

# Evolution Beyond Entailing Law:

## The Roles of Embodied Information and Self Organization

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### Abstract

It is argued that no law entails the evolution of the biosphere. Biological evolution rests on both quantum random and classical non-random natural selection and whole-part interactions that render the sample space of adjacent biological possibilities unknowable. This would seem to create an insurmountable problem for intelligent design in biology. Nonetheless, the evolution of ensembles of interacting systems can be modeled by statistical laws that have strong self-organizational properties. Some compelling examples modeling evolutionary self-organization in biology are presented and it is concluded that a new science of order and organization beyond entailing law is required.

**Key words:** Evolution, Entailing Law, Adjacent Possible, Quantum Randomness, Classical Non-randomness, Natural Selection, Kantian Wholes, Darwinian Pre-adaptations, Embodied Information, Intelligent Design, Ensemble Approach, Genetic Regulatory Networks, Autocatalytic Sets, Rugged Fitness Landscapes, Self Organization

### Introduction

I wish to make major claims in this article. Foremost, as presaged in the title, I claim that no law entails the evolution of the biosphere. We must be deeply careful of so large a claim, for if it is true, the Reductionist dream of a “final theory” that will entail all that happens in the universe is false. But this has been the dream, since the Greeks, through Newton, Einstein, and Schrodinger, to most recently, Steven Weinberg in his *Dreams of a Final Theory* [1].

If the claim is correct that no law entails the evolution of the biosphere, it will follow that we do not know the ever-changing phase space of the future evolution of the biosphere. F. Bailly and G. Longo [2] make this point emphatically in their *Mathematics and the Natural Sciences: The Physical Singularity of Life*, as do I, in *Reinventing the Sacred* [3].

From the fact that we do not know the ever-changing phase space of biological evolution, it will follow that we do not know the “sample space” of what I call the “Adjacent Possible” of the evolution of the biosphere. From this it follows that standard notions of Information Theory, such as Shannon and Kolmogorov, cannot be applied, since both require prestatement of the sample space of the process. For example, for Shannon, prestatement of the set of possible messages — the sample space — is needed to compute the entropy of the information of the Source. If we do not know the sample space of evolution, Shannon’s starting point is moot.

Moreover, if we do not know the sample space of the process of biological evolution, then probability calculations utilized by Intelligent Design scholars are also either moot, or deeply suspect.

These issues mean we need to invent a new concept of biological information. No adequate formulation now exists. I will propose the start (only) of such a formulation.

If no law entails the evolution of the biosphere, then we must ask what forms of laws, if any, we can have. One approach that I will discuss is the study of ensembles of systems [4]. For example, the study of (i) ensembles of model genetic regulatory networks controlling cell differentiation and ontogeny, (ii) ensembles of reaction networks capable of catalysis of the same reactions to form collectively autocatalytic sets for the origin of molecular reproduction and life, and (iii) ensembles of tunably rugged fitness landscapes [5]. Two major features of this ensemble approach are: (i) A search for statistical laws, despite the absence of entailing laws. As more facts are learned about the systems in question, more refined ensembles can be built for better statistical laws. (ii) Remarkable evidence for profound self organization has been found, for example, as typical, or generic, properties of ensembles of genetic regulatory networks. This self organization almost surely plays a role with selection in evolution. A generic phase transition has been found, in chemical reaction networks, to the self-organized emergence of collectively autocatalytic sets capable of molecular reproduction that are likely to play a role in the origin of life. Furthermore, a remarkable linkage has been found between species co-evolving on tunably rugged landscapes and the very structure of those landscapes also evolving, such that evolution itself can tune the structure of fitness landscapes on which evolution occurs, to lower or even perhaps minimize the rate of extinction, and hence maximize species lifetimes. In all these cases, we find both statistical laws without entailing laws for the evolution of the biosphere, and unexpected and powerful self organization that mingles with natural selection in the panorama of life’s becoming.

This article is organized as follows: In section 1, I discuss work with senior French/Italian mathematician Giuseppe Longo that is the strongest case we can currently make that no law entails the detailed evolution of life. Hence my

conclusion that this spells “the end of a physics worldview.” In this discussion, I expand on my own work [3] and that of F. Bailly and Longo [2], both of which claim and demonstrate that the phase space of evolving life persistently changes in ways we cannot say. In section 2, I discuss the stunning fact that evolution, without selection, creates its own “adjacent possible” empty niches, which it may fill. Hence evolution, in a kind of “natural magic”, builds the very possibilities it becomes. That is, I demonstrate the truly astonishing fact that, without natural selection acting at all, the evolving biosphere creates the ever new Adjacent Possible empty ecological niches that evolution may/will fill. Thus, without any selection acting to create this astonishing aspect of evolution, evolution itself is building the very possibilities that evolution becomes. Here the claim from Heraclitus that “Life Bubbles Forth” seems right and deeply new. In section 3, I lay out the claim that we do not know the sample space of the evolutionary process, so standard information theory is moot. In section 4, I relate the above results briefly to the hopes of the Intelligent Design community to demonstrate Irreducible Complexity [6], and its vast improbability by normal evolutionary processes [7]. In section 5, I describe three examples of the use of the “ensemble approach” to find statistical laws in the absence of entailing laws for the detailed becoming of the biosphere. I discuss models of ensembles of genetic regulatory networks, the emergence of collectively autocatalytic sets, and the statistical features of evolving fitness landscapes. All also exhibit the self organization alluded to above [5].

## I. Evolution Is Beyond Entailing Law

At the dawn of Western philosophy and science, some 2,700 years ago, Heraclitus declared, roughly, that “the world bubbles forth”. There is, in this fragment of thought, a natural magic, a creativity beyond the entailing laws of modern physics. I believe Heraclitus was right about the evolution of the biosphere and human life. We live beyond entailing law in a kind of natural magic we co-create.

Early sociologist Max Weber said that with Isaac Newton, we became disenchanting and entered Modernity. He was right. Before Newton, our tradition, from *Genesis*, saw a creator God whose divine agency, rather like the natural magic of Heraclitus, created the world also beyond entailing law.

With Newton’s three laws of motion, universal gravitation, and the differential and integral calculus, our world transformed profoundly. Given the initial conditions of billiard balls’ positions and momenta on the table, the boundary conditions of the shape of the table, and the motions of the balls given in differential equation form using the laws of motion, then integration, a form of deduction, yielded the entire future and past trajectories of the balls.

With Pierre-Simon Laplace, this became the bedrock of reductionism: Given the positions and momenta of all the particles in the universe, a vast intelligence could, using Newton's laws, deduce the entire future and past of the universe. For Laplace, the complete determinism of Newton's laws co-existed with a capacity for accurate prediction. With Poincaré and the three body gravitational problem, deterministic chaos was discovered. Here the system remains deterministic but unpredictable because of sensitivity to initial conditions and the fact that any measurements of initial conditions require a finite interval of space and time — a point that Bailly and Longo stress [2]. Thus, in modern classical physics, determinism does not imply predictability.

The framework of entailing laws remains in the twin pillars of twentieth-century physics — classical physics with General Relativity, and quantum mechanics — in both cases with differential equations and their entailed integration. Bailly and Longo [2], stress that in physics, it is always possible to prestate the phase space of the system, typically derived from its underlying symmetries. In classical physics, a least action principle assures that the actual behavior of the classical system in its “possible phase space” is always a unique “shortest path”, or geodesic, on some manifold. In quantum physics, given the indeterminism of quantum mechanics, the analogous behavior is a geodesic of a probability distribution. In short, the framework of physics prestates its phase space in which, via laws of motion in ordinary or partial differential equation form, initial and boundary condition, and integration, yield the entailed geodesic behavior of the system.

I believe we reach a terminus of this physics worldview at the watershed of life. As we will see, it seems Heraclitus was right: Life bubbles forth in a kind of “natural magic”. A purpose of this article is to spell out this natural magic, which exhibits itself as the evolving biosphere literally constructs, without selection, its own future possibilities.

*First*, and of truly central importance, evolution itself defies both the completeness of quantum mechanics and the completeness of classical mechanics, yet unites them both. We know this, but never say it. Mutations are often quantum random and indeterminate events yielding Darwin's heritable variations. Yet evolution itself is not random, as the phenomenon of convergent evolution demonstrates. For example, the eye has evolved independently eleven times. And the convergence of the independently evolved vertebrate and octopus camera eye to a stunning near identity, the result of powerful natural selection, is obviously not random. More examples are found in the convergent evolution of marsupials and mammals.

Thus, in blunt terms, biological evolution is neither quantum indeterminate random, nor deterministic classical mechanics. The living world really is “new”. Quantum mechanics alone and classical physics alone each seem to be incomplete.

The fact of evolution, mixing quantum and classical physics for which each alone is insufficient, is clear. What might this truth mean?

One very important possibility is that, after 85 years of unsuccessful attempts to unite quantum mechanics and General Relativity, it may really not be possible to unify them into the single theory whose “Dream” is that of Weinberg [1]. We may have to live with quantum mechanics and classical physics un-united. In this case, evolution itself demonstrates that both nevertheless “mix” together: quantum indeterminate yet random mutations united with the non-random effects of natural selection acting at the level, at least in part, of classical physics, and thus the camera eye evolved in octopus and vertebrates. But this requires something that seems not to be entailed in current physics: Let a quantum indeterminate random DNA mutation occur, then natural selection act to evolve toward the tuned camera eye. As this largely classical physics evolution occurs, different alleles of mutated genomes are selected in the evolving population. Thus, when quantum random and indeterminate mutations creating yet new alleles occur, the very possibilities of what those quantum event mutations might be, i.e., in which gene sequences they may occur, has changed due to largely classical physics natural selection. In turn, the quantum random indeterminate mutations alter what natural selection will do. Taken together, evolution is both quantum indeterminate and also non-random.

Given this mixture of quantum indeterminate random, and classical physics non-random natural selection, it seems very hard on this basis alone to conceive of a single law that entails the detailed evolution of the biosphere.

In a related intellectual effort to link quantum mechanics and the mind-brain system, inspired by Sir Roger Penrose, but taking a different track, I have proposed in “Answering Descartes: Beyond Turing” [8], that even in the mind-brain system, perhaps in synapses, a similar non-determinate yet non-random mixture of quantum indeterminate and yet non-random classical behavior can occur. It may be important that there now appears to be a Poised Realm, where systems, via decoherence and re-coherence, can hover back and forth between quantum coherence and classicality for all practical purposes (FAPP). This hovering may play a role in organisms and be indeterminate, yet non-random. There may also be no entailing law for this behavior.

In short, if we cannot unite quantum mechanics and General Relativity under a single law, this may not be an intellectual tragedy, but may free us, after the 350 years since Newton, from the dream of universal entailment. Then true novelty, beyond entailment, can arise. Life can “bubble forth”. I now discuss further reasons to believe that no law entails the evolution of the biosphere.

*Second*, biological evolution concerns “Kantian wholes” [9], where the whole exists for and by means of the parts and the parts exist for and by means of the whole. An instance is a collectively autocatalytic set of peptides, as produced by

Gonen Ashkenazi of Ben Gurion University in his nine-peptide autocatalytic set. This is a clean example of a Kantian whole. No peptide catalyzes its own formation from two fragments of itself, but instead catalyzes the formation of one of the other nine peptides from two fragments of that peptide. The set of peptides as a whole catalyses the entire set of reactions by which the set of nine peptides reproduces itself in a collectively autocatalytic set. If we call catalyzing a reaction a “catalytic task”, then the set achieves a “closure” in catalytic task space. All the reactions that require catalysis are catalyzed by one or more members of the set. Note that, given a Kantian whole, the “function” of a given peptide can be defined as its role in sustaining the reproduction of the whole nine peptide collectively autocatalytic set.

In his forthcoming book, *Incomplete Nature* [10], Terrence Deacon, a professor at U.C. Berkeley, points out that philosopher Jaegwon Kim has argued that even such Kantian wholes do not preclude deduction upward from particles to wholes. But, points out Kim, according to Deacon, who agrees, that argument rests on classical “materialism,” i.e., the classical physics of point particles and fields. Deacon rightly notes that quantum mechanics, as in Feynman’s sum over all possible pathways that, e.g., a photon might take through the two slits, obviates such a naive materialism. The position and momentum of a particle cannot be jointly measured with precision; quantum mechanics precludes point particles existing prior to measurement, and multi-particle quantum systems are, ineluctably, “wholes”. Thus the collectively autocatalytic set is a Kantian “Organized Being,” whose ever-changing atoms and molecules exist in the universe — when most complex things above atoms will never exist — as a united whole, an entity which is sustained existing in the universe by the linked dynamical classical and quantum processes of parts and whole enabling one another. The specific peptides may come and go, yet the Kantian whole remain as non-equilibrium, self-sustaining, partly quantum, partly classical, and perhaps partially Poised Realm, processes.

*Third*, a living, dividing cell is both a collectively autocatalytic set, and thus a Kantian whole. But of central importance, it achieves a task closure in a much wider set of tasks than mere catalysis. Proteins are vectored to specific cell locations, energy is transduced, pumps operate in work cycles, and chromosomes are separated in mitosis, completing a set of task closures in some wide set of tasks such that the dividing cell reproduces. The function of each such task, typically a subset of the causal consequences of the physical processes involved, is its role in sustaining the reproduction of the cell as a Kantian whole.

*Fourth*, and of deep importance is this: We cannot name all the causal consequences or uses of any object, say a screw driver, alone or with other objects. The set of uses appears to be both unbounded or “indefinite”, and un-orderable. But

that means we cannot know that we have ever “listed” all the uses of a screw driver alone or with other objects or processes.

Now consider an evolving cell in which one or more objects or processes, each with myriad causal consequences, finds a novel use that we cannot prestate, but which enhances the fitness of the cell, and so is grafted by natural selection into the evolving biosphere. This “finding of a novel use that we cannot prestate” occurs all the time. The famous flagellar motor of some bacteria made use, via Darwinian preadaptations or exaptations (discussed further below), of fragments of its flagellar proteins that were serving entirely different functions in other bacteria.

*Fifth*, Darwinian preadaptations are typically not prestateable. A Darwinian preadaptation is a causal consequence of a part of a process in an organism of no selective significance in the current environment that “finds a use” in a novel selective environment and is selected, typically, for a novel function. Preadaptations occur all the time in evolution. I give but one example. Some fish have swim bladders, sacs partly filled with air and water, whose ratio adjusts neutral buoyancy in the water column. Paleontologists believe that swim bladders evolved from the lungs of lung fish: water got into some lungs, and then there was a sac partly filled with air and water, poised to evolve into a swim bladder. I now raise three questions: (i) Did a new function come to exist in the biosphere? Yes. Neutral buoyancy in the water column. (ii) Did the evolution of the swim bladder alter the future evolution of the biosphere? Yes, the possibilities of new species with swim bladders, new proteins, and new ecological niches came into existence: for example, a bacterium or worm might evolve that is only able to live in swim bladders. I return to this example below. (iii) Do you think you could prestate all the possible Darwinian preadaptations just for humans in the next million years? We all say “no”. Here is why: We cannot finitely prestate all the possible uses of parts, alone or together, of an organism, for they are indefinite in number and unorderable. We cannot know we have completed the list of uses. Next, we cannot say all possible selective environments for which such uses might be found to be useful. How would we know we had listed all possible selective environments?

But this means something terribly important. Let me call the set of possible next Darwinian preadaptations the Adjacent Possible of the evolution of the biosphere via preadaptations. We do not know what this set of possibilities is! Thus, and of central importance, we do not know the “sample space” of the evolution of the biosphere by Darwinian preadaptations.

But the fact that we do not know the sample space means we cannot make normal probability statements. Consider instead flipping a fair coin 10,000 times and calculating the probability of 4698 heads using the Binomial theorem. We can do this, but notice that we know ahead of time “all possible outcomes”, all heads,

all tails, all 2 to the 10,000 power possible outcomes of our 10,000 flips. We know the sample space, so we can erect a probability measure.

In contrast, for the evolution of the biosphere by preadaptations, we do not know the sample space and so seem entirely unable make normal probability statements. In turn, I think this inability has its roots in the indefinite set of uses of any part or set of parts or processes in a cell or organism, which set is also unorderable. We cannot know we have listed all the possible uses, nor the set of all adjacent possible selective environments. We do not know what features alone or together in, say, a dividing cell, may find a novel use in some environment and be grafted by natural selection into the Kantian whole, creating a novel function and a novel Kantian whole in the evolving biosphere.

*Sixth*, mathematics requires that we have the concepts beforehand of the relevant variables, say, mass and length of a pendulum, for the law of the pendulum. The older view of mathematics as mere formal manipulation of syntactic symbol strings given uninterpreted axioms, has given way to a more modern “constructivist” mathematics, as Bailly and Longo argue [2], in which the settled concepts with their semantics, not just syntax, is central to the development of mathematics. For Newton,  $F = MA$  rested on a pre-Newtonian notion of “mass”.

But unlike physics, where the phase spaces are always predated, in evolution the phase space is always changing [2, 3], and as we shall see, even more stunningly, building without selection, the very possible ways it may change its phase space. Thus, for evolution of the biosphere by ever new causal consequences, which may “find some unprestatable use” by Darwinian preadaptations in evolving Kantian wholes that constitute cells with ever changing Task closure, we do not know the relevant variables, so we cannot write down the laws of motion for the evolving biosphere.

*Seventh*, we do not know ahead of time the emerging novel Adjacent Possible empty niches, such as the fish swim bladder into which some worm or bacteria could evolve to live. But those niches constitute the boundary conditions on natural selection shaping the evolution of the worm or bacterium to live in the swim bladder.

Newton taught us that we need the laws of motion, which by point six above we do not have, and we need the initial and the boundary conditions, to integrate the laws of motion for the trajectory of, say, the billiard balls on the billiard table. But we do not know the boundary conditions that the swim bladder, when it may evolve, will constitute, so we cannot integrate the laws of motion, (which we do not have anyway), for the evolution of the biosphere. Lacking the boundary conditions would be like trying to integrate the motions of the billiard balls with no idea of the shape of the billiard table. We do not even have a mathematical model if we lack the boundary conditions!



In summary of these points, first through seventh, no law entails the detailed evolution of the biosphere. If this is true, it is the end of a physics worldview.

## II. Life Bubbles Forth

Heraclitus was right: Life bubbles forth, beyond entailing law. Consider the evolution of the swim bladder above by a Darwinian preadaptation. Did natural selection act to craft a well-functioning swim bladder in an evolving population of fish? Of course. But did natural selection act to craft the new adjacent possible empty ecological niche that the swim bladder constituted? NO. No natural selection acted to create the new adjacent possible empty niche into which the worm or bacteria might evolve to live.

But this means that, without any selection at all, the biosphere is building its own adjacent possible pathways of evolution. The biosphere is building, without selection, its own future possibilities. By a kind of “natural magic”, the biosphere creates its own future. Heraclitus was right: Life bubbles forth beyond entailing law.

If the above is true, we must give up our deep belief, at least since Newton, if not the Greeks, that without entailing law, the world cannot become in a coherent way: The biosphere has been doing just fine for 3.7 billion years of becomings as Kantian wholes make their largely self-consistent but ever-changing worlds ever anew with one another. We need to think anew how this becoming, even with extinction avalanches, can be coherent without entailing law.

More, if Max Weber is right that with Newton we became disenchanting and entered Modernity, my hope is that the “natural magic” of life bubbling forth, and, a fortiori, human life, can re-enchant us. Perhaps we can move beyond Modernity.

## III. Beyond Standard Information Theory to Embodied Information

I begin with Shannon’s famous information theory [11]. Shannon chose, on purpose, to ignore any semantics, and concentrate on purely syntactic symbol strings, or “messages” over some pre-chosen symbol alphabet, most simply 0 and 1. Then he considered an Information Source filled with diverse bit string “messages”, say bit strings of length  $N$ . Each message might occur once or many times in the source. Let  $p_i$  be the frequency of the  $i^{\text{th}}$  message. Then  $-\sum p_i \ln(p_i)$  over the set of messages in the source is the “entropy” of the source. Given a measure of the entropy of the source and a noisy channel with a decoder at the far end, he could study information transmission down the channel from source to decoder.

It is clear that Shannon's invention requires that the ensemble of all possible messages, here the possible  $2$  to the  $N^{\text{th}}$  power bit strings length  $N$ , be stable head of time. Without this statement, the entropy of the information source cannot be defined.

Now let's turn to evolution. We saw above that we cannot prestate the adjacent possibilities of the evolution of the biosphere by Darwinian preadaptations. Thus, we cannot construct anything like Shannon's probability measure over the future evolution of the biosphere; thus, in turn, we cannot apply information theory in any obvious way to that evolution.

This blunt statement ignores further huge difficulties in applying Information Theory in biology. For Shannon, a bit is a bit, 0 or 1, hence the only "features" are the members of the alphabet of pre-chosen symbols, here 0 or 1. But in biological evolution, where we cannot finitely state the causal consequences of uses of any one or many features or processes in cells or organisms, where the set is both indefinite and unbounded, even if we prestated the "features" we could not state the alphabet of their relevant causal consequences or uses. It is precisely because of these causal consequences alone or together that "find a use" in an evolving cell or organism that these ever new features are grafted into the evolving biosphere.

More, what counts as a "feature"? Any causal consequence of "one" or many parts or processes which alone or together "find a use" that enhances fitness of the Kantian whole so enters the biosphere. We cannot even prestate what aspects of a cell may constitute a feature. In terms of Shannon, we don't even know the "alphabet".

The same concerns arise for Kolmogorov [12], who again requires a defined alphabet and symbol strings of some length distribution in that alphabet. Again, Kolmogorov uses only a syntactic approach. Life is deeply semantic with no prestated alphabet, no "Source", no definable entropy of a source, but unprestatable causal consequences which alone or together may find a use in an evolving Kantian whole of a cell or organism.

In summary, standard information theory, both purely syntactic and requiring a prestated sample space, is largely useless with respect to evolution. On the other hand, there is a persistent becoming of ever novel structures and processes that constitute specific novel and integrated functionalities in the Kantian wholes that co-create the evolving biosphere. Note that the causal consequences and uses in Kantian wholes have a deep semantic content in embodied cells and organisms living in an embodied physical world. We need a new theory of embodied functional information in a cell, ecosystem or the biosphere.

A start of such a theory is taken in Kauffman [13]. The issues include these: (i) How do we measure the diversity of functions embodied in one or a community of Kantian wholes making their worlds together at any point in their evolution?

(ii) How do we measure the “degree of organization” of the processes carried out in those embodied functions? Consider the heart. Its function is to pump blood. But it makes heart sounds and jiggles water in the pericardial sac. The function of the heart is to pump blood, not make heart sounds or jiggle water in the pericardial sac. Thus, the function of a part of an organism is typically a subset of its causal consequences.

In Kauffman [13] I propose the steps of: (i) Distinguishing the system into a set of “parts and processes”. (ii) For each of these, list its set of immediate causal consequences. (iii) Find that choice, for each of the distinguished “parts”, of that one of its causal consequence, such that, when taken over all the parts together, that choice of one causal consequence per part maximizes a measure of the total diversity of processes of the total system. This measure is called Set Complexity. This maximal Set Complexity measure with its identified single causal consequence, among all the causal consequences of each part, will hopefully pick out the causal consequence of each part which is the true functions of that part. Thereby this will measure the total diversity of functions in the total system. (iv) For work processes, measure the power efficiency per unit fuel consumed of that process as a macroscopic measure of the “degree of organization” of that functional work process. Power efficiency per unit fuel consumed for work processes picks out an optimal displacement from equilibrium, hence is of considerable interest as a measure of the degree of organization of a process. (v) Multiply each identified functional work process of each part by its power efficiency and sum over the parts in the system to get an overall measure of the total diversity of organized processes.

I do not know how to generalize this to functions in cells or organisms which are not work processes.

If we could invent a measure along these lines, we could measure the diversity of organized processes in an ecosystem, or even the biosphere, at any moment of time. Then this diversity is a natural measure of the “embodied information” in the Kantian wholes co-creating their worlds. With this measure, should we get it, we could measure the change, presumably an average secular increase over evolutionary time, of the embodied information of the biosphere.

#### **IV. Implications for Intelligent Design**

The underlying concept of Intelligent Design, ID, is perfectly sensible but perhaps in a restricted set of scientific contexts. For example, ID can be taken to ask: (i) given an alphabet and messages, is the set of received messages highly improbable given the entropy of the Shannon source? (ii) Alternatively, given

absorption or emission signals from atoms from stars, is the observed time sequence so improbable that it suggests “design”. SETI has just this legitimate problem.

At issue is whether Intelligent Design is well founded in asking this question of biology. Here there are at least two issues: First of all, Irreducible Complexity [6], exemplified by the bacterial flagellar motor, is a phenomenon said by ID advocates to be too specifically complex to have arisen by random variation and natural selection. But this approach ignores Darwinian preadaptations where old parts, selected for different purposes, are recombined for a new function — e.g., the flagellar motor itself, assembled, it is thought, from proteins serving different functions in different bacteria.

Secondly and more deeply, Intelligent Design seeks to accomplish the analogue of SETI. But if, as above, we can construct no probability measure for the emergence and evolution into the ever changing adjacent possible of the evolving biosphere, it would seem that such calculations are either moot or questionable at present.

Whether the attempt to show that evolution is, in some definable sense, more “ordered” than some new and yet to be defined measure of randomness concerning what the myriad branching pathways of evolution, with some confidence level, would allow, remains to be seen. It would seem that Intelligent Design researchers — indeed, all of us — need to begin to cope with the amazing bubbling forth of new niches without selection, allowing new directions of evolution as life itself bubbles forth.

## **V. The Ensemble Approach to Statistical Laws and Self Organization with No Entailing Law**

The “ensemble approach” [4] may prove useful. I will give four examples where it has been applied: (1) genetic regulatory networks, (2) the origin of life, (3) statistical features of “rugged fitness landscapes, and (4) in physics, spin glasses. I discuss the first in detail.

### ***The Ensemble Approach to Genetic Regulatory Networks***

As a young man, I thought about cell differentiation. How could different cells in us, all having the same genes, be different, liver, kidney, etc? It was known that in different cells types, different genes were active making specific and different sets of proteins. In 1961 and 1963, French microbiologists, F. Jacob and J. Monod,

cracked the problem when they showed that, in *E. coli* bacteria, one gene, say A, could make a protein, say A, that bound to a DNA region next to another gene, say the B gene, and turn on or turn off the B gene's formation of its own B protein. In a seminal 1963 paper [14], they argued that if two genes, A and B, each repressed, or turned off, the other gene, the little two gene circuit had two dynamical steady states: (1) A on and B off, or (2) A off and B on. Hence, they said, the SAME set of genes could express different proteins corresponding to two cell types [14].

All biologists recognize that Jacob and Monod set the now central question of Systems Biology: what is the genetic regulatory network among 23,000 human genes, of which about 2,200 genes coding for transcription factors, and others coding for microRNAs, regulate one another's activities and regulate the rest of the 23,000? Here we need to know which genes regulate which genes, and by what "dynamical rules". Then we need to "integrate" the equations of motion of such a network to discover its integrated behavior. Just as Newton's laws for billiard balls yield, upon integration with given initial and boundary conditions, the trajectory of the balls, so for a classical physics genetic network, the behavior of the system has a trajectory from each initial state, i.e., from each pattern of gene expression among all 23,000 genes. These flow through a sequence of patterns, or states of gene expression, and typically the flows, or "trajectories", end up on small subsets of states, called "attractors", each of which drains a "basin of attraction". Cell types probably correspond to attractors and differentiation corresponds to noise or signal induced flow among attractors [5, 15].

Here is the "ensemble approach": I wondered if natural selection had to struggle to create very specifically selected, hence "engineered", networks to achieve controlled differentiation from the fertilized egg, or zygote, called "ontogeny", or, I hoped, some broad class or "ensemble" of networks would all have "good enough" dynamical behavior to underlie ontogeny with just some tuning by natural selection.

To ask this question I idealized the behavior of a gene as an on-off device, a light bulb, and asked if there was a class of large genetic networks that yielded "orderly behavior". To ask this question is inherently to take the Ensemble Approach: it asks whether there are typical (i.e. generic) behaviors in different classes or "ensembles" of networks. In my case I imagined  $N$  genes, each with  $K$  inputs. There are vastly many networks, an entire "ensemble" of networks, with  $N = 23,000$  genes, and  $K =$  say 2 inputs per gene. To study the typical properties of this ensemble, one approach is to sample at random from this ensemble. Thus, I chose the  $K = 2$  inputs to each gene at random from among the  $N$ , and for each I assigned at random one of the 16 possible logical, or "Boolean functions" prescribing the behavior of the regulated gene at the "next time moment", given the on or off states of its two inputs at the current moment. The "AND" function

is such a Boolean function. It says the regulated gene will be “on” at the next moment only if both its inputs are “on” at the present moment.

To summarize many years of work by many on Random Boolean Networks, it turns out that they behave in three regimes: Ordered, Chaotic, and a “Critical” “edge of chaos” regime which is a phase transition between order and chaos.  $K = 2$  networks turn out to be critical for the ensemble of networks with randomly chosen Boolean functions. Critical networks can have other values of  $K$  greater than 2 by using non-random choices of Boolean functions of  $K$  [5].

Now three essential facts: (i) Critical and Ordered networks exhibit very ordered, and also multiple, attractors, hence the generic behaviors of these networks exhibits a new form of SELF ORGANIZATION — generic order in an Ensemble of systems. These ordered attractors are so ordered that the different attractors could explain the order of the different cell types in an organism. (ii) It is becoming clear that differentiated cell types are almost certainly “attractors” [14]. (iii). More amazingly, cells appear to be “Critical”, to live on the edge of chaos [16–19].

Note three essential feature of the Ensemble Approach: (i) There is a vast ensemble of  $NK$  Random Boolean Networks, or more realistic models of genetic networks, all of which are dynamically critical. In short, “criticality” is a feature of an entire ENSEMBLE of networks, not just of one. ii. Importantly, this means that the generic behaviors of this class of networks is independent of the physics of any specific member of the ensemble. iii. Critical networks are a subset of all Random Boolean Networks, those at the edge of chaos. If cells are critical, Natural Selection must hold networks at the edge of chaos for adaptive reasons — here is the mixture of Ensemble Self-Organization AND Natural Selection.

### ***The Ensemble Approach Can Yield Statistical Laws Beyond Entailing Laws***

As stressed at the start of this article, no law entails the detailed evolution of the biosphere, including the evolution of genetic regulatory networks. This means we cannot deduce *ab initio* what those networks are. But the Ensemble Approach allows statistical laws about the typical features and behaviors of the entire ensemble of critical networks. More profoundly, evolution does NOT follow geodesics. Thus evolution is NOT entailed. It follows myriad pathways mixing quantum random indeterminate mutations and non random natural selection. The Ensemble Approach is the natural way to seek statistical laws about the behaviors of genetic regulatory networks, without needing to know the details of any specific genetic regulatory network. As we learn more about real networks we can refine

the specifications of the ensemble, hence the generic behaviors of the refined ensemble, for better statistical predictions.

In short, the Ensemble Approach marries to the lack of entailing law for evolution, to yield one viable approach to statistical laws beyond entailing law.

### ***The Ensemble Approach to the Emergence of Collectively Autocatalytic Sets as a Generic Phase Transition in Complex Chemical Reaction Networks***

Perhaps the central problem concerning the origin of life is the onset of molecular reproduction, given a “soup” of prebiotic organic molecules such as amino acids, lipids, nucleotides and other organic molecules. These molecules may have been present on the early earth due to meteorite infall, abiotic synthesis on the early earth, or both.

Such small organic molecules, say in confined spaces such as tidal pools or rocks with interconnected hollow chambers, may be a necessary condition for the onset of molecular reproduction, but not sufficient. In 1971, the received view was that life must be based on template replication of arbitrary sequences of single stranded DNA, RNA, or similar molecules. The hope was that a single, say, RNA template strand would line up free A,U,C, and G nucleotides to Watson-Crick match the arbitrary single template strand, then the free nucleotides would be bonded by 3'–5' phosphodiester bonds to make a second complementary strand, then the two strands would melt apart and cycle. This would create, without enzymes, a self replicating arbitrary RNA sequence. Forty years of intense work has so far failed.

A current approach, pinioned on the observation that RNA molecules can act as enzymes, called ribozymes, is a search for an RNA ribozyme, single stranded, able to copy a second complementary RNA strand, then copy that complementary strand back into a copy of the initial strand. Such a ribozyme would, acting as a “polymerase”, be able to copy any single-stranded RNA molecule, including itself. Some progress has been made, but I have concerns: (i) Such molecules may exist but be very rare, so unlikely to arise by chance. (ii) How does such a molecule build the network of metabolism around itself? (iii) If the ribozyme is error prone, its copies will have more errors, and their copies yet more errors, and may create a runaway “error catastrophe” if the mutation rate is stronger than the selective advantage of the good ribozyme(s).

In 1971 [20, 21, 5], I took the ensemble approach based on a different conception. What was needed, I thought, was a set of molecules that were collectively autocatalytic, as is Gonen Ashkenasi's nine-peptide collectively

autocatalytic set [22]. His set, by the way, conclusively demonstrates that molecular reproduction need have nothing to do with DNA, RNA, or nucleotides.

To approach my question in an ensemble sense, I asked this: Given a set of molecules,  $M$  in number, with  $R$  reactions among them, and some distribution of which, if any, of the  $R$  reactions, each of the  $M$  might catalyze, could one find conditions under which, generically, collectively autocatalytic sets would arise? The answer can be yes. Under simple assumptions in which, as a 0<sup>th</sup> order hypothesis, each molecule among  $M$  has a probability  $P$  to catalyze each of the  $R$  reactions, it is a theorem that, as the diversity of  $M$  and the greater diversity of  $R$  and hence  $R/M$  increases, a phase transition is reached at which collectively autocatalytic sets emerge with probability near 1. Importantly, the same results arise with more realistic models of *which molecules catalyze which reactions* by a local “matching” rule [21, 5].

This work has been confirmed and extended in a number of ways. It is the ensemble approach, for it says that independent of the detailed chemistry and physics, it is a typical or generic property of complex reaction networks — whose molecules are also candidates to catalyze the reactions — that collectively autocatalytic sets will arise. (I emphasize that this remains theory and is not confirmed experimentally yet, but is fully open to being tested using libraries of random peptides, RNA, DNA, or mixtures of the above.) Here are the important features of this ensemble approach: (i) The emergence of collectively autocatalytic sets as a phase transition in complex reaction networks is a powerful example of self organization. (ii) Since DNA, RNA, and peptide collectively autocatalytic sets have been synthesized by good chemists [23, 24, 22], such sets are our only current examples of self reproducing molecular systems and are Kantian wholes as noted above. (iii) The theory of the emergence of such autocatalytic sets is again independent of the specific underlying physics, so it cannot be reduced to any specific physics, such as the choice of a specific set of molecules that happens to be one among trillions of collectively autocatalytic sets. The routes to molecular reproduction lie in chance and number, not specific physics. (iv) It now turns out that such systems in hollow lipid vesicles called liposomes can, *in silico*, synchronize the division of the liposome with that of the autocatalytic set [25], and can undergo open ended evolution [26]. (v) With the inclusion of inhibition of catalysis as well as catalysis, such systems can exhibit alternative attractors and critical dynamical behavior, like model genetic regulatory networks [26]. Thus, if critical autocatalytic sets are selectively advantageous, as I suspect, there will be a vast ensemble of such possible networks among a larger set of non-critical autocatalytic sets, so selection will have interacted with self organization to yield the useful ensemble, again a marriage of self organization and selection.



### **The Ensemble Approach to Tunably Rugged Fitness Landscapes**

The concept of fitness landscapes, introduced by Sewall Wright into biology [27], is well established. Briefly, in one concrete case, over a set of haploid genotypes, each has a fitness in some fixed environment. This fitness can be thought of as a “height” over a large-dimension space of all the gene sequences under consideration. Now, in genetics, it is known that the fitness contribution of one version, or allele, of a gene at one “locus”, may depend upon the alleles and other loci. This dependence is called “epistasis”. The ensemble approach I utilized was borrowed with modification from “spin glasses” in physics [28]. I presumed  $N$  genes, each with two alternative alleles, or versions. I assumed that each gene allele’s fitness contribution depended upon the allele of that gene and the alleles of  $K$  other genes. The rest of this  $NK$  model was randomly constituted, hence the ensemble approach. I assigned the  $K$  epistatic inputs to each gene at random among the  $N$ . I assigned the fitness contribution of a given gene,  $i$ , for each of the 2 to the  $K + 1$  alleles of that gene and the  $K$  other input genes, at random from the uniform interval from 0 to 1. I defined the fitness of a given vector, or list, or state of the alleles of the  $N$  genes, and the average of their fitness contributions. These simple ensemble assumptions yield, for each randomly built  $NK$  model, a fitness landscape over all 2 to the  $N^{\text{th}}$  power haploid genotypes. Hence any  $NK$  model is a random sample, having fixed  $N$  and  $K$ , of an entire ensemble of fitness landscapes with the same  $N$  and  $K$  [5].

The result is an ensemble of fitness landscapes, whose statistical properties depend upon  $N$  and  $K$ . Briefly, for  $K = 0$ , each allele of each gene makes a fitness contribution that is independent of all other genes. There is a Fujiyama fitness landscape with one peak and smooth sides. For  $K = N - 1$ , its maximum value, the fitness landscape is random, there are 2 to the  $N$  divided by  $(N + 1)$  local fitness peaks on the landscape, and many other statistical features. These features are tuned as  $N$  and  $K$  are tuned [5].

It is clear that the  $NK$  model inquires into the typical or generic properties of fitness landscapes only as a function of the epistatic coupling  $K$ , and the size of the system  $N$ .  $K$  captures conflicting constraints, hence as  $K$  increases the landscapes become more rugged. This model has found use in the economics of learning curves, maturation of the immune response, molecular evolution over rugged landscapes, and even in management models [27].

Surprisingly, if species co-evolve on  $NK$  landscapes and can both invade one another’s niches, and when they do, they carry their own landscape ruggedness parameter,  $K$ , which varies in the population and can itself evolve, the system evolves to a state that increases species life-time distributions, smooths landscapes

to an intermediate ruggedness, and yields a power law distribution of avalanches of extinction events matching the evolutionary record. Hence, evolution can modify the landscapes upon which evolution occurs [29].

## Conclusion

I have offered rather radical views. Most notably, it may well be true that there is no law which entails the evolution of the biosphere. If so, what I speak of is, in fact, the end of a physics worldview, of the dream of reductionism to find a fundamental “final theory” that entails all that occurs in the universe. This is a very large claim requiring careful investigation. But if true, it begins to appear that it is not the tragedy we may have feared for so long. In its place is a vast creativity in the living world, far beyond what we have imagined. In *Answering Descartes: Beyond Turing*, (8), I hope I have been able to articulate similar ideas that could give a new account of major problems in the philosophy of mind and neuroscience concerning how mind can act “acausally” on matter via decoherence, and how we might have a responsible free will by a similar marriage of quantum random indeterminism and classical determinism in what I call Trans-Turing systems operating in the Poised Realm that hovers reversibly between quantum-coherent and classicality-FAPP behaviors.

If no law entails the becoming of the biosphere, we do not know the sample space of evolution, for its phase space persistently changes. Hence, we need to invent a new form of Embodied Information, which is laden with the semantics of the functions of parts of Kantian wholes in sustaining the existence and co-existence of such Kantian wholes. I have proposed what may be a start of such embodied information that seeks the “diversity of organized processes” in a cell, organism, ecosystem, or the biosphere, as a measure of the embodied information in the biosphere and how it may grow over time. Such growth would be a true form of information creation, beyond entailing law, and since merely syntactic information in a pre-stated sample space is of no use in biological evolution, whose phase space, as stressed, keeps changing in ways we do not know.

Self organization, as in the emergence and evolution of collectively autocatalytic sets as a generic property in ensembles of complex chemical reaction networks, and in ensembles of genetic regulatory networks, must play a profound role in the emergence of functional order, beyond entailing law, in co-evolving Kantian wholes. With natural selection, the entire process, beyond entailing law, has created a functional biosphere that has persisted and flourished for 3.7 billion years. We are thus invited to new science and a new view of what is required for order and organization to emerge and flourish beyond entailing law.

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