

Complexity and Life

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Introduction

DURING THE last two decades of the 20th century, a new understanding of life emerged at the forefront of science. The intellectual tradition of systemic thinking, or ‘systems thinking’, and the models of living systems developed during the earlier decades of the century, form the conceptual and historical roots of this new scientific understanding of life.

Systemic thinking means thinking in terms of relationships, patterns, processes and context. Over the past 25 years, this scientific tradition was raised to a new level with the development of complexity theory. Technically known as nonlinear dynamics, complexity theory is a new mathematical language and a new set of concepts for describing and modeling complex nonlinear systems. Complexity theory now offers the exciting possibility of developing a unified view of life by integrating life’s biological, cognitive and social dimensions (Capra, 2002). In this article, I shall review the current achievements and status of complexity theory from the perspective of the new scientific understanding of biological life.

Metabolism – The Essence of Life

Let us begin with the age-old question: what is the essential nature of life in the realm of plants, animals and micro-organisms? To understand the nature of life, it is not enough to understand DNA, proteins and the other molecular structures that are the building blocks of living organisms, because these structures also exist in dead organisms, for example, in a dead piece of wood or bone.

The difference between a living organism and a dead organism lies in the basic process of life – in what sages and poets throughout the ages have called the ‘breath of life’. In modern scientific language, this process is called metabolism. It is the ceaseless flow of energy and matter through a

network of chemical reactions, which enables a living organism to continually generate, repair and perpetuate itself.

The understanding of metabolism includes two basic aspects. One is the continuous flow of energy and matter. All living systems need energy and food to sustain themselves; and all living systems produce waste. But life has evolved in such a way that organisms form communities, the ecosystems, in which the waste of one species is food for the next, so that matter cycles continually through the ecosystem.

The second aspect of metabolism is the network of chemical reactions that processes the food and forms the biochemical basis of all biological structures, functions and behavior. The emphasis here is on 'network'. One of the most important insights of the new scientific understanding of life is the recognition that networks are the basic pattern of organization of living systems. Ecosystems are organized in terms of food webs, that is, networks of organisms; organisms are networks of cells, organs and organ systems; and cells are networks of molecules. The network is a pattern that is common to all life. Wherever we see life, we see networks.

It is important to realize that these living networks are not material structures, like a fishing net or a spider's web. They are *functional* networks, networks of relationships between various processes. In a cell, for example, these processes are chemical reactions between the cell's molecules. In a food web, the processes are processes of feeding, of organisms eating one another. In both cases the network is a nonmaterial pattern of relationships.

Closer examination of these living networks has shown that their key characteristic is that they are self-generating (Capra, 1996: 95ff.). In a cell, for example, all the biological structures – the proteins, enzymes, the DNA, the cell membrane, etc. – are continually produced, repaired and regenerated by the cellular network. Similarly, at the level of a multicellular organism, the bodily cells are continually regenerated and recycled by the organism's metabolic network.

Living networks are self-generating. They continually create, or recreate, themselves by transforming or replacing their components. In this way they undergo continual structural changes while preserving their web-like patterns of organization.

Nonlinear Dynamics

The process of metabolism can be summarized in terms of the following four key characteristics of biological life.

1. A living system is materially and energetically open; it needs to take in food and excrete waste to stay alive.
2. It operates far from equilibrium; there is a continual flow of energy and matter through the system.
3. It is organizationally closed; a metabolic network bounded by a membrane.
4. It is self-generating; each component helps to transform and replace other components.

These four characteristics all have one thing in common: they are characteristics of a system whose dynamics and pattern of organization are nonlinear. Nonequilibrium systems are described mathematically by nonlinear equations; networks are nonlinear, multidirectional, patterns of organization. This is why complexity theory is so important for understanding living systems. As its technical name ‘nonlinear dynamics’ indicates, it is a nonlinear mathematical theory.

Nonlinear equations have properties that are strikingly different from those of the linear equations commonly used in science. In a linear differential equation, small changes produce small effects and large effects are obtained by adding up many small changes. Mathematically, this means that the sum of two solutions is again a solution, which makes linear equations relatively easy to solve. They are called ‘linear’ because they can be represented on a graph by a straight line. Nonlinear equations, by contrast, are represented by graphs that are curved, are very difficult to solve, and display a host of unusual properties.

In science, until recently, we always avoided the study of nonlinear systems because of the mathematical difficulties involved in the equations describing them.

Whenever nonlinear equations appeared, they were replaced by linear approximations. Instead of describing the phenomena in their full complexity, the equations of classical science deal with *small* oscillations, *shallow* waves, *small* changes of temperature and so on, for which linear equations can be formulated. This became such a habit that most scientists and engineers came to believe that virtually all natural phenomena could be described by linear equations.

The decisive change over the last 25 years has been to recognize the importance of nonlinear phenomena, and to develop mathematical techniques for solving nonlinear equations. The use of computers has played a crucial role in this development. With the help of powerful, high-speed computers, mathematicians are now able to solve complex equations that had previously been intractable. In doing so, they have devised a number of techniques, a new kind of mathematical language that revealed very surprising patterns underneath the seemingly chaotic behavior of nonlinear systems, an underlying order beneath the seeming chaos (Stewart, 1997).

Let me now review some of the main features of nonlinear dynamics, the theory of complexity (Capra, 1996: 112ff.; Mosekilde et al., 1988). When you solve a nonlinear equation with these new mathematical techniques, the result is not a formula but a visual shape, a pattern traced by the computer, known as an ‘attractor’. An attractor is a geometrical figure in two, three or more dimensions that represent the variables needed to describe the system. These dimensions form a mathematical space called ‘phase space’. Each point in phase space is determined by the values of the system’s variables, which in turn completely determine the state of the system.

In other words, each point in phase space represents the system in a particular state. As the system changes, the point representing it traces

out a trajectory that represents the dynamics of the system. The attractor, then, is the pattern of this trajectory in phase space. It is called ‘attractor’, because it represents the system’s long-term dynamics. A nonlinear system will typically move in a variety of ways in the beginning, depending on how it is started off, but then will settle down to a characteristic long-term behavior, represented by the attractor. Metaphorically speaking, the trajectory is ‘attracted’ to this pattern whatever its starting point may have been.

Over the past 20 years, scientists and mathematicians explored a wide variety of complex systems. In case after case they would set up nonlinear equations and have computers trace out the solutions as trajectories in phase space. To their great surprise, these researchers discovered that there is a very limited number of different attractors. Their shapes can be classified topologically, and the general dynamic properties of a system can be deduced from the shape of its attractor.

The analysis of nonlinear systems in terms of the topological features of their attractors is known as ‘qualitative analysis’. A nonlinear system can have several attractors, and they may be of several different types. All trajectories starting within a certain region of phase space will lead sooner or later to the same attractor. This region is called the ‘basin of attraction’ of that attractor. Thus the phase space of a nonlinear system is partitioned into several basins of attraction, each embedding its separate attractor.

When we try to assess the achievements and current status of complexity theory, we need to remember, first of all, that nonlinear dynamics is not a scientific theory, in the sense of an empirically based analysis of natural or social phenomena. It is a *mathematical* theory, that is, a body of mathematical concepts and techniques for the description of nonlinear systems. The most important achievement of nonlinear dynamics, in my view, is to provide the appropriate language for dealing with nonlinear systems. The key concepts of this language – chaos, attractors, fractals, qualitative analysis, etc. – did not exist 25 years ago. Now we know what kinds of questions to ask when we deal with nonlinear systems.

Having the appropriate mathematical language does not mean that we know how to construct a mathematical model in a particular case. We need to simplify a highly complex system by choosing a few relevant variables, and then we need to set up the proper equations to interconnect these variables. This is the interplay between science and mathematics. So, the creation of a new language is, in my view, the overall achievement of nonlinear dynamics; and then there are partial achievements in various fields. Among them I shall now concentrate on those achievements that have led to major breakthroughs in our understanding of biological life.

Theory of Dissipative Structures

The Russian-born chemist and Nobel Laureate Ilya Prigogine was one of the first to use nonlinear dynamics to explore basic properties of living systems. What intrigued Prigogine most was that living organisms are able

to maintain their life processes under conditions of nonequilibrium. During the 1960s, he became fascinated by systems far from equilibrium and began a detailed investigation to find out under exactly what conditions non-equilibrium situations may be stable.

The crucial breakthrough occurred, when he realized that systems far from equilibrium must be described by nonlinear equations. The clear recognition of this link between ‘far from equilibrium’ and ‘nonlinearity’ opened an avenue of research for Prigogine that would culminate a decade later in his theory of dissipative structures, formulated in the language of nonlinear dynamics (Capra, 1996: 172ff.; Prigogine and Glansdorff, 1971).

A living organism is an open system that maintains itself in a state far from equilibrium, and yet is stable: the same overall structure is maintained in spite of an ongoing flow and change of components. Prigogine called the open systems described by his theory ‘dissipative structures’ to emphasize this close interplay between structure on the one hand and flow and change (or dissipation) on the other. The farther a dissipative structure is from equilibrium, the greater is its complexity and the higher is the degree of nonlinearity in the mathematical equations describing it.

The dynamics of these dissipative structures specifically include the spontaneous emergence of new forms of order. When the flow of energy increases, the system may encounter a point of instability, or bifurcation point, at which it can branch off into an entirely new state where new structures and new forms of order may emerge.

This spontaneous emergence of order at critical points of instability, often simply referred to as ‘emergence’, is one of the most important concepts of the new understanding of life. Emergence is one of the hallmarks of life. It has been recognized as the dynamic origin of development, learning and evolution. In other words, creativity – the generation of new forms – is a key property of all living systems. And since emergence is an integral part of the dynamics of open systems, this means that open systems develop and evolve. Life constantly reaches out into novelty.

The theory of dissipative structures explains not only the spontaneous emergence of order, but also helps us to define complexity. Whereas traditionally the study of complexity has been a study of complex structures, the focus is now shifting from the structures to the processes of their emergence. For example, instead of defining the complexity of an organism in terms of the number of its different cell types, as biologists often do, we can define it as the number of bifurcations the embryo goes through in the organism’s development. Accordingly, the British biologist Brian Goodwin (pers. comm.) speaks of ‘morphological complexity’.

Cell Development

The theory of emergence, known technically as bifurcation theory, has been studied extensively by mathematicians and scientists, among them the American biologist Stuart Kauffman. Kauffman used nonlinear dynamics to construct binary models of genetic networks and was remarkably

successful in predicting some key features of cell differentiation (Kauffman, 1991, 1993; see also Capra, 1996: 194ff.).

A binary network, also known as Boolean network, consists of nodes capable of two distinct values, conventionally labeled ON and OFF. The nodes are coupled to one another in such a way that the value of each node is determined by the prior values of neighboring nodes according to some 'switching rule'.

When Kauffman studied genetic networks, he noticed that each gene in the genome is directly regulated by only a few other genes, and he also knew that genes are turned on and off in response to specific signals. In other words, genes do not simply act; they must be activated. Molecular biologists speak of patterns of gene expression.

This gave Kauffman the idea of modeling genetic networks and patterns of gene expression in terms of binary networks with certain switching rules. The succession of ON–OFF states in these models is associated with a trajectory in phase space and is classified in terms of different types of attractors.

Extensive examination of a wide variety of complex binary networks has shown that they exhibit three broad regimes of behavior: an ordered regime with frozen components (i.e. nodes that remain either ON or OFF), a chaotic regime with no frozen components (i.e. nodes switching back and forth between ON and OFF), and a boundary region between order and chaos where frozen components just begin to change.

Kauffman's central hypothesis is that living systems exist in that boundary region near the so-called 'edge of chaos'. He believes that natural selection may favor and sustain living systems at the edge of chaos, because these may be best able to coordinate complex and flexible behavior. To test his hypothesis, Kauffman applied his model to the genetic networks in living organisms and was able to derive from it several surprising and rather accurate predictions.

In terms of complexity theory, the development of an organism is characterized by a series of bifurcations, each corresponding to a new cell type. Each cell type corresponds to a different pattern of gene expression, and hence to a different attractor. Now, the human genome contains between 30,000 and 100,000 genes. In a binary network of that size, the possibilities of different patterns of gene expression are astronomical. However, Kauffman could show that at the *edge of chaos* the number of attractors in such a network is approximately equal to the square root of the number of its elements. Therefore, the human network of genes should express itself in approximately 245 different cell types. This number comes remarkably close to the 254 distinct cell types identified in humans.

Kauffman also tested his attractor model with predictions of the number of cell types for various other species, and again the agreement with the actual numbers observed was very good. Another prediction of Kauffman's attractor model concerns the stability of cell types. Since the frozen core of the binary network is identical for all attractors, all cell types

in an organism should express mostly the same set of genes and should differ by the expressions of only a small percentage of genes. This is indeed the case for all living organisms.

In view of the fact that these binary models of genetic networks are quite crude, and that Kauffman's predictions are derived from the models' very general features, the agreement with the observed data must be seen as a remarkable success of nonlinear dynamics.

Morphology

A very rich and promising area for complexity theory in biology is the study of the origin of biological form, known as morphology. This is a field of study that was very lively in the 18th century, but then was eclipsed by the mechanistic approach to biology, until it made a comeback very recently with the emphasis of nonlinear dynamics on patterns and shapes.

A key insight of the new understanding of life has been that biological forms are not determined by a 'genetic blueprint', but are emergent properties of an entire epigenetic network of metabolic processes.

To understand the emergence of biological form, we need to understand not only the genetic structures and the cell's biochemistry, but also the complex dynamics that unfold when the epigenetic network encounters the physical and chemical constraints of its environment. In this encounter, the interactions between the organism's physical and chemical variables are highly complex and can be represented in simplified models by nonlinear equations. The solutions of these equations, represented by a limited number of attractors, correspond to the limited number of possible biological forms. This technique has been applied to a variety of biological forms, from branching patterns of plants and the coloring of sea shells to the nest building of termites (Solé and Goodwin, 2000; Stewart, 1998).

A good example is the work of Brian Goodwin (1994: 77ff.), who used nonlinear dynamics to model the stages of development of a single-celled Mediterranean alga, called *Acetabularia*, which forms beautiful little 'parasol' caps. Like the cells of all plants and animals, the cell of this alga is shaped and sustained by its cytoskeleton, a complex and intricate structure of protein filaments. The cytoskeleton is subject to various mechanical stresses, and it turns out that a key influence on its mechanical state – its rigidity or softness – is the calcium concentration in the cell. The cytoskeleton is anchored to the cell wall, and its behavior under the mechanical stresses, therefore, gives rise to the alga's biological form.

Since the mechanical properties of the cytoskeleton at the molecular level are far too complex to be described mathematically, Goodwin and his colleagues approximated them by a continuous field, known in physics as a stress-tensor field. They were then able to set up nonlinear equations that interrelate patterns of calcium concentration in the alga's cell fluid with the mechanical properties of the cell walls.

These equations contain numerous parameters, such as the diffusion constant for calcium, the resistance of the cytoskeleton to deformation and

so on. In nature, these quantities are determined genetically and change from species to species, so that different species produce different biological forms.

Goodwin and his colleagues proceeded to try out a variety of parameters in computer simulations to explore the types of form that a developing alga could produce. They succeeded in simulating a whole sequence of structures that appear in the alga's development of its characteristic stalk and parasol. These forms emerged as successive bifurcations of the attractors representing the interplay between patterns of calcium and mechanical strain.

The lesson to be learned from these models of plant morphology is that biological form emerges from the nonlinear dynamics of the organism's epigenetic network as it interacts with the physical constraints of its molecular structures. The genes do not provide a blueprint for biological forms. They provide the initial conditions that determine which kind of dynamics – or, mathematically, which kind of attractors – will appear in a given species. In this way genes stabilize the emergence of biological form.

Developmental Stability

From the origin of biological form, I shall now turn to the development of an embryo (Capra, 2002: 152–3). Complexity theory may shed new light on an intriguing property of biological development that was discovered almost a hundred years ago by the German embryologist Hans Driesch. With a series of careful experiments on sea urchin eggs, Driesch showed that he could destroy several cells in the very early stages of the embryo, and it would still grow into a full, mature sea urchin. Similarly, more recent genetic experiments have shown that 'knocking out' single genes, even when they were thought to be essential, had very little effect on the functioning of the organism.

This very remarkable stability and robustness of biological development means that an embryo may start from different initial stages – for example, if single genes or entire cells are destroyed accidentally – but will nevertheless reach the same mature form that is characteristic of its species. The question is, what keeps development on track?

There is an emerging consensus among genetic researchers that this robustness indicates a redundancy in genetic and metabolic pathways. It seems that cells maintain multiple pathways for the production of essential cellular structures and the support of essential metabolic processes. This redundancy ensures not only the remarkable stability of biological development but also great flexibility and adaptability to unexpected environmental changes. Genetic and metabolic redundancy may be seen, perhaps, as the equivalent of biodiversity in ecosystems. It seems that life has evolved ample diversity and redundancy at all levels of complexity.

The observation of genetic redundancy is in stark contradiction to genetic determinism, and in particular to the metaphor of the 'selfish gene' proposed by the British biologist Richard Dawkins (1976). According to

Dawkins, genes behave as if they were selfish by constantly competing, via the organisms they produce, to leave more copies of themselves.¹ From this reductionist perspective, the widespread existence of redundant genes makes no evolutionary sense. From a systemic point of view, by contrast, we recognize that natural selection operates not on individual genes but on the organism's patterns of self-organization. In other words, what is selected by nature is not the individual gene but the endurance of the organism's life cycle.

Now, the existence of multiple pathways is an essential property of all networks; it may even be seen as the defining characteristic of a network. It is therefore not surprising that complexity theory, which is eminently suited to the analysis of networks, should contribute important insights into the nature of developmental stability.

In the language of nonlinear dynamics, the process of biological development is seen as a continuous unfolding of a nonlinear system as the embryo forms out of an extended domain of cells.² This 'cell sheet' has certain dynamical properties that give rise to a sequence of deformations and foldings as the embryo emerges. The entire process can be represented mathematically by a trajectory in phase space moving inside a basin of attraction toward an attractor that describes the functioning of the organism in its stable adult form.

A characteristic property of complex nonlinear systems is that they display a certain 'structural stability'. A basin of attraction can be disturbed or deformed without changing the system's basic characteristics. In the case of a developing embryo this means that the initial conditions of the process can be changed to some extent without seriously disturbing development as a whole. Thus developmental stability, which seems quite mysterious from the perspective of genetic determinism, is recognized as a consequence of a very basic property of complex nonlinear systems.

Origin of Life

The last example of my review of applications of complexity theory to problems in biology is not about an actual achievement but about the potential for a major breakthrough in solving an old scientific puzzle – the question of the origin of life on earth (Capra, 2002: 17ff.).

Ever since Darwin, scientists have debated the likelihood of life emerging from a primordial 'chemical soup' that formed 4 billion years ago when the planet cooled off and the primeval oceans expanded. The idea that small molecules should assemble spontaneously into structures of ever-increasing complexity runs counter to all conventional experience with simple chemical systems. Many scientists have therefore argued that the odds of such prebiotic evolution are vanishingly small; or, alternatively, that there must have been an extraordinary triggering event, such as a seeding of the earth with macromolecules by meteorites.

Today, our starting position for resolving this puzzle is radically different. Scientists working in this field have come to recognize that the flaw of

the conventional argument lies in the idea that life must have emerged out of a chemical soup through progressive increase of molecular complexity. The new thinking begins from the hypothesis that very early on, *before* the increase of molecular complexity, certain molecules assembled into primitive membranes that spontaneously formed closed bubbles, and that the evolution of molecular complexity took place inside these bubbles, rather than in a structureless chemical soup.

It turns out that small bubbles, known to chemists as vesicles, form spontaneously when there is a mixture of oil and water, as we can easily observe when we put oil and water together and shake the mixture. Indeed, the Italian chemist Pier Luigi Luisi (1996) and his colleagues at the Swiss Federal Institute of Technology have repeatedly prepared appropriate 'water-and-soap' environments in which vesicles with primitive membranes, made of fatty substances known as lipids, formed spontaneously.

The biologist Harold Morowitz (1992) has developed a detailed scenario for prebiotic evolution along these lines. He points out that the formation of membrane-bounded vesicles in the primeval oceans created two different environments – an outside and an inside – in which compositional differences could develop. The internal volume of a vesicle provides a closed micro-environment in which directed chemical reactions can occur, which means that molecules that are normally rare may be formed in great quantities. These molecules include in particular the building blocks of the membrane itself, which become incorporated into the existing membrane, so that the whole membrane area increases. At some point in this growth process the stabilizing forces are no longer able to maintain the membrane's integrity, and the vesicle breaks up into two or more smaller bubbles.

These processes of growth and replication will occur only if there is a flow of energy and matter through the membrane. Morowitz describes a plausible scenario of how this might have happened. The vesicle membranes are semi-permeable, and thus various small molecules can enter the bubbles or be incorporated into the membrane. Among those will be so-called chromophores, molecules that absorb sunlight. Their presence creates electric potentials across the membrane, and thus the vesicle becomes a device that converts light energy into electric potential energy. Once this system of energy conversion is in place, it becomes possible for a continuous flow of energy to drive the chemical processes inside the vesicle.

At this point we see that two defining characteristics of cellular life are manifest in rudimentary form in these primitive membrane-bounded bubbles. The vesicles are open systems, subject to continual flows of energy and matter, while their interiors are relatively closed spaces in which networks of chemical reactions are likely to develop. We can recognize these two properties as the roots of living networks and their dissipative structures.

Now the stage is set for prebiotic evolution. In a large population of vesicles there will be many differences in their chemical properties and structural components. If these differences persist when the bubbles divide,

we can speak of ‘species’ of vesicles, and since these species will compete for energy and various molecules from their environment, a kind of Darwinian dynamics of competition and natural selection will take place, in which molecular accidents may be amplified and selected for their ‘evolutionary’ advantages.

Thus we see that a variety of purely physical and chemical mechanisms provides the membrane-bounded vesicles with the potential to ‘evolve’ through natural selection into complex, self-producing structures without enzymes or genes in these early stages. A dramatic increase in molecular complexity must have occurred when catalysts, based on nitrogen, entered the system, because catalysts create complex chemical networks by inter-linking different reactions. Once this happens, the entire nonlinear dynamics of networks, including the spontaneous emergence of new forms of order, comes into play.

The final step in the emergence of life was the evolution of proteins, nucleic acids and the genetic code. At present, the details of this stage are still quite mysterious. However, we need to remember that the evolution of catalytic networks within the closed spaces of the protocells created a new type of network chemistry that is still very poorly understood. This is where complexity theory could lead to decisive new insights. We can expect that the application of nonlinear dynamics to these complex chemical networks will shed considerable light on the last phase of pre-biotic evolution.

Indeed, Morowitz points out that the analysis of the chemical pathways from small molecules to amino acids reveals an extraordinary set of correlations that seem to suggest, as he puts it, a ‘deep network logic’ in the development of the genetic code. The future understanding of this network logic may become one of the greatest achievements of complexity theory in biology.

Notes

1. See Goodwin (1994: 29ff.) for a critical discussion of the ‘selfish gene’ metaphor.
2. I am grateful to Brian Goodwin for clarifying discussions on this subject.

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