Quantification of Microscopic Events in the Process of Long-Term Evolutionary Dynamics

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Abstract
This paper describes a new standpoint to further understanding the evolvability of A-life systems, that is, quantification of the dependency of system constituents. If a system exhibits evolutionary activity, new events, including the development or extinction of systems constituents, may emerge one after the other. The occurrence of new events would involve a changing complexion in the course of the future direction of system behaviors. In this respect, there have been a considerable number of studies on capturing long-term dynamics in A-life systems in terms of, for example, population dynamics. On the other hand, we focus on the quantification of relational concepts between constituents to clarify the occurrence of fundamental events affecting long-term course of evolution. We apply a quantification method to our A-life simulation model. Sequential analysis of the obtained results enables us to visualize its long-term evolutionary dynamics. We discuss the effectiveness of our approach and the quantified evolutionary dynamics.

Introduction
Many A-life models have been proposed so far for the understanding of behaviors of living systems. Some of them have given us new insights to divine the fundamentals of living things, and some have been successfully applied to the development of artifacts that can perform life-like activity.

A-life research usually consists of the conception of a model, its realization through artificial media, and observation of simulated behavior in a collection of experiments. One of the characteristics of A-life that attracts researchers in this community is the emergent or evolutionary activity of a system observed in simulation runs, though the meanings of these terms are still debatable.

While a number of simulation models have been proposed, one important future issue in A-life research would be the development of tools to analyze and evaluate the emergent activity of A-life systems. In particular, the most striking and mystical term, emergence, should be reconsidered in respect of how to quantify evolutionary dynamics so that we can compare emergent behaviors and specify an event crucial for the future course of evolution. The terms emergence and evolution are frequently used for behaviors of A-life systems. However, excessive use of these terms without the establishment of criteria for defining the activities of emergence and evolution is likely to devalue their significance.

There seems to be two major streams of research related to the above issue. One is a human diagnosing approach similar to the Turing Test in the realm of artificial intelligence. Ronald et al. recently proposed an emergence test consisting of the criteria of design, observation and surprise for diagnosing emergence (Ronald, Sipper, and Casacarrere 1999). They have tried to establish an emergence test by assessing surprise on the basis of how easy (or how difficult) it is for an observer to bridge the gap from design to observation. In their study, they administered the test to some major A-life models and assessed their emergence levels.

The other major stream of research is a more statistical approach. This approach is usually related to evolutionary dynamics in an objective model. Bedau et al. devised a way of measuring evolutionary activity from the viewpoint of population genetics (Bedau and Packard 1992), and they then applied their methodology to the fossil data obtained from the real biosphere (Bedau et al. 1997). Their research progressed to the classification of long-term evolutionary dynamics (Bedau, Snyder, and Packard 1998), similar to Wolfram’s famous work on cellular automata (Wolfram 1984). Following on from Bedau’s work, Taylor investigated the role of contingency by mutation in the evolutionary dynamics of his A-life model (Taylor and Hallam 1998). Furthermore, from the viewpoint of computational complexity, we have described self-organized complexity of our A-life model through an increase in the complexity of interactions among constituents of the system (Yoshii, Ohashi, and Kakazu 1998a).

The latter approaches described above are statistical in the sense that those approaches analyze simulated behaviors by measuring some variables that appear at the stage of design of a model or observation in terms of Ronald’s test criteria. However, we question whether the measurement of such anticipatorily selected variables is appropriate for understanding emergence. As for the concept of emergence, there is a consensus that a holistic context may change depending on the local behavior of each system constituent and, on the other hand, each local behavior is affected by the holistic context. The holistic context of such systems as...
a whole is dynamically organized through alteration in the relations among the constituents that interact with each other. In other words, the holistic context of a system is not determined before the system actually begins to function.

In this respect, we do not think that measurement based on anticipatory criterion variables is sufficient to aid in the capturing of essences of emergence. Rather, we think that a new standpoint is necessary. We therefore focus on alteration in the dependency relationship of system constituents following microscopic events involving their generation and extinction.

Since a dependency relationship is qualitative rather than quantitative, a method for transforming qualitative data into quantitative data is needed. In addition to this, criterion variables for statistical analysis of a holistic context are not available before the system functions. Thus, this paper introduces a method developed by Hayashi for quantifying a dependency relationship. Among the various methods developed by Hayashi, a method called Quantification Type IV (QTIV) can be applied to problems for which no criterion variables are available in advance (Hayashi 1964).

In this paper, we apply the QTIV to our A-life model for quantifying and clarifying microscopic events in the process of the long-term course of evolution. We represent the concept of a dependency relationship as a preference described with an ordinal scale. Preference data will be gathered from interactions between system constituents in the evolutionary process. Then, those data will be analyzed using the QTIV to generate a point that will be plotted on a dependency projection space (DPS). Based on the results of quantification, we show the process of changes in relations between the system constituents through long-term evolutionary dynamics.

Next, we briefly describe our A-life model, named PROTEAN, and then we describe the QTIV method. Lastly, we show some quantified evolutionary dynamics obtained by the QTIV and end up with discussion.

Our A-life Model: PROTEAN

Our test model for quantification of evolutionary dynamics, named PROTEAN (Platform for Recursive Ontogenetic Turing-machine Ecosystem for Autopoietic Networks), is an A-life system aimed at simulating autopoietic behaviors of computer programs described in the form of a Turing machine (TM) (Yoshii, Ohashi, and Kakazu 1998b). In the PROTEAN, survival games take place on a universal Turing machine (UTM), with dynamically changing ecological resources being competed for. The essential features of the PROTEAN are the implementation on a UTM, the interaction procedure between constituents, and the constitution of the system as a whole. Although some of its characteristics are similar to the models in former works by Ray (Ray 1991) and Adami (Adami 1994), the PROTEAN has the following unique characteristics.

- Universal Encoding of Algorithms by UTM

For the realization of a universal model for complex adaptive systems, the PROTEAN implements the notion of a UTM. Conceptually speaking, the PROTEAN has the capability of describing and producing any kind of algorithm computable by TM.

We call a system constituent of the PROTEAN a scheme. A scheme as a tape for the UTM is nothing more than the coded version of a TM that performs the task desired of the UTM. We can regard a scheme as a genotype that encodes the Turing machine's functionality, while a scheme decoded as a TM on the UTM is called a phenotype because it is dictated completely by that scheme.

- Interaction between Turing Machines

Figure 1 illustrates an overview of an interaction. First, a scheme, $g_i$, is interpreted by the UTM and it is then decoded into a phenotype (i.e., a specific TM, $T_i$). Next, the decoded TM, $T_i$, reads and operates on another scheme, $g_j$, as an input tape operated. If this tape is accepted, a new scheme is generated through the following template matching procedure. The newly generated genotype will dictate a new scheme, or in other words, a new TM. This means that such an interaction can realize a process whereby a program can directly operate on the description of another program to generate a new algorithm.

- Parallel Processing to Avoid the Halting Problem

There is no way to tell in advance whether a TM will accept its input tape or not. In order to avoid this insoluble problem, known as the halting problem, the PROTEAN uses parallel processing and compulsory termination: All of the schemes reside in a static amount of memory called an ecosystem, and each scheme occupies its own memory block dependent on its description length. Each scheme reads and operates, in parallel, the other schemes chosen at random. When a scheme accepts an input tape and some partition is vacant, the parent scheme allocates a memory block for its child there. On the other hand, if another scheme or schemes have already occupied that memory block, the parent can terminate their interaction process and rewrite the memory. Consequently, those schemes that are likely to face the halting problem are eliminated from the ecosystem.

Figure 1: Interaction between schemes.
Furthermore, there are no arbitrary rules for self-organization or self-reproduction, as well as no special metaphors derived from living systems. Intrinsically, the PROTEAN modeling does not restrict the possibilities for algorithms: any kind of algorithm can be produced theoretically.

The Quantification Method

Originally, the QTIV was developed for the field of sociometry. When a preference table by paired comparison is given, the purpose of the QTIV is to quantify so that a pair of similarities come close to each other and to arrange each element in the minimum dimension possible. The unique aspect of the QTIV is that it is applicable even when there is no advance information that is directly helpful for spatial arrangement.

Let \( e_i \) (\( i \neq j \)) be the degree of preference of an element \( i \) for \( j \). In order to simplify the explanation of the QTIV, one-dimensional quantification is first described.

Now, giving one-dimensional coordinate value to each element, consider a Euclid square distance \( (x_i - x_j)^2 \) as a value denoting a distance between a pair of objective elements. In order to approximate a pair of similarities, in other words, a pair whose preference for the other is very great, and to under a pair whose preference for the other is small, determine \( \{x_i\} \) that maximizes the following value \( Q \):

\[
Q = -\sum_{i=1}^{n} \sum_{j=1}^{n} e_{ij} (x_i - x_j)^2.
\]

(1)

\( Q \) is the inner product of \(-e_i\) (negative preference) and a Euclid square distance that denotes the degree of difference between the objective elements. To maximize \( Q \) is equivalent to determining the quantity \( \{x_i\} \) by which the non-preference \(-e_i\) and its Euclid square distance have the closest agreement. Here, for the normalization of data, let the average of \( \{x_i\} \) be

\[
\frac{1}{n} \sum_{i=1}^{n} x_i = 0,
\]

and let the variance be

\[
\frac{1}{n} \sum_{i=1}^{n} (x_i - \bar{x})^2.
\]

(2)

In equation (1), the greater the preference of a pair of elements is for each other, the larger the value of \( e_{ij} \) becomes. As a result, the smaller a Euclid square distance \( (x_i - x_j)^2 \) is, the larger \( Q \) becomes. On the other hand, if a preference between a pair of elements is small, \( e_{ij} \) becomes small, and, thus, if a Euclid square distance \( (x_i - x_j)^2 \) is larger, the value of \( Q \) becomes larger.

Now, to determine the quantity \( \{x_i\} \) results in solving an eigenvalue problem for a matrix \( H = (h_{ij}) \) that appears in the following equation:

\[
\sum_{j=1}^{n} h_{ij} x_j - \beta x_i, \quad (i = 1, 2, \ldots, n).
\]

(4)

The matrix \( H(h_{ij}) \) is defined by \( e_{ij} \), which denotes preference as follows:

\[
h_{ij} = h_{ji} = e_{ij} + e_{ji},
\]

\[
h_{ii} = -\sum_{j \neq i} h_{ij} = -\sum_{j \neq i} e_{ij}.
\]

(5)

It follows that \( \{x_i\} \) is equivalent to an element of an eigenvector for the largest eigenvalue \( \beta \) in equation (4).

When multidimensional quantification is required, first, a \( q \)-dimensional quantity for \( i \) is defined as \( \{x_i^{(r)}, x_i^{(s)}, \ldots, x_i^{(q)}\} \). In this context, consider the maximization of

\[
Q = -\sum_{i=1}^{n} \sum_{j=1}^{n} e_{ij} \left( (x_i^{(r)} - x_j^{(r)})^2 + (x_i^{(s)} - x_j^{(s)})^2 + \cdots + (x_i^{(q)} - x_j^{(q)})^2 \right).
\]

(6)

By solving the above equation, elements of an eigenvector for eigenvalues, each of which is from the largest one to the \( q \)-th largest, become quantities of \( \{x_i^{(r)}, x_i^{(s)}, \ldots, x_i^{(q)}\} \) respectively.

Quantified Evolutionary Dynamics

In this section, the quantification method QTIV is applied to simulation results obtained through runs of the PROTEAN.

Preference data gathered from local interactions are analyzed to generate points in a DPS. This paper uses two-dimensional analysis, because there is general agreement that up to the second largest eigenvector in the QTIV calculation is enough to quantify objective data. The position of each scheme in the 2-D DPS changes with time during their reproductive processes. Thus, quantified evolutionary dynamics are demonstrated.

We first begin with an example of a self-developmental process of a scheme that is deliberately chosen because of its interesting process in interaction, and then we demonstrate quantification of a more complicated case of evolution in the self-developmental process. The evolutionary dynamics of the population of schemes in the PROTEAN induces a set of orbits in the DPS. Different types of long-term evolutionary dynamics are discussed using the collection orbits across the sequential DPS.

Microscopic Snapshot of Dependency Relationship in Pure Self-Developmental Process

Here, a pure self-developmental process that starts from scheme 100101100010101010110011110010110010 is examined. The reason we call the self-developmental process discussed here "a pure self-developmental process" is that we check all of the possible interactions in advance and then use its step-by-step results for the demonstration of the effectiveness of the quantification method.

In the following, a 100-adic notation system is adopted for scheme descriptions, using 100 characters such as \( \{0, 1, \ldots, 9, \ldots, \bar{9}, \ldots, 9, \ldots, \bar{0}, \ldots, 0\} \), as the length of a bit-string does not allow full representation. The above scheme, for example, is described as \( \bar{9}9062 \) under the notation system.

The characteristic of a series of interactions beginning from scheme \( \bar{9}9062 \) is that the scheme first generates a
new one operating on its own description, and then such an interaction process automatically progresses with the resources generated as follows:

\[
\begin{align*}
\text{BAWHrl} \odot \text{BAWHrl} & \rightarrow \text{CBtpPh} \quad \cdots \quad (1) \\
\text{CBtpPh} \odot \text{BAWHrl} & \rightarrow \text{Ecngxt} \quad \cdots \quad (2) \\
\text{Ecngxt} \odot \text{BAWHrl} & \rightarrow \text{IfbONF} \quad \cdots \quad (3) \\
\text{IfbONF} \odot \text{BAWHrl} & \rightarrow \text{QVDtQ} \quad \cdots \quad (4) \\
\text{QVDtQ} \odot \text{BAWHrl} & \rightarrow \text{hXGHy} \quad \cdots \quad (5) \\
\text{hXGHy} \odot \text{BAWHrl} & \rightarrow \text{QVDtQ} \quad \cdots \quad (6) \\
\text{QVDtQ} \odot \text{BAWHrl} & \rightarrow \text{hXGHy} \quad \cdots \quad (7) \\
\text{BDtYK} \odot \text{BAWHrl} & \rightarrow \text{CHiCHOM} \quad \cdots \quad (8) \\
\text{CHiCHOM} \odot \text{BAWHrl} & \rightarrow \text{FPTFPyQ} \quad \cdots \quad (9) \\
\text{FPTFPyQ} \odot \text{BAWHrl} & \rightarrow \text{KgnKgP} \quad \cdots \quad (10) \\
\text{KgnKgP} \odot \text{BAWHrl} & \rightarrow \text{OmbUNwp} \quad \cdots \quad (11) \\
\text{OmbUNwp} \odot \text{BAWHrl} & \rightarrow \text{QVDtQ} \quad \cdots \quad (12) \\
\text{QVDtQ} \odot \text{BAWHrl} & \rightarrow \text{hXGHy} \quad \cdots \quad (13) \\
\text{hXGHy} \odot \text{BAWHrl} & \rightarrow \text{QVDtQ} \quad \cdots \quad (14) \\
\text{QVDtQ} \odot \text{BAWHrl} & \rightarrow \text{CHiCHOM} \quad \cdots \quad (15)
\end{align*}
\]

where \( g_i \odot g_j \rightarrow g_k \) denotes an interaction, in which a scheme \( g_i \) that is decoded into \( T_j \) reads the other scheme \( g_j \) and then newly generates a scheme \( g_k \).

These equations are a series of possible interactions that are likely to occur through a run of the PROTEAN with a seed of scheme BAWHrl. Although the interactions executed by the above schemes are actually quite trivial from a computational point of view, the interacting processes are sufficient for demonstrating the developmental dependency relationship.

Suppose there are \( n \) schemes that interact with each other. When an interaction \( g_i \odot g_j \rightarrow g_k \) occurs, giving one integer point to \( g_i \) and \( g_j \) for \( g_k \), an \( n \times n \) matrix is obtained. The way of scoring means \( g_k \) owes its generation to \( g_i \) and \( g_j \). In this way, a preference table denoting the dependency relationship is defined.

For example, Table 1 shows a preference table of the interactions from (1) to (3) in the above series of interaction. Thus, by applying the quantification method QTIV to the preference table, a 2-D diagram of DPS is then obtained, as depicted in Figure 2. Note that the coordinate real value itself of each element in the DPS is not important. What has to be noted is the spatial arrangement of elements based on their degree of preference to other elements. A pair of elements that are close to each other has an affinitive relationship. A relational concept, which is qualitative data, must now be transformed into quantitative data with a scale described in the form of a Euclid distance.

<table>
<thead>
<tr>
<th></th>
<th>BAWHrl</th>
<th>CBtpPh</th>
<th>Ecngxt</th>
<th>IfbONF</th>
</tr>
</thead>
<tbody>
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<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>CBtpPh</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Ecngxt</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>IfbONF</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 1: Preference table obtained for interactions at the early stage.

Figure 2: 2-D dependency projection space obtained by application of QTIV to the interactions in Table 1.

Figure 3: 3-D diagram that quantifies the self-developmental process and one close-up DPS snapshot selected among those sequential analyses.
Furthermore, a sequential collection of DPS by quantification through to interaction (15) is shown in Figure 3. The 3-D diagram that converges in a spiral form can be seen. One DPS snapshot among the sequential view is also depicted in Figure 3. It illustrates that affinitive relationships among the elements are represented as a curve consisting of a set of crowded dots.

Note that this figure is just drawn from the above data for a sample demonstration of a fact that the quantified method works well with our intuitive expectation. The actual evolutionary dynamics through a run of the PROTEAN is examined next.

Quantification of Evolutionary Dynamics through Computer Simulation

A significant difference in an evolutionary process from the above pure self-developmental process shown in Figure 3 is that the existing schemes have to now compete with the others for a static amount of resources, that is, memory space in the PROTEAN. Their fitness is dynamically dependent on their relations to others and the consequent environment thereof. At the same time, extinction of each scheme is now likely to occur.

Figure 4 illustrates evolutionary dynamics that starts from an interaction of scheme BAGHLE on the basis of the same quantification procedure as that used in the former experiment. As space is limited, abbreviations of the whole dynamics are shown in this figure. The reason the observed complexion is quite different in spite of beginning from the same seed as in the case of Figure 3 is because of the effect of survival games taking place under a dynamically changing selection pressure and because those local interactions and the environment thereof are, then, organizing a holistic context. The combination of a top-down selection pressure and a bottom-up local interactions makes the

![Figure 4: Long-term evolutionary dynamics that involve microscopic events obtained through the quantification of the dependency relationship of system constituents: (a) the generation of new system constituents at the early stage of evolution; (b) the extinction of a system constituent involving an alteration in the following evolutionary dynamics; (c) the generations of new constituents and drastic changes in the dependency relationship subsequent to those events; (d) a simple extinction; (e) transition from a stationary state to the generation rush of new constituents.](http://direct.mit.edu/books/book/chapter-pdf/268092/9780262291071_cba.pdf)
evolutionary dynamics more complicated than that of Figure 3.

Although the dynamics is complicated, Figure 4 shows some interesting patterns in the long-term evolution. Next, let us turn to the investigation of each case.

A Gradual Acceptance. Figure 4 (a) depicts dynamics at the early stage of evolution. Some schemes, such as $QLd1c$ and $hXqGpY$, are newly generated from the initial seed. Scheme $IFdONe$ is once left out of the others and then takes a hand again in them by degrees after the generation of scheme $hXqGpY$. Remember that the closer to the center in each $2-D$ DPS the location of a constituent is, the more affinitive is the relationship that it has to the others. Scheme $IFdONe$ is thought to have an important role in the subsequent dynamics.

Events Involving Drastic Changes. Figure 4 (b) and (c) show examples of the extinction and generations of schemes, respectively. Figure 4 (b) shows a process in which scheme $BdKdD$ loses its adaptivity. That scheme eventually becomes extinct, and it follows from that event that the dependency relationship of the remaining schemes has been expanded. On the other hand, In Figure 4 (c), the schemes of $tKpdKplNC$, $QGyYVdWrC$, and $tQGwNvBy$ are generated. Drastic changes in the dependency relationship coincide with those events, implying that those generations are stimulatory in the evolutionary dynamics.

A Desolate Extinction. Unlike the case in Figure 4 (b), scheme $18KdWobYqI$ disappears in a long-term stationary state as depicted in Figure 4 (d). Very few changes occur, meaning that this scheme already has no importance for the current evolutionary dynamics at this moment.

Calm before Rush of Generation. While a stationary state is continuous, as shown in the upper part of Figure 4 (e), the generation of scheme $LqKnNtZsWwErsGy$ led to the birth of its offspring. However, the evolutionary dynamics shows that the ecosystem manages to absorb those newcomers.

Discussion

We have described the quantification of evolutionary dynamics observed in computer simulations of an A-life model. In this section, the effectiveness of this quantification approach and future prospects are discussed.

The QTIV is a method for representing the relational concept between objective elements as their spatial arrangement through quantification of their relationships. The figures shown in the former section illustrate the dependency relationship of each element: An element that has affinitive to the others is located close to the origin in the DPS because of the minimization of Euclidian distances to those elements. Furthermore, the sequential analysis of such spatial arrangements has enabled us to visualize long-term evolutionary dynamics from the viewpoint of local interactions.

In this paper, a simple self-developmental process has been described for demonstration of the quantified evolutionary dynamics. The following results were obtained. When a system constituent is newly generated in the system, it appears far from the origin. If this constituent is subsequently capable of interacting with other constituents, it gradually comes close to those constituents. On the other hand, a constituent that is likely to become extinct goes away from the origin and disappears. At this moment, if a drastic alteration in the spatial arrangements follows, the extinct constituent is thought to have had an affinitive relationship with the other constituents. On the other hand, no distinctive change occurs when a constituent that has already lost its existence value becomes extinct. The extent of dynamics change following generation or extinction depends on the holistic constitution of the system at that time.

An important point is that the quantification of the dependency relationship indicates the possibility of clarifying microscopic events capable of influencing the future course of evolution. It could be said, for example, that the appearance of a new constituent in the spatial arrangement of DPS corresponds to emergence in a narrow sense. At the same time, the following changes in evolutionary dynamics are thought to show a complexion in which the holistic complexity is re-organized. In some previous works on evolutionary dynamics, a certain criterion for quantifying a holistic complexion has been introduced in advance. As described before, the anticipatory definition of such a criterion would not intrinsically agree with the essence of emergence and evolution. On the other hand, we have tried to represent ongoing dynamics of a system from the microscopic point of view, free from any pre-embodiment of criterion variables.

Motivated by such an intention, we dealt with a simple self-developmental process in this study. From the formal point of view, it is no more than a simple step-by-step developmental process. The results of simulation, however, revealed complex aspects ongoing in the system, unlike a pure step-by-step process. In the previous section, we described some interesting patterns among its long-term evolutionary dynamics. We are currently studying evolutionary dynamics consisting of schemes that execute more interesting computation in the theoretical sense, and we have confirmed that this quantification approach is effective even in more complex problems.

Lastly, let us now turn to another characteristic of the quantification approach, that is, the normalization of data. As shown in equations (2) and (3), the results obtained from this method are always normalized. The relative quantity through the normalization may be able to be applied in the future to calculation of the fitness value of each constituent. In the field of evolutionary computation, the fitness value is given absolutely from a certain pre-defined equation. On the other hand, some studies on experimental biology insist each system constituent defines its adaptivity as a dynamically changing relative value to the others (Matsumo 1989). Such a school argues in favor of an approach based on the normalized relational concept.
To summarize, an approach of quantification of local interactions has been presented as a possible tool for future research in A-life. Evolutionary dynamics of our A-life model have been represented in the form of the sequential transition of quantified local interactions. Evolutionary dynamics and the usefulness of our approach were discussed on the basis of results of computer simulations.

References


