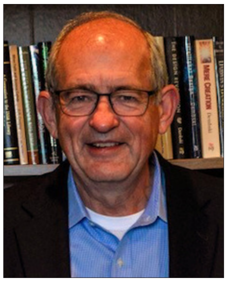

Randy Isaac

Stephen Freeland

Article

DOI: https://doi.org/10.56315/PSCF3-23Isaac

Rethinking Abiogenesis: Part III, Meaning in the Light of Complexity, Information, and Simplification

Randy Isaac and Stephen Freeland

This article concludes a three-part series on abiogenesis that suggests meaningful configurations of organic components can arise spontaneously, leading to organisms that successfully survive and reproduce. While the complexity of the disorganized abiotic world makes it appear to some that such a feat of organization would require the nonnatural intervention of an intelligent mind (including but not limited to supernatural intervention), we suggest that careful considerations of thermodynamics and information lead to the plausibility of a natural occurrence. No specific, complete pathway for abiogenesis has yet been identified, but the fundamental processes that enable such a path can be articulated more clearly now than ever before as a result of new and continuing research in multiple disciplines. This concluding article centers on the way in which complex states of molecular organic information can be generated to produce the most meaningful configurations.

Keywords: Abiogenesis, origin of life, information, complexity, simplification, evolution, systems chemistry, natural selection

The quest to understand the origin of life may be as ancient as humanity itself. With little physical evidence to guide understanding, most early cultures evolved narratives of origins that reflected the interaction of a spiritual world with our physical universe.[1] The biblical account of creation forms the basis for the dominant narrative of origins in the western world. The interpretation of that account varies widely from a literal interpretation of a specific English translation to a deeply metaphorical perspective. One particular dichotomy of assumptions about the transition from nonlife to life concerns us here. On the one hand, many are convinced that the biblical account reflects one or more miraculous occurrences that do not conform to any discernible scientific process.[2] On the other hand, many think that God created the universe to enable a natural transition from a nonliving universe to a world teeming with an amazing diversity of species.[3] Scientific observations do not, as yet, provide compelling evidence for irrefutably distinguishing between these two perspectives. While God is certainly capable of using any means of God's choosing for the creation of life, it is the conviction of the authors that it is demonstrably worthwhile to explore plausible naturalistic paths by which God may have enabled the appearance of life from nonlife.

Randy Isaac *is Executive Director Emeritus of the American Scientific Affiliation. He holds a PhD in physics from the University of Illinois at Urbana-Champaign. His career was 28 years at IBM Research where he became Research Vice-President of Systems, Science, and Technology.*

Stephen Freeland *(PhD, Cambridge University) is professor of biology, director of the Interdisciplinary Studies Program, and associate dean of undergraduate academic affairs at the University of Maryland, Baltimore County. His research uses computers to study life's early evolution, especially the evolution of the amino acid alphabet with which organisms construct genetically encoded proteins.*

In Part I, we argued that it may be useful, even important, to perceive the origin of life as a seamlessly continuous (and arguably incomplete) process. This contrasts with a more traditional view that abiogenesis refers to a specific point in time or evolutionary history.[4]

In Part II, we proposed that life may be considered as a simplification of the nonliving universe, such that the beginning of life (abiogenesis) may be usefully perceived as a reduction of complexity from the randomness of the prebiotic world.[5] This stands in sharp contrast to a more typical view of perceiving life as an increase in complexity from simpler molecules. Certainly, the intuitively awesome intricacy of life as we know it is remarkable, especially compared with what seems to some a less interesting, nonliving universe. And yet, the perspective of asking about increasing complexity (e.g., through synthetic chemistry or artificial life) has not yet yielded a plausible, comprehensive pathway from nonlife to life. This difficulty leads some to conclude that a supernatural agent or cause must have been necessary for the appearance of life.[6]

In this Part III, we delve deeper into definitions of information, complexity, and meaning so as to offer more explicit precision about how simplification in the prebiotic world enables the possibility of a natural pathway for abiogenesis.

In the first section of this article, we explore the concepts of complexity and meaning, comparing them with the concept of information. Next, we seek to show that in at least some clear sense(s) of the word, simplification through natural selection is as much an inherent aspect of the evolutionary process as increasing complexity. By turning next to consider abiogenesis explicitly, we conclude by arguing why it may be instructive to consider the importance of simplification in the prebiotic world in the sense of forming a relatively stable and more ordered structure from a disorganized, complicated environment.

The Complicated Concept of Complexity as It Relates to Information and Meaning

There is no single, universal definition of complexity within science,[7] and that important fact is a foundation for the more nuanced ideas we seek to introduce here. Put another way, a range of possible interpretations must be placed into context before careful discussion may proceed. Such discussion can helpfully consider *complexity* in comparison with two related concepts, namely *information* and *meaning*. In what follows, we explain from where we derive the following brief distinctions:

Information is a measure of the uncertainty in any system that can exist in a number of different states. The uncertainty is resolved when the state of the system is determined.[8] The amount of information reflects the number and probabilities of all possible alternative states. This is often called "Shannon information." Unless specified otherwise, in this article, the word "information" will refer to Shannon information.

Complexity refers to the minimum work required to describe a particular state of information.[9] States with a higher diversity of components are more complex than those with lower diversity because the former are more difficult to describe.

Meaning, from the perspective of information theory, is the value or usefulness of a particular state of information.[10] It may, for example, refer to matching a preconceived pattern or blueprint, conveying knowledge or an idea, or causing a particular biological function.[11] Meaning is often determined by an "interpreter" that exhibits the usefulness.[12] This definition of *meaning* overlaps with what, in common usage, we often call "information," (e.g., "Detectives have received information leading to a number of arrests"). This overlap offers ample opportunity for confusion, leading Claude Shannon and Warren Weaver to caution against confusing the two.[13]

To illustrate the definitions given above, their overlap and their differences, let us consider the popular game Wordle.[14] The Wordle website selects a secret five-letter word that the player seeks to determine by a series of guesses. After each guess, the website responds by identifying which letters in the guess occur in the secret word and whether or not they are in the right location. The player wins if the secret word is determined in six or fewer guesses. Wordle helps us illustrate the way in which context is essential to all of the three concepts under consideration (information, complexity, and meaning).

Beginning with *information,* we may determine how much is contained in each secret word of this game. The answer depends on a number of assumptions in setting up the game.

1. Of which language will we use the alphabet (e.g., English, French, Ancient Greek)?
2. Are special symbols allowed (such as accents, hyphens, or spaces)?
3. Can any five-letter sequence be used or must the word exist within a specified dictionary?

In light of these assumptions, it becomes clear that the amount of information depends on the context. In our word game, if we assume that we use the contemporary English alphabet with no special symbols and it need not be a word, then there would exist 26^5 possibilities. The amount of information is 23.5 bits.[15] But if we restrict the combinations of letters to those that comprise a 5-letter word, then there exist only 12,478 possible words[16] and the amount of information is reduced to 13.6 bits. There is less information because of interdependence between the letters. Sequence matters. For example, if the first letter is a "b," then the second letter is most likely a vowel or one of only a few consonants. Many consonants have zero probability of occurring. Because there are fewer possible states, the amount of information decreases as well as the complexity, but the capacity for meaning is maintained or increased. Other changes to our assumptions can significantly change the amount of information. Increases could come from choosing to allow hyphenated words or choosing to recognize the typeface, font size, or font color. Anything that can be different may be employed in an information system. For this reason, context is essential.

Once the context is fixed, it is possible to physically change both the amount and the state of *information.* A physical change in the sequence of the letters in the example of Wordle changes not only the word, or state of information but potentially the amount of information as well. In general, any physical energy flux (i.e., input or output of energy) in a system can modify and increase or decrease information.[17]

Complexity, in contrast, deals with a single, specific state of the system. One of the most common metrics for complexity is "Kolmogorov complexity."[18] This measures the number of bits of the shortest possible lines of code that a universal coding machine (e.g., a Turing machine) would need to describe the state of a system. This is the primary type of complexity used in algorithmic information theory.[19] It can be thought of as measuring the diversity of the specific information states of the system. But Kolmogorov complexity, like information, depends on the assumptions being used. Like information, the complexity of a given sequence of letters decreases if we know ahead of time that the letters must form a word in a specified language, since only a few of the letters may be needed to determine the rest. More generally then, a repetitive sequence is less complex than one that is all random.

Turning to considering *meaning* brings new challenges to thinking clearly about both *information* and *complexity*. In Wordle, the secret word is restricted to the set of words preselected by the author of the game. In contrast to the case of a random set of five letters, relationships between the letters and their sequences are important. If there is a high degree of repetition of letters, not only is the complexity low, but there is less likelihood of having a meaning. A random set of letters with no pattern, on the other hand, will have high complexity while also having a low likelihood of meaning. In the intermediate range where there is some degree of order, the complexity is medium, but the potential for having a meaning is higher.

Warren Weaver, one of the earliest scientists/mathematicians to address complexity, recognized the role of order in complexity in 1947.[20] He suggested a primary distinction between two types of complexity: disorganized complexity and organized complexity. Disorganized complexity occurs wherever a system involves minimal order between components, such as a collection of letters for which there is no particular sequence. Organized complexity occurs wherever the ordering between elements of the system is very important; for example, if those same letters occur in a sequence, such that one ordering produces a word whereas another produces a nonsense anagram of that word, then there is organized complexity.

To measure complexity that accounts for organization within the system, Charles Bennett proposed a related measure called "logical depth."[21] It attempted to quantify the role of meaning, or "message value" as he put it. The logical depth can be thought of as the time required, rather than the minimum size, for a universal computing machine to compute a string of elements for the Kolmogorov complexity. More recently, Terrence Deacon and Spyridon Koutroufinis sought to offset shortcomings of "logical depth" by proposing a measure of "dynamical depth."[22] They seek to account for nested interacting organization levels rather than just the structural complexity.

When the presence of *meaning*, or message value, is part of the context for considering information, we need to think carefully about what kind of meaning is relevant. Stephen Meyer stresses the importance of distinguishing between meaning that conveys "a piece of knowledge known by a person" versus "a sequence of characters or arrangements of something that produce a specific effect" and that "it is also necessary to distinguish Shannon information from information that performs a function or conveys a meaning."[23] The latter is typically called "specified complex information."

For our discussion of abiogenesis and evolution, the difference between these two aspects of meaning is crucial. While conveying a piece of knowledge requires an intelligent agent as an interpreter, producing a specific effect or function is different. That which enables an organism to survive and reproduce is a self-sustaining interpretation or meaning created between an organism and its environment, for which no intelligent receiver or interpreter is required.[24]

This point may be clarified by comparing the word-game we have been discussing with human genetics. When one player thinks of a five-letter word, they may write it down with pencil and paper, in which case the meaning has been transformed from one medium to another through the agency of an intelligent mind. A dictionary might pass superficially for a non-intelligent agent that validates this meaning, but considered more carefully, it is merely documentation of the abstract relationships to which intelligent minds have previously agreed.

In contrast, the human genome contains a segment of DNA, called a "gene," that codes for a specific protein.[25] A suite of molecular machinery, coordinated by the ribosome, translates this sequence of nucleotides (i.e., the gene) into a corresponding sequence of amino acids, which link together to form a protein. More accurately, the protein is a complex, 3-dimensional shape formed when the linked sequence of amino acids folds up spontaneously, because the shape (of the folded protein) yields both structure and function.[26] Protein sequences with meanings (functions) that tend to help the genome achieve successful replication are, by definition, those which "reward" their corresponding genes to flow forward in time and increase in frequency. Such functions often involve catalyzing specific (bio)chemical reactions to occur faster than they would otherwise. In this sense, we may say that the genome has an embodied meaning to build proteins. But there is no need or process for the meaning of the protein (or genome) to involve matching any predetermined specification. A theologically and philosophically interesting discussion about *meaning* must look far deeper than a limited view of genomes (or proteins) creating meaning: it must instead explore whether and how one might perceive an intelligent **agency** causing and sustaining the fundamental physics of the universe. In the words of Loren Haarsma, in a 1995 letter on behalf of the American Scientific Affiliation to the National Association of Biology Teachers,

> While each of these mechanisms can be modeled as a purely natural process, this does not tell us whether the entire evolutionary process is ultimately supervised or unsupervised. That question goes beyond the realm of science, into philosophy and religion.[27]

To illustrate the difference, we note that some have argued a role for abstract interpretation within the genetic code by which genes are translated into proteins.[28] From the perspective of natural science, here we find nothing more than a straightforward chain of cause and effect. Translation involves the interpretation of a nucleotide gene sequence by molecular machinery (mainly tRNA molecules coordinated by a ribosome) as a set of mini-sequences, each of them 3 nucleotides in length. Each mini-sequence is known as a codon; every possible codon that can be constructed from an "alphabet" of 4 nucleotides ($4^3 = 64$) *means* a specific amino acid, so that the set of possible codons and their meanings together compose an elaborate genetic code.[29] Like the example with an intelligent mind, genetic information is transformed from one physical medium (nucleotides/gene) to another (amino acids/protein). But unlike the example with an intelligent mind, the meaning of the gene and protein sequence requires no abstract interpretation. Abstract interpretations by human researchers may, however, see deeper by moving to other disciplinary perspectives, but in doing so, they change assumptions as they move to arguments about meaning of the material universe, and they lose any unique need for direct, intelligent agency within molecular biochemistry or life's origins.

To summarize the core concepts from which we now proceed, *information, complexity,* and *meaning* are all contextual and depend on the assumptions and the variables being assessed. Information reflects the uncertainty arising from the number of different possible states of the system while complexity reflects the effort required to describe the structure, relative ordering, and dynamic interaction of a particular state of the system. A particular state of the system may have meaning either by conforming to a predesignated (abstract) state or by causing a specific physical effect.

Complexity and Simplification in the Evolution of Living Organisms

Before turning to consider the origin of life, it is helpful to see first how the concepts of information, complexity, and meaning apply to changes over time in the biological world that we observe today. For this part of the discussion, our focus will be the change in complexity over one generation of a population, from birth until these offspring produce the next generation.

Let the collective set of genomic and epigenomic information of all members of a given generation, g0, be characterized by a reference complexity, c0. Once that population undergoes a reproductive cycle, there will be a new collective set of information of the offspring generation, g1, that is characterized by complexity, c1. Usually, this new set of information will be more complex ($c1 > c0$). Typical causes for this increased complexity include increased population size (since the number of offspring is often greater than the number of parents) and increased genetic diversity (as mutations of all kinds create new variations of genetic material[30]).

By most measures of complexity, more individuals and/or more genetic diversity represent an increase in the total complexity of genomic and epigenomic information of the next generation. This increase is, however, temporary. As the offspring generation, g1, progresses through its life cycle, the effects (changes in function) of different genetic variations become manifest. Members of that population carrying variations which produce functions that are less well adapted to their environments will contribute less, by reproduction, to the next generation: at an extreme, their carriers may die before reproduction. In this way, the complexity of the information of g1 reduces over time, from fertilization until the second offspring generation, g2, is produced ($c1_{\text{at time of reproduction}} < c1_{\text{at time g1 is created}}$). The complexity, c2, of g2 is, again, greater than c1 ($c2_{\text{at time g2 is created}} > c1_{\text{at time of reproduction}}$). Generation 2 undergoes simplification, though, depending on the degree and type of adaptation; the ultimate complexity, c2, at time of reproduction may be greater than that of g1 at time of reproduction ($c2_{\text{at time of reproduction of g2}} > \sim c1_{\text{at time of reproduction of g1}}$).

A detailed example that illustrates this concept is presented in box 1. Within this life cycle, the complexity reduction phase is a simplification through selective elimination, commonly called "natural selection." But in the terminology of information theory, the selection process of simplification is effectively a feedback mechanism that injects meaning into the system. It identifies what genomic information is most capable of persisting in a given environment. Thus, nature itself provides a go/no-go decision on the subset of genomic information (the sequence of genetic chemical structures) which continues to the next reproductive cycle. More broadly, organized complexity may gradually increase by iteration of complexification and simplification. Nature explores a wider and more complex set of configurations in each generation and the competition for resources ("survival of the fittest") results in finding a set that has good persistence.

From within the perspective of the natural sciences, the *meaning* of the sequence and configuration of the genome and epigenome is the ability of the organism to survive and reproduce. This ability reflects the relationship between function and environment. The result of repeatedly iterating a sequence of complexification and simplification can result in an increase in organized complexity. Complexification occurs naturally in the interaction between the environment and the reproducing organisms. Simplification occurs naturally in the ability to survive and reproduce. This is the core process of evolution by natural selection that Charles Darwin proposed in the nineteenth century.

Box 1: Example of Simplification in a Generation of Humans

Consider a generation, g0, consisting of a theoretical population of 10,000 humans, half of which are men and half are women, all of whom remain alive during their reproductive years. This generation comprises 10,000 unique genomes and is characterized by a complexity, c0. There is a spectrum of differences between these genomes and some theoretical reference genome that characterizes the entire population. According to the Population Reference Bureau's 2021 World Population Data Sheet, the global total fertility rate of women was 2.3 births per woman, down from 3.2 in 1990.[1] Assuming a value of 3 for our example, we would expect 15,000 births to occur in this theoretical g0. It is estimated that approximately 30–40% of all conceptions result in miscarriage.[2] Taking 1/3 as an average number, we would expect a total of 22,500 conceptions to have taken place. This means that the 10,000 people in g0 would produce 22,500 fertilized eggs comprising the offspring generation, g1. This set of genomes has greater complexity, $c1_{\text{at time of conception}}$, than that, c0, of the genomes of g0 for two primary reasons. One is the larger number of genomes. The other is that each genome of g1 differs from every other genome in g1 due to crossover in gamete formation and mutations such as SNP's, HGT's, and retroviruses.[3]

It is further estimated that approximately half of the 30–40% miscarriage rate is due to some type of chromosomal abnormality. This most likely corresponds to significant harmful deviations from a viable genomic sequence. The miscarriages of 7,500 fertilized eggs in our example is the first and largest selection process that eliminates the genomes that cannot survive. Following birth, the infant mortality, currently approximately 0.9%, partially reflects genomic structures that are less able to survive. Additional selection occurs through an approximately 10% infertility rate. The population of g1 that is able to reproduce to create the second offspring generation, g2, would be about 13,365. Thus, we have a simplification of the population of g1 from 22,500, $c1_{\text{at time of conception}}$, to 13,365, $c1_{\text{at time of birth}}$. This simplification process produces a set of g1 genomes that may contain individuals with more complexity than those of g0, in which the more complex changes enable better survival in the slightly modified environment of g1 compared with g0.

For humans, as with most species that reproduce sexually, there is an additional cycle of complexification and simplification in the pre-fertilization phase. On average, a man produces on the order of a trillion (10^{12}) sperm in his lifetime. Each sperm contains a gamete with a single set of chromosomes formed through meiosis. A woman is born with about a million (10^{6}) ovarian follicles that potentially could become mature eggs, of which there are ultimately about 500 in a lifetime. Each follicle contains a gamete that similarly has a single set of chromosomes formed through meiosis. The set of sperm from each man and follicles from each woman comprises a vast complexification from their respective genomic sequences. The dominant process of simplification is the selection of which sperm and which egg will mature and be able, given the opportunity, to produce a fertilized egg. This means that each fertilized egg is selected from about 10^{18} potential combinations, each with a genomic sequence that did not exist before and, unless selected, will never occur again. While the numbers are different for each species, the process is essentially the same—a combinatorial complexification with mutations from which a very few are selected; this is effectively a simplification that can be expressed by the relation $c1_{\text{potential gamete combinations}} >> c1_{\text{fertilization attempts}} >> c1_{\text{at time of conception}} >> c1_{\text{at time of birth}} > c1_{\text{at time of reproduction}}$. This simplification of g1 leads to a $c1_{\text{at time of reproduction}}$ that may be greater than the $c0_{\text{at time of reproduction}}$ of g0.

Notes

[1]Population Reference Bureau, "Impact of COVID-19 Pandemic on Global Birth and Death Rates Unclear, with Many Countries Lacking Reliable Data," August 17, 2021, accessed November 16, 2021, https://www.prb.org/news/2021-world-population-data-sheet-released/.

[2]Department of Gynecology and Obstetrics, The Johns Hopkins University School of Medicine, Baltimore, Maryland, *The Johns Hopkins Manual of Gynecology and Obstetrics,* 4th edition (New York: Lippincott Williams & Wilkins, 2012), 438–39.

[3]Ultimately the source of all genetic variation is mutation. Although introductory textbooks might distinguish genetic crossover (if dealing with sexual reproduction between diploid organisms that undergo meiosis) from mutations (e.g., Single Nucleotide Polymorphisms, insertions, and deletions) and even exotic events which involve the addition or deletion of genetic letters through horizontal gene transfer or the action of retroviruses, none of these would introduce new information had not mutation acted somewhere in their evolutionary history.

Life as Simplification of the Nonliving Universe

Having first introduced information, complexity, and meaning, then discussed how these concepts apply to evolution by natural selection, we now turn to asking how far this framework of understanding can go in describing a plausible pathway to the emergence of life within a nonliving universe: abiogenesis.

The Russian physical chemist Ilya Prigogine pioneered a field of study in statistical mechanics, identifying a category of systems he called "dissipative structures." Prigogine received the 1977 Nobel Prize in Chemistry[31] for his work on these systems which are thermodynamic systems that exist in a state far from equilibrium.[32] For example, a harbor on the ocean is a body of water in equilibrium at sea level. A lake in the mountains is far from equilibrium due to its gravitational potential energy. In the language of thermodynamics, this lake would be called "a metastable state" because it is stable, but at a higher state of energy than the global equilibrium (sea level). When containment of the lake is breached, water rushes toward sea level, exhibiting behavior very different from that of water in equilibrium. As long as meteorological conditions sustain a cycle of ocean evaporation and condensation in the mountains to replenish the lake, the system of rushing water, converting potential energy to kinetic energy, will be a steady state of flow which can be called "a dissipative structure." Prigogine's insight was that there exist physical dissipative systems far from equilibrium that self-organize into metastable states which may exhibit lower entropy.

In his chapters on thermodynamics in *The Mystery of Life's Origin*, Walter Bradley's critique was that nothing here could speak meaningfully to life's origins because dissipative systems fail to account for the configurational work needed to assemble life.[33] Work is needed to bring order from chaos: to find, from within a vast entropy, a specific configuration of molecules that reproduces and evolves. Bradley's specific focus was on the component organic molecules that must be assembled in a particular configuration (sequence) out of nearly countless possibilities.

In 2022, we may address the criticism by placing Prigogine's ideas into an interdisciplinary sandwich formed by subsequent work in two related (but distinguishable) subfields (fig. 1). On one side lie developments in non-equilibrium physics; on the other side lie developments in systems chemistry. Combined with the foundations laid by Prigogine, this body of theory argues for the relevance of exactly the sort of experiments in organic synthetic chemistry that we find currently at the leading edge of abiogenesis research.

From physics, the pioneering work of Jeremy England shows how thermodynamics allows nonliving systems to transition to lower states of entropy in the presence of an energy source: a cyclical driving force can modify a system in remarkable ways that simply cannot happen at equilibrium. In more precise, technical terms, non-equilibrium thermodynamics can enable an open system (i.e., one that is absorbing a flux of energy) to move to any of a large number of metastable states, some of which are likely to have lower entropy.[34] Metastable states with lower entropy might well have a shorter lifetime,

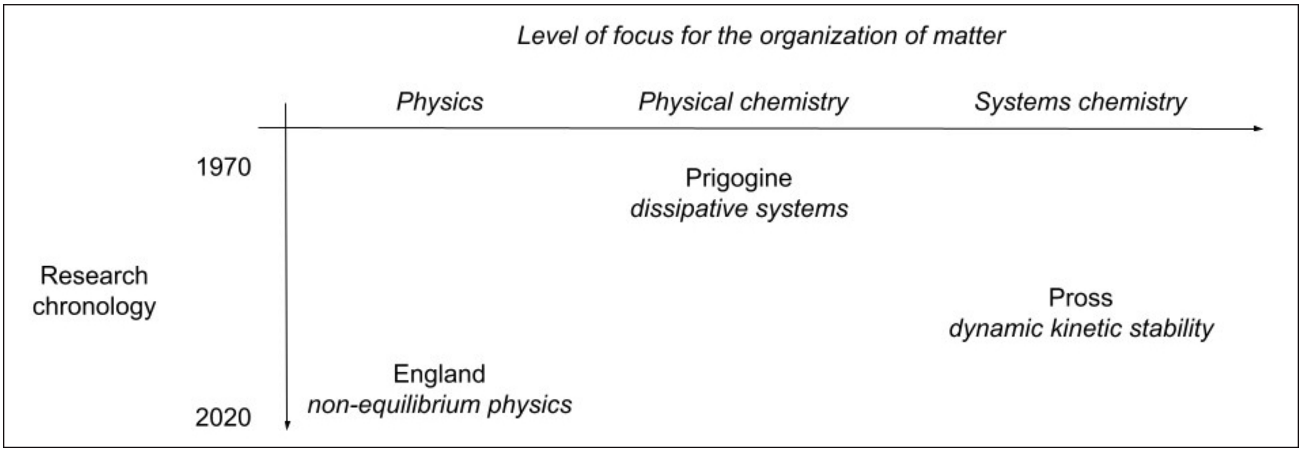

Figure 1. Three overlapping areas of research have emerged since the late twentieth century to explain how matter can self-organize into states which exhibit organized complexity and lower entropy.

but they may also modify the system's response to the incoming energy flux. Modifications which dissipate energy more efficiently can stabilize the lower entropy state. Writing about all this for a lay audience, England uses his Jewish faith to notice and use the metaphor of the bush which Moses saw burning, without becoming consumed: contrary to our lived experience, within this vision it is the very act of burning which stabilizes the persistence of the bush. Indeed, the centrality of this metaphor to his work comes across from the title of his book: *Every Life Is on Fire*.

In more precise, technical language England's research team has studied simple physical systems to which an oscillating energy source is applied. One study modeled 20 idealized particles that make and break catch-bond springs[35] with each other,[36] another simulated spin glasses responding to time-driven external fields.[37] In all cases, the system showed the capability (which may appear to some as *agency*) to restructure itself into a new steady state that alters how further energy is received. The spectrum of work absorption can shift to either increased or decreased energy absorption, and the direction of this shift depends upon the specific parameters of the driving force relative to the spring characteristics. Of particular interest, when a large concentration of elements is repeatedly exposed to cyclical energy sources, it will find the most efficient configurations for maintaining metastable states. In other words, a simplification process will eliminate those states that are least stable and select a state that persists in the presence of that driving force.

Complementing these foundations in physics we find the systems chemistry of Addy Pross, and specifically the concept of "dynamic kinetic stability" (DKS) by which non-equilibrium, open systems can sustain metastable states.[38] Living organisms are metastable systems that are more efficient than nonliving metastable systems in utilizing energy flux to sustain their existence, and are therefore favored to develop. Pross illustrated DKS with the example of a river. A river is stable even though the water molecules that compose a river are constantly moving and changing (no man can cross the same river twice!). The river has dynamic kinetic stability. As described previously, it is a metastable, non-equilibrium system that is sustained by energy flux. Warmed by the sun, water in the ocean evaporates. Winds convey the water vapor to higher land where the cooler air causes the water to condense as rainfall in mountainous regions. Gravity compels the water to find its way back to the ocean. Before any riverbed existed, the paths for water to flow down were varied and complex. Those paths that were most favorable underwent the greatest erosion, gradually increasing their ability to facilitate the flow of water. Eventually the most favorable path became a riverbed, establishing a river with dynamic kinetic stability as a result of a process of simplification. (By the way, there was no sense in which an intelligent agent was required to identify this optimal or near optimal path to the ocean).

Pross argues that while natural selection as we know it in the biological world cannot act in the prebiotic world, there is an equivalent process of "kinetic selection." He points to work by Sol Spiegelman[39] and Gerald Joyce[40] to show how competitive exclusion operates in the chemical world of organic systems just as it does in natural selection. Building on that perspective, Pross goes on to show that the biological concept of fitness is the same principle as DKS in the prebiotic world. This is consistent with our perspective on continuity in the origin of life. If one looks backward from a biological perspective, it is hard to see reproduction with variation and survival of the fittest occurring in the prebiotic world. But if one looks forward from the competitive world of organic chemical reactions, the principles of kinetic selection and DKS can be seen as the basis for natural selection and fitness in the far more complex world of living organisms.

But back to our major theme: we might re-express the shifts to new steady states of energy absorption shown by England and colleagues, in the language of systems chemistry, as examples of dynamic kinetic stability. Thus, recent physics tells us that nonliving systems can transition into lower states of entropy in the presence of an energy source, particularly a cyclical driving force. Physical chemistry tells us that low entropy states can exist as stable states far from equilibrium so long as they dissipate energy into entropy. Systems chemistry tells us that non-equilibrium, open systems can be sustained in metastable states. From this theoretical framework in physics and chemistry (fig. 1), we finally may turn to consider explicitly those studying the sort of organic synthetic chemistry which produces molecular biochemistry.

Turning to Abiogenesis

The research community tackling abiogenesis comprises many different approaches and disciplines. One useful way to sketch a map of this sprawling frontier is to distinguish those who choose to work "top down" and those who work "bottom up."[41] Here "bottom up" research focuses on the chemistry and physics of the nonliving universe, often asking what processes and conditions are conducive to forming the two classes of biological polymer that are central to life as we know it: nucleic acid and protein. "Top down" research comprises those who work backwards toward the prebiotic world from these central facts of "modern" (post-LUCA) biology: genes, proteins, and the molecular machinery that translates the former into the latter. Within this schema, at the interface where top down meets bottom up, lies a subcommunity of researchers who have explored for decades the extent to which "wet/dry cycles" can cause monomeric building blocks—amino acids and nucleotides—to join together into polymers: RNA and protein (DNA is thought to have arisen later as a derivative of RNA).

Wet/dry cycles, as the name implies, refer to an environment in which watery conditions alternate with periods of evaporation/drying. In various incarnations,[42] this environment has been pictured as the shoreline of a primordial ocean, streams that flow ephemerally after rain, springs or pools of water with drying edges, or even their opposite counterpart of geothermal fields where water sinks into the crust and dries as it encounters ever hotter depths.[43] What unites all such specific instances is that the organic chemistry of an aqueous solution shifts back and forth with the different organic chemistry that takes place as water is removed from the system.

The regime of wet/dry cycles was first conceived as one conducive to the formation of biopolymers simply because the chemical reaction which forms both nucleic acids from nucleotides, and proteins from amino acids, involves the removal of water molecules (see fig. 2).[44] Simply put, the relevant monomers form under a range of different chemistries and pathways within an aqueous solution, and the subsequent removal of water favors these monomers further reacting together to form polymers.

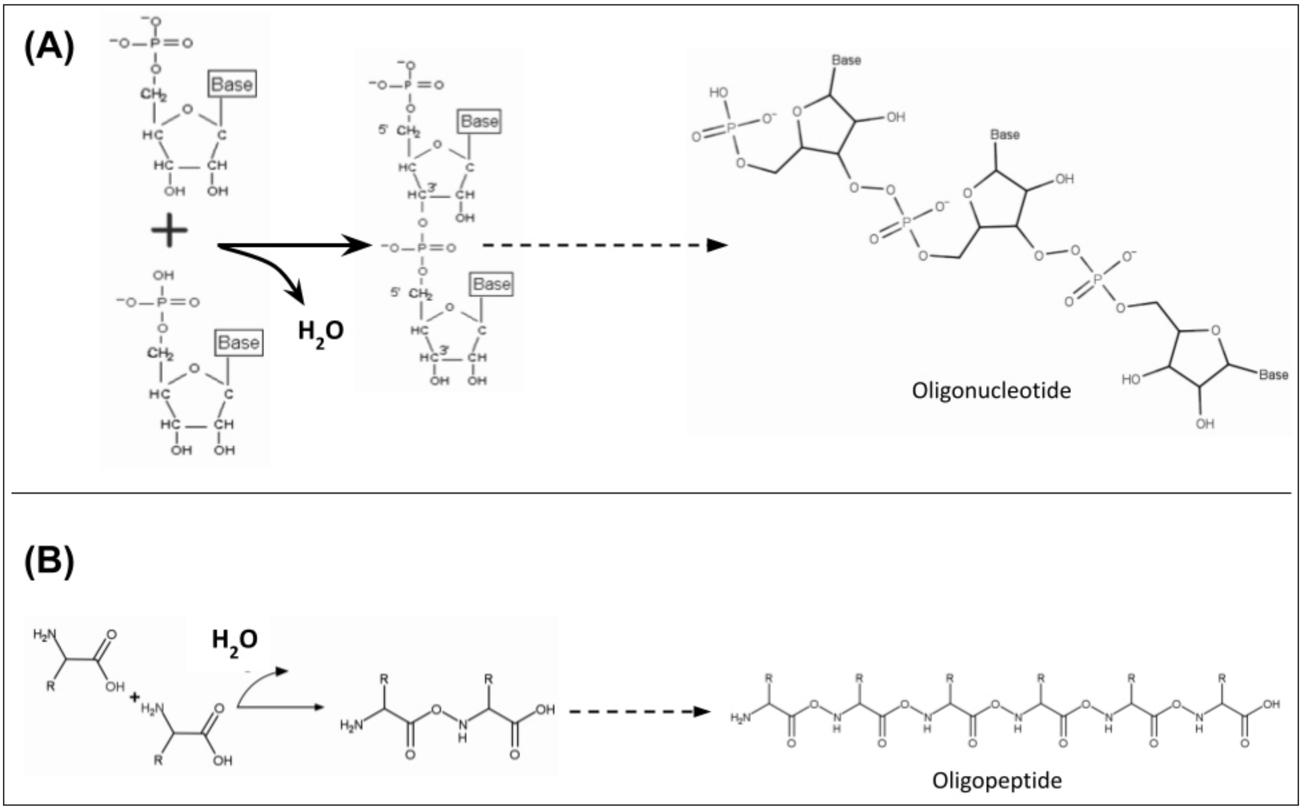

Figure 2. The chemical reactions by which life's chemical building blocks form into polymers involve the removal of water molecules. **(A)** nucheotides link together through a phosphodiester linkage into sequences of RNA; **(B)** amino acids link together through peptide bonds to form proteins.

As such, the concept of wet/dry cycling has been applied over the decades to study every aspect of biopolymer formation, from the "dehydration condensation" reaction at the heart of polymerization,[45] to processes involving spontaneous self-purification of the resulting polymers[46]—it even offers another pathway towards monomer formation.[47] But from an initial motivation of chemistry (seek a process that favors the removal of water molecules) it is interesting to note how pioneers of this approach have increasingly come to absorb and reflect the maturing physics and chemistry of non-equilibrium systems. We may, for example, illustrate how seamlessly and directly wet/dry cycling research meshes with all we have written about how meaningful complexity is generated. To do so, let us consider the specific case study of Bruce Damer and David Deamer who have explored iterative wet/dry cycles around pools fed by hot springs.[48] They present the rationale for their approach as follows.

> Energy-driven cycles are central to life's ability to maintain itself in a far-from-equilibrium state against the trend toward ever increasing entropy. Therefore, it is reasonable to consider the possibility that life's origin also depended on cycles … Significantly, cycling also drives a series of natural experiments that undergo combinatorial selection in the form of encapsulated polymers.[49]

They go on to examine in detail a variety of energy-driven cycles. One is the distillation process resulting from evaporation and condensation. Another is the alternate drying and hydration of pools. They describe the process this way:

> Hydrothermal pools undergo wet-dry cycles resulting from precipitation and fluctuating water levels … Polymers are synthesized by condensation reactions occurring within these dried films … During the hydration phase, vesicles bud off, encapsulating systems of polymers to form protocells … This process generates random sets of polymers captured in vesicles to form vast numbers of protocells. Frequent cycling of these populations initiates the combinatorial selection process that drives chemical evolution and enables the emergence of ever more robust protocells. As the protocells continue to undergo the stresses of cycling, most will be disrupted, their components leaking out or dispersing through disrupted membranes, but a rare few are likely to contain polymers that enhance their survival … The products of selection that cycling systems generate can lead to the stepwise emergence of increasingly functional polymers …"[50]

Note that the "combinatorial selection process" to which they refer is directly equivalent to the configurational entropy work that Walter Bradley identified as missing from the body of thought developed by Prigogine.

It remains to be seen how fruitful Damer and Deamer's particular scenario will be in showing the plausibility of abiogenesis. Other researchers explore how life began with the formation of RNA,[51] or RNA fragments,[52] or RNA-like fragments.[53] We, along with Damer and Deamer, would argue however that this gradual dissipation over time of strong claims for "RNA first" within the scientific literature has much further to go, and would look for energy flux to produce a sequence of chemistries that lead onward toward RNA. Rather than RNA first, we would hypothesize RNA itself as an evolutionary outcome. For the purposes of this manuscript, it matters little. Whichever molecule or starting point is considered, a perceived increase in complexity comes only from limiting one's focus to the evolving genetic content. But genetic, hereditary material is changing over time in response to the environment, and once we broaden our vision to embrace this broader system, we can perceive the genetic material as a simplified representation of the environment. In this light, the work of Damer and Deamer illustrates how some of the earliest steps might have involved a drying, aqueous environment favoring monomers to join together. A dimer looks more complex than two monomers, but is (from our perspective) a simplified, coded reflection of the environment.

Indeed, the words of Damer and Deamer express, in a different disciplinary language, the ideas of non-equilibrium physics from England. We might, for example, re-express Damer and Deamer's ideas as suggesting that energy flux from various sources, such as the cyclical driving force from the sun, seasons, tides, etc., provides the iterative complexification/simplification process that is inherent in the reproduction with variation/natural selection cycle of true biological evolution. In non-equilibrium systems, an increase in energy enables the system to explore a complex set of states with higher energy, many of which may have lower entropy. A dissipation in energy allows the system to settle into a metastable state which may be a lower entropy simplification from the higher energy complexity. Those metastable states that are capable of persisting (Pross's DKS) modulate the system response to the driving force (England's non-equilibrium physics), and thereby are those which evolve into primitive precursors of life. The local environment provides the information necessary to guide which polymer sequences persist and multiply. This has created the specified complexity we find in gene sequences. The gene sequence is an encoding of the environment, and the encoding is simpler than the full environment in all its dimensions. As successive rounds of selection proceed, the encoding may grow in scope but always as a fraction of the information which it now reflects. There is no need for an intelligent interpreter at any point.

Conclusion

Within this series on "Rethinking Abiogenesis," we have described ideas traditionally presented from a perspective and language of evolutionary biology in the different disciplinary language of information and complexity theory, in order to show how they integrate in a fully consistent, broader framework of scientific research, including the leading edge of abiogenesis research.

Part I of this series on abiogenesis emphasized the continuity in time of the transition from nonlife to life.[54] That continuity is exemplified in our inability to offer a clear demarcation between nonlife and life. Part II expanded that view to consider continuity in space with a close connection between life and the external environment.[55] It was suggested that this connection is helpful to perceive life as simplification, whereby the complexity inherent to an environment is incorporated over time into a biological structure that is increasingly robust within the environment at that time. In this sense, life is a reflection of its environment—and reflections contain less information than that which they reflect.

Here in Part III, by considering carefully the definition of complexity, we discussed in detail the cyclical process of complexification and simplification that produces this reflection. The prebiotic world is high in random, disorganized information with a wide diversity of elements and molecules, both organic and inorganic. Given an environment with multiple high-energy driving forces (whether incoming radiation from the sun on a prebiotic shoreline, or dissipation of interior planetary energy from a hydrothermal vent), a process of self-organization can occur that is effectively one of simplification. Configurations that are simpler and more orderly than the random environment are possible when they modify the system response to the energy flux. Configurations that are more stable have an enduring existence (persistence) that forms the basis for further cycles of complexification and simplification. This can be perceived as a forerunner to the process of reproduction with heritable variation that is ubiquitous to evolution by natural selection, as science currently understands that phrase within biology.

Implicitly, this perspective suggests that abiogenesis should not be sought in the immediate, spontaneous assembly of structures seen within modern life, but rather, in the process which led to such structures over time. In this explicit sense, we suggest that for research into the origins of life, it may be instructive to consider the importance of simplification in the prebiotic world in the sense of forming a relatively stable and more ordered structure from a highly random environment.

Our account of the prominent role of a cycle of complexification and simplification in abiogenesis claims no novel process or mechanism. Rather, it uses the language of information and complexity theory to describe the familiar concept of differential reproductive success in evolutionary theory. While the challenge of understanding abiogenesis remains far from being resolved, we suggest that this account teaches us that a naturalistic origin of life cannot be ruled out and merits further study. We suggest that readers of this journal recognize that the mainstream scientific community studying the origin of life pursues naturalistic abiogenesis, not primarily because of a bias against supernatural intervention, but because of its potential plausibility. ☼

Acknowledgment

We gratefully acknowledge the helpful and thoughtful suggestions by two reviewers and are grateful to ASA member Larry Funck for pointing us to the work of Addy Pross.

Notes

[1]Philip Freund, *Myths of Creation* (New York: Washington Square Press, 1965).

[2]Several examples include the following: Young-Earth Creationism—Dr. Terry Mortenson, "Young-Earth Creationist View Summarized and Defended," in *Answers in Depth*, February 16, 2011, https://answersingenesis.org/creationism/young-earth/young-earth-creationist-view-summarized-and-defended/; Reasons to Believe Model (aka Old Earth Creationism or Progressive Creationism)—Hugh Ross, "Summary of Reasons to Believe's Testable Creation Model," Reasons to Believe, updated March 1, 2022, https://reasons.org/explore/publications/articles/summary-of-reasons-to-believes-testable-creation-model-1; and Intelligent Design—"What Is Intelligent Design?," accessed January 16, 2023, https://intelligentdesign.org/whatisid/.

[3]Evolutionary Creation aka Theistic Evolution—https://biologos.org/common-questions/what-is-evolutionary-creation.

[4]Emily Boring, J. B. Stump, and Stephen Freeland, "Rethinking Abiogenesis: Part 1, Continuity of Life through Time," *Perspectives on Science and Christian Faith* 72, no. 1 (2020): 25–35, https://www.asa3.org/ASA/PSCF/2020/PSCF3-20BoringStumpFreeland.pdf.

[5]Emily Boring, Randy Isaac, and Stephen Freeland, "Rethinking Abiogenesis: Part II, Life as a Simplification of the Nonliving Universe," *PSCF* 73, no. 2 (2021): 100–113, https://www.asa3.org/ASA/PSCF/2021/PSCF6-21BoringIsaacFreeland.pdf.

[6]In a 2010 survey of American Scientific Affiliation members, while 60.2% accepted compelling evidence of evolutionary development for all life from a common ancestral form, only 39.6% accepted a form of abiogenesis. "ASA Survey on Origins: Final Results June 1, 2010," https://cdn.ymaws.com/network.asa3.org/resource/resmgr/OriginsResults.pdf.

[7]Charles H. Bennett stated, "… the problem of defining complexity is itself complex, and there are many satisfactory definitions of different kinds of complexity" in "Complexity in the Universe," in *Physical Origins of Time Asymmetry,* ed. J. J. Halliwell, J. Pérez-Mercader, and W. H. Zurek (Cambridge, UK: Cambridge University Press, 1996), 33–46.

[8]Claude Shannon, "A Mathematical Theory of Communication," in *The Bell System Technical Journal* 27, no. 3 (July 1948): 379–423, https://doi.org/10.1002/j.1538-7305.1948.tb01338.x.

[9]Called Kolmogorov-Solomonoff-Chaitin complexity, this definition can be traced back to A. N. Kolmogoroff, "On Tables of Random Numbers," *Theoretical Computer Science* 207, no. 2 (November 6, 1998): 387–95, https://doi.org/10.1016/S0304-3975(98)00075-9, which is a reprint of Kolmogorov's original Russian paper in 1960.

[10]Charles H. Bennett, "Logical Depth and Physical Complexity," in *The Universal Turing Machine – A Half-Century Survey,* ed. Rolf Herken (New York: Oxford University Press, 1988), 227–57.

[11]Francis Crick, "On Protein Synthesis," in *Symposia of the Society of Experimental Biology* 12 (Cambridge, UK: Cambridge University Press, 1958), 138–63; and Sahotra Sarkar, "Decoding 'Coding': Information and DNA," *BioScience* 46, no. 11 (1996): 857–64, https://doi.org/10.2307/1312971.

[12]Peter R. Wills, "Genetic Information, Physical Interpreters and Thermodynamics; The Material-Informatic Basis of Biosemiosis," *Biosemiotics* 7, no. 1 (2014): 141–65, https://doi.org/10.1007/s12304-013-9196-2.

[13]Claude Shannon and Warren Weaver, *The Mathematical Theory of Communication* (Urbana, IL: University of Illinois Press, 1949), 8.

[14]In 2021, Josh Wardle introduced a word game called Wordle, now owned by the *New York Times,* https://nytimeswordle.io/. It is similar to games like MasterMind and Bulls and Cows in the information sense.

[15]The equation $I = -\sum_{i=1}^{i=N} p_i \log_2 p_i$ is for the amount of information where N is the number of states in which a system can be, p_i is the probability that the system is in state i, and I is given in number of bits, from Shannon and Weaver, *The Mathematical Theory of Communication*.

[16]List of All Five Letter Words, accessed August 20, 2022, https://www.bestwordlist.com/5letterwords.htm. This number depends on the specific dictionary used and the extent to which uncommon words are excluded.

[17]Here, and throughout the discussion that follows, we use the word "system" to refer to any collection of objects that comprises focus of attention, from atoms to individuals within a population. Every possible physical state of a system, including its very existence, constitutes information, but we can choose to confine our usage and analysis to a much more convenient subset of possible states.

[18]Peter Grünwald and Paul Vitányi, "Shannon Information and Kolmogorov Complexity," arXiv:cs/0410002v1, August 8, 2005, https://arxiv.org/pdf/cs/0410002.pdf; https://arxiv.org/abs/cs/0410002; https://doi.org/10.48550/arXiv.cs/0410002.

[19]Ray Solomonoff, *A Preliminary Report on a General Theory of Inductive Inference* (US Air Force, Office of Scientific Research, February 4, 1960), https://std.com/~rjs/rayfeb60.pdf. Revision published November 1960, http://raysolomonoff.com/publications/z138.pdf.

[20]Warren Weaver suggested that the two main types of complexity were disorganized and organized complexity. Warren Weaver, "Science and Complexity," *American Scientist* 36, no. 4 (1948): 536–44, https://www.jstor.org/stable/27826254.

[21]Charles H. Bennett, "Information, Dissipation, and the Definition of Organization" and "Dissipation, Information, Computational Complexity and the Definition of Organization," in *Emerging Syntheses in Science*, ed. David Pines (Santa Fe, NM: The Santa Fe Institute Press, 1985), 297–313.

[22]Terrence Deacon and Spyridon Koutroufinis, "Complexity and Dynamical Depth," *Information* 5, no. 3 (2014): 404–23, https://doi.org/10.3390/info5030404.

[23]Stephen C. Meyer, *Signature in the Cell: DNA and the Evidence for Intelligent Design* (New York: HarperOne, 2009), 91.

[24]Randy Isaac, "The Significance of *The Mystery of Life's Origin*," *Perspectives on Science and Christian Faith* 73, no. 3 (2021): 158–62, https://www.asa3.org/ASA/PSCF/2021/PSCF9-21Isaac.pdf.

[25]George W. Beadle, Edward L. Tatum, and Joshua Lederberg, The Nobel Prize in Physiology or Medicine 1958, https://www.nobelprize.org/prizes/medicine/1958/summary/. See also George W. Beadle and Edward L. Tatum, "Genetic Control of Biochemical Reactions in Neurospora," *Proceedings of the National Academy of Sciences* 27, no. 11 (1941): 499–506, https://doi.org/10.1073/pnas.27.11.499.

[26]Christian B. Anfinsen, Stanford Moore, and William H. Stein, The Nobel Prize in Chemistry 1972, https://www.nobelprize.org/prizes/chemistry/1972/summary/. See

also Christian B. Anfinsen, "Principles That Govern the Folding of Protein Chains," *Science* 181, no. 4096 (1973): 223–30, https://doi.org/10.1126/science.181.4096.223.

[27]Loren Haarsma, "Letter to the National Association of Biology Teachers," November 22, 1996, https://www.asa3.org/ASA/resources/Haarsma1996.pdf.

[28]Meyer, *Signature in the Cell*, 91.

[29]Har Gobind Khorana, The Nobel Prize in Physiology or Medicine 1968, https://www.nobelprize.org/prizes/medicine/1968/summary/.

[30]Ultimately the source of all genetic variation is mutation. Although introductory textbooks might distinguish genetic crossover (if dealing with sexual reproduction between diploid organisms that undergo meiosis) from mutations (single nucleotide polymorphisms, insertions and deletions) and even exotic events which involve the addition or deletion of genetic letters through horizontal gene transfers or the action of retroviruses, none of these would introduce new information had not mutation acted somewhere in their evolutionary history.

[31]Ilya Prigogine—Facts, https://www.nobelprize.org/prizes/chemistry/1977/prigogine/facts/.

[32]See some of his work in Ilya Prigogine and Isabelle Stengers, *Order out of Chaos: Man's New Dialogue with Nature* (Toronto, ON: Bantam Books Canada, 1984); Gregoire Nicolis and Ilya Prigogine, *Exploring Complexity* (New York: W. H. Freeman and Company, St. Martin's Press, 1989); Gregoire Nicolis and Ilya Prigogine, *Self-Organization in Nonequilibrium Systems: From Dissipative Structures to Order through Fluctuations* (Hoboken, NJ: John Wiley & Sons, 1977); and William C. Schieve and Peter M. Allen, editors, *Self-Organization and Dissipative Structures: Applications in the Physical and Social Sciences* (Austin, TX: University of Texas Press, 1982).

[33]Charles Thaxton, Walter Bradley, and Roger Olsen, *The Mystery of Life's Origin: Reassessing Current Theories* (New York: Philosophical Library, 1984).

[34]Jeremy England, *Every Life Is on Fire: How Thermodynamics Explains the Origins of Living Things* (New York: Basic Books, 2020).

[35]Catch-bond springs have increased bond lifetime when mechanically stretched. See Micah Dembo et al., "The Reaction-Limited Kinetics of Membrane-to-Surface Adhesion and Detachment," *Proceedings of the Royal Society of London Series B Biological Sciences* 234, no. 1274 (1988): 55–83, https://doi.org/10.1098/rspb.1988.0038; and Yuriy V. Pereverzev et al., "The Two-Pathway Model for the Catch-Slip Transition in Biological Adhesion," *Biophysical Journal* 89, no. 3 (2005): 1446–54, https://doi.org/10.1529/biophysj.105.062158.

[36]Tal Kachman, Jeremy A. Owen, and Jeremy L. England, "Self-Organized Resonance during Search of a Diverse Chemical Space," *Physical Review Letters* 119, no. 3 (2017): 038001, https://doi.org/10.1103/PhysRevLett.119.038001.

[37]Jacob M. Gold and Jeremy L. England, "Self-Organized Novelty Detection in Driven Spin Glasses," arXiv:1911.07216v1, November 17, 2019, https://doi.org/10.48550/arXiv.1911.07216.

[38]Addy Pross, *What Is Life? How Chemistry Becomes Biology* (Oxford, UK: Oxford University Press, 2012), chapter 7.

[39]D. R. Mills, R. L. Peterson, and S. Spiegelman, "An Extracellular Darwinian Experiment with a Self-Duplicating Nucleic Acid Molecule," *PNAS* 58, no. 1 (July 1, 1967): 217–24, https://doi.org/10.1073/pnas.58.1.217.

[40]Sarah B. Voytek and Gerald F. Joyce, "Niche Partitioning in the Coevolution of 2 Distinct RNA Enzymes," in *PNAS* 106, no. 19 (May 12, 2009): 7780–85, https://doi.org/10.1073/pnas.0903397106.

[41]H. James Cleaves, *The Origins of Life: A Review of Scientific Inquiry* (West Conshohocken, PA: John Templeton Foundation, 2020), https://www.templeton.org/wp-content/uploads/2021/07/JTF_Origins_of_Life_Final.pdf.

[42]N. Lahav and D. H. White, "A Possible Role of Fluctuating Clay-Water Systems in the Production of Ordered Prebiotic Oligomers," *Journal of Molecular Evolution* 16, no. 1 (September 1980): 11–21, https://doi.org/10.1007/BF01732066.

[43]Thomas D. Campbell et al., "Prebiotic Condensation through Wet-Dry Cycling Regulated by Deliquescence," *Nature Communications* 10 (2019): article number 4508, https://doi.org/10.1038/s41467-019-11834-1.

[44]N. Lahav and S. Chang, "The Possible Role of Solid Surface Area in Condensation Reactions during Chemical Evolution: Reevaluation," *Journal of Molecular Evolution* 8, no. 4 (1976): 357–80, https://doi.org/10.1007/BF01739261.

[45]Ben K. D. Pearce et al., "Origin of the RNA World: The Fate of Nucleobases in Warm Little Ponds," *Proceedings of the National Academy of Sciences USA* 114, no. 43 (2017): 11327–32, https://doi.org/10.1073/pnas.1710339114.

[46]Jay G. Forsythe et al., "Ester-Mediated Amide Bond Formation Driven by Wet-Dry Cycles: A Possible Path to Polypeptides on the Prebiotic Earth," *Angewandte Chemie* 54, no. 34 (2015): 9871–75, https://doi.org/10.1002/anie.201503792.

[47]Sidney Becker et al., "Wet-dry Cycles Enable the Parallel Origin of Canonical and Non-Canonical Nucleosides by Continuous Synthesis," *Nature Communications* 9 (2018): article 163, https://doi.org/10.1038/s41467-017-02639-1.

[48]Bruce Damer and David Deamer, "The Hot Spring Hypothesis for an Origin of Life," *Astrobiology* 20, no. 4 (2020): 429–52, https://www.liebertpub.com/doi/10.1089/ast.2019.2045.

[49]Ibid., 435–36.

[50]Ibid., 441.

[51]Michael P. Robertson and Gerald F. Joyce, "The Origins of the RNA World," *Cold Spring Harbor Perspectives in Biology* 4, no. 5 (2012): article 003608, https://doi.org/10.1101/cshperspect.a003608.

[52]Paul G. Higgs and Niles Lehman, "The RNA World: Molecular Cooperation at the Origins of Life," *Nature Reviews Genetics* 16, no. 1 (2015): 7–17, https://doi.org/10.1038/nrg3841.

[53]Nicholas V. Hud et al., "The Origin of RNA and 'My Grandfather's Axe,'" *Chemistry & Biology* 20, no. 4 (Apr 18 2013): 466–74, https://doi.org/10.1016/j.chembiol.2013.03.012.

[54]Boring, Stump, and Freeland, "Rethinking Abiogenesis: Part 1, Continuity of Life through Time."

[55]Boring, Isaac, and Freeland, "Rethinking Abiogenesis: Part II, Life as a Simplification of the Nonliving Universe."