Formulating a Mathematical Model for Living Systems

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ABSTRACT

Prigogine's 1978 concept of dissipative structures, drawing parallels with living systems, forms the basis for exploring life's unique traits. However, these identified similarities prove insufficient in capturing the entirety of life. To address this gap, our proposed modeling approach emphasizes the distinctive ability of living organisms to observe other systems—an attribute intricately tied to quantum mechanics' "measurement" processes, as highlighted by Howard Pattee. This article introduces a comprehensive mathematical model centered on quantum dynamical dissipative systems, portraying living systems as entities defined by their observational capacities within this framework. The exploration extends to the core dynamics of these systems and the intricacies of biological cells, including the impact of membrane potentials on protein states. Within this theoretical structure, the model is expanded to multicellular living systems, revealing how cells observe quantum dynamical systems through protein state changes influenced by membrane potentials. The conclusion acknowledges the current theoretical status of the model, underscoring the crucial need for experimental validation, particularly regarding the superposition state of membrane proteins under the influence of an electric field.

1 Introduction

In 1978, Prigogine delineated dissipative structures[1], which exhibit several traits shared with living systems, such as self-assembly[2–4]. However, these parallels do not encompass all the characteristics of life. Many dissipative systems exist that are not living organisms, such as cyclones and turbulent flows. Therefore, it is essential to explore additional tools for modeling life, focusing on characteristics unique to living organisms rather than generic dissipative structures.

To distinguish living organisms from other dissipative systems, we must identify a defining property exclusive to life. I propose that a key characteristic of living organisms (referred to as living systems) is their ability to observe other systems in their surroundings. This observation process is intricately linked to the concept of "measurement" in quantum mechanics.

The acquisition of information about the physical universe heavily relies on the process of "measurement"[5]. Howard Pattee has emphasized that "measurement" processes must inherently connect with living systems[6].

2 Mathematical model

2.1 Quantum dynamical dissipative systems

Most mathematical concepts are founded on set theory. To mitigate the risk of paradoxes in the model, it is crucial to adhere to the notion of a 'pure set,' excluding entities like proper classes. Therefore, I assume $\mathscr{M}$ to be a Grothendieck universe, defined as the universe comprising only 'pure sets'[7]. In this context, $\mathscr{H}$ represents the set of all linear maps from $\mathscr{M}$ to $\mathbb{R}$, and $\mathscr{I} \subseteq \mathbb{R}$ is a finite set consisting of specific (finite) values $h(x)$ for some $x \in \mathscr{M}$ and certain linear maps $h \in \mathscr{H}$. This assumption of a finite set is based on the hypothesis that living systems, including humanity, cannot yield infinite values when measuring anything.

Let $\mathscr{M}_H \subseteq \mathscr{M}$ be a Hilbert space equipped with a norm $\|x\| = \sqrt{\langle x,x\rangle}$ and a distance function $d(x,y) = \|x-y\|$ defined for each $x,y \in \mathscr{M}_H$. Then M_H is also a Banach space, and the set of all (Lipschitz) continuous linear maps from $\mathscr{M}_H$ to $\mathbb{R}$ is the dual space of $\mathscr{M}_H$ (denoted by $\mathscr{M}_H^*$). $\mathscr{M}_H^*$ is also a Hilbert space[8,9].

Let $\mathscr{I}_H \subseteq \mathscr{I}$ be a set of finite eigenvalues of operators on $\mathscr{M}_H$, then $\mathscr{I}_H$ is finite. Let $X \subseteq \mathscr{M}_H$ be a closed subset of $\mathscr{M}_H$, S_t be an evolution operator, and $B \subseteq X$ be an absorbing set. Then (X, S_t, B) is a dynamical dissipative system[10]. According to Riesz-Fréchet Representation Theorem[8], for each $f \in X^*$, there is a unique $x \in X$ such that $f(y) = \langle x,y\rangle$ for all $y \in X$. We denote f as $\langle x|$, y as $|y\rangle$, and $\langle x,y\rangle$ as $\langle x|y\rangle$. Additionally, we define a set U_X of evolution operators represented by

$$\begin{aligned} &U_{t-t_0} : X \to X, \\ &\quad |x_{t_0}\rangle \mapsto |x_t\rangle, \end{aligned}$$

where $t, t_0 \in \mathbb{T}_X \subseteq \mathscr{I}_X$ and $t \geq t_0$. The operators in U_X satisfy the following properties: $U_{t-t}|x\rangle = U_0|x\rangle = |x\rangle, U_{t-t_1} \circ$

$U_{t_1-t_0}|x\rangle = U_{t-t_0}|x\rangle$, where $\circ$ is the composition of operators. These operators are known as the time-evolutions or the propagators[9]. Each element U_{t,t_0} of U_X can be represented by the pair (t,t_0).

An absorbing set of X is a closed set $B_X \subseteq X$ which has the following property: for any bounded set $D \subseteq X$, there exists $t_D \in \mathbb{T}_X$ such that $U_{t-t_0}(D) \subseteq B_X$ for all $t,t_0 \in \mathscr{I}_X$ with $t \geq t_D \geq t_0$, where $U_{t-t_0}(D) = \{U_{t-t_0}|x\rangle \,\big|\, x \in D\}$.

A system (X,U_X) is called a quantum dynamical system, and (X,U_X,B_X) is called a quantum dynamical dissipative system, where X is a closed subset of a Hilbert space, U_{t-t_0} is the time evolution operator, and B_X is an absorbing set of X.

2.2 Living systems

A living system has properties of a dissipative structure, therefore it is a quantum dynamical dissipative system. Let (X,U_X,B_X) be a quantum dynamical dissipative system, and let X_Y be a subset of X. Suppose that every element of X_Y can be represented as x_{ij}, where $i,j \in \mathbb{Z}_+$ and $i \leq j$. Let $*$ is a binary operator defined on X_Y such that $x_{ij} * x_{jk} = x_{ik}$ whenever x_{ij},x_{jk},x_{ik} are in X_Y. The set X_Y is not necessarily closed under $*$, as there may exist x_{ab},x_{bc} in X_Y such that x_{ac} does not belong to X_Y.

The distinctive characteristic of living systems lies in their capacity for "observing" the motion in their surroundings, which is characterized by evolution operators. Considering a living system denoted as (X,U_X,B_X) observing a quantum dynamical system (Y,U_Y), I posit that X acquires all the information regarding the motion of Y, encompassing the properties of the evolution operators U_Y. Consequently, there exists a subsystem X_Y within the system X such that $(U_Y,\circ)$ is isomorphic to $(X_Y,*)$—signifying a bijection $F : U_Y \to X_Y$ where, for all $u,v \in U_Y$, if $u \circ v \in U_Y$, then $F(u) * F(v) \in X_Y$ and $F(u) * F(v) = F(u \circ v)$. In such cases, we assert that Y is observed by X, designating the system (X,U_X,B_X) as a living system.

Living organisms cannot be immortal; they are destined to experience mortality and cease functioning at a specific time. In this context, a living system X is deemed to be dead at a designated time t_d if it ceases to manifest the defining characteristics of a living system for all times $t \geq t_d$.

2.3 The core of a living system

Cells constitute the fundamental units of a living organism, and the information within a cell is stored in ribonucleic acids such as DNAs or RNAs, which I term the "core" of the cell. Consequently, it becomes essential to establish a mathematical definition for the "core" in the context of living systems. Consider a living system denoted as (X,U_X,B_X), where C_X and X^0 function as subsets of X. Assuming (X^0,U_X) is isomorphic to (C_X,U_X) and there exists a subset $B_X^0 \subseteq X^0$ transformed to an absorbing set $B_X \subseteq X$ by operators $P_1,\cdots,P_n$, the subset C_X is designated as the core of X. The time evolution operator $U_{t'-t}$ acts on the core C_X at time t and transforms it into the new core C'_X at time t'. This temporal evolution of the core serves as the fundamental mechanism underpinning the overall evolution of living systems.

The cell has the ability to multiply or generate copies through the information encoded in its ribonucleic acids. In the context of a living system denoted as (X,U_X,B_X), if there exists a subset $C_{X'}$ of X such that $(C_{X'},U_X)$ is isomorphic to $(C'X,U_X)$, and CX' serves as the core of a living system $(X',B_{X'},U_{X'})$, then we designate the living system X' as a copy of X. The operator responsible for transforming C_X in the space $\mathscr{M}_H$ into the pair $(C'_X,C_{X'})$ in the space $\mathscr{M}_H \times \mathscr{M}_H$ is referred to as a copy operator, symbolized by $\hat{C}$.

3 Biological cells

We consider a biological cell denoted as B_X. Let $\mathbb{T}_X = \{t_0,t_1,\cdots,t_n\}$ be its lifespan, where t_0 is the time of its inception and t_n is the time of its termination. Let X be the set of all entities (such as mass or energy quanta) absorbed by B_X (or in B_X) at time $t_i \in \mathbb{T}_X$. The elements of X are represented by (x_k,t_i). The time evolution operators on X are represented by

$$U^X_{t_j-t_i}(x_k,t_i) = (x_k,t_j),$$

where $t_i,t_j \in \mathbb{T}_X, t_j \geq t_i$ and $(x,t_i),(x,t_j) \in X$. Then (X,U_X,B_X) is a quantum dynamical dissipative system, where U_X is the set of time operators on X and B_X can be considered as an absorbing set of X. The nucleic acids (such as DNA and RNA) inside the nucleus of the cell B_X along with relevant entities in X (such as energy quanta, amino acids, phospholipids, ...), can be considered as its core.

Defining a binary operator in mathematics is straightforward, but finding a real-world analogue poses challenges. To address this, I leverage the concept of superposition states in quantum mechanics and exploit the properties of membrane proteins within cells. The structure of proteins, such as p_0 on the cell membrane, can be influenced by a low-strength electric field[11,12]. The presence of a membrane potential[13] has the potential to induce alterations in the structure of proteins on the membrane of B_X. Considering a protein on the membrane, denoted as p_0, I define the set $P = p_0,p_1,\cdots,p_m$ encompassing all structures of protein p_0 that can be modified by membrane potential (remaining unchanged if the membrane potential is insufficient, denoted as p_0). This modification is contingent upon the cell being alive, ensuring $m \leq n$. Assuming the protein exists in state

p_i at time t_j, where i and j are selected from the set $0,1,\cdots,m$ with the condition that $j \geq i$, I postulate that at time $t_k \geq t_j$, the protein's state evolves into a superposition state, a composition of both p_j and p_i. Subsequently, at time $t_l > t_k$, the protein's state undergoes a transition to the state p_k.

If we denote the state p_j at time t_j as (p_i,t_j), we can define a binary combination (denoted by $*$) between two such state as follows

$$(p_i,t_j)*(p_j,t_k) = (p_i,t_k).$$

It is evident that the set P_t, consisting of all such state (p_i,t_j), is a subset of X. The set P_t with the binary combination $*$ is isomorphic to the set U_Y of time operators defined on a quantum dynamical system Y. Therefore, (X,U_X,B_X) is a living system.

Let's represent the state p_i by the vector $|p_i\rangle$, for $i = 1,\cdots,m$. Suppose all the neighboring states $|p_i\rangle, |p_{i+1}\rangle$ are orthogonal (i.e., $\langle p_i|p_{i+1}\rangle = 0$), and the protein is in state p_i at time instant τ_i. Then, the set P of such states of proteins can be considered as a quantum clock[14–16] with a time resolution given by

$$\tau_{i+1} - \tau_i = \delta\tau_i \geq \frac{\hbar}{2\Delta E_i},$$

where ΔE_i is the corresponding energy uncertainty. This implies that quantum clocks can exist in every living cell containing membrane proteins that can change states over time.

Numerous individual living systems (X_i,U_{x_i},B_{X_i}) can combine to form a living system (X,U_X,B_X), where $X = \bigcup_i X_i, U_X = \bigcup_i U_{X_i}, B_X = \bigcup_i B_{X_i}$.

If the protein cannot return to the initial state p_0, we say that it has undergone degeneration. If the proteins within the cell membrane cannot enter a superposition state, the cell wouldn't observe any quantum dynamical system and thus cannot be considered as a living system. Without the membrane potential, the proteins would remain unaffected by the electric fields, preventing necessary structural changes for entering a superposition state. The presence of an environment conducive to membrane potential, facilitated by water, becomes essential. This elucidates why living systems need water.

4 Conclusions

In conclusion, while this mathematical model of life may not comprehensively encapsulate all the intricacies of living organisms, it stands as a vital link that unites fundamental physics theories with biology. Significantly, it enables the distinction between living and non-living systems. While certain facets are presently confined to theoretical descriptions, their validation through experimentation is imperative, particularly concerning the superposition state of membrane proteins influenced by a low-strength electric field. This model lays the groundwork for further exploration and empirical validation, fostering a deeper understanding of the complex dynamics inherent in living systems.

5 Acknowledgments

I express my sincere gratitude to my parents and my wife for their unwavering support. Special thanks go to my younger brother, Nguyen Dac Khoi Nguyen, for his invaluable contributions through critical discussions and assistance in discovering pertinent mathematical textbooks.

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