Botanical Development System in 3D Euclidean Space

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Abstract

This paper describes an alternative trial to simulate evolutionary and developmental process of multi-cellular plants in 3D Euclidean space. Starting from a seed on the surface of the ground, each individual grows by spawning daughter cells of each active cells. The rule set of growth is encoded as a gene on the chromosome that indicates the orientation of daughter cell and state transition. The model is very simple but includes a type of metabolism for absorbing water at the root underground and photosynthesis at the cells above the ground. Through the computer simulation of evolutionary process by a genetic algorithm with a fitness measure given by the number of cells, a variety of phenotypic shapes which similar to moss have emerged.

Introduction

It is a feasible view that the growth of multi-cellular plants is realized by an iteration of cell division, cohesion, enlargement, reformation, and death. These activities are triggered by some chemical and physical events on the cell itself guided by the genetic information on the chromosomes it contains. Through a lot of efforts of biologists, some details of species-specific developmental process have been revealed, and the wide variety of complicated strategies of development aresometimes surprising. To deepen our understanding of the foundations of life, it is also important to build mathematical models of biological activities on a more abstract level, while investigating concrete organisms in more detail.

One of the remarkable mathematical models of growth of multi-cellular plants is the *L-system* (Lindenmayer 89), which provides a formal method with a type of *rewrite rule set* to describe recursive processessuch as growth. It has been widely used to draw computer graphics images of many types of plants of both real and imaginary species. L-system and its extended framework are very useful not only for drawing but also for understanding formal aspects of morphology by clarifying how wide a variety of shapes a simple rule set can generate.

In real biological organisms, the rule set for developmental processes is encoded on the chromosomes: the
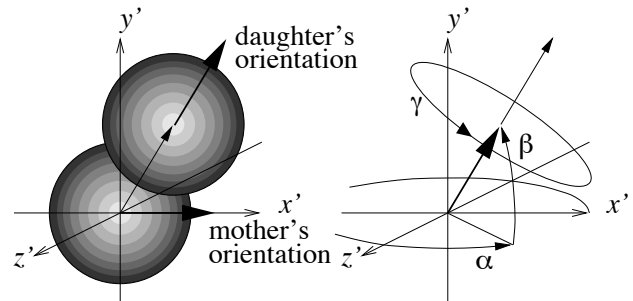

Figure 1: Spawning a daughter cell in 3D space.

genotype, which has changed from simple to sophisticated through billions of years of evolutionary processess by adapting to its environment. It will be helpful to combine models of evolution and development from the stand point of *Artificial Life* in which we move towards the intrinsics of life through synthesis. We designed a model of the evolution of the development process, and examined it via computer simulation.

For real natural organisms, various types of features of physical and chemical entities and events affect the cell activities. To avoid the complicated task to build a realistic model, many types of physical features are ignored such as gravity, shade, weather, seasons, and so on. Our model presented below does not use a discrete grid world, but a continuous three-dimensional Euclidean space because it theoretically provides an infinite number of degrees of freedom to form a shape. This feature is important to investigate evolution of sophisticated strategies, although it consumes more computational resources.

In the following sections, we examine morphology, metabolism, and evolution of our proposed model, and then describe experimental simulations, the results and close with some remarks.

Morphology

At an abstract level in the developmental process, each cell decides its action according to the rules on the gene conditioned by its own status. For a mathematical model of cell division, we assume that the orientation of di-

vision is determined by two kinds of information: the internal state, and the genetic information the cell contains. Because of the difficulty of simulating all of these complicated features, we assumed that (1) the cell shapae be a sphere, (2) the cell size is constant, (3) cells do not split but spawn daughter cells at an adjoining side, (4) cells do not move from the original position where they were born, (5) cells spawn daughter cells only if there is enough empty space, and (6) each cell has its own direction as one of the attributes.

Each cell has an attribute indicating whather it is active or inactive. An active cell intends to spawn its daughter cell at an adjoining side where the gene corresponding to the current state designates the relative orientation. The internal states are represented by four bit integers of which the most significant bit indicates active (=0) or inactive (=1). The conditional part of the development rule contains the current internal state. The action part contains the relative orientation from the cell's direction to spawn a daughter cell, the daughter's initial internal state, and next internal state of itself. Each information to decide the orientation of a daughter cell requires a triplet of angles in 3D space as shown in Figure 1. The total action part of each rule includes two more four-bit integers and three eight-bit integers, that is, $4 \times 2 + 8 \times 3 = 32$ bits. Thus, one genome consists of $32 \times 8 = 256$ bits. Actually, we employ a look-up table to represent these rules as shown in Figure 2.

On the initial seed, the state is zero, and the orientation is vertically upward.

Metabolism

The above model is very simple, but we added a type of metabolism to

1. absorb water from root,

2. photosynthesize glucose for cells above ground,

3. evaporate water from cells above ground,

4. move water and glucose between mother and daughter cell, and

5. consume an amount of water and glucose when spawning.

Each cell keeps track of the amount of water W and glucose G it contains. These parameters are normalized and range from zero to one. A cell under ground absorbs water according to

$$\Delta W = P_w(1.0 - W) \qquad (1)$$

for each step, where P_w is a constant. A cell above ground looses water through evaporation by
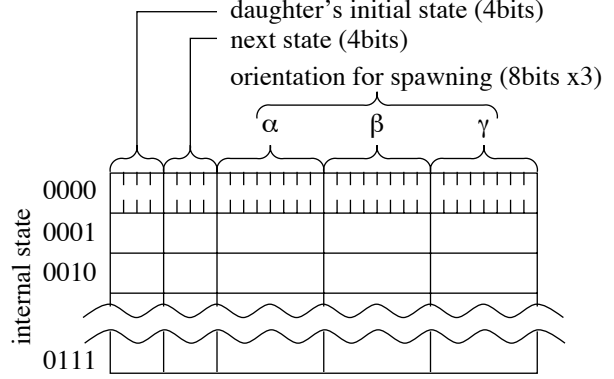
$$\Delta W = -P_v W \qquad (2)$$

Figure 2: Form of chromosome and gene.

for each step, where P_v is a constant. It also increases glucose content through photosynthesis by

$$\Delta G = P_g(1.0 - G) \qquad (3)$$

for each step, where P_g is a constant. Both water and glucose move between mother cell and daughter cell according to

$$\Delta W_m = -\Delta W_d = M_w(W_d - W_m) \qquad (4)$$
$$\Delta G_m = -\Delta G_d = M_g(G_d - G_m) \qquad (5)$$

for each step, where M_w and M_g are constants, W_m and G_m are the values of the mother's parameters and W_d and G_d are the daughter's parameters. Each cell can spawn its daughter cell only when it is active, if it has enough water and glucose ($W > \theta_w, G > \theta_g$), and if there is enough empty space for the daughter. After spawning the daughter, water and glucose decrease by

$$\Delta W = -\theta_w \qquad (6)$$
$$\Delta G = -\theta_g \qquad (7)$$

where θ_w and θ_g are threshold values.

Photosynthesis of glucose consumes water via its chemical reaction

$$6CO_2 + 12H_2O \rightarrow C_6H_{12}O_6 + 6O_2 + 6H_2O . \qquad (8)$$
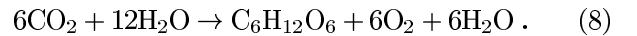
However we ignore this phenomeon here because a decrease of water through evaporation can account for this. We also ignored other materials such as nitrogen and other essential elements, because they will not affect the shape as the result of the development process in this simple model.

Evolution

The evolutionary process of natural organisms strongly depends on inter-species interactions such as the food web. Starting from the simplest settings, we examined evolution by a Genetic Algorithm (GA) (Goldberg 89) with pre-defined fitness function.
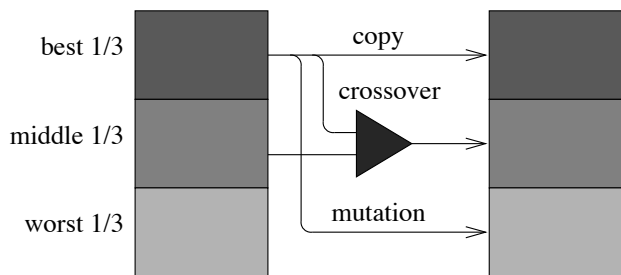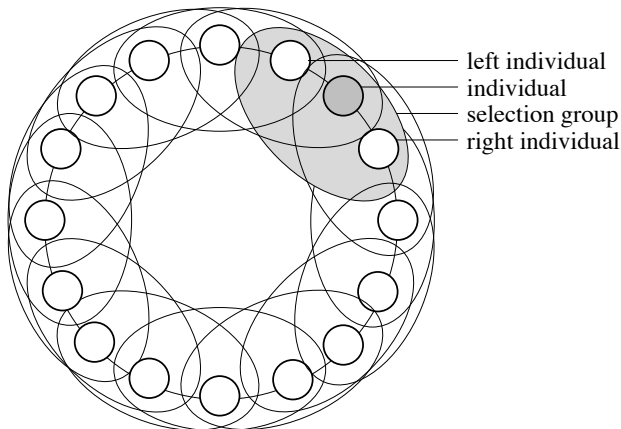
Figure 3: *1/3 selection.*

Figure 4: Local selection using ring.

We use two types of generational GA in which every individual in the population is initialized by a random genotype and is tested through selection process to decide whether it remains in the next generation or not. First, to accelerate the evolutionary process, we did not employ ordinary selection algorithms widely used in GAs (such as roulette-wheel selection, ranking selection, or any other probability-based selection mechanism) but instead used a *1/3 selection* algorithm as shown in Figure 3. In this algorithm:
(1) The best third of the population remains in the next generation without any modification of genotype,
(2) the middle third of the population is replaced with individuals generated using crossover operation between the best third individuals and the middle third individuals, and
(3) the worst third of the population is replaced with mutants of the best third individuals.

In our second type of GA, we use a type of local selection where individuals are arranged along a ring as shown in Figure 4. The algorithm is similar to the 1/3-selection described above, but selection is done among local neighbors, that is:
(1) after evaluating the fitness, each individual obtains for comparison the values of its nearest (left and right) neighbors.
(2) it remains in the next generation without any modi-

fication if it is the best among these three individuals,
(3) it is replaced with the one generated by crossover with the best one; and
(4) it is replaced with a mutant of the best one.

As some researchers pointed out, GAs with local selection have an advantage to approach the global optimal solution because they can keep more diversity in the population than global selection (Sarma 97). It is better not only as an optimization algorithm but also as a model of natural selection, because the competition among real organisms must always be local.

Experiments

Using as fitness measure the number of cells after allowing growth for a constant number of steps, the results of our simulations showed a wide variety of phenotypic shapes as shown in Figure 5.

State transition networks of development rules for individuals can be drawn as shown in Figure 6, viewing the active part of gene as an automaton. Networks in Figure 6 correspond to phenotypes shown in Figure 5. From this figure, we can see that the genotype of larger phenotypes includes cyclic transitions which can produce a recursive structure of development.

Evolutionary processes using fifty distinct random number sequences for each selection strategy are shown in Figure 7. It is clear that local selection leads to better fitness more often than global 1/3-selection.

Conclusion

We designed a model to study the evolution of botanical development in 3D Euclidean space and a simple metabolism, and examined the evolution with two types of selection algorithms. Via experiments described above, we observed that a variety of phenotypic shapes reflecting effective strategies for efficient body growth have emerged. These shapes resemble a kind of moss because they tend to spread on the ground. Comparing two different strategies for selection, local selection appears to be better than global selection for reaching better solutions.

The results of the simulations presented above are only a sample of forms we found. Though one might conclude that this provides possible evidence for the diversity of forms that emerged through evolution, we should investigate more thoroughly the effects that different parameters have on the process of evolution, before more fruitful results can be obtained from the point of view of biology.

We are also considering some directions to extend the model described above, such as physical interaction, chemical diffusion, differentiation, life cycle and ecology. A combination of this research with other morphological research such as (Fleischer 96) and (Onitsuka 96), and artificial botany such as (Colasanti 97) might provide the inspiration for progress with this research in the
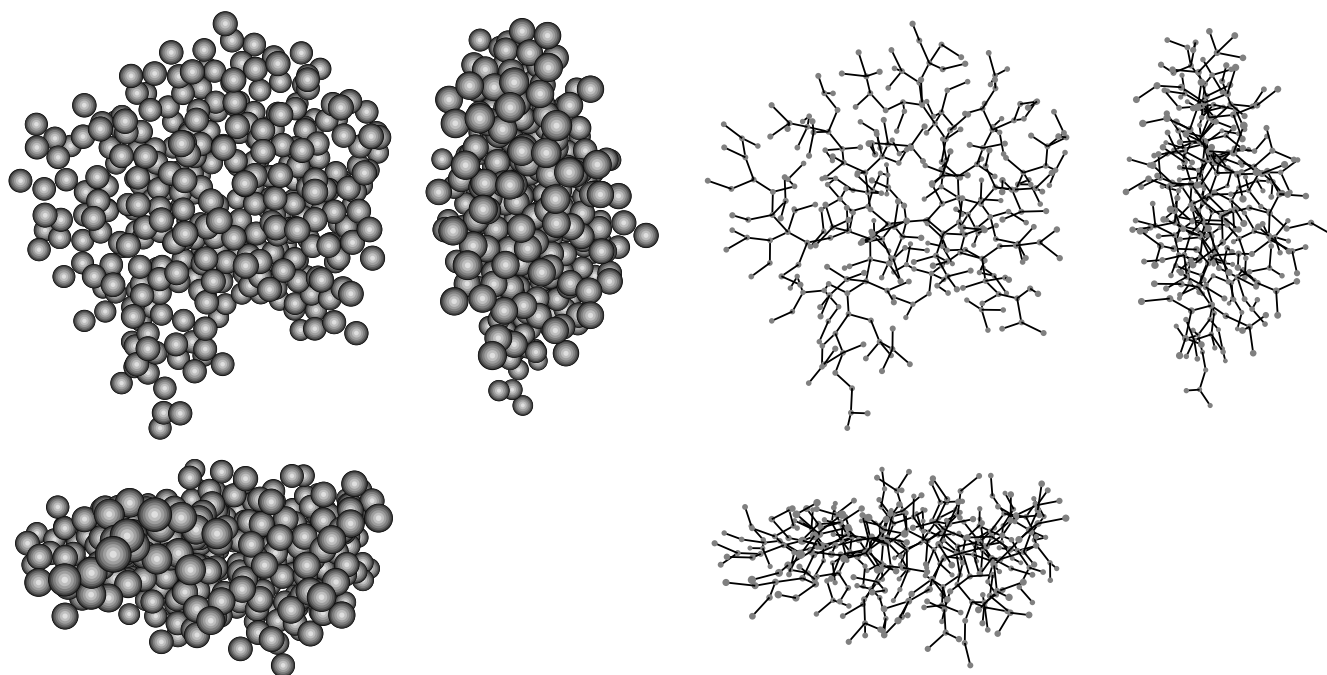
Global 1/3 selection, 378 cells.
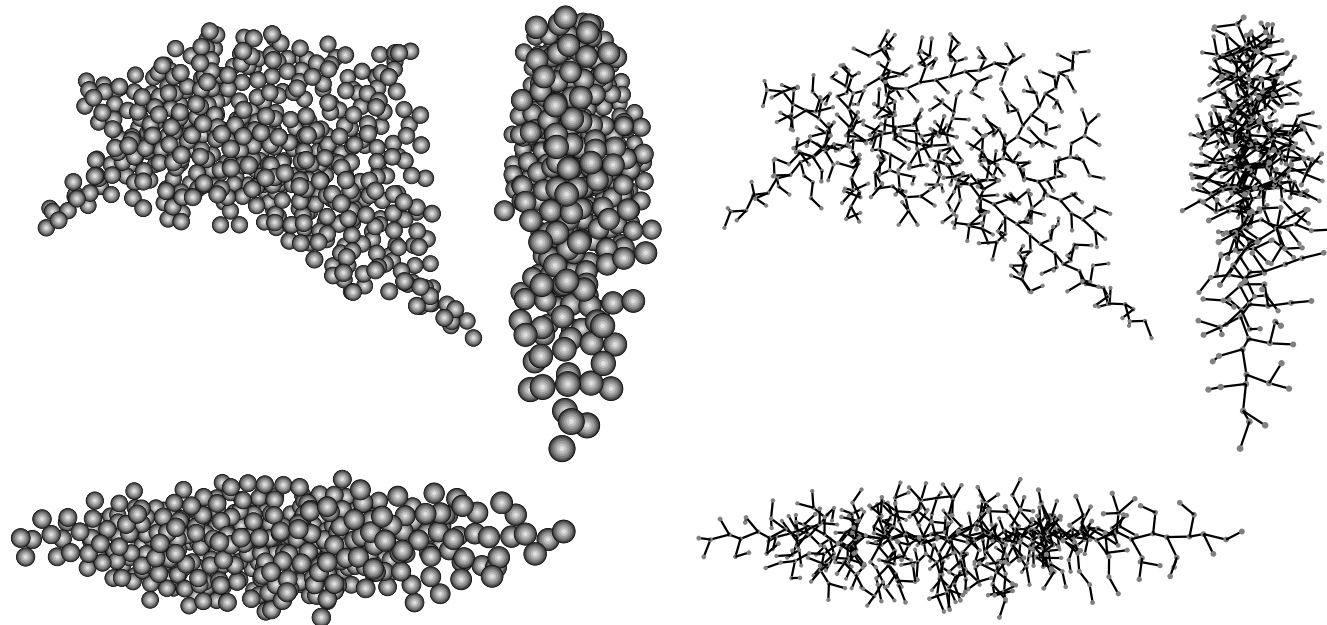
Local selection, 542 cells

Figure 5: Typical phenotypes that emerged from evolution through 500 generations in 400 steps per one generation, whith a population size 36. Cells are drawn as spheres in the lef thand figure, while line segments between the centers of mothers and daughters are drawn in the right hand figure. The upper left figure of each is the top view, the right figure is the right view, and lthe ower figure is the front view. The parameter settings are: $P_w = 0.1, P_v = 0.01, P_g = 0.1, M_w = 0.02, M_g = 0.02, \theta_w = 0.2, \theta_g = 0.2$.
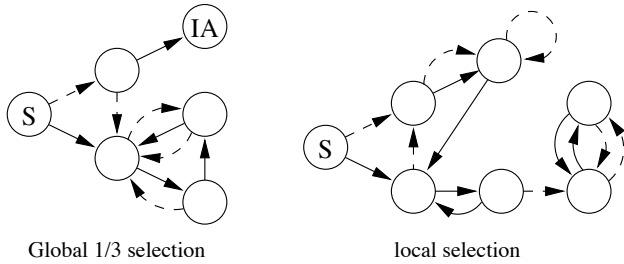
Global 1/3 selection   local selection

Figure 6: State transition networks of development rules produced through evolution. S indicates the initial seed, and IA indicates inactive. Dashed arrows indicate transitions from mother to daughter. These networks are generated for the phenotypes shown in Figure 5.

near future.

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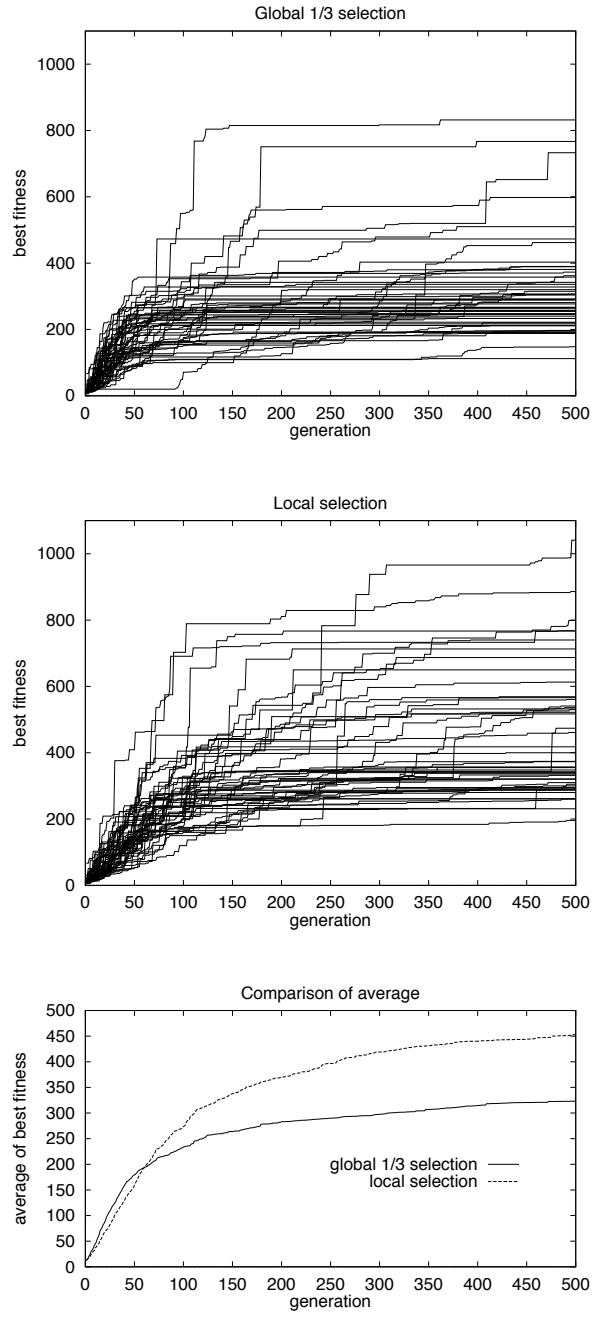
Figure 7: Evolutionary processes of fifty distinct random number sequences, and comparison between average values of best fitness of global and local selection.