SIVA: ARTIFICIAL LIFE BASED ON PROGRAMMED SELF-DECOMPOSITION MODEL

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In 1987, Oohashi et al. proposed a biological hypothesis "programmed self-decomposition (PSD) model"[3], which assumes that a mechanism of decomposing itself and restoring substances and space to the environment is intrinsically programmed in every cell of terrestrial life. I have developed a simulator "SIVA-2 (Simulator for Individuals of Virtual Automata 2)" as an application for AP1000+ and examined the effects of the self-decomposition mechanism through computer simulations of an ecosystem of artificial life (ALife) based on the PSD model[5]. The method of implementation of parallel ALife and the newest results of experiments are reported in this article.

1 Background

1.1 Programmed self-decomposition model

Terrestrial life including human beings has continued to survive and evolve for these about 3.5 billion years on the surface of the earth, where space and substances have been surely limited. This fact tells us that the terrestrial life has continued to re-utilize the same limited space and substances for such a long time.

Ecology so far explains the restoration mechanism of the environment to be achieved mainly by the function of the *food chain*. This is a circulation of nutrients and energy in the inter-individual and inter-species network including many kinds of paths such as primary excretion by predators, microbial decomposition of detritus, direct cycling from plant to plant through symbiotic microorganisms, and so on[2]. Though the food chain takes a very important part in the restoration mechanism of the current ecosystem, such explanations based on inter-dependence of creatures have great difficulty in explaining the continuous self-reproduction and evolution of life within the limited environment before the appearance of such a complex network.

At that time the restoration mechanism must have been not in the system but in the structure of individuals of life.

A biological hypothesis "programmed self-decomposition model", proposed by Oohashi et al. in 1987[3], is a proposal of an additional explanation for the restoration mechanism of the terrestrial ecosystem. It assumes that every cell of terrestrial creatures has intrinsically installed with a fundamental ability to decompose itself and restore to the environment the space and substances it had possessed. It is expected that this hypothesis can explain with less contradiction how primitive life had continued to reproduce and evolve themselves at the ancient time before an ecosystem emerged.

It was already reported that this new model could be expressed as a variation of von Neumann's self-reproductive automaton model[3, 6]. Oohashi named this expanded automaton model "selfreproductio-selfdecomposition (SRSD) system".

1.2 Artificial life

Biochemical analysis of actual creatures has so far been an effective way to examine a biological hypothesis. An analytic approach certainly tells us whether the actual life is organized according to the examined hypothesis or not. That is much enough for biology intended for creatures now existent. Once the subject of the hypothesis becomes expanded to the evolutionary behavior of life, however, the analytic approach is inadequate for examination of it, because the subject creatures are often only in an imaginary world or had been already distinguished away from the present earth.

Artificial life (ALife) appeared as a new field of science to be the supplement of biology with

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its "synthetic" methodology. The field of ALife involves any kinds of interdisciplinary attempts to create life-like systems artificially by theoretical models, software on computers, hardware on robotics, and so on. A synthetic approach of ALife enables us to organize new creatures in accordance with the examined hypothesis and investigate them as experimental subjects. To couple these two different approaches — analysis and synthesis of life — may generalize biology for *life-as-it-could-be*[1].

2 Parallel simulator SIVA-2

2.1 ALife based on PSD model

With the background referred in the previous section, I have attempted to clarify the effect of the self-decomposition function in the ecosystem and comprehend the transitional process of evolution through ALife simulations in direct collaboration with Prof. Oohashi[4, 5]. Concretely, I have bred ALives of both von Neumann's self-reproductive automaton and Oohashi's SRSD system respectively within the same limited virtual space.

On the beginning of this study, a preliminary simulator SIVA based on a simple model was developed first[4]. The main works processed by SIVA were simulation of the behaviors of virtual individuals and calculation of diffusion of substances. Since both of them could be processed locally, they were quite suitable for parallel processing. So then I tried to implement SIVA-2 — the expanded version of SIVA for the parallel processing, on a super-parallel computer Fujitsu AP1000+[5]. AP1000+ I used this time consists of 1 host workstation (SUN 4) and $16 \times 16 = 256$ processors (SuperSPARC chips).

2.2 Design

The virtual world of SIVA-2 is assumed to be a regular finite lattice which consists of 256×256 pixels (*Cf.* fig. 1). Since the left edge of this space is connected to the right one, the space is similar to a side surface of a circular cylinder. Temperature is defined at each pixel differently according to its y ordinate to realize heterogeneity of the environment. This world can be regarded as a surface of a tiny planet where it is hottest in the North Pole and coldest in the South Pole. This world is provided with four kinds of finite substances diffusing within it.

The structure of each individual is constructed as fig. 1. These individuals will reproduce themselves using substances in the space for materials to construct their bodies. When an individual reproduces itself, there is a probability of mutation — a change of values of genes on a chromosome. Furthermore, the individual of SRSD system will decompose itself and return the components of its body to the environment, when it is triggered by either aging or unfitness of temperature.

2.3 Mapping

Parallelized tasks in SIVA-2 are simulation of the behaviors of virtual individuals and calculation of diffusion of substances. There are many ways to decompose and map them to processors. Three typical methods are as follows:

1. Domain decomposition (1) — Block mapping: The whole space is decomposed into the same number of blocks as that of processors. Each block belongs to a processor in a one-to-one correspondence. By this method the amount of communication among processors can be minimized when the subject problem can be processed locally. However, the load balance among processors may be quite disproportionate when the elements of the problem clusters in particular parts of the space.

2. Domain decomposition (2) — Cyclic mapping: The whole space is decomposed cyclically along coordinate axes so that the pixels mapped to a certain processor distributes uniformly to every area of the space. The load balance among processors is kept to be proportionate by this method even when distribution of the elements is unbalanced. The drawback of this method is that the communication between processors occurs much more frequently than in other methods because neighboring pixels always belong to different neighboring processors.

3. Functional decomposition — Managed mapping: The processing of elements is separated with that of the space. A manager processor decides the correspondence

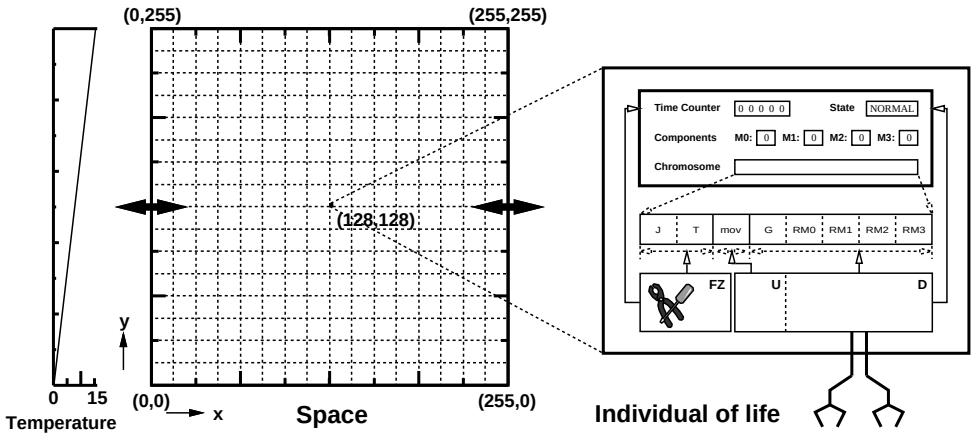

Figure 1: Design of SIVA-2

between elements and worker processors. By this method load balance among worker processors can be controlled almost completely by the manager processor. However, it is difficult to detect and settle the conflicts between the elements affecting to the same pixel at the same time.

I adopted block mapping for this simulator, because most parts of calculations in SIVA-2 are related only to neighboring pixels. Concretely in SIVA-2, each of cell processors of AP1000+ (i.e., $16 \times 16 = 256$ processors) is provided with a task to simulate one of 16×16 blocks which the whole space is decomposed into. The communication between neighboring processors is realized by T-Net in AP1000+.

2.4 How to get deterministic results

It was demanded for SIVA-2 to lead the same result deterministically when started from the same initial state, regardless the condition of computers. This demand is for making it easy to debug the simulator and analyze results of simulation. Some devices were added in implement of SIVA-2 to satisfy that demand.

First, the method of asynchronized parallel simulation of individuals, in which each individual was created as a process really executed in parallel by UNIX OS, was not adopted because the result would become indefinite. The pseudo-parallel simulating system was actually realized in which individuals were sequentially simulated by a list structure in each processor and the order of the list was randomized by shuffling it after every iteration.

The more serious problem is how to select deterministically the winner of conflict among individuals willing to occupy the same pixel at the same time, for its self-reproduction or movement, on the boundary area of neighboring blocks.

If the whole simulation were calculated within a single workstation, the "first-come-first-served" method would be easy for the attainment of deterministic simulation, and also it would be good for reduction of the amount of computation. In the case the simulation is calculated by parallel processors, however, the result of simulation on the first-come-first-served method may be indefinite, because the "first-comer" may change in the boundary area of neighboring blocks by the influence of the condition of processors such as load balance, and further, the first-come-first-served method generates the difference between a property of the space near the boundary of neighboring blocks and that in the middle of a block. This is not desirable for a simulation model of uniform space.

For the settlement of these problems, in SIVA-2, the winner of conflict is randomly selected from individuals which want to self-reproduce or move onto some pixel, after all the requests from them have been bid to that pixel. The requests are issued whether the individual exists on the boundary of the block or not, and all of them are treated by the same processing routine. It guarantees the property of the space to be uniform at any point of the block concerning the

settlement of conflicts.

Concretely, the simulation flow of each individual is separated into five phases shown in fig. 2 and synchronized at the important points. As a result of several times of trial and error, it turned to be most efficient to synchronize all processors five times per an iteration as shown in fig. 2, for the speedup and stabilization of the simulator. Diligent synchronization at the end of each phase of processing may be desirable for parallel processing which is difficult to be overlapped like this case.

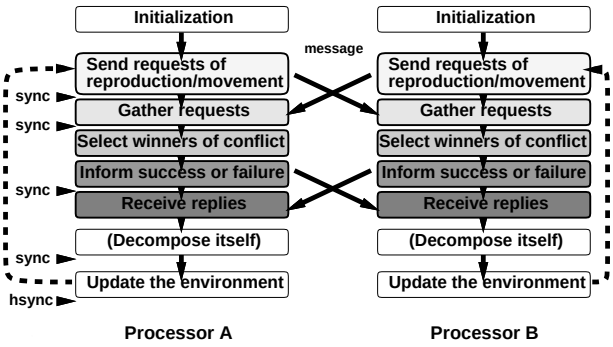

Figure 2: 5 phases of parallel processing of SIVA-2

Through the above-mentioned techniques of implementation, it was guaranteed that SIVA-2 surely led deterministically the same result when started from the same initial state including the seed of random numbers.

2.5 Effect of parallelization

The parallelization of SIVA-2 contributes to the improvement of the performance of the simulator. The simulated space of SIVA-2 is expanded to be about 26 times as large as that of SIVA. The running time for 5000 iteration of simulation by SIVA-2 is reduced as about a fifth of that by SIVA, when executed on a cell processor of AP1000+ with no output generating. It seems not efficient that the reduction of running time $\left(\frac{1}{5}\right)$ exceeds the reduction of the number of pixels per a processor $\left(\frac{16 \times 16}{50 \times 50} = \frac{1}{9.77}\right)$. This may be caused by the overhead of communication among processors and load unbalance at the beginning of simulation.

The scalability of SIVA-2 was measured in accordance with increase of the number of processors, while the total size of simulated space was fixed. The result of measurement is shown in fig. 3. In the case when 4 or 16 processors was used, the speedup exceeded the ideal estimate because of rising of cache-hitting ratio. The speedup became most efficient in the case of 16 processors, when the number of pixels per a processor was $16 \times 16 = 256$. SIVA-2 used for actual experiments is designed to make the number of pixels per a processor the same as this.

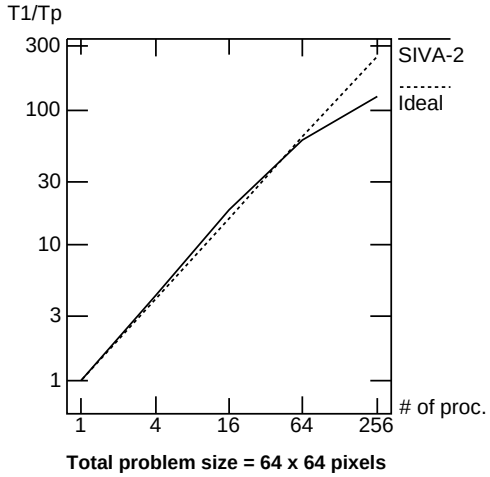

Figure 3: Scalability of SIVA-2

3 Results

3.1 Evolutionary adaptability

Simulations of ALife based on both the PSD model and the non-PSD model were made by SIVA-2. Transitions of spatial distribution of individuals are shown in fig. 4. The horizontal axis is the passage of time, and the vertical axis is the index of a probability of mutation in a logarithmic scale. This index is a logarithm on the base 2 of the probability of mutation in copying a gene on self-reproduction. Each square picture of the matrix represents a spatial distribution of individuals with given probability of mutation and time. Individuals are painted in a different gray tone according to the best-fit temperature for it.

The upper half of fig. 4 shows that frequent mutation provides high evolutionary adaptability to individuals based on the non-PSD model, and on the contrary, that the evolutionary

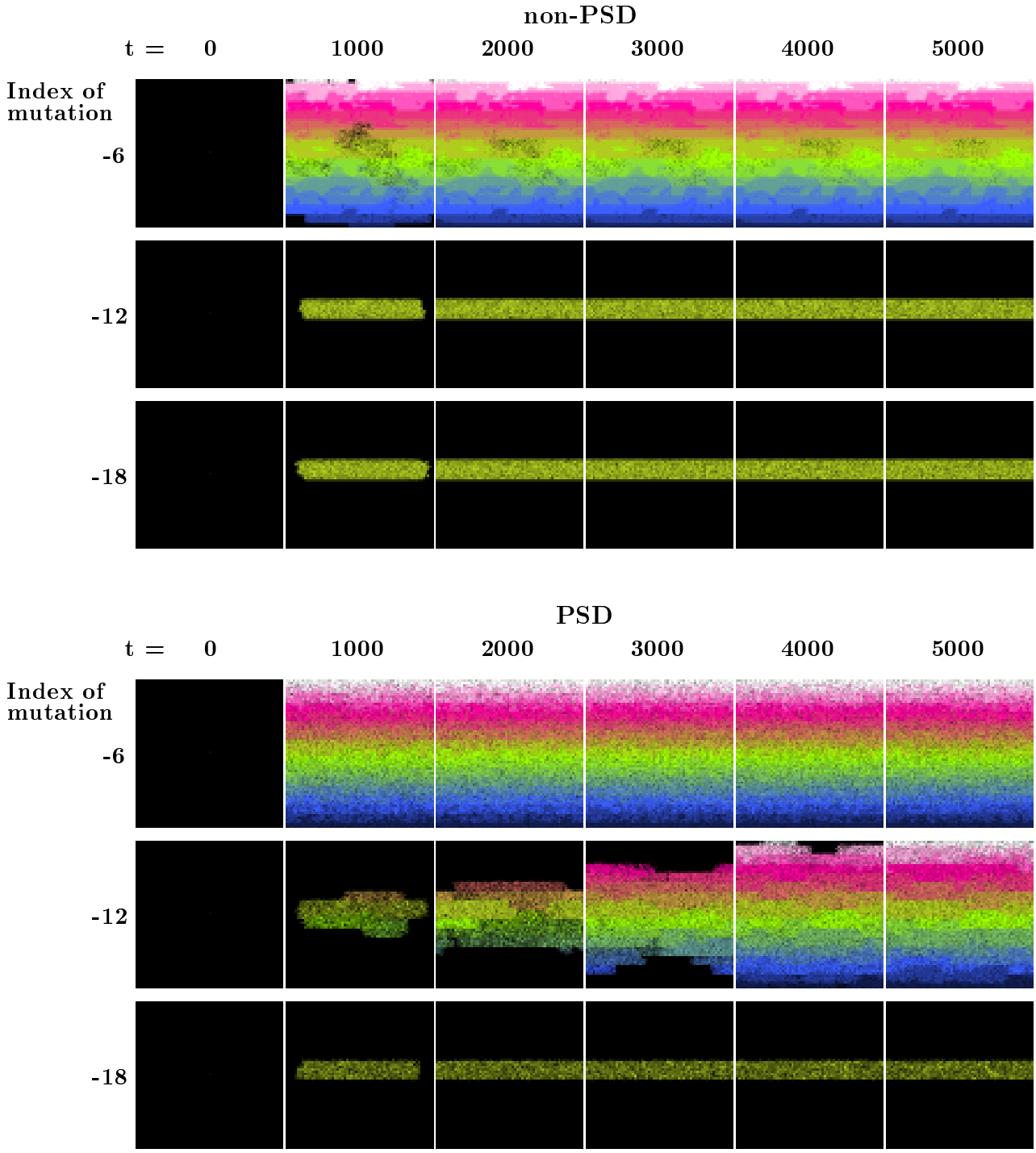

Figure 4: Transitions of spatial distribution of individuals in SIVA-2

adaptability is practically nothing under rare mutation.

Transitions of spatial distribution of individuals based on the PSD model is shown in the lower half of fig. 4. This shows that, the more frequent mutation occurs, the higher the evolutionary adaptability of individuals becomes. However, the remarkable point is that the evolutionary adaptability of individuals is not lost even when the index of mutation is small, because the individuals are able to catch the rare chances of mutation efficiently by repeating self-reproduction and self-decomposition.

For more objective investigation, I measured quantitatively the evolutionary adaptation in the both cases of the PSD model and the non-PSD model. The number of individuals in the space was adopted as the index of the evolutionary adaptation. The transitions of the number of individuals were recorded 10 times for the calculation of the average, with a respectively different seed value of random numbers for each condition of the respective index of mutation. $2 \times 13 \times 10 = 260$ times of simulation were made in total. Experiments with such large quantities of computation became possible by the improvement of parallelization of SIVA-2.

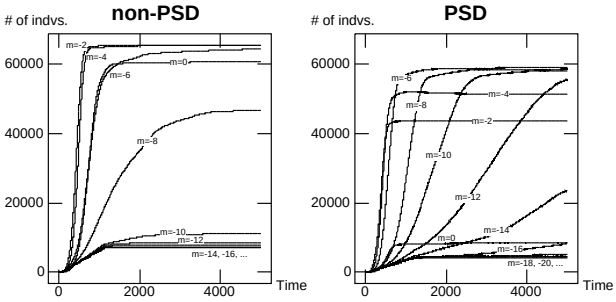

Figure 5: Transitions of populations in SIVA-2 (1)

The transitions of populations under different probabilities of mutation are shown in fig. 5. This figure shows that there is an obvious and substantial difference between the behavior of the evolutionary adaptation on the non-PSD model and that on the PSD model.

In the case on the non-PSD model, when the probability of mutation is large, it is observed that individuals adapted quickly to the whole space. When the probability of mutation is smaller, however, the ecosystem fell into a static state with no evolutionary adaptation after the region in which they could live had been filled up with individuals because of their one-way self-reproduction. That is, it can be said that the probability of mutation on the non-PSD model is directly connected to the limit of the environmental condition to which the individuals are able to evolutionarily adapt before they are forced to be inactive in short of the space or the substances.

On the other hand in the case of the PSD model, it was quite different from the non-PSD model in that the evolutionary adaptation advanced with no stagnation in the most cases. Exceptionally there are some cases that the adaptation stalled before the individuals adapted to the whole space when the probabilities of mutation were respectively $2^0, 2^{-2}, 2^{-4}$. This is because, under such a large probability of mutation, it happened in some simulation trials that all the individuals became extinct in the early stage of the simulation. Except for these cases, the advance of evolutionary adaptation was observed even in the case the probability of mutation was as small as 2^{-18}.

Fig. 6 is a redraw of fig. 5 from a different viewpoint, for the purpose of clarifying the substantial difference between the non-PSD model and the PSD model. The horizontal axis of fig. 6 is the probability of mutation. This figure shows the transitions of relation between probabilities of mutation and populations of individuals along the passage of time.

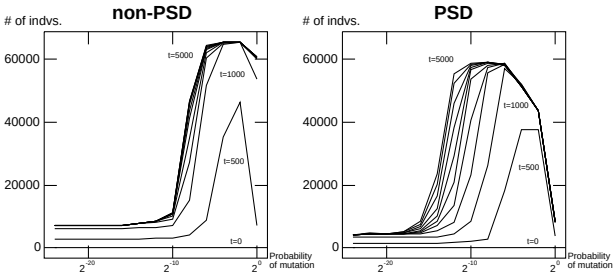

Figure 6: Transitions of populations in SIVA-2 (2)

The difference between two models became more conspicuous in this figure than before. In brief, curves of the non-PSD model gradually converge to a limit curve as time passes, while the left slope of curves of the PSD model continues to move to the left, which means that

increase of population in the case with smaller probability of mutation, as time passes. In other words, individuals on the non-PSD model reproduce and evolve themselves toward a static state determined by a probability of mutation, and individuals on the PSD model evolutionarily adapt to every area of the space even when with rare mutations, by accumulating rare mutations through long-term repetition of self-reproduction and self-decomposition.

3.2 Consideration on fatal mutation

It seems that the behaviors of individuals on the non-PSD model can be separated generously into two patterns as below, by the boundary at probability of mutation= 2^{-8}: (1) Reclamation of new space through evolutionary adaptation usually advances faster than consumption of it through self-reproduction. Individuals can reproduce themselves and adapt infinitely to everywhere unless they fill up the whole space. (2) Reclamation of new space through evolutionary adaptation becomes eventually outdistanced by consumption of it through self-reproduction. Then the individuals fall into a static state.

Now let us consider here whether the pattern (1) actually exists. In SIVA-2, the self-reproduction mechanism is treated as a black box and guarded from frequent mutations. For the actual creatures, however, frequent mutations may destroy essential mechanisms of life, such as self-maintenance and self-reproduction, and also may remarkably reduce the fitness of that creature. Therefore the results of the experiments by SIVA-2 in this thesis must be revised with reflection on such a harmful influence to life.

Here, I assumed a simple chromosome model for consideration on the relation between probability of mutation and evolutionary adaptation. This chromosome model contains l ($l > 0$) genes. In this chromosome, there is a "fixed region" which consists of s ($l > s > 0$) genes and contains serious contents to maintain sound activities of life. When any mutation occurs within the fixed region, the individual will stop its life activities. The other part of the chromosome is named a "variable region" which consists of $l - s$ genes. The mutation within this region has no bad influence to the activities of the individual. Therefore, the evolutionary adaptation to different environments may be attained by accumulation of mutations in the variable region.

When the probability of mutation per a copy of a gene is defined as 2^m, the evolutionary adaptability of an individual may become in proportion to [probability that no mutation occurs within a fixed region] $\times$[average of the number of mutations within a variable region]. i.e.,

$$\text{Adaptability}(m) \quad = \quad C(1-2^m)^s \cdot 2^m(l-s)$$

On the basis of this consideration, the results of experiments are revised under the assumption that each individual in SIVA-2 had a fixed region which consists of 50 genes. The number of individuals is approximated to be in proportion to their evolutionary adaptability. Fig. 7 is the revised results by multiplication of $(1-2^m)^{50}$ to fig. 6. In fig. 7 the pattern (1) of the non-PSD model mentioned above disappears, and the behaviors of individuals on this model become the pattern (2) in all cases. In the case on the PSD model, though this revision lets the curves of the PSD model be a little small, it makes the increase of population under a small probability of mutation more conspicuous than before.

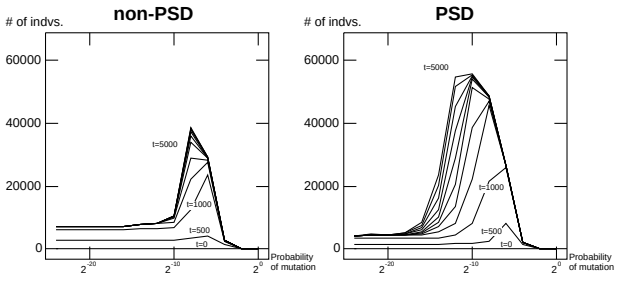

Figure 7: Transitions of populations in SIVA-2 (2, Revised)

3.3 Significance of the self-decomposition mechanism

These results are to be summarized as follows: The large probability of mutation makes the evolutionary adaptability high but the stable maintenance of self-reproduction difficult. On the contrary, the small probability of mutation makes the evolutionary adaptability low but the stable maintenance of self-reproduction easy. If this antinomy could be satisfied at the same time by any strategy, it would become possible to create the favored "family" of life with the evolutionary-historic advantage.

From such a standpoint, it may be said that the self-decomposition mechanism has the function to attain both the stable maintenance of self-reproduction ability and the maintenance of evolutionary adaptability at the same time, by catching efficiently such rare mutations that it has no damage for life, and pushing up the evolutionary adaptability of life during the greatly prolonged repetition of self-reproduction and self-decomposition utilizing the limited space and substances.

4 Summary

This study aims at the examination of the effect of a biological hypothesis "programmed self-decomposition (PSD) model", proposed by Oohashi et al., on the evolutionary history of life. I had developed the simulator SIVA and SIVA-2 for this work, and made experiments of simulation to breed and evolve both von Neumann's self-reproductive automata and Oohashi's selfreproductio-selfdecomposition (SRSD) system respectively in the same environment provided with heterogeneity on temperature and limited space and substances.

The results of these experiments showed that, on one hand individuals without the self-decomposition mechanism continued to remain a static state with neither self-reproduction nor evolution, after they had exhausted limited space and substances. On the other hand, individuals with the self-decomposition mechanism attained the restoration of the environment by re-utilizing limited space and substances through self-decomposition, and repeatedly reproduced themselves. Such a large number of self-reproduction provided the individuals with many chances of mutation. At last appeared the species which had adapted evolutionarily to every region of the heterogeneous world.

It became possible by SIVA-2 to simulate many cases under various conditions with different probabilities of mutation, because SIVA-2 achieved to make the simulation speed faster and the simulated space larger than SIVA by the improvement of parallelization. The results showed that the self-decomposition mechanism has an effect to keep the evolutionary adaptability of life even when the frequency of mutation is small.

Furthermore, I measured quantitatively the evolutionary adaptability of life under many conditions with various probabilities of mutation and different seed values of random numbers. The results of the measurement suggested that the self-decomposition mechanism would function as a survival strategy to attain the following two inconsistent things at the same time: the stable maintenance of self-reproduction ability and that of evolutionary adaptability. Verification of this insight will be made using a new simulator being developed now.

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