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Automatic Creation of 3D Artificial Flowers with Interactive Evaluation on Evolutionary Engine

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Abstract— **Directed graph and Lindenmayer system (L-system) are two major encoding methods of representation to develop creatures in an application field of artificial life. It is difficult to structurally define real morphology using the L-systems which are a grammatical rewriting system because they represent genotype as loops, procedure calls, variables, and parameters. This paper defines a class of representations called structured directed graph and interactive genetic algorithm for automatically creating 3D flower morphology. The experimental results show that natural flower morphology can be created by the proposed method.**

I. Introduction

Artificial life (A-life) is the study of life and life-like processes having autonomy, adaptation, self-replication and self-repairing, and literally a field that seeks to increase the role of synthesis in the study of biological phenomena [1]. Among the representative applications for A-life research, a study of creating artificial creatures using evolutioniary algorithm is actively promoted. It can automatically create artificial characters having action or morphology satisfied with user, and has also advantage to generate new population that is not predicted by user. In recent years, A-life research has fostered new applications in the computer graphics, creating of game characters, design, arts and edutainment [2].

The representative method of genotype for creating populations using evolutionary algorithm are directed graph and Lindenmayer system (L-system). Each of creatures is represented by composition of nodes and edges in directed graph that is proposed by K. Sims for creating 3D creatures [3]. It is convenient to define morphological structure of population more quickly and easily and users can intuitively know about real morphology of genotype represented by directed graph.

L-systems pioneered by Lindenmayer are a grammatical rewriting system in which the rewriting rules are applied in parallel to all symbols in a string [4]. The sequence in L-system begins with the first rule and the sequences of strings below it are the strings generated after each iteration of parallel replacement. The last string of symbols is the assembly procedure used for generating a creature. L-systems specify creatures in terms of local growth rules and can easily generate artificial creatures of symmetric structure.

In this paper, we present a method for automatically creating creatures using genotypic representations as a kind of structured directed graph and interactive genetic algorithm.

II. Creating 3D Artificial Flowers

L-system has been worked for generating plants or flowers by J. Pollack and P. Prusinkiewicz [5][6]. L-systems may be intuitive for biologists since they easily specify plants through parameters and iterations of local growth rules, but from the modeling point of view the global characteristics of plants have to be dealt directly with. Also, it is difficult to apply the conventional evolutionary algorithm since humans' emotional evaluation is required for creating more natural morphology of flowers. Therefore, in this paper we present the structured directed graph as the genotypic representation of real morphology and interactive genetic algorithm (IGA) for automatic creation of natural flower morphology. Figure 1 shows the entire process of the proposed method creating genotype of population and evaluating through interactive genetic algorithm.

A. Structured Directed Graph

The structures of populations are composed of nodes and edges in directed graph. Each node in the directed graph contains the information describing rigid part such as dimension and color of each part, and each edge also contains the information of position and orientation connecting each part and the sum of edges in each part. Figure 2 shows the genotypic representation through directed graph.

Directed graph $DG = (V, E)$ has a set of vertices and a set of edges between the vertices. Each vertex and edge in directed graph described in figure 2 is defined as follows.

$$V(DG) = \{stem, twig, sepal, petal, leaf\}$$

$$E(DG) = \{< stem, stem >, < stem, twig >, < stem, sepal > \\ < twig, twig >, < twig, leaf >, < sepal, petal >\}$$

We represent adjacency matrix of DG to 5×5 matrix because $DG = (V, E)$ and $|V| = 5$, and each element of this matrix is defined as follows.

$$a_{ij} = \begin{cases} n, & (v_i, v_j) \in E(DG) \\ n/r, & (v_i, v_i) \in E(DG) \\ 0, & \text{otherwise} \end{cases}$$

where n and r represent the number of edges and recursion count respectively.

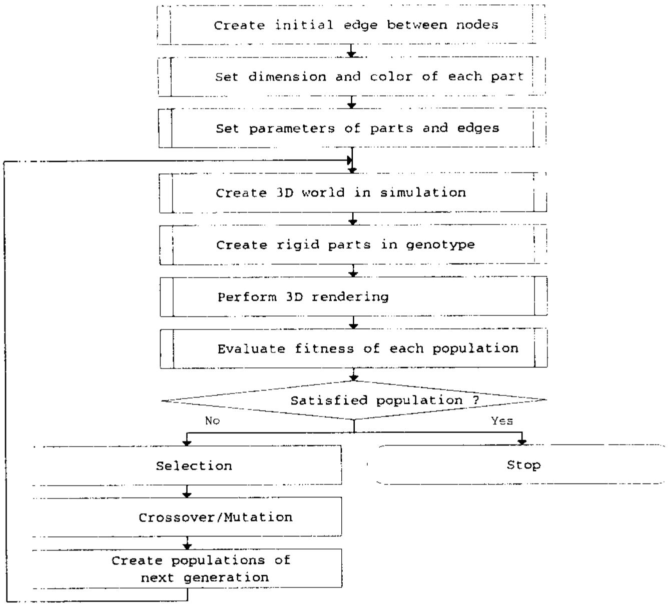

Fig. 1. Process of the proposed method.

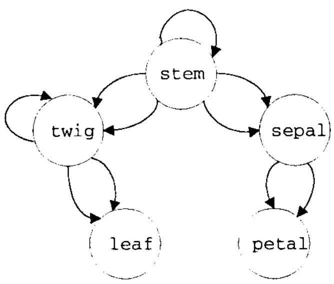

Fig. 2. Genotypic representation of flower.

B. Modeling 3D Morphology

The position and orientation of each part in the representation of phenotype are defined by Newton's law, and a more efficient method for obtaining rotation about a specific axis is to use a quaternion representation for the rotation transformation. In a three-dimensional homogeneous coordinate representation, a point is translated from position $P = (x, y, z)$ to position $P' = (x', y', z')$ by using the matrix operation, and this matrix representation is equivalent to the three equations

$$x' = x + t'_x, \quad y' = y + t'_y, \quad z' = z + t'_z$$

where t'_x, t'_y and t'_z are translation distances for the coordinate directions x, y, and z and assigned any real values. We can get new position by using the following matrices respectively.

$$\begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & cos(\theta) & -sin(\theta) & 0 \\ 0 & sin(\theta) & cos(\theta) & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} cos(\theta) & -sin(\theta) & 0 & 0 \\ sin(\theta) & cos(\theta) & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

node	stem	twig	sepal	petal	leaf
stem	3	2	1	0	2
twig	0	2	1	0	4
sepal	0	0	0	10	0
petal	0	0	0	0	0
leaf	0	0	0	0	0

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node	stem	twig	sepal	petal	leaf
stem	2	2	1	0	0
twig	0	2	1	0	2
sepal	0	0	0	12	0
petal	0	0	0	0	0
leaf	0	0	0	0	0

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node	stem	twig	sepal	petal	leaf
stem	2	2	1	0	2
twig	0	2	1	0	2
sepal	0	0	0	10	0
petal	0	0	0	0	0
leaf	0	0	0	0	0

node	stem	twig	sepal	petal	leaf
stem	3	2	1	0	0
twig	0	2	1	0	2
sepal	0	0	0	12	0
petal	0	0	0	0	0
leaf	0	0	0	0	0

Fig. 3. An example of crossover operation in IGA.

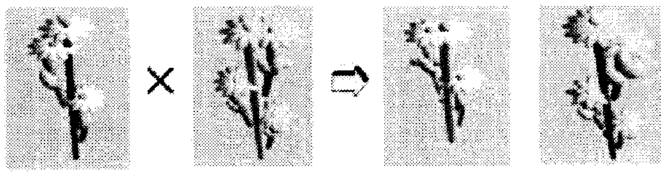

Fig. 4. An example of phenotypic representations with crossover operation.

$$\begin{bmatrix} cos(\theta) & 0 & -sin(\theta) & 0 \\ 0 & 1 & 0 & 0 \\ sin(\theta) & 0 & cos(\theta) & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

Using a quaternion representation of orientation in three-dimension, we can get w, x, y, and z values in $quaternion(w, x, y, z)$ by the following equations if the position $P = (x', y', z')$ is rotated about y axis and rotation angle θ [7].

$$w = cos(\frac{\theta}{2})$$

$$x = x' \times sin(\frac{\theta}{2})$$

$$y = y' \times sin(\frac{\theta}{2})$$

$$z = z' \times sin(\frac{\theta}{2})$$

C. Interactive Genetic Algorithm

GA proposed by John Holland in early 1970s applies some of natural evolution mechanisms such as crossover, mutation, and selection of the fittest to optimization and machine learning. GA provides very efficient search method working on population, and has been applied to many problems of optimization and classification [8]. In IGA that is the similar method as GA except fitness evaluation, user evaluates fitness to each individual in a population. IGA can interact with user and can inspire user's emotion or preference in the course of evolution [9]. Therefore, IGA is suitable for solving problems that cannot be easily solved by GA, like the evaluation of natural flower morphology in this paper. We fix the number of nodes with pre-defined parts of detail structure in genotypic

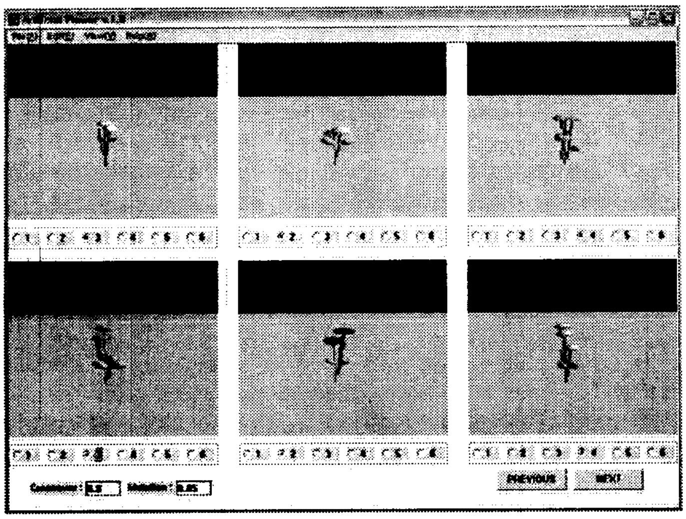

Fig. 5. Interface of the proposed system.

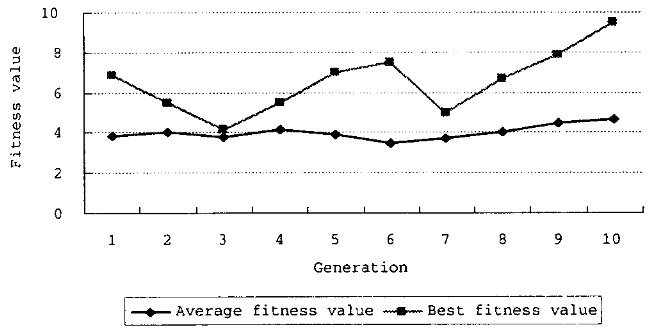

Fig. 6. Flower fitness changes on searching for natural flower.

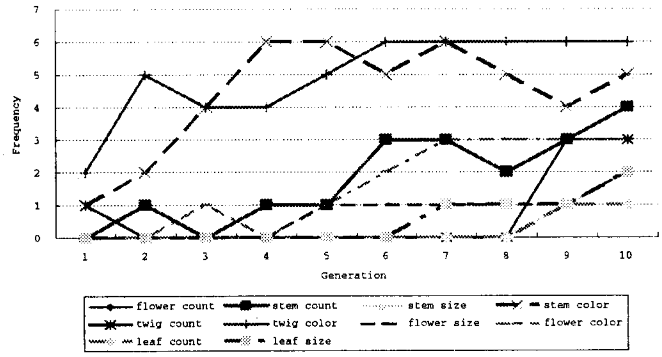

Fig. 7. The variation in generations of frequency of schemas.

representation for IGA operations, and can create various morphologies from basic structure of flower by changing values of parameters in edges and nodes. For example, if (stem, twig) and (sepal, petal, leaf) of nodes having 5 nodes composed of stem, twig, sepal, petal, and leaf in directed graph are crossed over, each node and the parameters about nodes and edges of selected 2 individuals are crossed over. The relations of nodes and edges in directed graph are represented by matrix, and an example of IGA is shown in figure 3 and figure 4 using this matrix.

III. Experimental Results

In this section we present the experimental set-up to generate flower morphologies by the proposed method. First of all, we define the genotype of flower structure by directed graph. Secondly, we represent each individual acquired to get by changing parameters in edges and nodes of each part, and evaluate each individual from IGA up to last generation. We use API program named 3D MathEngine that is now used in commercial to represent morphology and locomotion of individuals [10]. Using this program, we can represent and define position and orientation in 3D space by applying Newton's physical law. We use fundamental shapes given by MathEngine such as cube, cylinder, ellipsoid, and corn for each part of morphology.

We have developed the interface of the prototype system as shown in figure 5, and in IGA we have defined 6 individuals, 10 generations, and 5 levels of fitness evaluation. Nodes in directed graph are divided into 5 parts which are stem, twig, sepal, petal, and leaf, and each node is connected with edges by randomly generated parameters. In this experiment, the conditions of IGA is given as follows.

- The number of individuals is 6,
- The generation of individuals is 10,
- The crossover rate is 80%,
- The mutation rate is 5%,
- The fitness value is a rate on a scale of 1 to 10 (the worst to the best correspond to 1 to 5), and
- IGA evaluation by 13 subjects

Since IGA differs from general GA due to humans" subjective evaluation, it is difficult to show the convergence of IGA. Therefore, we have carried out convergence test, schema analysis, and Shéffe's pair-comparision to evaluate the performance of this system.

A. Convergence Test

Convergence test uses the variation of mean values of fitness evaluation by subjects. To show the convergence of the method as an experimental result, we have requested 13 subjects to find natural flower morphology using this system. Figure 6 shows the variations of fitness on average and the best, while subjects are searching for more natural morphology. In this figure, x-asis is the number of generations and y-axis is fitness values from 1 to 10. By the iteration of generation in IGA, we can observe that more natural flower is generated.

B. Analysis of Schemas

This analyzes the frequency of each part of individuals in the last population, which shows how the best characteristic schema is inherited from IGA. Figure 7 shows the variation in each generation of frequency of schemas included in approximate solution. We have defined schemas as the elements composed of each part such as shape, color, and count of

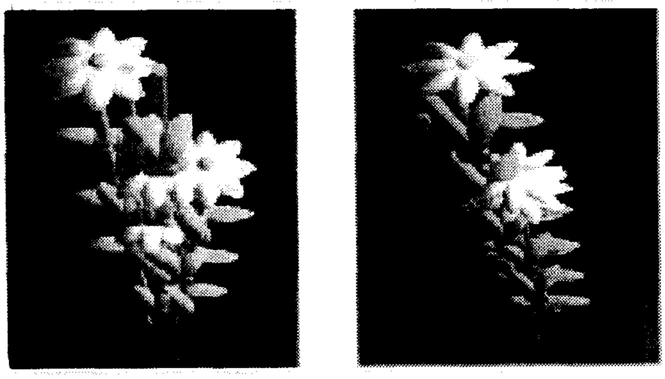

Fig. 8. Examples of natural flower.

nodes in directed graph. Each node consists of stem, twig, sepal, petal, and leaf, and morphology of flower may differ each other by defined schemas. We have randomly selected an individual in those of last population through the evaluation of convergence test, and the figure shows the variation of each schema in selected individuals through generations. In this figure, we can notice that the characteristic schemas which do not appear in individuals of the first generation are increased. For analyzing these schemas, we select any individual randomly in those of the course of IGA evaluating more natural look. Next, we suppose the approximation is the individual acquired to the best fitness value in the last population. Lastly we analyze schemas in selected individual through the IGA process. In this experiment, since we define ellipsoid shape for leaf, petal, and sepal and cylinder shape for stem and twig, the schema for shape of each part is determined by size. Figure 8 shows examples of natural flower selected in the last population for this analysis.

C. *Satisfiability Test*

We have used paired comparison of Shéffe for this test of how much the user is satisfied with the system performance. It prevents subjects from evaluating searched morphology too subjectively by requesting them to compare each morphology with some relatively objective ones, pair to pair. For this test, subjects randomly select individuals which are created by this system, and relative criteria of samples are selected from those of selected individuals. Firstly, we have randomly selected 200 sample individuals from entire search space, and requested 3 subjects to evaluate the sample morphology with more natural look into 5 degrees from 1 to 5. From their average scores, 10 most natural morphologies are selected as criteria of evaluation.

Next, we have requested 13 subjects to select natural flower in the last population using this system. After 10 generations, 13 subjects have selected the best one from the last population, and compare it with the criteria made by an earlier process, pair to pair. This score has 7 degrees from -3 to 3, and this result is analyzed statistically. Figure 9 shows the degree of user's satisfaction at 95% and 99% of reliability, respectively. If this system is not converged using IGA, the selected result

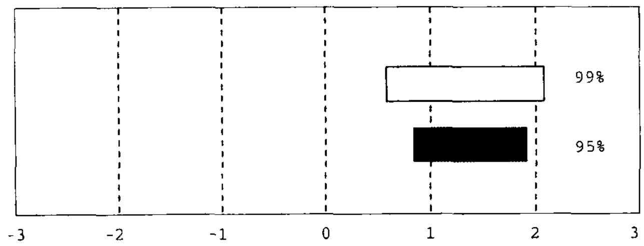

Fig. 9. The degree of satisfaction at 95% and 99% of reliability.

by 13 subjects and before criteria would be similar, and degree of reliability approaches 0. We can observe relatively good satisfaction to the selected morphology since we get 1.3 at 95% and 99% of reliability.

IV. Conclusion

We presented an automatic creation method of morphology by using IGA which is suitable for sensitive problems due to humans' evaluation, and a creation of natural morphology to real character with structured directed graph which can create structure similar to real shape. We have created artificial flowers in three-dimensional world with the evoluationary processes.

We can reproduce the best characteristic parts by iteration of nodes in genotypic representation using directed graph. Moreover, in contrast to previous approaches our system lets users get direct feedback because it is represented structurally by directed graph. In future work we will focus on a representation of natural locomotion and the creation of other morphologies using directed graph.

Acknowledgment

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