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Abstract

Motivating the study of constructing a formal neuron in computer, we propose a logic-based dynamical theory for a genesis of biological threshold which specific proteins like ion channel proteins or their network can be responsible for. By viewing such a protein or a protein network as a computation machine, the statements concerning the states of reaction chains which eventually activate or inactivate the protein are treated. Introducing dynamical systems, associated with an inference process on the statements with continuous truth values, we investigate invariant characters of such a dynamics, thereby we obtain a sigmoidal function for an invariant distribution function of the truth values. The domain of solutions of functional equations regarded as a representation of the self-description of proteins or protein networks as a machine indicates the emergence of threshold, namely the realization of dyadic value, 0 or 1, based on the continuous truth values takes place. The results obtained may highlight the mechanism of neuronal threshold in the framework different from population dynamics. The derived dynamical systems may also provide a simple model of "demon" rectifying the thermal fluctutions to drive unidirectional movements.

Keywords: Threshold; Patchy and folding map; Logic-dynamics transformation; Internal observer; Chaotic functional map.

1 Introduction

We propose a new dynamical theory which provides an explicit description concerning a logic which may underlie the dynamic behaviors of complex networks consisting of macromolecules. The present study is motivated by the constructive approaches to neural systems, where at least a formal neuron must be constructed in computer. An indication of formal neuron is provided by the existence of threshold.

On the other hand, the mechanism of threshold in excitable cells like neurons is still unclear. Usually, one can conceive for a dynamical representation of excitability the appearance of a pair of saddle and node via saddle-node bifurcation, where stable manifold of the saddle plays a role of threshold. This mechanism was actually found in an exothermic reaction (Murakami and Tomita, 1979). This is, however, difficult to apply to biological excitable cells at physiological conditions. Hodgikin-Huxley's (HH) equations (1952) and later proposed FitzHugh-Nagumo's equations (FitzHugh, 1961; Nagumo *et al*, 1962) for action potential showed threshold-like behavior of dynamical orbits in phase space, but the dynamical mechanism is quite different from the one of exothermic reaction. The case of the above neuron models adopted at physiological conditions is due to the nonuniformity of orbital density. Though there is a parameter region where saddle exists, this case becomes bistable and does not express the excitability, or be far from physiological conditions. Though these equations simulate well the phenomena relating to the presence of threshold such as neuron's spike and impulse travelling, they do not effectively work to clarify a genesis of threshold since they are phenomenological equations.

Our aim here is to propose the third possibility for the mechanism of threshold, namely a possible logical basis of biological threshold. We take into account, in the model study, ion channel proteins activated or inactivated by kinase-phosphatase network. This system has a rich complexity such as a complex enzymatic reactions. In spite of this complexity, one can extract the underlying logic in these reactions. In the present approach, we neglect the details of reactions, rather try to express the logical sturucture of the reactions as a statement. Thus reaction scheme is converted to an inference process of the statements, and then the inference process is replaced by dynamical system, thereby we obtain logic-based dynamical systems showing curious behaviors. We will conclude that the situation of open-and-close of ion channel proteins or their networks expressed by a specific logic can be a cause of threshold if they "read" the network behaviors as a self-referential statement according to a continuous logic like Lukasiewicz logic (for example, Rescher, 1969).

2 Observer-Oriented Model for Kinase-Phosphatase Network

In this section, we briefly summarize several typical roles of a network consisting of kinase and phosphatase (Albert *et al* 1994), and also address five assumptions for modelling such a system.

2.1 Kinase-Phosphatase Network and Its Function

The kinase-phosphatase (k-p) networks are well-known to play an important role for functional manifestation of specific proteins like ion channel proteins, accesory proteins of DNA, and so on (Albert *et al*, 1994). Enzymatic reactions proceed inside this network, where phosphorylation, namely a delivery of phosphoric acid intervenes in the process. Consequently, it is viewed that some kinase activate or some others inactivate other kinase, phosphatase and proteins, while some phosphatase inhibit or some others disinhibit other phosphatase, kinase and proteins, depending on the proteins' internal states.

For ion channel proteins, the k-p network plays a role of initiation of the process for morphological changes of the protein, say a change of morphology A to B and *vice versa*. For accessory proteins of DNA, the k-p network works for the activation of accessory proteins, and eventually may lead to a variety of phenotype.

The functional form of the proteins can be described even by dyadic value $\{0 \text{ or } 1\}$, in spite of complex chemical reactions involved in continuous medium. The dyadic value representation may lead to the threshold for excitable cells.

Hypothetical roles of k-p networks have also been addressed (Albert *et al*, 1994). For instance, k-p networks might be incorporated in the genesis of timing for cell division. Furthermore, it has been hypothesized that a variety of k-p networks may create a variety of time scales of chemical reactions involved in the cells.

Since k-p network-related reactions are too complicated, it seems to be practically impossible to model this system precisely, including a whole reaction process. One possible way, which has been actually taken, is to model with population dynamics, where average populations, for instance, of active and inactive channels are taken into account. The Hodgikin-Huxley's (HH) equations were proposed to explain the mechanism of neuron's firing, that is, of impulse generation, whose equations include this type of populations which bring about the dynamics of the voltage-dependent sodium and potassium conductance (Hodgikin and Huxley, 1952). Since HH equations include empirically determined functions of membrane potential, it is difficult to analyze mathematically. FitzHugh-Nagumo's (FN) equations (FitzHugh, 1961; Nagumo *et al*, 1962) are a simpler model to provide a neuron's firing, and it is easier to analyze mathematically.

Computer simulations of HH equations (FitzHugh, 1969) and dynamical systems analysis of FN equations FitzHugh, 1969) show that these dynamical systems have no saddle point when showing the excitability, where the saddle point can be responsible for the threshold by its stable manifold called separatrix, instead the threshold-like behavior for firing is produced by only one stable fixed point such that it has a specific orbital structure in its neighborhood in phase space.

It is not the present purpose to propose an alternative model of the HH equations or the FN equations. Rather our approach is based on a complementary aspect. The population dynamics approach is based on the notion of "external observations", while the present approach is based on the notion of "internal observations". The former can give an appropriate (but not always adequite) explanation for the underlying system, in terms of macroscopic or coarse-grained variables. The latter can give a constructive (but not always productive) description for the system, based on the logic consistent to the phenomena. Especially, the former approach is effective in the case that significant variables represent averaged quantities. On the other hand, the situation happens in the reactions of macromolecules that one specific molecule can play a key role of activation or inactivation of reaction chains even if its concentration is extremely low. Thus both approaches are complementary.

We here take into account, in particular, the model system consisting of the k-p network and ion channel proteins in order to clarify the functional significance of the model. The present approach is, however, universal in the sense that the theory is not restricted to some specific system but easily applied to any system such as described by logical statements. In particular, the network acting on the proteins is not necessarily the k-p network, but Ca-systems, other modified proteins, *etc* can also be taken into account. In the following model study, we will use the terms "kinase", "phosphotase", and "k-p network", but these can be replaced by other biological substance which possess similar reaction-specific properties.

Our model equations showing an indication of threshold are derived from simple axiomatic formulation. We try to extract an essential minimum of formal logic which likely underlies the process of functional manifestation of proteins or their networks initiated by k-p networks. For this formulation, at least five assumptions are necessary, as shown in the following subsection.

2.2 Assumptions for Modelling

Five assumptions are addressed in order to make an appropriate statement for k-p networks. We here view the protein as a computation machine for the state of k-p networks. In the following, the term "protein" implies protein's network as well as a single protein, since protein's network can be viewed as another protein.

Assumptions:

(1) *The protein works as an observer for k-p networks.*

(2) *The observation process is expressed as an inference process for the statement concerning the state of k-p networks. The records are kept until the functional manifestation of protein occurs.*

(3) *The protein calculates the truth values of statements and the process itself according to a basic logic like Lukasiewicz logic.*

(4) *For the protein, molecules are indistinguishable from others of the same kind.*

(5) *There is only one kination site for each of kinase, phosphatase and protein.*

The k-p network eventually activates or inactivates the protein. It is likely thought that this process depends on internal states of protein. Then, the protein will behave like an observer for k-p network. This is what is meant by the assumption (1).

The assumption (2) means that the protein possesses sufficiently complex structure to encode the behaviors of k-p network in a compressed manner. We will not deal with any physical mechanisms – what force works for the protein "observing" k-p network, what physical structure is necessary for such internal descriptions, *etc.* Instead, we will derive a biologically significant result only with a simple mathematical formulation.

The assumption (3) is concerning what logical statements are permitted within the system. This means the presence of restrictions on actual processes within the protein. The mechanism of such a process is not known, hence we adopt a formal logic for this restriction.

The assumption (4) is the indistinguishability assumption. The k-p network itself can be viewed as one protein. Thus for the protein, which kinase or phosphatase could work effectively is meaningless. Then, the assumption (4) is plausible for the present internal observer's model.

The assumption (5) is not essential, which was introduced for simplicity. Actually, it is known that there are also kinase, phosphatase, and proteins with two or three kination sites (Albert *et al* , 1994). In our framework, a plural kination site simply increases a number of variables. In order to avoid such an unnecessary complication of the model, we here assume only one kination site for each molecule. Though our model is actually primitive by this asumption, rather it can represent the essence of the internal logical process which might be hidden in simplified external observations.

3 Basic Logic and Its Transformation to Dynamical Systems

We deal with a basic logic, and further introduce the notion of "time" associated with an inference process. The basic logic adopted here is known as Lukasiewicz logic (for example, Rescher, 1969), especially in the field of fuzzy logic.

Let A and B be the statement, and $v(X)$ be the truth value of statement X.

Basic Logic:

$$\begin{aligned} v(\neg A) &= 1 - v(A), &(1)\\ v(A \land B) &= min[v(A), v(B)], &(2)\\ v(A \lor B) &= max[v(A), v(B)], &(3)\\ v(A \rightarrow B) &= min[1, 1 - v(A) + v(B)], &(4)\\ v(A \leftrightarrow B) &= 1 - |v(A) - v(B)|. &(5)\end{aligned}$$

Here, $\neg$ denotes *negation*, $\land$ *conjunction*, $\lor$ *disjunction*, $\rightarrow$ *imply*, and $\leftrightarrow$ *if and only if.* The truth value is defined on the unit interval, [0,1], namely a continuous truth value is here adopted. As is well known, only by two operations, *negation* and *conjunction*, any other operations are uniquely derived in case of dyadic logic. Since the truth value is extended to the real values on unit interval, the uniquness of interpretation for operations does no longer hold. One can have a plural expression of the right hand side of the above equations, all of which are identical in case of dyadic truth value. In the above logic, the operation $\lor$ is derived from two operations $\neg$ and $\land$, and the operation $\leftrightarrow$ is derived from the operation $\rightarrow$ but not derived from $\neg$ and $\land$. The operation $\rightarrow$ derived from $\neg$ and $\land$ has a different form from the above. Therefore, a general question in case of continuous truth value is how one defines *imply.* Actually, several interpretations have been proposed (Zadeh, 1975; Rescher, 1969). Among others, we choose the above form, since we believe it would be natural in biological operation.

Let us further introduce the notion of *time*, whereby the transformation from logic to dynamics is assured. This idea is not new, but first proposed by Spencer-Brown (1969) in the context of *laws of form*. Recently, a similar idea has been proposed by Nicolis and Tsuda (1985), Basti and Perrone (1992; 1995; Perrone, 1995), and also by Grim (1993) in the context of cognition of self-referential statements. These recent studies have been devoted to chaotic dynamical systems as what representing self-referential statements. Nicolis and Tsuda have addressed chaotic dynamics as one possible representation of cognitive process for self-referential and self-embedded statements, and derived a potential number of logical depth seen in human inference process for self-referential statements. Grim has derived chaotic maps corresponding to self- or mutual-reference with the Lukasiewicz logic. Taking, at the first stage of the theory, a self- or mutual-referential statement, Grim adopted linguistic truth value for such a statement, and then converted an inference process of the linguistic truth value to map.

It has not been, however, shown a general scheme for the transformation of logical statements expressing "events" to dynamical systems. On the other hand, Basti and Perrone have proposed a new scheme for computations with chaotic dynamical systems, introducing a notion of " dynamic axiomatization". In such a formalization, the undecidability problems that appear in formal axiomatic system are avoided due to an adaptive change of axioms depending on the context. Our present approach is deeply related with their approach, though we simply deal with a fixed logic in this paper. Actually, we will show that the Lukasiewicz logic is useful to obtain the biological threshold and sigmoidal function, but another logic reflected by population dynamics is useless for this purpose. It will not, however, be elucidated in the present paper whether or not the Lukasiewicz logic could provide the most appropriate model. There will be a possibility that actual biological systems use a dynamic axiomatization in Basti-Perrone's sense. This is left as an open question in this paper.

We introduce a dynamical system for the inference process concerning the truth value of statements describing the occurrence of events, as in the Grim's framework(1993). Let us consider the closed system S. Suppose N events occur in S. We make N statements, each of which is for a respective event. The closed system here means that each of N statements has at most N variables, that is, each statement does not refer to any other events than the events occuring within the system S. We are concerned with the determination process of their truth values. Each statement $P_j(e_1, e_2, \cdots, e_N)$ concerning events $\{e_i\}$ is viewed as *premise.* The corresponding *consequence* $C_j(e_j)$ is defined by the statement concerning the event e_j. Such an inference process is shown in Fig.1. The truth value of the statement P_j at time n determines the truth value of the statement C_j at time $n+1$. Thus we obtain n-dimensional dynamical systems (maps):

$$v_{n+1}(C_j(e_j)) = v_n(P_j(e_1, \cdots, e_N)), j = 1, \cdots, N. \tag{6}$$

Let us call the dynamics transformed from a logical statement a *logic dynamics*, generally, and, in particular, a *logic map* in case of map.

–Fig.1–

4 Analysis and Simulation of Logic Dynamics

4.1 Construction of Logic Maps

We adopt the formula of inference process developed in the previous section in order to describe the states of k-p network. Then dynamics obtained is viewed as an "observation process" by supposed protein. There can be several possibilities of statements, depending on the level of this internal description. We deal with two levels of statements. Let $< k >$ and $< p >$ be the statement that "kinase is active" and that "phosphatase is active", respectively. The following is the lower level of statement.

The statement 1

$$\begin{array}{ccc} Consequence & & Premise \\ < k > & \Leftarrow & < k > \wedge < \neg p >, \qquad (7) \\ < p > & \Leftarrow & < k > \wedge < \neg p > . \qquad (8) \end{array}$$

These are a simple self-referential statement if premise and consequence are identified. Since a molecule cannot be distinguished among molecules of the same kind due to the assumption (4), the statement that 'kinase is active' can be derived from the statement that 'kinase is active and phosphatase is inactive'. The statement about phosphatase is similarly obtained.

The equations of motions are provided as follows.

$$x_{n+1} = min[x_n, 1 - y_n], \tag{9}$$

$$y_{n+1} = min[x_n, 1 - y_n], \tag{10}$$

where we simply use the symbol x and y for the truth values of $< k >$ and $< p >$, respectively. Hence, the equation

$$x_{n+1} = \begin{cases} x_n & (0 \leq x_n < \frac{1}{2}) \\ 1 - x_n & (\frac{1}{2} \leq x_n \leq 1) \end{cases} \tag{11}$$

holds. Neutral fixed line $x_{n+1} = x_n$ $(0 \leq x_n \leq 1/2)$ appears. One possible interpretation of continuous truth values is a *certainty* of truth or an *uncertainty* of falseness. In this sense, a decision point of truth or falseness would likely be 1/2 if a final decision follows a dyadic truth value. Under this judgment, it is concluded for this statement that the protein cannot work, for the protein is assumed to work only when the kinase is active and the phosphatase is inactive. Furthermore, it is even true for this statement that the kinase and the phosphatase cannot be distinguished by the protein. Then we proceed to the further step, that is, to a higher level's statement in order to describe the situation of the protein being functional.

The statement 2

$$\begin{array}{ccc} \mathit{Consequence} & & \mathit{Premise} \\ < k > & \Leftarrow & < k > \leftrightarrow < k > \wedge < \neg p >, \end{array} \tag{12}$$

$$< p > \ \Leftarrow \ < p > \leftrightarrow < k > \wedge < \neg p > . \tag{13}$$

These statements are self-referential if premise and consequence are identified as in the statement 1, but much more complicated due to the presence of the *if and only if* operation. The statement that 'kinase is active' is derived from the statement that the statement 'kinase is active' is equivalent to the statement 'kinase is active and phosphatase is inactive'. The statement about phosphatase is similarly obtained. The premise for kinase leads to $1 - |x - min(x, 1 - y)|$, and for phosphatase $1 - |y - min(x, 1 - y)|$. Hence, the line $x + y = 1$ devides the unit square into two regions, called region I ($x + y < 1$) and region II ($x + y \geq 1$), respectively. Therefore, the equations of motions are as follows.

$$\begin{aligned} x_{n+1} &= 1, && (14) \\ y_{n+1} &= y_n && (15) \end{aligned}$$

in region I, and

$$\begin{aligned} x_{n+1} &= 2 - x_n - y_n, && (16) \\ y_{n+1} &= 1 - |1 - 2y_n| && (17) \end{aligned}$$

in region II.

In region I the dynamics brings about a uniform contraction of area, and chaos-driven dynamics appears in region II. Especially in region II, y-variable obeys a tent map which gives rise to chaos. Hence, the resultant dynamics is a composition of contraction and chaos-driven dynamics, which can give rise to nowhere-differentiable attractors (Kaplan and Yorke, 1979; Grebogi *et al*, 1984; Rössler *et al*, 1992, 1995; Rössler and Hudson, 1984). The present dynamical system provides a fruitful result for dynamics itself and for computational capability, too.

4.2 Dynamical Features of the Logic Map

It is easily verified that the above dynamical system possesses two fixed points, both of which are unstable. Fixed points are $(x^*, y^*) = (2/3, 2/3), (1, 0)$. It turns out by linear stability analysis that each fixed point is neutral in one eigendirection and unstable in another eigendirection. The fixed point (1, 0) is just an admissible truth value of the statement 2 in the case of dyadic logic. Thus an extension of the truth value to real numbers makes dyadic logic unstable.

Since orbits consisting of successive dynamical truth values must be bound in the unit square, a set of orbits forms a nontrivial geometrical object. Actually, we obtain a geometry as in Fig.2. The Jacobian is 0 in region I ($x+y<1$), and in region II it is 2 for $y \geq 1/2$ and -2 for $y<1/2$. As shown in Fig.3, however, the region II (the upper triangle in the figure) is mapped to the trapezoid with folded triangle. Since the region I shrinks onto the line $x=1$, the entire unit squre is mapped to the same trapezoid, thus the phase volume is contracted. This fact leads to an attracting invariant set. The construction of invariant set is made as follows. A point is mapped on the line $x=1$ whenever it enters in the region I. The line $x=1$ is mapped to the folded line $y=1-|1-2x|$. The mapped lines are successively mapped to another lines. The portion of the mapped line drop in the region I, which is mapped again to $x=1$, but the other portion remains in the region II, where phase volume is expanded. By this expansion of phase volume in region II, the orbits leave this region before long and come into the region I. Thus a set of lines mapped successively, starting from $x=1$ forms an invariant set.

–Fig.2–

–Fig.3–

Complexity of dynamics stems not only from this point but also from the structure of mapping the line $x=1$. The lower half portion of this line ($y<1/2$) is mapped to the line $y=2-2x$, keeping the order of y-direction, while the upper half ($y \geq 1/2$) is mapped to the line $y=2x$, converting the y-direction. This way of mapping $x=1$ gives rise to a mixing property of orbits as well as the presence of overlapping region seen in region II.

A specific feature of the invariant set is an intersection of the manifold, which is unusual in ordinary chaotic dynamics, namely it is not seen in strange attractors. It seems that there exist infinitely many intersections. Nowhere-differentiable or singular-continuous nowhere-differentiable attractors are typical in chaos-driven contraction maps. This class of dynamical systems have been widely investigated by Yorke and his colleagues (Kaplan and Yorke, 1979; Grebogi *et al*, 1984), and more recently by Rössler and his colleagues

(Rössler *et al*, 1992, 1995; Rössler and Hudson, 1984). The present dynamics is similar to this class but slightly different in the sense that the dynamics is a composite of uniformly contraction dynamics and chaos-driven neutral dynamics.

Furthermore, the map possesses a discontinuity on the line $x+y=1$. Thus it is a patchy and folding map. The presence of intersection of unstable manifold itself stems from this discontinuity. A patchy and folding map was first investigated by Moore (1990, 1991) to elucidate an computational capability of dynamical systems. The present dynamical system is similar to a generalized shift invented by Moore.

4.3 Computational Features of the Logic Map

Moore studied a piecewise-linear map, called a generalized shift in order to elucidate a computational power of dynamical systems. In a machine representation of chaos, an orbital instability is replaced by the motion of "machine head" such that it moves on "tape" by α bits per iteration in average, where α is a positive number. On the other hand, one can construct a generalized shift such that the head moves on tape by α bits per logarithm of iteration. This means the power divergence of nearby orbits. This character of generalized shift stems from a composite dynamics of the patchy and folding. By this mechanism, not unpredictability by orbital instability but undecidability is assured in the following sense. Provided some appropriate subset of a domain of definition, ask when orbits enter into this region, or ask if orbits eventually arrive there. These questions are undecidable in the specific generalized shift as well as in a universal Turing machine. A universal machine mimics any other machines' behaviors. Correspondingly, a universal computation with dynamical systems requires a variety of well-formed domains, where the symbolic dynamics must not be interfered by another symbolic dynamics defined on another domain. This means that a decimal point in symbolic dynamics must not move even by one bit in average, which gives rise to zero-Lyapunov exponent. A power divergence of nearby orbits provides the upper limitation of this case. Actually, a power divergence can restrict the domain for each well-formed initial condition, where the supposed "machine head" moves .

Moore adopted horseshoe map (Smale,1967), where one direction in phase space is responsible for contraction (exponential convergence) and another for expansion (exponential divergence). This is a typical structure of chaos. In horseshoe map, linealy stable and unstable manifold is identical to the globally stable and unstable manifold, respectively. Thus, the calculation of eigenvalue in each eigendirection determines a positive or a negative Lyapunov exponent. In case of a generalized shift, however, exponential divergence and convergence are mixed in each eigendirection by means of a patchwork of phase space. By this mechanism, a power divergence, that is, an exponential divergence in logarithmic time scale can take place in some special case of generalized shift, namely the case that divergence and convergence completely cancel out in tangent space along the orbits.

We calculated the Lyapunov exponents in our logic map. The largest exponent $\lambda = 0.56$, and the second one is -∞. In usual *differentiable* dynamical systems, it is difficult to get a power divergence of nearby orbits. Because an exponential divergence apparently appears if at least a linear term of dynamical equations is present. Moore proved that the generalized shift which possesses a power divergence can be embedded in three-dimensional *differentiable* dynamical systems (Moore, 1991). Even in this case, if one calculates the exponent in three-dimensional full space, using Jacobian matrix in tangent space, one would obtain a positive Lyapunov exponent. On the other hand, it would be rather easy to get a power divergence in a *projected* dynamics of differentiable dynamical systems possessing exponential divergence, for it can behave like a random noise.

Then, we took a specific direction along which the local divergence of nearby orbits were calculated at every time step. Thus the second exponent is meaningless in this scheme. This scheme gives the exponent for the projected dynamics to this direction. It is, however, unknown to specify precisely what projected dynamics appears. Hence, from a computational viewpoint, it is situated that we have introduced an *oracle* such that the dynamical system projected to that direction is well-defined and we can always specify the dynamical orbits. Assuming this kind of oracle, we can obtain an almost power divergence in our logic map in the direction $(cos\pi/b, sin\pi/b)$, which may give rise to universal computation.

Figure 4 indicates the power α for an average local divergence of nearby orbis with the logarithmic scale, n^α, in the case of $b = 11.3$. Since the orbits do not diverge up to around 100,000 time steps, various kinds of machine codes can be embedded up to this time. The time within which the orbits do not diverge can be extended unlimitedly by adjusting the parameter b. Hence, this projected dynamics has an capability of universal computation, provided the oracle that projected dynamics is precisely described. The necessity of strong oracle like this apparently weakens the computational power of the present dynamics. On the other hand, there is no necessity of any oracle for a universal computation in Moore's generalized shift. This problem is left for further studies.

–Fig.4 (a) and (b)–

4.4 Emergence of Sigmoidal Function – A Precursor of Threshold

We investigated an invariant measure of the map. This study elucidates a probability measure of the truth values for kinase and phosphatase. Figure 5 shows this invariant character.

–Fig.5 (a) and (b) –

As seen in the figure, the probability density for kinase $p(x)$ is roughly a sigmoidal function, and $p(y)$ for phosphatase is an inverse-sigmoidal function, if we neglect fine structures. This means that for kinase the truth value larger than 0.5 is realized with high probability, while the truth value for phosphatase smaller than 0.5 is relatively probable.

Therefore, the phosphatase is likely inactive, whereas the kinase is likely active in the inference process on the statement 2 based on the Lukasiewicz logic. By the assumptions, this gives rise to the activation of ion channel protein. The ion channel protein can become active probabilistically according to the dynamics. The sigmoidal function obtained here provides the probability of this activity, and it also seems to provide a decision point beyond which it becomes active. A question arises: where should the decision point be?

Generally, a sigmoidal function is found in excitable media as what producing all-or-none response of the system. A typical system is a neuron or even a neuron assembly (Freeman, 1975). Actually, in neuronal modelling a sigmoidal function is usually used, where it indicates firing probabilities for given membrane potential. The present sigmoidal function also represents probabilities for given truth values of the statement about kinase and phosphatase. Although the emergence of sigmoidal function suggests the presence of threshold, the sigmoidal function itself does not provide the dynamical threshold. Nevertheless, this function can provide a basis to produce a threshold. In this sense, we call the sigmoidal function obtained here a "precursor" of threshold.

Furthermore, it would not be reasonable to think that the protein actually follows the sigmoidal function in order to make itself be functional. Because if it is so then the protein must have a mechanism to calculate the truth values over a long time and to average the truth values. Some mechanism for transformation of this computational complexity in time axis to that in spatial axis is needed for an effective functional manifestation.

In the next section, we will show the emergence of threshold in the domain of solutions of functional equations constructed for "self-description" of the protein, whereby the transformation of computational complexity to the spatial domain can also be obtained.

5 Functional Map with Dynamical Variables – An Emergence of Threshold

A hypothetical diagram for "self-description" is depicted in Fig.6. A new assumption for protein is introduced.

–Fig.6–

Assumption:

(6) *The protein has a code for self-description.*

The self-description here is performed by mimicing the dynamics expressed as a protein's description for the k-p networks. Therefore, it is natural to represent the self-description by functional maps with dynamical variables representing the description for the k-p network, eqs. (14)-(17). We made such functional equations, adopting the additional relation that has been widely used in fuzzy logic (see for example Grim (1993)).

$$Z_{false}(x) = Z_{true}(1 - x). \tag{18}$$

The function $Z(x)$ implies a *certainty of description* Z with respect to the truth value x. In fuzzy logic, this relation is introduced to imply $Z(x)$ by a fuzziness of the truth value x, thus the assumption of the above symmetric relation is natural. In our case, the symmetric relation is used simply because of simplicity of the model, thus by this relation one kind of interpretation is introduced. Let us write functional maps for the statement 2, based on the Lukasiewicz logic.

$$\begin{aligned} f_{n+1}(x_{n+1}, y_{n+1}) &= 1, & (19) \\ g_{n+1}(x_{n+1}, y_{n+1}) &= g_n(x_n, y_n) & (20) \end{aligned}$$

in region I, and

$$\begin{aligned} f_{n+1}(x_{n+1}, y_{n+1}) &= 1 - |f_n(x_n, y_n) - g_n(x_n, 1 - y_n)|, & (21) \\ g_{n+1}(x_{n+1}, y_{n+1}) &= 1 - |g_n(x_n, y_n) - g_n(x_n, 1 - y_n)| & (22) \end{aligned}$$

in region II.

Here, f is the certainty of self-description for the truth value x of kinase affected by phosphatase through the equations of motions of x and y, *i.e.*, eqs.(14)-(17). The function g is a similar one for the truth value of phosphatase. Thus the functions f and g have both arguments x and y, respectively. We call the dynamics of x and y a *lower dynamics*, and the dynamics of f and g a *higher dynamics*. Here a lower and a higher dynamics are almost identical, only the difference of which comes from the relation (18).

A fixed function in functional space is $f(x, y) = x$ and $g(x, y) = y$ which are trivial solutions. The implication of these solutions is an identical self-description for the truth values of kinase and phosphatase. Our concerns here are nontrivial solutions. Since the arguments change their values chaotically in each time, there is no unique asymptotic functional value for each function, f or g. Furthermore, in order to solve the functional equations at n-time step, one needs n times inverse mappings for lower dynamics, which gives rise to at most 2^n solutions, except for the inverse mappings of $x = 1$ which provide a continuously infinite number of solutions. This point is made clearer, if one takes into account the following functional equations on $[0,1] \times [0,1]$.

$$h_{n+1}(z_{n+1}) = \tilde{F}(h_n(z_n)), \tag{23}$$

$$z_{n+1} = F(z_n), \tag{24}$$

where z $\in [0,1] \times [0,1]$. The formal solution at n-time step is given by

$$h_n = \tilde{F}^{(n)} \circ h_0 \circ F^{(-n)}, \tag{25}$$

where h_0 is a given initial function. Although the argument $1 - y$ on the right hand side of our functional maps is included, corresponding to the argument y on the left, the above form h_n represents the main structure of solutions without loss of generality.

The lower dynamics, eqs.(14)-(17), transforms the unit square to the trapezoid (hatched region) as shown in Fig.3. Hence, if the inversely-mapped point drop on the residual region, that is, a triangle region in the figure, the inverse mappings are no longer defined. Actually, the domain of definition for the functional equations, eqs.(19)-(22) shrinks rapidly and eventually to zero. This process is shown in Fig.7.

–Fig.7 (a), (b), (c), and (d)–

In order to solve the functional equations, avoiding this difficulty, we assume some function for each of f and g in the undefined region of inverse mappings. Since the solution at each time step is the multivalued due to multivaluedness of the inverse mapping of the lower dynamcs, what we should be concerned with is the domain of solutions. In Fig.8 we show this domain after convergence, where we used a MonteCarlo simulation. In this figure, we adopted $f_0(x,y) = g_0(x,y) = (x+y)/2$ and the same functions as an assigned function for the undefined region.

–Fig.8 (a) and (b)–

For almost all truth values in the well-defined region, the solutions are bound to the domain greater than 0.5, except for the solutions at $x = 1.0$. Since the truth value $x = 1.0$ has infinitely many numbers of inversely mapped points, this is excluded from our discussion. The figure shows a certainty f is greater than 0.5 for the truth values of kinase that is greater than the value a, and a certainty g is also greater than 0.5 for the truth values of phosphatase that is less than the value b. We see here the threshold as a restriction of functional values. The values a and b vary moderately and continuously by a change of the cross-section perpendicular to y- and x-axis, respectively. According to the rapid (around ten steps) convergence to zero measure of well-defined domains of functional solutions in case without assigned functions, the restricted domain in case with assigned functions converges rapidly (around ten to fifteen steps).

We also performed the simulations with .various combinations of the initial and the assigned functions, and concluded the appearance of threshold in the above sense, although the value of threshold varies depending on the functional form of initial and assigned functions. It would be interesting to note that the threshold value is easily controled by choosing the constant-valued assigned functions.

From the computational viewpoint, the long-term memory necessary for the description of sigmoidal functions appeared in invariant measure is here replaced by the spatial memory. One may conceive that the geometrical (structural) complexity of proteins might be necessary for this spatial complexity of computations.

6 Summary, Related Topics and Outlook

We proposed a possible scheme to understand a mechanism of dynamic behaviors in complex networks. In particular, a kinase-phosphatase network so called "kinase-kinase" was treated as one example, provided that ion channel proteins or their network becoming to manifest a specific function by kinations can be viewed as a molecular machine such as describing that network. In order to represent this description explicitly, we dealt with a logical statement concerning the network characteristics, whose statement was assumed to be encoded by proteins. This assumption would be rational if the machinery within proteins to read and write the reactions affecting the protein itself by means of some code such as seen in DNA of DNA-proteins complex is allowed. We could not designate here its physical mechanism, but instead we obtained biologically significant results only with the dynamics according to the logical statements.

In relation with this dynamics, we introduced a transformation from logical statement to dynamical systems, assuming a basic logic and one time-step delay in obtaining consequence from premise. The dynamical variable was a truth value defined on the unit interval. A natural extension from dyadic truth values to continuous truth values was developed. Accordingly, the lower level's statements had a consistent truth value with a dyadic logic. This led, however, to the conclusion that kinase is inactive, which gives rise to the mulfunction of protein. The truth value of the higher level's statements represented by the fixed point of converted dynamical systems was just identical to the truth value in case of dyadic logic. In this case, the fixed point was unstable, giving rise to a chaotic behavior. It should be noted that this is a consistent statement in a dyadic logic. It would be interesting to note that in general an inconsistent and self-referential statement is converted to periodic orbits, whereas chaotic orbits are derived from a consistent and self-referential statement in the sense of linguistic truth value (Grim, 1993). Actually, our higher level's statement is consistent and self-referential.

Our dynamical system is not a differentiable, but a patchy and folding map by the presence of discontinuity on the decision line $x + y = 1$. In this sense, we discussed a similarity of our dynamics to a generalized shift from a computational viewpoint. It turns out that our dynamical system is a universal machine with oracle. At the moment, our oracle is too strong which makes our system be weak as a computation machine. Studying the oracle and reducing its power are left for future studies.

The invariant measure of the truth values showed a sigmoidal and an inverse-sigmoidal function for kinase and for phosphatase, respectively. The appearance of sigmoidal function indicates that a precursor of threshold can be derived in the present scheme. We further introduced a dynamics-dependent functional map in order to elucidate an effect of self-description, whereby a threshold was obtained, which is defined by the borderline beyond which the solutions of functional equations exist.

The mechanism of threshold in excitable cells like neurons has not been clearly known. In both Hodgikin-Huxley's equations and later proposed FitzHugh-Nagumo's equations for action potential, the presence of nonuniformity of orbital density is viewed as a dynamical mechanism of threshold. Our approach is complementary to these studies in the following sense. In place of population dynamics which is actually used in their equations, the logic map was adopted, based on the notion that proteins do not always work as a population but often work as individual. This is the reason that we regarded the proteins as a computational machine on real numbers. In this context, we obtained the nonuniformity of orbital density in the space of truth value representing a computational capability as a machine.

Our theory provides the following view concerning neuron's firing. Proteins have four kinds of code concerning $< k >$, $< p >$, f and g. The value within the domain of definition of f and g is determined in time by the value of $< k >$ and $< p >$ at that time, therby whether the polarization occurs is determined. Therefore, the poteins do not necessarily memorize all the values of the functionals, but sufficiently process the value at each time. Furthermore, the present formalization can be applied to various levels of processings such as proteins, a single neuron, neuron assemblies and even human behavior.

There are still several issues left to be discussed. In the following, we will adrress these issues and discuss them in more details, and also discuss some other related topics.

(1) *Another Basic Logic*

Our results depend on the kind of basic logic. It would be interesting to know what happens if one changes basic logic. The following logic was made, taking into account a population dynamics.

logic p:

$$\begin{aligned} v(\neg A) &= 1 - v(A), \qquad (26) \\ v(A \wedge B) &= v(A)v(B), \qquad (27) \end{aligned}$$

$$\begin{aligned} v(A \vee B) &= 1-(1-v(A))(1-v(B)), && (28) \\ v(A \rightarrow B) &= 1-v(A)(1-v(B)), && (29) \\ v(A \leftrightarrow B) &= 1-v(A)-v(B)+v(A)v(B)(3-v(A)-v(B)-v(A)v(B)). && (30) \end{aligned}$$

Here, the operations $\neg$ and $\wedge$ are used in the derivation of other operations. The difference from Lukasiewicz logic lies in the definition of 'AND'. Defining 'AND' by *product* makes us imagine a probability. Actually, the truth value $v(P)$ here can be viewed as the probability of the occurance of event P. This corresponds to the aspect that the populations of kinase and phosphatase are taken into account when determining their truth values. Let us briefly see the dynamic behaviors when adopting this logic.

The equations of motions concerning the truth values are as follows for the statement 1.

$$\begin{aligned} x_{n+1} &= x_n(1-y_n), && (31) \\ y_{n+1} &= x_n(1-y_n). && (32) \end{aligned}$$

Hence, one-dimensional map follows.

$$x_{n+1} = x_n(1-x_n). \tag{33}$$

This is just the case of $a = 1$ in so called logistic map $x_{n+1} = ax_n(1-x_n)$. The asymptotically stable truth value is obviously $x = y = 0$. This indicates that the statement 1 is false. This is also intuitively correct. This asymptotically stable consequence implies that the protein describing the k-p network with the lower level's statement cannot work. One reason for this inability is that the protein cannot even distinguish kinase from phosphatase. Another reason is that zero-truth value for kinase indicates the inactivation of protein.

For the statement 2, the equations of motions are as follows.

$$\begin{aligned} x_{n+1} &= 1-x_n-x_n(1-y_n)+(3-x_n-x_n(1-y_n)-x_n^2(1-y_n))x_n^2(1-y_n), && (34) \\ y_{n+1} &= 1-y_n-x_n(1-y_n)+(3-y_n-x_n(1-y_n)-x_ny_n(1-y_n))x_ny_n(1-y_n). && (35) \end{aligned}$$

There are two fixed points, one of which is (1, 0). This "true" fixed point is unstable also in this case, but another fixed point is stable, thus dynamical orbits converge to this stable fixed point. No chaotic orbit appears, therefore, no threshold function was obtained. The probabilities of kinase and phosphatase being active are simply determined. Hence, the present approach will give no useful information in case with this logic.

(2) *Self-Reference and Threshold*

For the present study, a choice of Lukasiewicz logic is essential. It should be, however, noted that the operation *min* is not a direct cause of the emergence of threshold, but indirectly related. This operation provides a patchy dynamics.

In the logic map, eqs.(14)-(17), the chaotic component stems from the tent map in y-variable (eq.(17)), which possesses a uniform invariant measure. The tent map stems from a self-reference of the statement. In region II, x-variable conserving a measure by itself is driven by chaotic y-variable. By one iteration of the dynamics in region II, an area restricted to $y < 1/2$ increases relatively as three times an area restricted to $y > 1/2$. On the other hand, region I permits the y-value to conserve. Thus, the measure in y-direction is roughly estimated to be biased to lower values of y-variable by the composite dynamics in whole space. The measure in x-direction is roughly determined by the term $1 - y$, whereby it can be biased to higher values of x-variable. Hence, the appearance of sigmoidal functions, thus the threshold, too, is due to both the self-referential statement and a specificity of Lukasiewicz logic such as giving a piecewise linear map.

(3) *Linear Demon*

It would be worth relating the emergence of sigmoidal function to the generation of unidirectional movements from randomly varied environments such as observed in actomyosin system (Ishijima *et al*, 1991), and in flagella motor system (Murase, 1992). This is also to find a mechanism of *demon* within proteins similar to Maxwell's demon (McClare, 1971).

A particle in one-dimensional symmetric potential can statistically move in one-direction (a break of detailed balance in nonequilibrium conditions (for this break due to effective asymmetric potential in muscle contraction, see Mitsui *et al*, 1988) if the particle is additionally driven by random motions derived from some chaos (Hondo and Sawada, 1995). This is due to higher ordered correlations or high probabilities of successive increase (or decrease) of dynamical increments of orbits in chaotic systems (Hondo and Sawada, 1995).

The dynamical demon was proposed (Zaslavsky, 1995) in another context that dynamical orbits possess high probabilities to stay in some region of phase space according to a power law distribution, even if the initial distribution is uniform.

Let us discuss another *demon* related to our model. Suppose a random motion represented by chaotic dynamics with uniform measure. As a possible mechanism of rectifying a random motion, one can propose a linear system with a resetting mechanism. The "demon" described by linear equation, say, $x_{n+1} = 2 - x_n$ is simply driven by a random motion and records x_{n+1} if $x_{n+1} \leq 1$, and otherwise it initializes the value of itself. Only by this simple mechanism, the random motion is rectified, namely the transformation from uniform measure to biased measure appears in x-variable of this *linear demon*. Thus, unidirectional movements of proteins can be created if this biased measure is directly transformed to the motion.

The work of *linear demon* is actually cheap, since any judgment about the values of random variable is not required. Only the judgment is on the value of itself. The record of the values of demon itself can be *rough* as the same degree as the digital computations. Moreover, this record can be discarded whenever the new value is recorded. For discarding the record, the heat will be taken inside.

A similar mechanism has been proposed in terms of neural networks with a resetting mechanism to simulate a dynamically successive association of memory (Tsuda, 1991a; 1991b; 1992; 1994) , where the random resetting gives rise to chaotic itinerancy (Ikeda *et al*, 1989; Kaneko, 1990; Tsuda, 1991). It would be worth elucidating the detailed relations between dynamical demon and chaotic itinerancy in this context.

(4) *Learning*

The issues proposed here will be useful also for understanding a learning mechanism in brain. Recent studies about the long-term potentiations (LTP) and the long-term depressions (LTD) in hippocampal pyramidal cells have proven an internal mechanism for the dynamics of memorizing process. Especially, kinase-phosphatase networks play an important role for the interactions of NMDA- and AMPA-receptors (Tsumoto, 1992). The studies for this issue within the proposed framework will be published elsewhere.

(5) *Description Level*

The proposed framework will be useful for understanding a complex system such as macromolecules' networks, metabolic networks, neural networks, and so on, where a huge amount of descriptions is demanded if one tries to explicitly write down the details of the reactions. Even if one could possess the details of the network, it would not be useful for understanding the system to adopt the all of those descriptions. In such a situation, one useful way is to find a macroscopic description, thereby a macroscopic averaged behavior can be extracted. The success of this description is guaranteed only when the time scales are separated at macroscopic and microscopic levels.

In complex systems, however, the dynamic behaviors such that the elementary dynamics does not necessarily obey the population have been observed. Among others, chaotic itinerancy (Ikeda *et al*, 1989; Kaneko, 1990; Tsuda, 1991) has been widely investigated, even in brain dynamics (Tsuda, 1991a; 1991b; 1992; 1994; Nara and Davis, 1992; 1995; Freeman, 1994; 1995; Kay *et al*, 1995). The appearance of chaotic itinerancy can be an indication of the presence of interplay between macroscopic and microscopic events. Then, usual population dynamics approach is insufficient for better understanding of the system. Our approach adopted here will provide an explicit description of such an interplay.

(6) *Description Stability*

The formulation of self-description in terms of functional equations treated in the last section leads to the notion of *description stability* (Tsuda, 1990; Kaneko and Tsuda, 1996). This is also a generalization of pseudo-orbit-tracing properties in dynamical systems.

Let f be a continuous map on compact space M. Let x be a point in this space. The point x is transformed to $f(x)$, $f^2(x)$, and so on. This transformation defines a dynamical orbit. Let us conceive an "observation" of this orbit with numerical simulations or experiments. The observed orbit is not always identical with the dynamical orbit, because of contaminations by round off errors or by accidental pertubations. Let $\{y_i\}_{i=0,1,\cdots}$ be an observed orbit. If there exists $\alpha > 0$ such that $f(y_{i-1})$ is in the α neighborhood of y_i for any i, then $\{y_i\}_{i=0,1,\cdots}$ is called an α pseudo-orbit. Furthermore, if for some $x \in M$ there exists $\beta > 0$ such that $f^n(x)$ is in the β neighborhood of y_n for any n, then the pseudo-orbit $\{y_i\}_{i=0,1,\cdots}$ is β-traced by x. If any α pseudo-orbit is β-traced, then (f, M) has a pseudo-orbit-tracing property. This scheme is shown in Fig.9(a). The pseudo-orbit-tracing property indicates the stability of dynamical systems associated with observations, which is related to structural stability (Smale, 1967).

Our functional equations have a similar scheme, which is shown in Fig.9(b). Here, a function $f(x)$ is viewed as a description. If a map F and a function f are continuous on compact space M and X, respectively, our scheme can be reduced to the similar formulation to pseudo-orbit-tracing property. Our scheme is, however, not restricted to the stability associated with obervations, but generally deal with the stability associated with descriptions concerning the system itself. One may say in the following. Suppose a dynamical system F and a described system $\tilde{F}$. If there exists $\alpha > 0$ such that $F \circ f_{i-1}^{-1} \circ \tilde{F}^{i-1}$ is in the α neighborhood of $\tilde{F}^i$ for any i, then we say that $\{\tilde{F}^i\}_{i=0,1,\cdots}$ is α pseudo-dynamical system. Furthermore, if for some description $g_0 \in X$ there exists $\beta > 0$ such that $F^n \circ g_0^{-1} \circ \tilde{F}^0$ is in the β neighborhood of $\tilde{F}^n$ for any n, then we say that pseudo-dynamical system $\{\tilde{F}^n\}$ is β-traced by g_0. If any α pseudo-dynamical system is β-traced, let us say that (F, M) has a pseudo-dynamical system-tracing property, or a *description stability*.

Our functional equations have a trivial solution $f^n(x) = x$ for any n. A slight perturbation for this identity function makes the descriptions deviate far from the original dynamical system F. Therefore, our system would be in the class of description instability. On the other hand, the question arises: what dynamical systems are they in the class of description stability? This question is still immature and vague. We have to refine this idea.

–Fig.9 (a) and (b)–

(7) *Internal Observer*

The present system was derived, based on the supposed internal structure of proteins viewed as a machine. Thus, the present theory can be viewed as an observer-oriented theory. This viewpoint has been widely investigated in several contexts. Matsuno (1989) has pointed out that for the understanding of biological functions the machinery embedded in macromolecules must be reconstructed in a different framework from ordinary physical law. He named biology to be investigated at this standpoint *protobiology* (Matsuno, 1989). Gunji (1994) has followed Matsuno's idea and tried to construct an observer-oriented theory by means of category theory. Earlier, Rosen (1986; 1993), and Shimizu (Shimizu and Yamaguchi, 1987) independently started to formulate an internal observer theory in order to study a genesis of *relation* formation which is essential in functional manifestations of biological organisms.

These theories and our present theory are related with *endophysics* proposed by Finkelstein (1983), and Rössler (1987). An object of endophysics is, however, a Hamilton system which does not hold in almost biological systems, where instead dissipative systems (Nicolis and Prigogine, 1977) can be an appropriate model. Our present theory might be viewed as what could first provide concrete and biologically significant results at the standpoint of internal observers.

From "*endo*viewpoints", our theory is related to molecular computations (Pattee, 1973; Conrad, 1973; Liberman, 1979). Intracellular molecular networks can be viewed as a computation machine, where various functions of cells are realized by parallel and/or serial processes of reactions giving rise to specificity. The present theory also provides a logical basis of *specificity* seen in molecular computations.

(8) *The Possibility of Actual Proof*

The present theory is a formal theory, not a biophysical one for a genesis of biological threshold, in the sense that we simply proposed a possible causation. Therefore, it would rather be surprising that the Lukasiewicz logic and the inference process were thus effective to bring about a sigmoidal and also a threshold function. Is there any possibilities that the present theory will be substantiated by biological experiments?

All assumptions adopted here are related to microscopic structures and dynamic behaviors of proteins. Taking into account a tactile process of proteins (Liberman, 1975; Conrad, 1985), it would be reasonable to think that proteins may behave like a digital computer to some degree. Here, a digital computation will be done in both a serial and a parallel manner (Conrad, 1985). Therefore, if the internal structure and microscopic dynamics of proteins are sufficiently investigated, then the mechanism of computations proceeding within the proteins will be clarified. At this stage, the biological implications of the assumptions in our theory can be judged if they could actually make sense. In particular, the theory will be partially verified by studying the correlations between the change at, for instance, kination sites and the change of internal structure of the proteins.

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Figure captions

Fig.1 Inference process for the truth values of N statements concerning N events occuring in the closed system S.

Fig.2 Attractor of the logic map (eqs.(14)-(17)) derived from the statement 2. Simulations of the tent map were performed by replacing the value 2 by $2 - \varepsilon$ ($\varepsilon = 10^{-6}$), otherwise the map gives the value 0 after some iterations, for the tent map is just a binary computation.

Fig.3 Transformation of phase space by one iteration of the logic map (eqs.(14)-(17)). See also Fig.7(a).

Fig.4 Almost power divergence of nearby orbits seen in the projected tangent space to the direction $(cos\pi/b, sin\pi/b)$, where $b = 11.3$. Abscissa denotes a discrete time n, and ordinate a power α when the divergence is measured by n^{α}. If the scale is taken as exponential divergence, the exponent is calculated as almost zero, *i.e.*, the order of 10^{-6}. (a) up to 30,000 time steps, and (b) up to 100,000 time steps.

Fig.5 Invariant probability distribution $p(x)$ in x-direction ((a)), and $p(y)$ in y-direction ((b)) for the logic map (eqs.(14)-(17)). Here x is the truth value of kinase, and y the one of phosphatase. Since the density at $x = 1$ is extremely high by the dynamical rule adopted, the density at $x < 1$ is shown in (a).

Fig.6 A scheme for self-description of the system. "Protein" indicates a single protein or protein networks.

Fig.7 The existence regions denoted by dots at each time step n of the functional values of the functional map (eqs.(19)-(22)). (a) n=1, (b) n=3, (c) n=5, and (d) n=8.

Fig.8 A set of the functional values of the functional map (eqs.(19)-(22)) with assigned functions $f_0(x,y) = g_0(x,y) = (x+y)/2$. (a) The invariant domain of solutions for $f(x,y)$ at the cross-section $y = 1.0$. (b) The invariant domain of solutions for $g(x,y)$ at the cross-section $x = 0.3$. The inverse mappings at $x = 1$ form vertical segments or domains, depending on the value of cross-section, which are omitted in the figure. For numerical solutions of the functional equations, the Monte Carlo simulation was adopted for 1,000 by 1,000 subregions in the figure.

Fig.9 (a) Pseudo-orbit-tracing property. (b) Description stability.

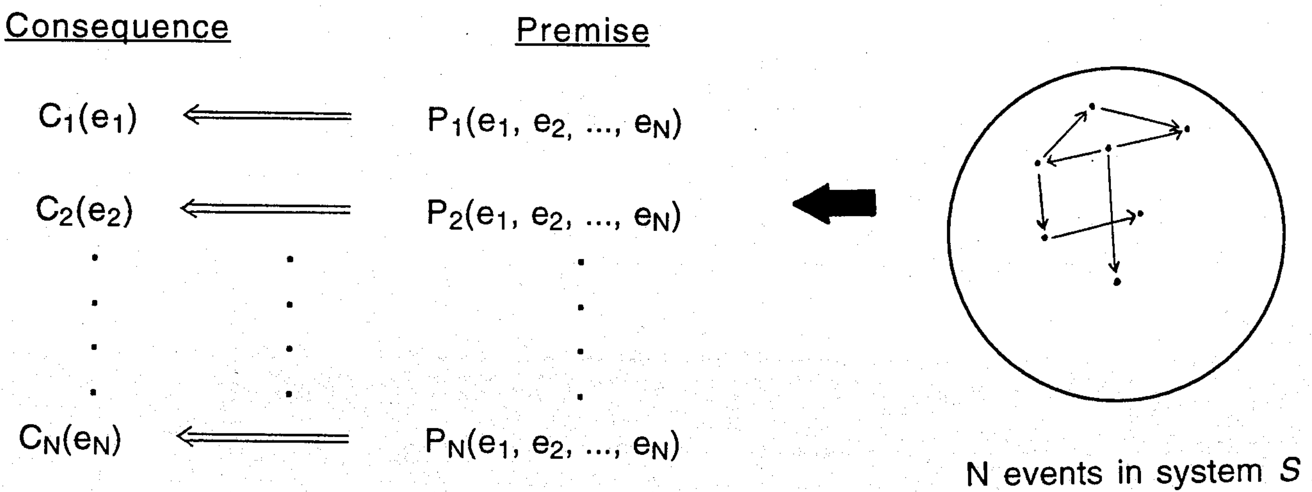

Fig. 1.

I. Tsuda & K. Tadaki

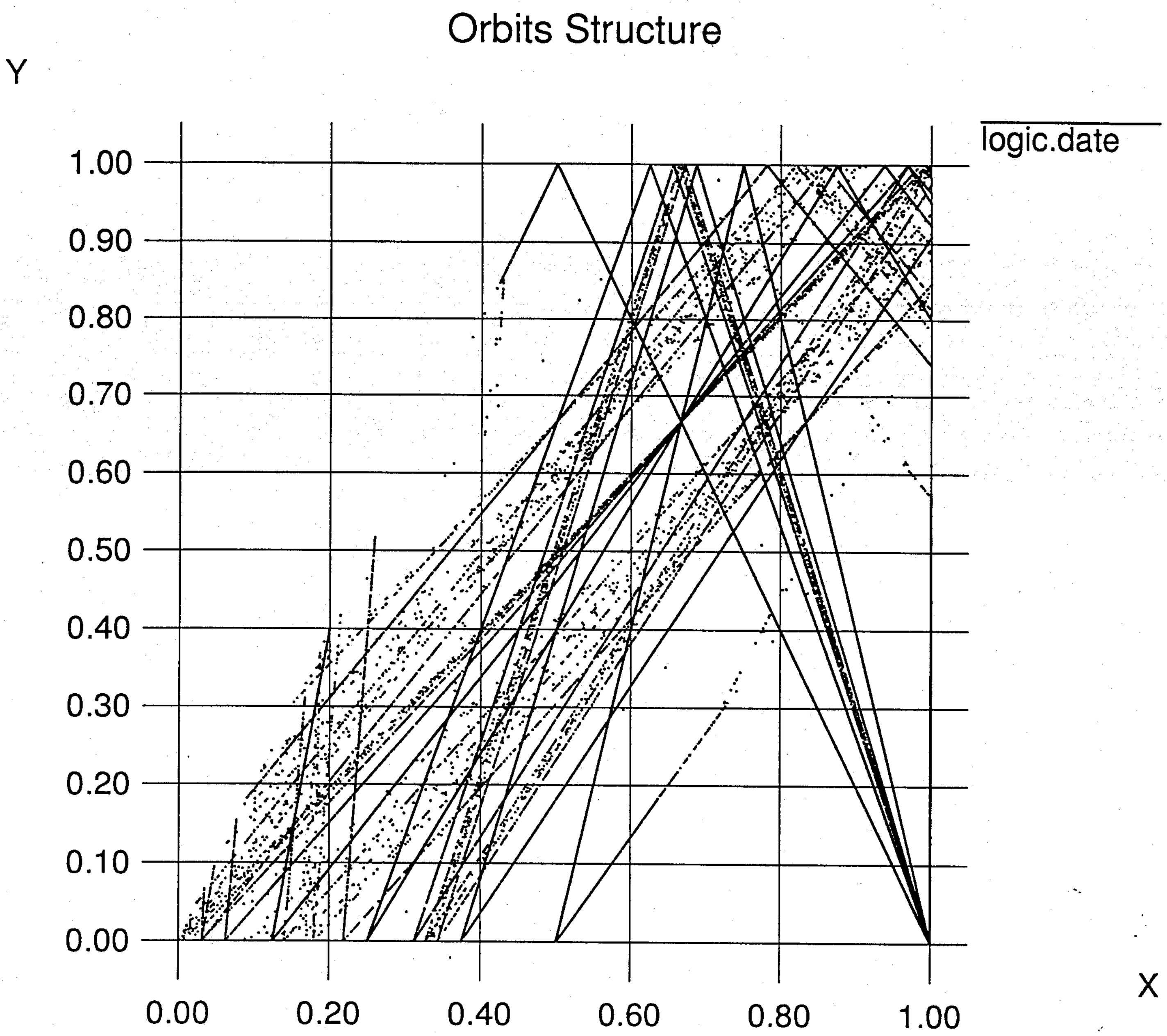

Fig 2.

Tsuda & Tadaki

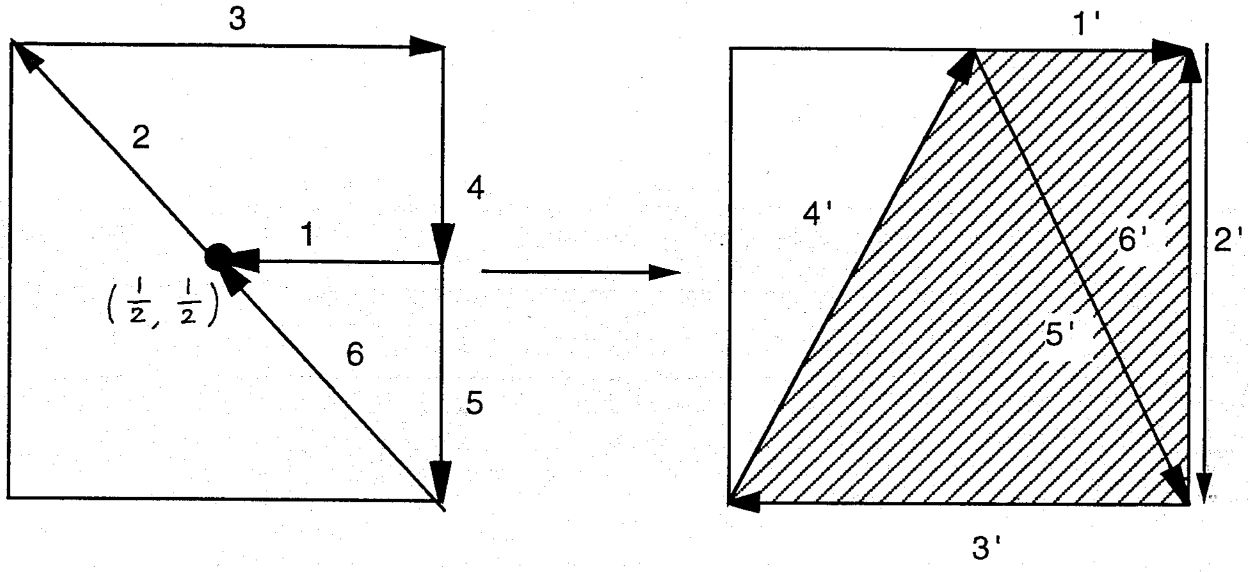

Fig 3

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(a)

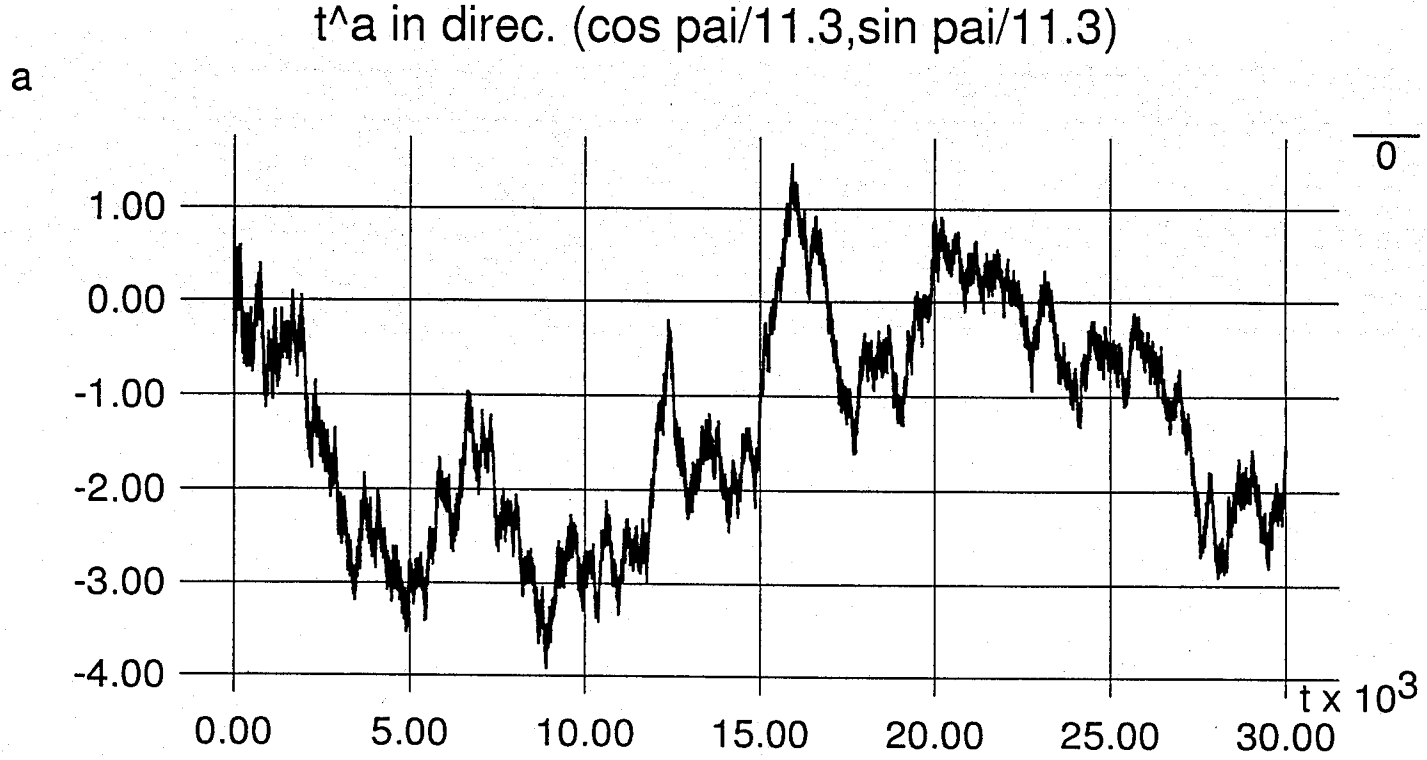

Fig 4 (a)

Tsuda & Tadaki

(b)

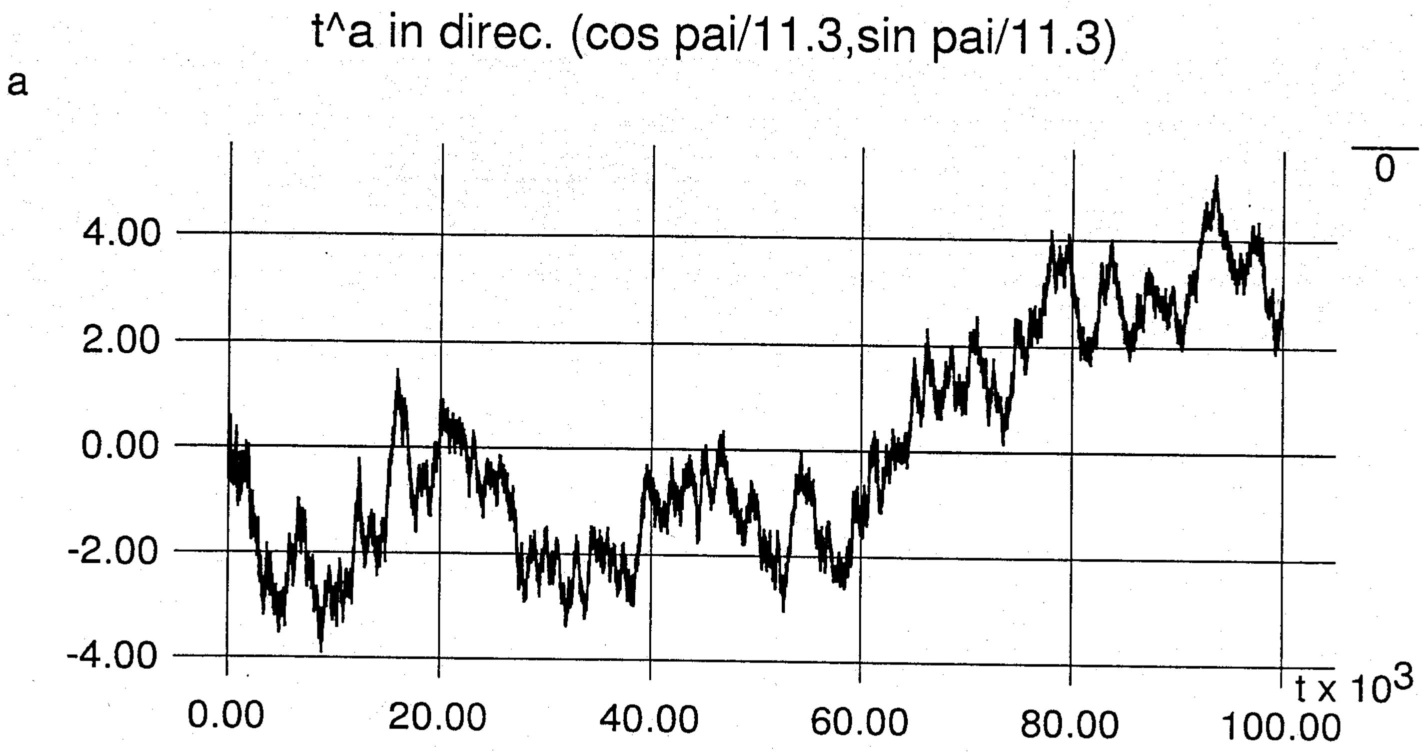
t^a in direc. (cos pai/11.3,sin pai/11.3)

Fig 4. (b)

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(a)

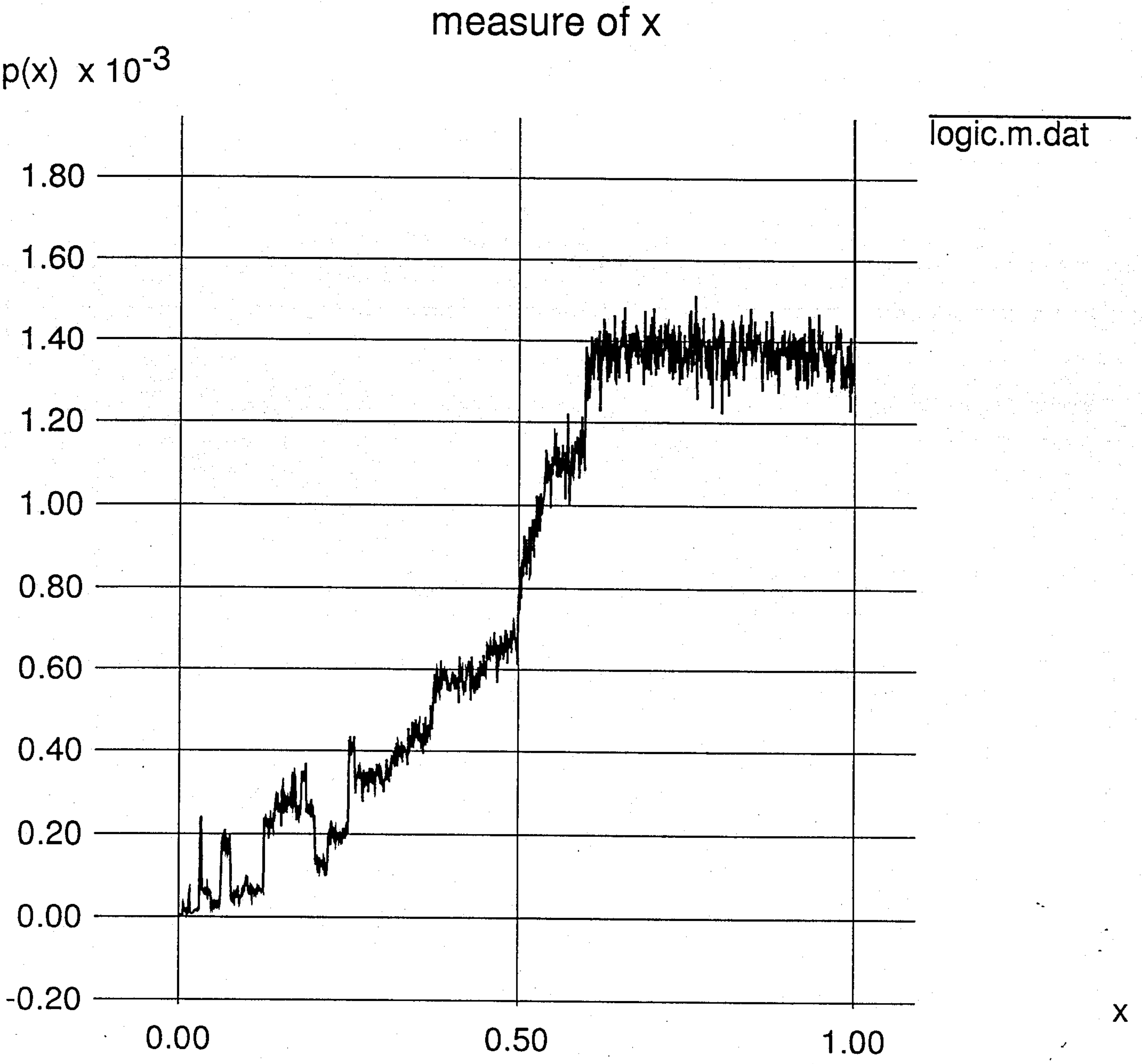

Fig 5 (a)

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(b)

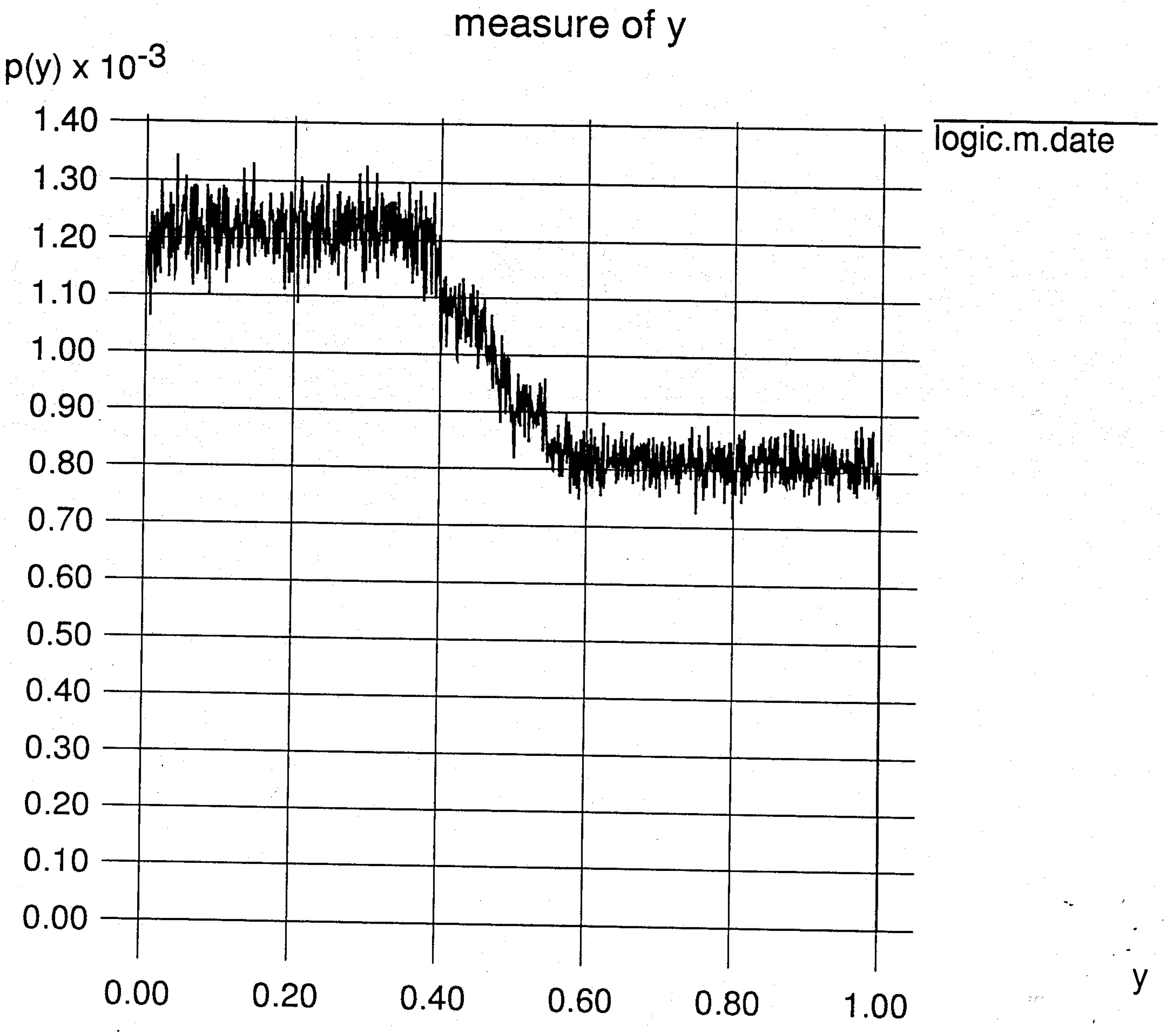

Fig 5 (b)

Tsuda & Tadaki

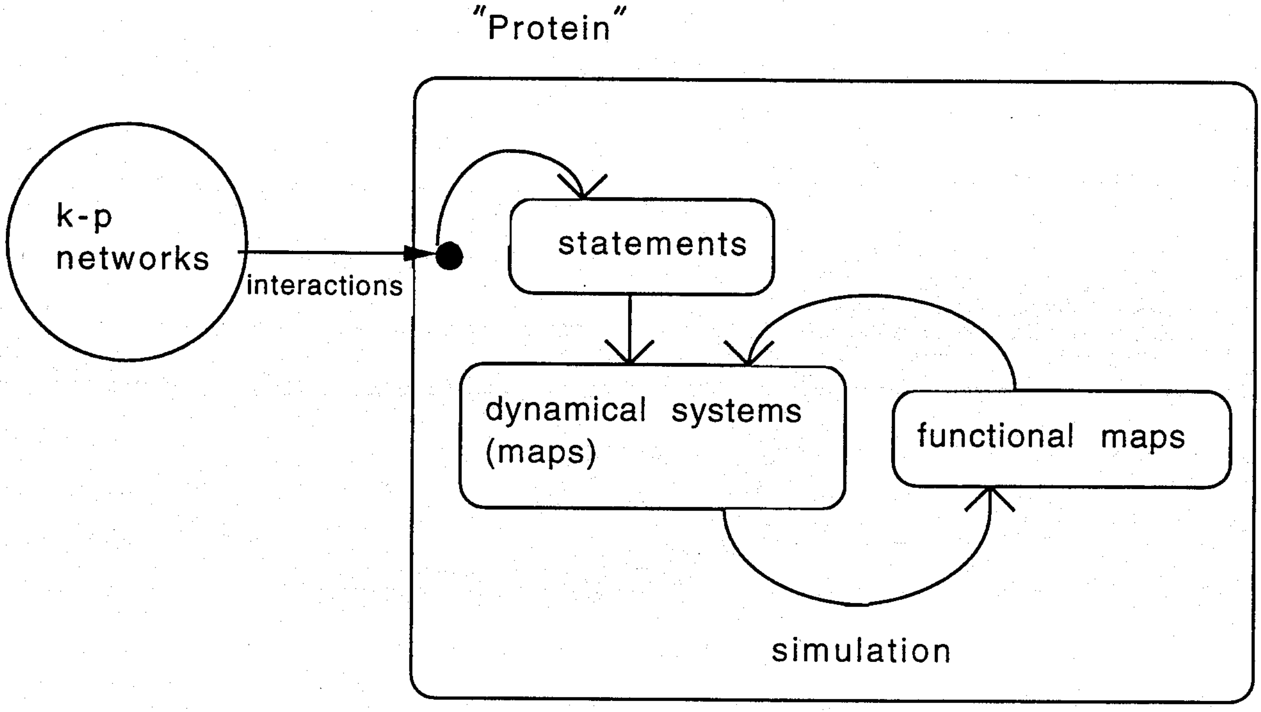

Fig 6.

Tsuda & Tadaki

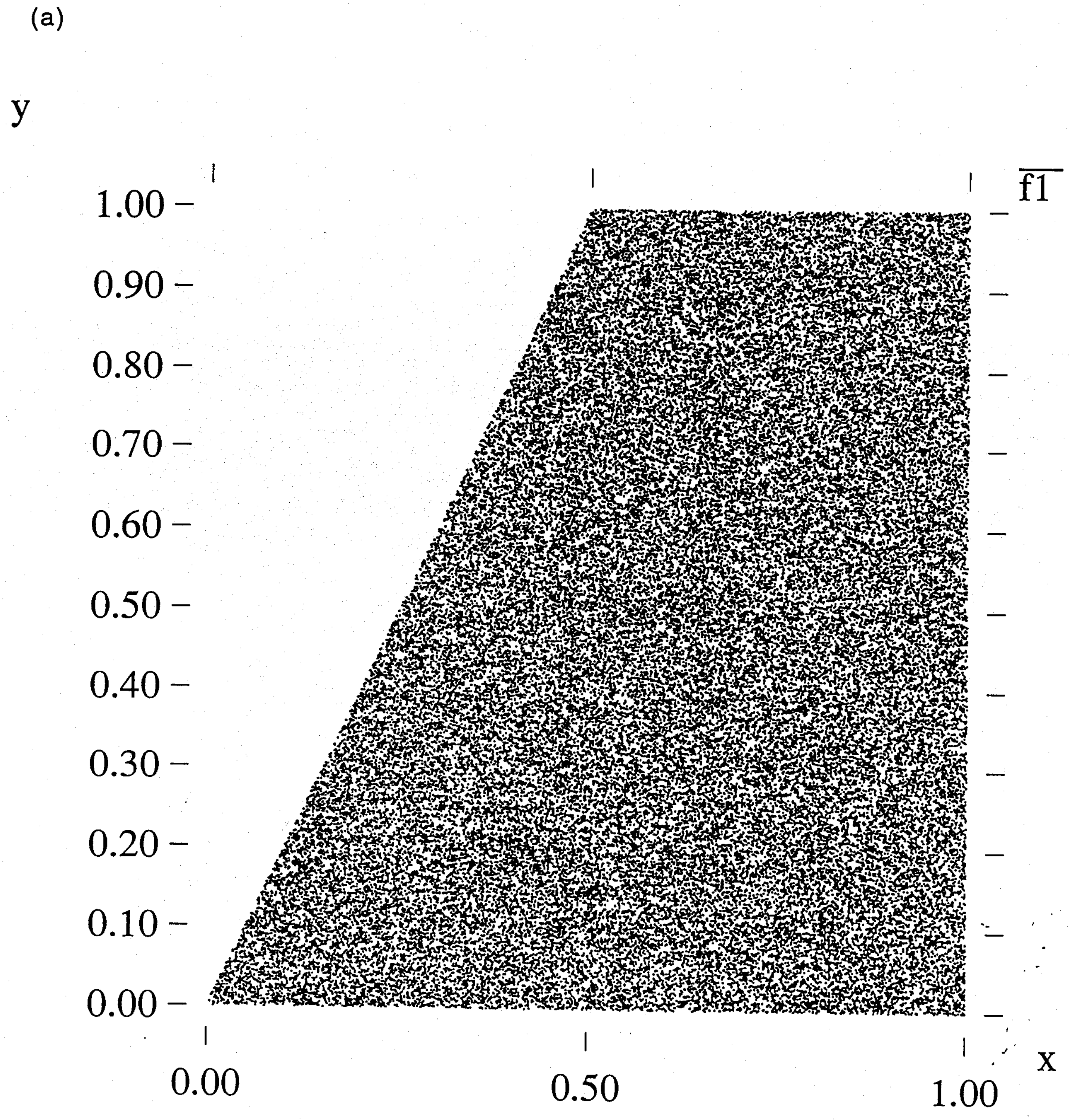

Fig 7. (a)

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(b)

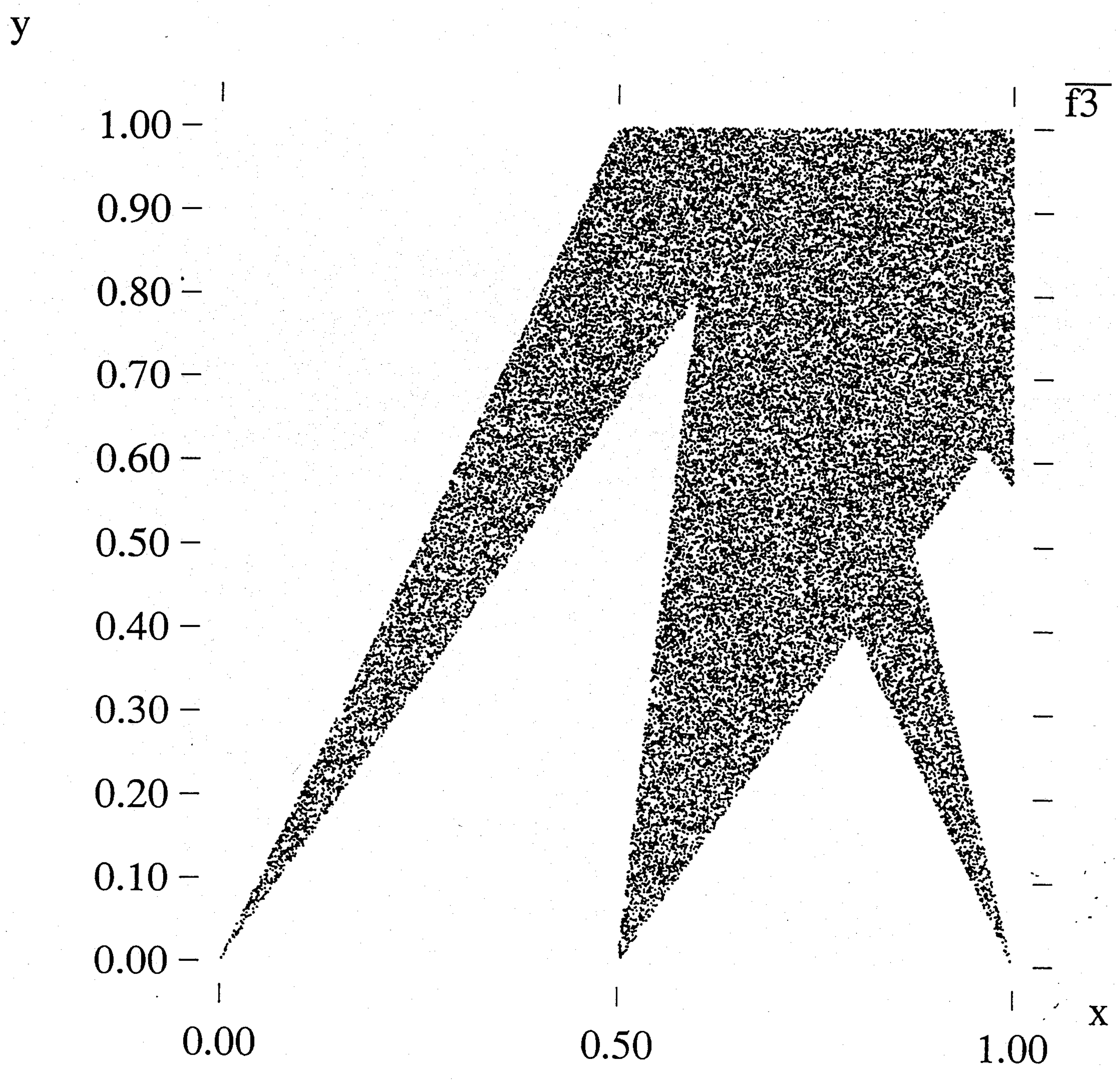

Fig 7 (b)

Tsuda & Tadaki

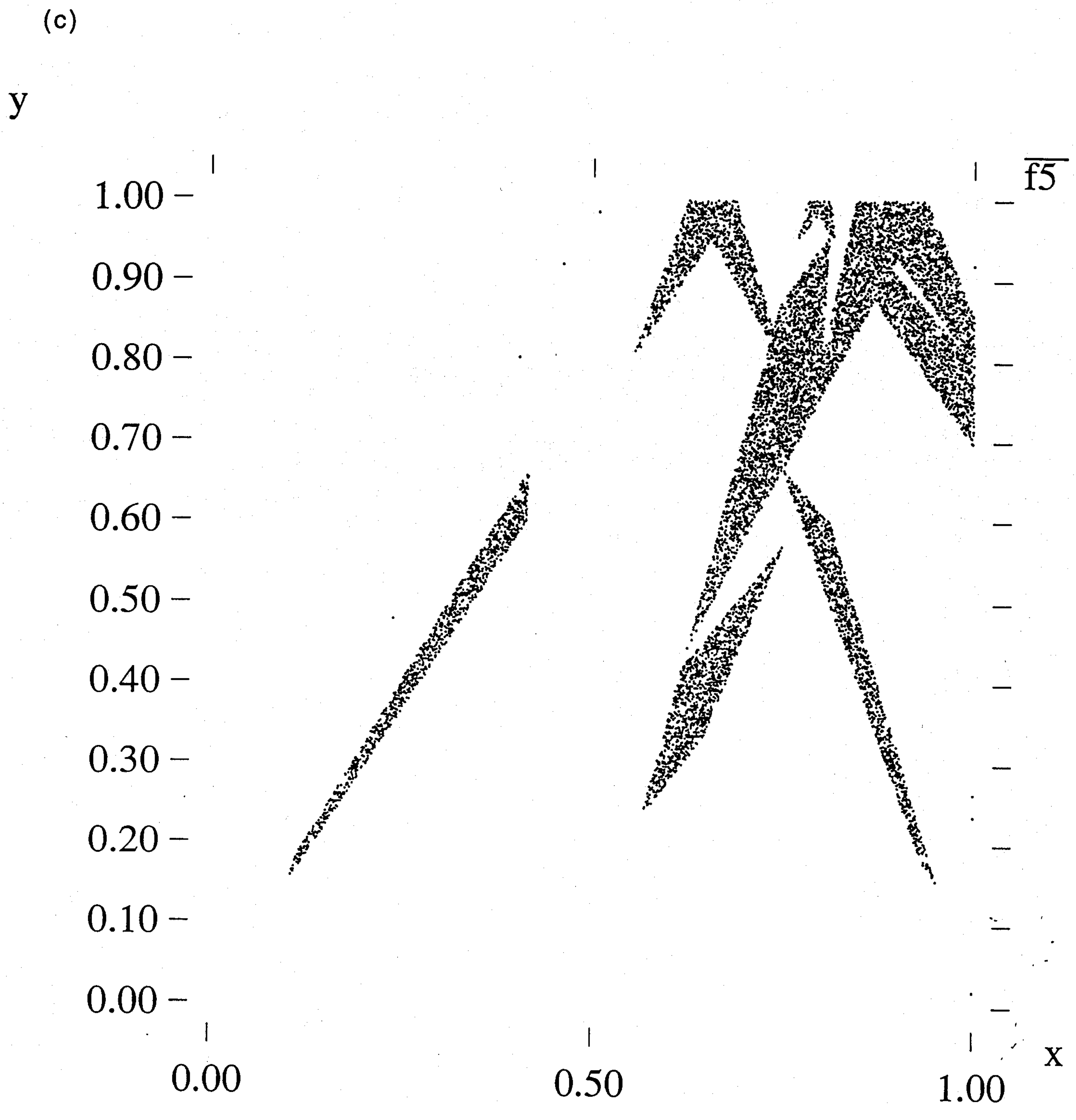

Fig 7 (c)

Tsuda & Tadaki

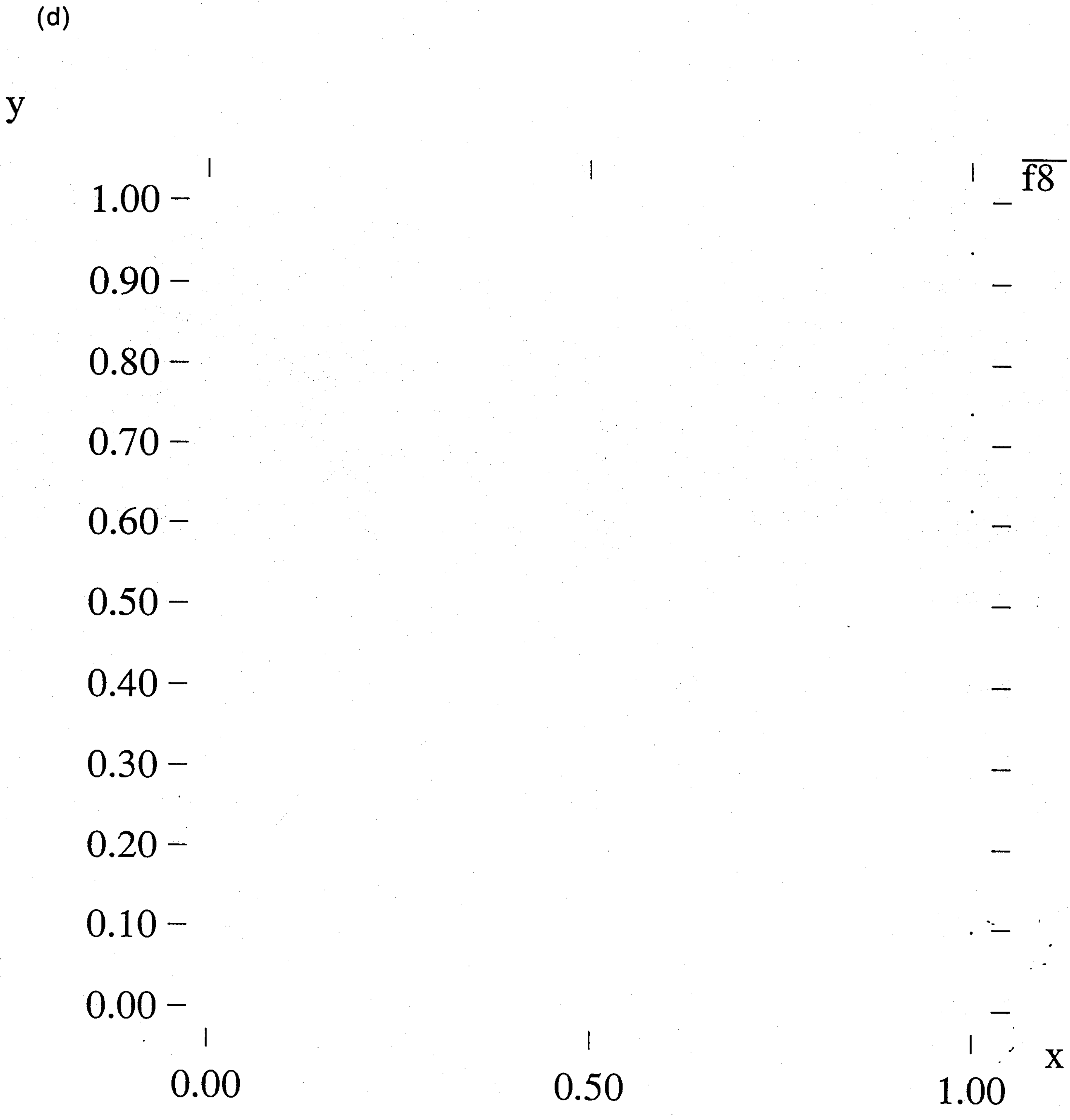

Fig 7 (d)

Tsuda & Tadaki

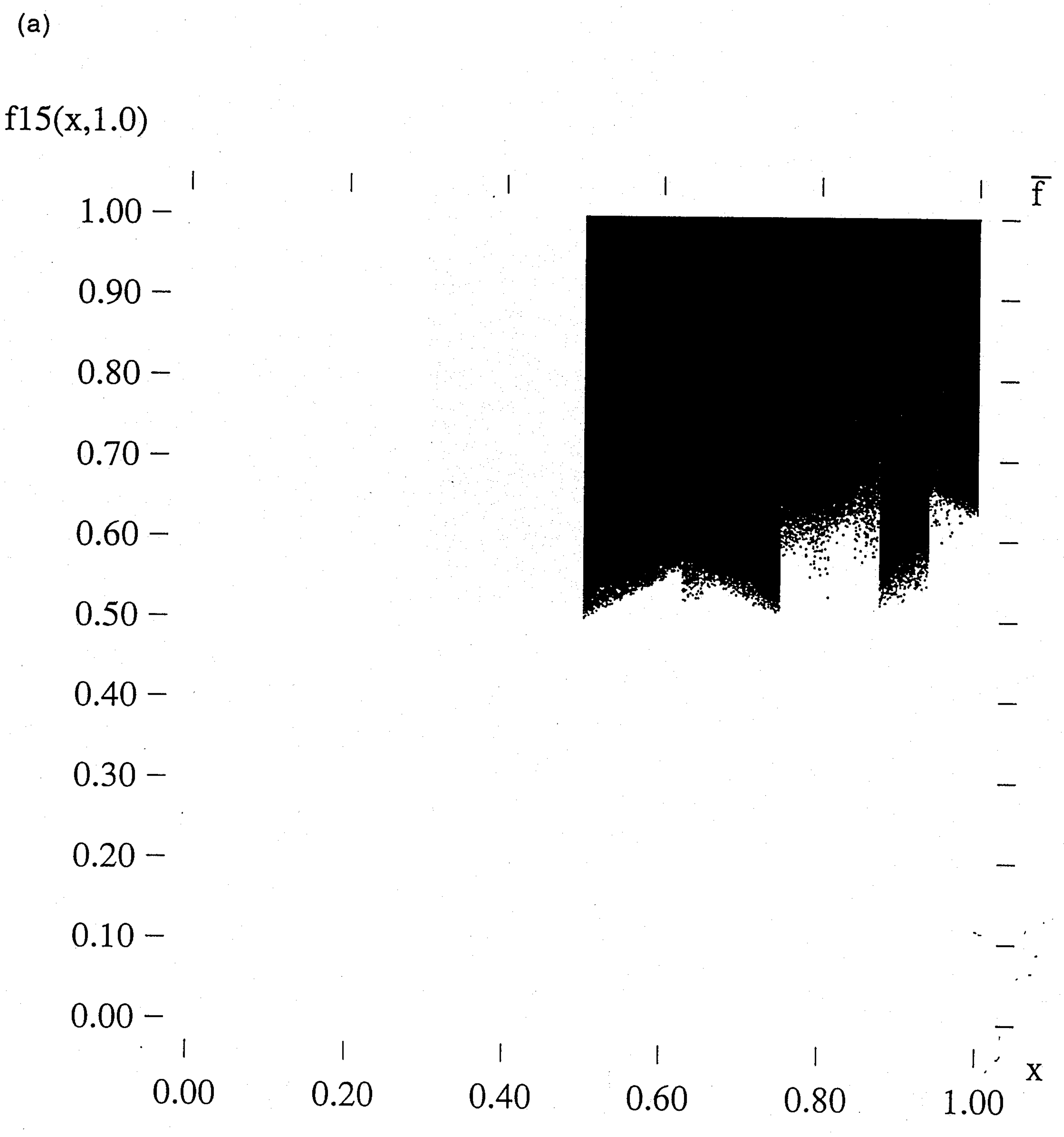

Fig 8 (a)
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(b)

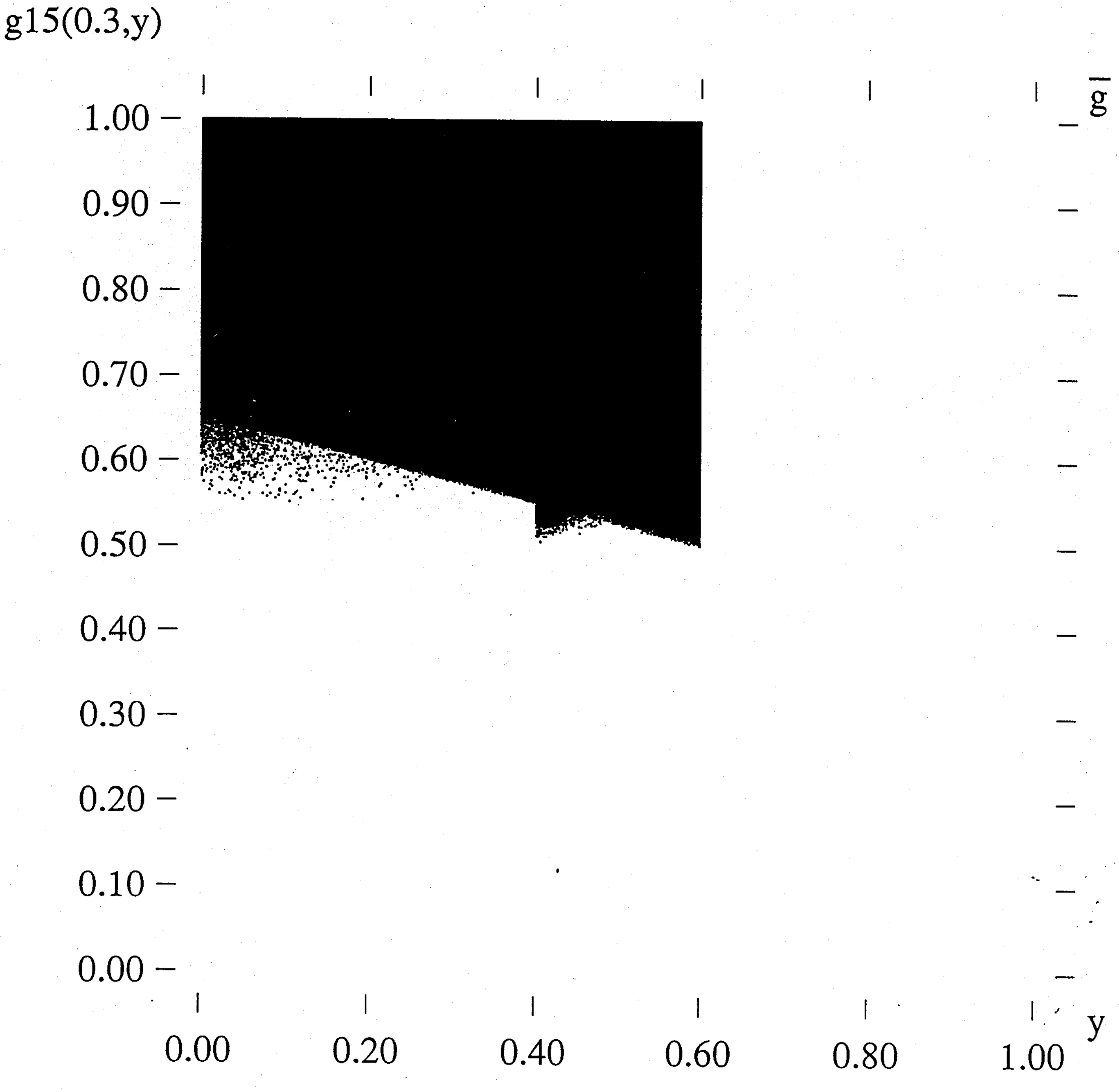

Fig 8 (b)

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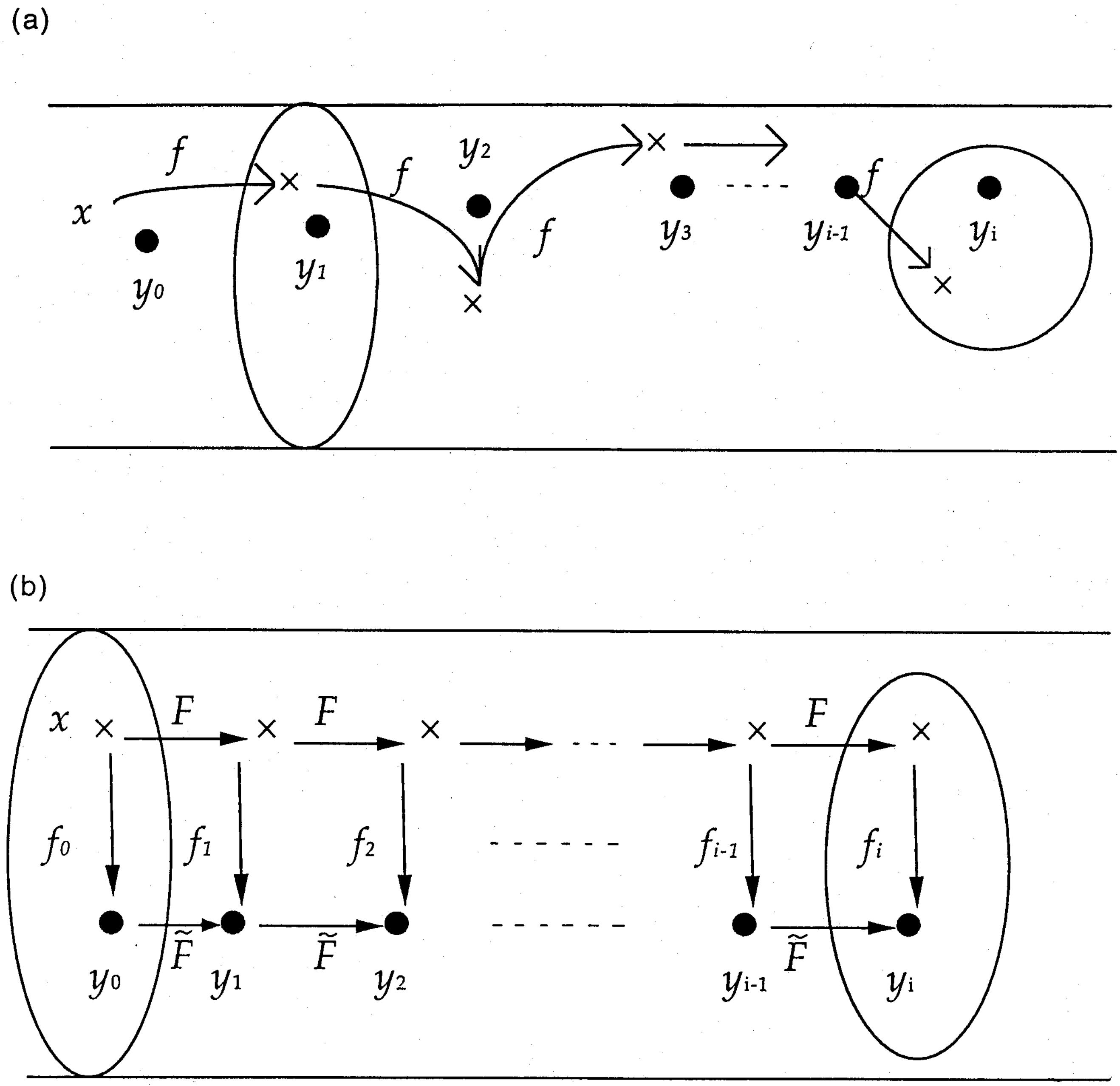

Fig 9 (a) & (b)

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