DNA BY DESIGN

AN INFERENCE TO THE BEST EXPLANATION FOR THE ORIGIN OF BIOLOGICAL INFORMATION

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INTRODUCTION

In the second chapter of his recent book *Philosophy and Biology*, Elliott Sober, warns historians and philosophers of biology against the danger of anachronism. In particular, he notes that many contemporary evolutionary biologists regard the design hypothesis as inherently untestable and, therefore, unscientific in principle, simply because it does not any longer command scientific assent. He notes that while logically unbeatable versions of the design hypothesis have been formulated (involving, for example, a "trickster God" who creates a world that appears undesigned), design hypotheses in general need not assume an untestable character. A design hypothesis could, he argues, be formulated as a fully scientific "inference to the best explanation." He notes that scientists often evaluate the explanatory power of a "hypothesis by testing it against one or more competing hypotheses."[1] On these grounds, he notes that Paley's version of the design hypothesis was manifestly testable, but was rejected precisely because it could not explain the relevant evidence of then contemporary biology as well as the fully naturalistic theory of Charles Darwin. Sober then casts his lot with the neo-Darwinian explanation on evidential rather than methodological grounds. But the possibility remains, he argues, "that

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[1] Sober (1993) 44.

there is some other version of the design hypothesis that both disagrees with the hypothesis of evolution and also is a more likely explanation of what we observe. No one, to my knowledge, has developed such a version of the design hypothesis. But this does not mean that no one ever will."[2]

This paper will present a design hypotheses, not as an explanation for the origin of species, but as an explanation for the origin of the information required to make a living system in the first place. Whereas Darwinism and neo-Darwinism address the former question, theories of chemical evolution have addressed the latter question of the ultimate origin of life. This essay will argue against the causal adequacy of chemical evolutionary theories whether based upon "chance," "necessity," or their combination. Instead it will suggest design as the best explanation for the origin of the information present in large bio-macromolecules such as DNA, RNA and proteins. In the process, this paper will bring together developments from molecular biology and the information sciences, including the some analytical concepts that have been developed in another NTSE conference paper by William A. Dembski entitled "Intelligent Design as a Theory of Information."

To develop my case for design as the best explanation for the origin of biological information, I will trace developments in origin-of-life research from the 1950s to the present. As it happens, the recent history of this discipline can be understood nicely by reference to Jacques Monod's categories of "chance and necessity." From the 1920s to the mid-1960s origin of life research relied on theories that emphasized the creative role of random variations, i.e., chance. Since the late 1960s, theorists have instead invoked deterministic self-organizational laws or properties, i.e., necessity. This paper will argue that a third type of explanation—design—provides a better explanation. To paraphrase Sober, this paper will present a design hypothesis that disagrees with the theory of *chemical* evolution and provides a better explanation for the observed complexity of the simplest living organisms.

CHEMICAL EVOLUTIONARY THEORY AND THE PROBLEM OF LIFE'S ORIGIN

After Darwin published the *Origin of Species* in 1859, many scientists began to think about a problem that Darwin had not addressed,[3] namely,

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[2]Sober (1993) 45-46.

[3]Darwin's only speculation on the origin of life is found in an unpublished 1871 letter to Joseph Hooker. In it he sketched the outlines of the chemical evolutionary idea, namely, that life could have first evolved from a series of chemical reactions "It is often

how life had arisen in the first place. While Darwin's theory purported to explain how life could have grown gradually more complex starting from "one or a few simple forms," it did not explain, nor did it attempt to explain, where life had first originated. Yet evolutionary biologists in the 1870s and 1880s such as Ernst Haeckel and Thomas Huxley assumed that devising an explanation for the origin of life would be fairly easy. For one thing, they assumed that life was essentially a rather simple substance called protoplasm that could be easily constructed by combining and recombining simple chemicals such as carbon dioxide, oxygen and nitrogen. Their early theories of abiogenesis reflected this simplistic view. Haeckel likened cell "autogony," as he called it, to a process of inorganic crystallization.[4] Haeckel's English counterpart, T.H. Huxley, proposed a simple two-step method of chemical recombination to explain the origin of the first cell.[5]

A more fully Darwinian approach to this problem did not emerge until the 1920s and 1930s, when the Russian biochemist Alexander I. Oparin would devise a theory of evolutionary abiogenesis or "chemical evolution." Oparin had a much more accurate understanding of the complexity of cellular metabolism than his nineteenth century counterparts, but neither he, nor any one else in the 1930s, fully appreciated the complexity of the molecules such as protein and DNA that make life possible. Oparin, like his nineteenth century predecessors, suggested that life could have first evolved as the result of a series of chemical reactions. Unlike his predecessors, however, he envisioned that this process of chemical evolution would involve many more chemical reactions, chance interactions and hundreds of millions (or even billions) of years.

Oparin's theory envisioned a series of chemical reactions (See Figure 1) that he thought would enable a complex cell to assemble itself gradually and naturalistically from simple chemical precursors. Oparin believed that simple gases such as ammonia (NH_3), methane (CH_4), water (H_2O), carbon dioxide (CO_2) and hydrogen (H_2) would have rained down to the early oceans and combined with metallic compounds extruded from the core of

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said that all the conditions for the first production of living organisms are now present, which could ever have been present. But if (and oh! what a big if!) we could conceive in some warm little pond, with all sorts of ammonia and phosphoric salts, light, heat, electricity, etc., that a proteine compound was chemically formed ready to undergo still more complex changes, at the present such matter would be instantly devoured or absorbed, which would not have been the case before living creatures were formed." Cambridge University Library, Manuscripts Room. Darwin Archives. Letter to Hooker February, 1871. Courtesy Peter Gautrey.

[4]Haeckel (1866) 179-80, (1892) 411-13. Kamminga (1980) 60,61.

[5]Huxley, (1869) 138-39.

the earth.[6] With the aid of ultraviolet radiation from the sun, the ensuing reactions would have produced energy-rich hydrocarbon compounds.[7] These in turn would have combined and recombined with various other compounds to make amino acids, sugars, phosphates and other "building blocks" of the complex molecules (such as proteins) necessary to living cells.[8] These constituents would eventually arrange themselves by chance into simple cell-like enclosures that Oparin called coacervates.[9] Oparin then proposed a kind of Darwinian competition for survival among his coacervates. Those that, again by chance, developed increasingly complex molecules and metabolic processes would have survived and grown more complicated. Those that did not would have dissolved.[10]

Thus, cells would have become gradually more and more complex as they competed for survival over billions of years. Like Darwin, Oparin employed time, chance and natural selection to account for the origin of complexity from initial simplicity. Moreover, nowhere in his scenario did "mind" or "intelligent design" or "a Creator" play any explanatory role. Indeed, for Oparin—a Marxist[11]—such notions were explicitly precluded from scientific consideration. Matter interacting chemically with other matter, if given enough time and the right conditions, could produce life. Complex cells could be built from simple chemical precursors without any guiding personal or intelligent agency.

THE MILLER-UREY EXPERIMENT

The first experimental support for Oparin's hypothesis came in December of 1952. While doing graduate work under Harold Urey at the University of Chicago, Stanley Miller conducted the first experimental test of the Oparin chemical evolutionary model. Miller circulated a gaseous mixture of methane (CH_4), ammonia (NH_3), water vapor ($H_2 0$) and hydrogen (H_2) through a glass vessel containing an electrical discharge chamber.[12] Miller sent a high voltage charge of electricity into the chamber via tungsten filaments in an attempt to simulate the effects of ultraviolet light on prebiotic atmospheric gases. After two days, Miller found a small (2

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[6]Oparin (1938) 64-103.

[7]*Ibid.*, 98,107,108.

[8]*Ibid.*, 133-35.

[9]*Ibid.* 148-159.

[10]*Ibid.* 195-96.

[11]Graham (1973) 262-63. Araujo, (1981) 19.

[12]Miller, (1953) 528-29.

percent) yield of amino acids in the U-shaped water trap he used to collect reaction products at the bottom of the vessel. While Miller's initial experiment yielded only three of the twenty amino acids that occur naturally in proteins, subsequent experiments performed under similar conditions have produced all but one of the others. Other simulation experiments have produced fatty acids and the nucleotide bases found in DNA and RNA, but not the sugar molecules deoxyribose and ribose necessary to build DNA and RNA molecules.[13]

Miller's success in producing biologically relevant "building blocks" under ostensibly prebiotic conditions was heralded as a great breakthrough. His experiment seemed to provide experimental support for Oparin's chemical evolutionary theory by showing that an important step in Oparin's scenario—the production of biological building blocks from simpler atmospheric gases—was possible on the early earth. Miller's work inspired many similar simulation experiments and an unprecedented optimism about the possibility of developing an adequate naturalistic explanation for the origin of life. Indeed, thanks largely to Miller's experimental work, chemical evolution is now routinely presented in both high school and college biology textbooks[14] as the accepted scientific explanation for the origin of life. Yet as we shall see, chemical evolutionary theory is now known to be riddled with difficulties; and Miller's work is understood by the origin-of-life research community itself to have little, if any, relevance to explaining how amino acids—let alone proteins or livings cells—actually could have arisen on the early earth.

PROBLEMS WITH THE OPARIN/MILLER HYPOTHESIS

Despite its status as textbook orthodoxy, the Oparin chemical evolutionary theory has in recent years encountered severe, even fatal, criticisms on many fronts. First, geochemists have failed to find evidence of the nitrogen-rich "prebiotic soup" required by Oparin's model.[15]

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[13] Thaxton and Bradley (1994) 182. Shapiro (1988) 71-95. Ferris (1987) 30. Thaxton, et. al. (1992) pp. 24-38. Harada and Fox (1964) 335. Lemmon, (1970) 95-6.

[14] See, for example, Alberts, *et al.,* (1983) 4. Lehninger (1975) 23.

[15] As the result of geological and geochemical studies of the earliest Precambrian rocks scientists now question whether an oceanic medium full of biological precursors— i.e., the so-called "prebiotic soup" required by Oparin's scenario—ever existed. In 1973, two scientists Brooks and Shaw argued that if an amino and nucleic acid-rich ocean had existed, it would have left large deposits of nitrogen rich minerals (nitrogenous cokes) in metamorphosed Precambrian sedimentary rocks. No evidence of such deposits exists, however. In the words of Brooks, "the nitrogen content of early PreCambrian organic

Second, the remains of single-celled organisms in the very oldest rocks testify that, however life emerged, it did so relatively quickly—i.e. fossil evidence suggests that chemical evolution had little time to work before life emerged on the early earth.[16]   Third, new geological and geochemical evidence suggests that prebiotic atmospheric conditions were hostile, not friendly, to the production of amino acids and other essential building blocks of life. Fourth, the revolution in the field of molecular biology has revealed so great a complexity and specificity of design in even the "simplest" cells and cellular components as to defy materialisticexplanation. Even scientists known for a staunch commitment to materialistic philosophy now concede that materialistic science in no way suffices to explain the origin of life.[17] As Francis Crick has written: "An honest man, armed with all the knowledge available to us now, could only state that in some sense, the origin of life appears at the moment to be almost a miracle, so many are the conditions which would have had to have been satisfied to get it going."[18]

To understand the crisis in chemical evolutionary theory, it will be necessary to explain in more detail the latter two difficulties, namely, the

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matter is relatively low (less than .015%). From this we can be reasonably certain that: there never was any substantial amount of 'primitive soup' on Earth when PreCambrian sediments were formed; if such a soup ever existed it was only for a brief period of time." Brooks (1985) 118.

[16]Though in 1936 Oparin did not specify when he believed life first emerged, the gradual process of evolutionary development he described clearly implied that the earth had long existed in a lifeless state (perhaps several hundreds or even thousands of million years) in order to allow for the gradual development of molecular and metabolic complexity via natural selection. After the 1960s, however, a series of new fossil finds forced scientists to revise progressively downward their estimates of the time available for chemical evolution on earth. (Schopf and Barghorn, (1967) 508-11. Brooks and Shaw, (1973) 267-305, 361. Dickerson, (1978) 70. Knoll and Barghoorn, (1977) 396-98. Lowe, (1980) 441-43. Walter, *et al.*, (1980) 443-45. Brooks, (1985) 104-116. Hayes (1996) 21-22. Mojzsis, *et. al.* (1996) 55-59.). Fossilized mats of stromatolites and the remains of various one-celled microorganisms were found in some of the world's oldest Precambrian rocks in Australia, South Africa and Greenland. These finds suggested that one-celled life first existed at least as early as 3.5 billion, and perhaps as early as 3.85 billion, (Pflug and Jaeschke-Boyer, (1979) 483-86. Bridgewater, *et al.* (1981) 51-3) years ago or within as few as 150 million years of the earth's cooling according to geological and astronomical estimates. (Maher and Stevenson (1988) 612-14. Brooks and Shaw, (1973) 73. Thaxton, et. al. (1992) 69-72.) This drastic diminution of the time considered available for the occurrence of chemical evolution challenged the plausibility of Oparin's assumption of a long-lifeless terrestrial environment. It has also calls into question all chemical evolutionary theories that rely heavily on time and chance to explain the origin of biological complexity.

[17]Dose (1988) 348-356. Shapiro (1986).

[18]Crick (1981) 88.

problem of hostile pre-biotic conditions and the problem posed by the complexity of the cell and its components.

When Stanley Miller conducted his experiment simulating the production of amino acids on the early earth, he presupposed that the earth's atmosphere was composed of a mixture of what chemists call reducing gases such as methane (CH_4), ammonia (NH_3) and hydrogen (H_2).   He also assumed that the earth's atmosphere contained virtually no free oxygen. Miller derived his assumptions about these conditions from Oparin's 1936 book.[19]   In the years following Miller's experiment, however, new geochemical evidence made it clear that the assumptions that Oparin and Miller had made about the early atmosphere could not be justified. Instead, evidence strongly suggested that neutral gases such as carbon dioxide, nitrogen and water vapor[20]—not methane, ammonia and hydrogen— predominated in the early atmosphere. Moreover, a number of geochemical studies showed that significant amounts of free oxygen were also present even before the advent of plant life, probably as the result of volcanic outgassing and the photodissociation of water vapor.[21]

This new information about the probable composition of the early atmosphere has forced a serious re-evaluation of the significance and relevance of Miller-type simulation experiments. As had been well know even before Miller's experiment, amino acids will form readily in an appropriate mixture of reducing gases. In a chemically neutral atmosphere, however, reactions among atmospheric gases will not take place readily and those reactions that do take place will produce extremely low yields of biological building blocks as simulation experiments under thes morte realistic conditions have confirmed. Further, even a small amount of atmospheric oxygen will quench the production of biologically significant building blocks and cause any biomolecules otherwise present to degrade rapidly.

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[19] Miller, (1953) 528-29.

[20] Walker, (1977) 210, 246. Walker, (1978) 222. Kerr, (1980) 42-3. Thaxton, *et. al.* (1992) 73-94.

[21] Berkner and Marshall, (1965) 225. Brinkman, (1969) 5355. Dimroth and Kimberly, (1976) 1161. Carver, (1981) 136. Holland, *et al.*, (1986) 27-33. Kastings, et. al. (1979) 3097-3102. Kerr (1980) 42-3. Thaxton, *et. al.* (1992) 73-94.

THE MOLECULAR BIOLOGICAL REVOLUTION AND THE ORIGIN OF INFORMATION

Yet a more fundamental problem remains for all chemical evolutionary scenarios. Even if it could be demonstrated that the building blocks of essential molecules could arise in realistic prebiotic conditions, the problem of assembling those building blocks into functioning proteins or DNA chains would remain. This problem of explaining the specific sequencing and thus, the information, within biopolymers, lies at the heart of the current crisis in materialistic evolutionary thinking.

In the early 1950s, the molecular biologist Fred Sanger determined the structure of the protein molecule insulin. Sanger's work made clear for the first time that each protein found in the cell comprises a long and definitely arranged sequence of amino acids.[22] The amino acids in protein molecules are linked together to form a chain, rather like individual railroad cars comprising a long train. Moreover, the function of all such proteins (whether as enzymes or as structural components in the cell) depends upon the specific sequencing of the individual amino acids,[23] just as the meaning of an English text depends upon the sequential arrangement of the letters. The various chemical interactions between amino acids in any given chain will determine the three-dimensional shape or topography that the amino acid chain adopts. This shape in turn determines what function, if any, the amino acid chain can perform within the cell. For a functioning protein, its three-dimensional shape gives it a "hand-in-glove" fit with other molecules in the cell, enabling it to catalyze specific chemical reactions or to build specific structures within the cell. Thus, the function of a protein ultimately derives from the precise sequencing of its amino acid building blocks.

The discovery of the complexity and specificity of protein molecules has raised serious difficulties for chemical evolutionary theory, even if an abundant supply of amino acids is granted for the sake of argument. Amino acids alone do not make proteins, any more than letters alone make words, sentences or poetry. In both cases, the sequencing of the constituent parts determines the function (or lack of function) of the whole. In the case of human languages the sequencing of letters and words is obviously performed by intelligent human agents. In the cell, the sequencing of amino acids is directed by the information—the set of biochemical instructions—encoded on the DNA molecule.

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[22] Portugal and Cohen (1977) 307.

[23] Alberts, *et. al.* (1983) 91-141.

INFORMATION TRANSFER: FROM DNA TO PROTEIN

During the 1950s and 60s, at roughly the same time molecular biologists began to determine the structure and function of many proteins, scientists were able to explicate the structure and function of DNA, the molecule of heredity. After James Watson and Francis Crick elucidated the structure of DNA in 1953,[24] molecular biologists soon discovered how DNA directs the process of protein synthesis within the cell. They discovered that the specificity of amino acids in proteins derives from a prior specificity within the DNA molecule—from information on the DNA molecule stored as millions of specifically arranged chemicals called nucleotides or bases along the spine of DNA's helical strands. (See Figure 2) Chemists represent the four nucleotides with the letters A, T, G, and C (for adenine, thymine, guanine and cytosine).

As in the case of protein, the sequence specificity of the DNA molecule strongly resembles the sequence specificity of human codes or languages. Indeed, just as the letters in the alphabet of a written language may convey a particular message depending on their sequence, so too do the sequences of nucleotides or bases in the DNA molecule convey precise biochemical instructions that direct protein synthesis within the cell. Whereas the function of the protein molecule derives from the specific arrangement of twenty different amino acids (a twenty-letter alphabet), the function of DNA depends upon the arrangement of just four bases. Thus, it takes a group of three nucleotides (or triplets as they are called) on the DNA molecule to specify the construction of one amino acid. This process proceeds as long chains of nucleotide triplets (the genetic message) are first copied during a process known as DNA replication and then transported (by the molecular messenger m-RNA) to a complex organelle called a ribosome.[25] There at the ribosome site, the genetic message is translated with the aid of an ingenious adaptor molecule called transfer-RNA to produce a growing amino acid chain.[26] (See Figure 3) Thus, the sequence specificity in DNA begets sequence specificity in proteins. Or put differently, the sequence specificty of proteins depends upon a prior specificity—upon information—encoded in DNA.

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[24] Watson and Crick (1953) 737.

[25] Borek (1969) 184.

[26] Alberts, *et. al.* (1983) 108-09.

NATURALISTIC APPROACHES TO THE PROBLEM
OF THE ORIGIN OF INFORMATION

The explication of this system by molecular biologists in the 1950s and 1960s, has raised the question of the ultimate origin of the specificity—the information—in both DNA and proteins. Many scientists now refer to the information problem as the "Holy Grail" of origin-of-life biology.[27] As Bernd-Olaf Kuppers recently stated, "the problem of the origin of life is clearly basically equivalent to the problem of the origin of biological information."[28] As mentioned previously, the information contained or expressed in natural languages and computer codes is the product of intelligent minds. Minds routinely create informative arrangements of matter. Yet since the mid-nineteenth century scientists have sought to explain all phenomena by reference to exclusively material causes.[29] Since the 1950s, three broad types of naturalistic explanation have been proposed by scientists to explain the origin of information.

BIOLOGICAL INFORMATION: BEYOND
THE REACH OF CHANCE

After the revolutionary developments within molecular biology in the 1950s and early 1960s made clear that Oparin had underestimated the complexity of life, he revised his initial theory. He sought to account for the sequence specificity of the large protein, DNA and RNA molecules (known collectively as biomacromolecules or biopolymers). In each case, the broad outlines of his theory remained the same, but he invoked the notion of natural selection acting on random variations *within the sequences of the biopolymers* to account for the emergence of their specificity within these molecules.[30] Others invoked the idea of a chance formation for these large information-bearing molecules by speaking of them as "frozen accidents."[31]

While many outside origin-of-life biology may still invoke "chance" as a causal explanation for the origin of biological information, few serious

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[27] Thaxton and Bradley (1994) 190.

[28] Kuppers (1990) 170-72.

[29] Gillespie (1983). Meyer (1996). Meyer (1994) 67-112. Meyer (1994) 29-40. Meyer (1993) A14. Johnson (1991). Ruse (1982) 72-78.

[30] Kamminga (1980) 326. Oparin (1968) 146-47.

[31] Crick (1968) 367-79. Kamminga (1980) 303-04.

researchers[32] still do. Since molecular biologists began to appreciate the sequence specificity of proteins and nucleic acids in the 1950s and 1960s, many calculations have been made to determine the probability of formulating functional proteins and nucleic acids at random. Various methods of calculating probabilities have been offered by Morowitz, Hoyle, Cairns-Smith, Prigogine, Yockey and more recently, Robert Sauer.[33] For the sake of argument, these calculations have generally assumed extremely favorable prebiotic conditions (whether realistic or not) and theoretically maximal reaction rates among the constituent monomers (i.e. the constituent parts of the proteins, DNA and RNA). Such calculations have invariably shown that the probability of obtaining functionally sequenced biomacromolecules at random is, in Prigogine's words, "vanishingly small . . .even on the scale of . . .billions of years."[34] As Cairns-Smith wrote in 1971:

> Blind chance...is very limited. Low-levels of cooperation he [blind chance] can produce exceedingly easily (the equivalent of letters and small words), but he becomes very quickly incompetent as the amount of organization increases. Very soon indeed long waiting periods and massive material resources become irrelevant.[35]

Consider the probabilistic hurdles that must be overcome to construct even one short protein molecule of about one hundred amino acids in length. (A typical protein consists of about 300 amino acids, and some are very much longer).[36]

First, all amino acids must form a chemical bond known as a peptide bond so as to join with other amino acids in the protein chain. Yet in nature many other types of chemical bonds are possible between amino acids; in fact, peptide and non-peptide bonds occur with roughly equal probability. Thus, at any given site along a growing amino acid chain the probability of having a peptide bond is roughly 1/2. The probability of attaining four

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[32] de Duve (1996) 112. See especially, Crick (1981) 89-93.

[33] Morowitz, (1968) 5-12. Cairns-Smith, (1971) 92-96. Hoyle and Wickramasinghe, (1981) 24-27. Shapiro, (1986) 117-31. Yockey (1981) 13-31. Yockey (1992) 246-258. Bowie and Sauer (1989) 2152-2156. Bowie, Reidhaar-Olson, Lim, Sauer (1990) 1306-1310. Reidhaar-Olson, and Sauer (1990) 306-316.

[34] Prigogine, *et al.*, (1972) 23. Prigogine's statement in full is: "The probability that at ordinary temperatures a macroscopic number of molecules is assembled to give rise to the highly ordered structures and to the coordinated functions characterizing living organisms is vanishingly small. The idea of spontaneous genesis of life in its present form is therefore highly improbable, even on the scale of the billions of years during which prebiotic evolution occurred."

[35] Cairns-Smith (1971) 95.

[36] Alberts, *et. al.* (1983) 118.

peptide bonds is: (1/2 x 1/2 x 1/2 x 1/2)=1/16 or $(1/2)^4$. The probability of building a chain of 100 amino acids in which all linkages involve peptide linkages is $(1/2)^{100}$ or roughly 1 chance in 10^{30}.

Second, in nature every amino acid has a distinct mirror image of itself, one left-handed version or L-form and one right-handed version or D-form. These mirror-image forms are called optical isomers. Functioning proteins tolerate only left-handed amino acids, yet the right-handed and left-handed isomers occurs in nature with roughly equal frequency. Taking this into consideration compounds the improbability of attaining a biologically functioning protein. The probability of attaining at random only L-amino acids in a hypothetical peptide chain 100 amino acids long is again $(1/2)^{100}$ or roughly 1 chance in 10^{30}. The probability of building a 100 amino acid length chain at random in which all bonds are peptide bonds and all amino acids are L-form would be $(1/4)^{100}$ or roughly 1 chance in 10^{60} (zero for all practical purposes given the time available on the early earth).

Functioning proteins have a third independent requirement, the most important of all; their amino acids must link up in a specific sequential arrangement just the letters in a meaningful sentence must. In some cases, even changing one amino acid at a given site can result in a loss of protein function. Moreover, because there are twenty biologically occurring amino acids the probability of getting a specific amino acid at a given site is small, i.e. 1/20. (Actually the probability is even lower because there are many non-proteineous amino acids in nature). On the assumption that all sites in a protein chain require one particular amino acid, the probability the probability of attaining a particular protein 100 amino acids long would be $(1/20)^{100}$ or roughly 1 chance in 10^{130}.

We know now, however, that some sites along the chain do tolerate several of the twenty proteineous amino acids, while others do not. The biochemist Robert Sauer of M.I.T has used a technique known as "cassette mutagenesis" to determine just how much variance among amino acids can be tolerated at any given site in several proteins. His results have shown that, even taking the possibility of variance into account, the probability of achieving a functional sequence of amino acids[37] in several functioning proteins at random is still "vanishingly small," roughly 1 chance in 10^{65}—an astronomically large number.[38] (There are 10^{65} atoms in our galaxy). In light of these results, biochemist Michael Behe has compared the odds of

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[37] Actually, Sauer counted sequences that folded into stable three dimensional configurations as functional, though many sequences that fold are not functional. Thus, his results actually underestimate the probabilistic difficulty.

[38] Reidhaar-Olson, and Sauer (1990) 306-316.

attaining proper sequencing in a 100 amino acid length protein to the odds of a blindfolded man finding a single marked grain of sand hidden in the Sahara Desert, not once, but three times.[39] Moreover, if one also factors in the probability of attaining proper bonding and optical isomers, the probability of constructing a rather short functional protein at random becomes so small as to be effectively zero (1 chance in $10^{135)}$ even given our multi-billion year old universe.[40] All these calculations, thus simply reinforce the opinion that has prevailed since the mid-1960s within origin of life biology: chance does not provide an adequate explanation for the origin of biological specificity.

Recent theoretical and experimental work on the so-called "minimal complexity" required to sustain the simplest possible living organism suggests a lower bound of some 250-400 genes and their corresponding proteins.[41] The nucleotide sequence space corresponding to such a system of proteins exceeds 4^{300000}. No matter how one makes the calculation, the improbability corresponding to this measure of molecular complexity, easily exceeds the most conservative estimates of the so-called small probability threshold of 1 chance in $10^{150,}$ the point at which appeals to chance become absurd given the "probabilistic resources" of the entire universe.[42] Thus, when one considers the full complement of functional biomolecules required to maintain minimal cell function and vitality, one can see why chance-based theories of the origin of life were abandoned. What Mora said in 1963 still holds:

> Statistical considerations, probability, complexity, etc., followed to their logical implications suggest that the origin and continuance of life is not controlled by such principles. An admission of this is the use of a period of practically infinite time to obtain the derived result. Using such logic, however, we can prove anything.[43]

PRE-BIOTIC NATURAL SELECTION: A CONTRADICTION IN TERMS

Of course, even early theories of chemical evolution did not rely exclusively on chance as a causal mechanism. A.I. Oparin's theory, in particular, invoked prebiotic natural selection as a complement to chance

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[39] Behe (1994) 68-69.

[40] Borel (1962) 28. Dembski (1996) 54, 196-97.

[41] Pennisi (1996) 1098-99. Mushegian and Koonin (1996) 10268-10273. Bult et. al. (1996) 1058-1072.

[42] Dembski (1996) 153-215.

[43] Mora (1963) 215.

interactions. This approach allegedly helped to overcome the difficulties attendant pure chance by providing a mechanism for preserving complexity-increasing events. Yet at the same time that most researchers became disenchanted with a reliance upon "chance" as an explanation, theories of pre-biotic natural selection also fell out of favor. Indeed, it became clear that prebiotic natural selection does nothing to meet the probabilistic challenges to achieving a minimally complicated self-replicating system..

A revised version of Oparin's theory published in 1968 claimed, for example, that natural selection acted upon random polymers as they formed and changed within his coacervate protocells.[44] As more complex molecules accumulated, they presumably survived and reproduced more prolifically. Nevertheless, Oparin's discussion of differential reproduction seemed to presuppose a pre-existing mechanism of self-replication. Self-replication in all extant cells depends upon functional (and, therefore, to a high degree sequence-specific) proteins and nucleic acids. Yet the origin of these molecules is precisely what Oparin needed to explain. Thus, many rejected the postulation of prebiotic natural selection as question begging.[45] Functioning nucleic acids and proteins (or molecules approaching their complexity) seemed necessary to self-replication, which in turn seemed necessary to natural selection. Yet Oparin invoked natural selection to explain the origin of proteins and nucleic acids. As the evolutionary biologist Dobzhansky would proclaim, "prebiological natural selection is a contradiction in terms."[46] Or as Pattee put it:

> . . . there is no evidence that hereditary evolution occurs except in cells which already have the complete complement of hierarchical constraints, the DNA, the replicating and translating enzymes, and all the control systems and structures necessary to reproduce themselves.[47]

In any case, as just discussed, functional sequences of amino acids—i.e. proteins—cannot be counted on to arise via random events, even if some means of selecting them exists after they have been produced. Natural selection can only select what chance has first produced and chance, at least in a prebiotic setting, seems an implausible agent for producing the information present in even a single functioning protein or DNA molecule. Oparin attempted to circumvent this problem by claiming that the sequences of monomers in the first polymers need not have been highly specific in

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[44] Oparin (1968) 146-47

[45] Mora (1965) 311-12. Bertalanffy (1967) 82.

[46] Dobzhansky (1965) 310.

[47] Pattee (1970) 123.

their arrangement. But this claim raises doubts about whether self-replication (and thus, natural selection) could have proceeded at all. The mathematician Von Neumann[48], for example, showed that any system capable of self-replication would need to contain sub-systems that were functionally equivalent to the information storage, replicating and processing systems found in extant cells. His calculations and similar ones by Wigner,[49] Landsberg,[50] and Morowitz,[51] showed that random fluctuations of molecules in all probability (to understate the case) would not produce the minimal complexity needed for even a primitive replication system. Indeed, as noted above, the improbability of developing a replication system vastly exceeds the improbability of developing the protein or DNA components of such system. As P.T. Mora put it:

> To invoke statistical concepts, probability and complexity to account for the origin and the continuance of life is not felicitous or sufficient. As the complexity of a molecular aggregate increases, and indeed very complex arrangements and interrelationships of molecules are necessary for the simplest living unit, the probability of its existence under the disruptive and random influence of physico-chemical forces decreases; the probability that it will continue to function in a certain way, for example, to absorb and to repair, will be even lower; and *the probability that it will reproduce*, [is] still lower.[52]

For this reason most scientists now dismiss appeals to pre-biotic natural selection as essentially indistinguishable from appeals to chance.

Nevertheless, Richard Dawkins[53] and Bernd-Olaf Kuppers[54] have recently attempted to resuscitate pre-biotic natural selection as an explanation for the origin of biological information. Both accept the futility of naked appeals to chance and invoke what Kuppers calls a "Darwinian optimization principle." Both use a computer to demonstrate the efficacy of pre-biotic natural selection. Each selects a target sequence to represent a desired functional polymer. They then create a crop of randomly constructed sequences, and generate variations among them at random. They then program the computer to select those sequences that match the target

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[48] Von Neumann (1966).

[49] Wigner (1961) 231-35.

[50] Landsberg (1964) 928-30.

[51] Morowitz (1966) 446-59, (1968) 10-11.

[52] Mora (1963) 215.

[53] Dawkins (1986) 47-49.

[54] Kuppers (1987) 355-369.

sequence most closely. The computer then amplifies the production of those sequences, inhibits the production of the others (thus simulating differential reproduction) and repeats the process. As Kuppers puts it, "Every mutant sequence that agrees one bit better with the meaningful or reference sequence. . .will be allowed to reproduce more rapidly."[55]   In Kuppers case, after a mere 35 generations, his computer succeeds to spelling his target sequence, "NATURAL SELECTION."

Despite such superficially impressive results, these "simulations" conceal an obvious flaw: molecules *in situ* do not have a target sequence "in mind." Nor will they confer any selective advantage, and thus differentially reproduce, until they combine in a functional arrangement. Thus, nothing in nature corresponds to the role that the computer plays in selecting non-functional sequences that happen to agree "one bit better" than others with a target sequence. The sequence "NORMAL ELECTION" may agree more with "NATURAL SELECTION" than does the sequence "MISTRESS DEFECTION," but neither of the two yield any advantage in communication over the other, if, that is, we are trying to communicate something about "NATURAL SELECTION." If so, both are equally ineffectual. Similarly, a non-functional polypeptide would confer no selective advantage on a hypothetical proto-cell, even if its sequence happens to "agree one bit better" with an unrealized target protein than some other nonfunctional polypeptide.

And, indeed, both Kupper's[56] and Dawkin's[57] published results of their simulations show the early generations of variant phrases awash in non-functional gibberish.[58] In Dawkins simulation, for example, not a single functional English word appears until after the tenth iteration. Yet to make distinctions on the basis of function among sequences that have no function whatsoever would seem quite impossible. Such determination can only be made if considerations of proximity to possible future function are allowed, but this requires foresight that molecules do not have. But a computer, programmed by a human being, can perform these functions. To imply that molecules can as well only illicitly personifies nature.   Thus, if these computer simulations demonstrate anything, they subtly demonstrate the need for intelligent agents to elect some options and exclude others—that is, to create information.

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[55] Kuppers (1987) 366.

[56] Kuppers (1987) 366.

[57] Dawkins (1986) 47-49.

[58] Nelson (1996) 12.

SELF-ORGANIZATIONAL SCENARIOS

Because of the difficulties with chance-based theories, including those that rely upon pre-biotic natural selection, most origin-of-life theorists after the mid-1960s attempted to address the problem of the origin of biological information in a completely new way. Christian de Duve explains the logic in a recent *American Scientist* article:

"A single, freak, highly improbable event can conceivably happen. Many highly improbable events—drawing a winning lottery number or the distribution of playing cards in a hand of bridge—happen all the time. But a string of improbable events—drawing the same lottery number twice, or the same bridge hand twice in a row—does not happen naturally. All of which lead me to conclude that life is an obligatory manifestation of matter, bound to arise where conditions are appropriate."[59]

Indeed, from the late 1960s to the present, the perspective that de Duve describes has dominated theoretical work on the origin of life. Researchers have increasingly repudiated chance and pre-biotic natural selection, and looked for laws and properties of chemical attraction that might explain the origin of information in DNA and proteins. Thus, most origin of life theorists since the late-1960s have advocated self organizational models for the origin of life. Rather than invoking chance, these theories invoke necessity.

In particular, by the late 1960s origin of life biologists had begun to assert that deterministic forces (stereochemical "necessity") made the origin of life not just probable, but inevitable. Some suggested that simple chemicals might possess "self-ordering properties" capable of organizing the constituent parts of proteins, DNA and RNA into the specific arrangements they now possess.[60] Steinman and Cole, for example, suggested that differential bonding affinities or forces of chemical attraction between certain amino acids might account for the origin of the sequence specificity of proteins.[61] Just as electrostatic forces draw sodium ($Na+$) and chloride ions ($Cl-$) together into a highly-ordered patterns within a crystal of

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[59] de Duve (1995b) 437.

[60] Morowitz (1968).

[61] Steinman and Cole (1967) 735-741. Steinman (1967) 533-539. For recent criticism see, Kok, *et al.* (1988) 135-42.

salt (NaCl), so too might amino acids with special affinities for each other arrange themselves to form proteins. This idea was developed in a book called *Biochemical Predestination* by Kenyon and Steinman in 1969. They argued that the origin of life might have been "biochemically predestined" by the properties of attraction that exist between constituent chemical parts, particularly between amino acids in proteins.[62]

In 1977, another self-organizational theory was proposed by Prigogine and Nicolis based on a thermodynamic characterization of living organisms. In their book *Self Organization in Nonequilibrium Systems*, Prigogine and Nicolis classified living organisms as open, nonequilibrium systems capable of "dissipating" large quantities of energy and matter into the environment.[63] They observed that open systems driven far from equilibrium often display self-ordering tendencies. For example, gravitational energy will produce highly ordered vortices in a draining bathtub; thermal energy flowing through a heat sink will generate distinctive convection currents or "spiral wave activity." Prigogine and Nicolis then argued that the organized structures observed in living systems might have similarly "self-originated" with the aid of an energy source. In essence, they conceded the improbability of simple building blocks arranging themselves into highly ordered structures under normal equilibrium conditions. But they suggested that, under non-equilibrium conditions, where an external source of energy is supplied, biochemical building blocks might arrange themselves into highly ordered patterns.

More recently, Stuart Kuaffman[64] and Christian de Duve[65] have proposed self-organizational theories with somewhat less specificity. Kauffman invokes so-called "autocatalytic properties" that he speculates may emerge from very particular configurations of simple molecules in a massive "chemical minestrone." De Duve's self-organizational proposals seem to derive from an extra-evidential principle, his so-called "Cosmic Imperative."

ORDER V. INFORMATION

For many current origin-of-life scientists self-organizational models now seem to offer the most promising approach to explaining the origin of biological information. Nevertheless, critics have called into question both the plausibility and the relevance of self-organizational models. Ironically,

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[62] Kenyon and Steinman (1969) 199-211, 263-66.

[63] Prigogine and Nicolis (1977) 339-53,429-47.

[64] Kauffman (1993) 285-341.

[65] de Duve (1995a). de Duve (1995b) 428-437.

perhaps the most prominent early advocate of self-organization, Professor Dean Kenyon, has now explicitly repudiated such theories as both incompatible with empirical findings and theoretically incoherent.[66]

First, empirical studies have shown that some differential affinities do exist between various amino acids (i.e., particular amino acids do form linkages more readily with some amino acids than others).[67] Neverthless, these differences do not correlate to actual sequencing in large classes of known proteins.[68] In short, differing chemical affinities do not explain the multiplicity of amino acid sequences that exist in naturally occurring proteins or the sequential ordering of any single protein. In the case of DNA this point can be made more dramatically. Figure 4 shows the structure of DNA depends upon several chemical bonds. There are bonds, for example, between the sugar and the phosphate molecules that form the two twisting backbones of the DNA molecule. There are bonds fixing individual (nucleotide) bases to the sugar-phosphate backbones on each side of the molecule. There are also hydrogen bonds stretching horizontally across the molecule between nucleotide bases making so-called complementary pairs. These bonds, which hold two complementary copies of the DNA message text together, make replication of the genetic instructions possible. Most importantly, however, notice that there are *no* chemical bonds between the bases that run along the spine of the helix. Yet it is precisely along this axis of the molecule that the genetic instructions in DNA are encoded.[69]

Further, just as the letters in a Scrabble game can be combined and recombined in any way to form various sequences, so too can each of the four bases A, T, G, and C attach to any site on the DNA backbone with equal facility, making all sequences equally probable (or improbable). Nor are their differential affinities between any of the four bases and the binding sites along the sugar-phosphate backbone. The same type of (so-called "n-glycosidic") bonds occur between the base and the backbone regardless of which base attaches. All four bases are acceptable, none is preferred. As Kuppers has noted, "the properties of nucleic acids indicates that all the combinatorially possible nucleotide patterns of a DNA are, from a chemical point of view, equivalent." Thus, "self-organizing" bonding affinities can not explain the sequential ordering of the nucleotide bases along the spine of the DNA because there are no *differential* affinities between the backbone

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[66] Kok, *et. al.* (1988) 135-142.

[67] Steinman and Cole (1967) 735-741. Steinman (1967) 533-539.

[68] Kok, *et. al.* (1988) 135-142.

[69] Alberts, *et. al.* (1983) 105.

and various bases that could explain variations in sequencing. Because the same holds for RNA molecules, researchers who speculate that life began in an "RNA world," have also failed to solve the sequencing problem[70]—i.e., the problem of explaining how information present in all functioning RNA molecules could have arisen in the first place.

For those who want to explain the origin of life as the result of self-organizing properties intrinsic to the material constituents of living systems, these rather elementary facts of molecular biology have devastating implications. The most logical place to look for self-organizing properties to explain the origin of genetic information is in the constituent parts of the molecules carrying that information. But biochemistry and molecular biology make clear that forces of attraction between the constituents in DNA, RNA and proteins do not explain the sequence specificity of these large information-bearing biomolecules. We know this, for among other reasons, because of the multiplicity of variant polypeptides and gene sequences that exist in nature and that can be made in the laboratory. The properties of the monomers comprising nucleic acids and proteins simply do not make a particular gene, let alone life as we know it, inevitable.

Yet if self organizational explanations for the origin of biological information are to have any theoretical import, they must claim just the opposite. And, indeed, they often do, albeit without much specificity. In de Duve's words "the processes that generated life" were "highly deterministic" making life as we known it "inevitable" "given the conditions on the prebiotic earth." Yet grant self-organizational theorists the most favorable prebiotic conditions. Given a pool of all four DNA nucleotides, and all necessary sugars and phosphates, would any particular genetic sequence have to arise? Given all necessary monomers, would any particular functional protein or gene, let alone a specific genetic code, replication system or signal transduction circuitry, have to arise?

To ask the question is to evoke the answer. As origin-of-life biochemists have taught us, monomers are "building blocks." And building blocks can be arranged and rearranged in innumerable ways. The properties of the blocks do not determine the construction of buildings. Indeed, the properties of *biological* building blocks allow a vast ensemble of possible

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[70]A recent article heralding a breakthrough for "RNA world" scenarios makes this clear. After telling how RNA researcher Jack Szostak had succeeded in engineering RNA molecules with a broader range of catalytic properties than previously known, science writer John Horgan makes a candid admission: "Szostak's work leaves a major question unanswered: How did RNA, self-catalyzing or not, arise in the first place?" Horgan (1996) 27. Shapiro (1988) 71-95. Zaug and Cech, (1986) 470-75. Cech (1989) 507-508.

configurations, the overwhelming majority of which have no biological function whatsoever. Those that do possess biological function are no more chemically inevitable or determined, than the configuration of bricks and mortar making, say, Independence Hall in Philadelphia. To anthropomorphize, neither building blocks, nor letters in a written text, nor biomonomers "care" how they are arranged. In each case, the properties of the constituents remain largely indifferent to the innumerable specific configurations or sequences that they can adopt. Thus, conversely, the properties of nucleotide bases and amino acids do not make any specific sequences "inevitable" as self-organizationalists must claim.

Significantly, information theory makes clear that there is a good reason for this. If chemical affinities between the constituents in the DNA message text determined the arrangement of the text, such affinities would dramatically diminish the capacity of DNA to carry information. To illustrate, imagine receiving the following incomplete message over the wire. The "q-ick brown fox jumped over the lazy dog." Obviously someone who knew the conventions of English could determine which letter had been rubbed out in the transmission? Because "q" and "u" always go together by grammatical necessity, the presence of one indicates the probable presence of the other in the initial transmission of the message. The "u" in all English communications is an example of what information theorists call "redundancy." Given the grammatical rule 'u' must always follow 'q', the addition of the "u" adds no new information, when "q" is already present. It is "redundant" or unnecessary to determining the sense of the message (though not to making it grammatically correct).

Now consider what would happen if the individual nucleotide "letters" (A, T,G, C) in a DNA molecule *did* interact by *chemical* necessity with each other. Every time adenine (A) occurred in a growing genetic sequence, it would likely drag thymine (T) along with it.[71] Every time cytosine (C) appeared, guanine would follow. As a result, the DNA message text would be peppered with repeating sequences of A's followed by T's and C's followed by G's. Rather than having a genetic molecule capable of unlimited novelty with all the unpredictable and aperiodic sequences that characterize informative texts, we would have a highly repetitive text awash in redundant sequences—much as happens in crystals. Indeed, in a crystal the forces of mutual chemical attraction do completely explain the sequential ordering of the constituent parts and consequently crystals cannot convey novel information. Sequencing in crystals is highly ordered or repetitive,

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[71] This, in fact, happens where adenine and thymine do interact chemically in the complementary base pairing *across* the message bearing axis of the DNA molecule.

but not informative. Once one has seen "Na" followed by "Cl" in a crystal of salt, for example, one has seen the extent of the sequencing possible. In DNA, however, where any nucleotide can follow any other, innumerable novel sequences are possible, and a countless variety of amino acid sequences can be built.

The forces of chemical necessity, like grammatical necessity in our "q-and-u" example above, produce redundancy or monotonous order, but reduce the capacity to convey information and create novelty. As chemist Michael Polanyi has said:

> Suppose that the actual structure of a DNA molecule were due to the fact that the bindings of its bases were much stronger than the bindings would be for any other distribution of bases, then such a DNA molecule would have no information content. Its code-like character would be effaced by an overwhelming redundancy. . . Whatever may be the origin of a DNA configuration, it can function as a code only if its order is not due to the forces of potential energy. It *must be* as physically indeterminate as the sequence of words is on a printed page.[72] [emphasis added]

So, if chemists had found that bonding affinities between the nucleotides in DNA produced nucleotide sequencing, they would have also found that they had been mistaken about DNA's information-bearing properties. To put the point quantitatively, to the extent that forces of attraction between constituents in a sequence determine the arrangement of the sequence, to that extent, will the information carrying capacity of the system be diminished.[73] As Dretske has explained:

> "As $p(s_i)$ [the probability of a condition or state of affairs] approaches 1 the amount of information associated with the occurrence of s_i goes to 0. In the limiting, case when the probability of a condition or state of affairs is unity [$p(s_i) = 1$], no information is associated with, or generated by, the occurrence of s_i. This is

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[72]Polanyi (1968) 1309.

[73]The information carrying capacity of any symbol in a sequence is inversely related (by a negative logarithm function) to the probability of its occurrence. The informational capacity of a sequence as a whole is inversely proportional to the product of the individual probabilities for each member in the sequence. Since chemical affinities between constituents ("symbols") increase the probability of the occurrence of one given another (i.e., necessity increases probability), such affinities decrease the information carrying capacity of a system in proportion to the strength and relative frequency of such affinities within the system.

merely another way to say that no information is generated by the occurrence of events for which there are no possible alternatives."[74]

Bonding affinities, to the extent they exist, militate against the maximization of information.[75] They can not, therefore, be used to explain the origin of information. Affinities create mantras, not messages.

The tendency to conflate the qualitative distinction between "order" and "information" has characterized self-organizational research efforts and calls into question the relevance of such work to the origin of life. As Yockey has argued, the accumulation of structural or chemical order does not explain the origin of biological complexity (i.e., genetic information).[76] He concedes that energy flowing through a system may produce highly ordered patterns. Strong winds form swirling tornados and the "eyes" of hurricanes; Prigogine's thermal baths do develop interesting "convection currents"; and chemical elements do coalesce to form crystals. Self-organizational theorists explain well what doesn't need explaining. What needs explaining is not the origin of order (in the sense of symmetry or repetition), but the origin of information—the highly improbable, aperiodic, and yet specified sequences that make biological function possible.

To illustrate the distinction between order and information compare the sequence "ABABABABABABAB" to the sequence "Help! Our neighbor's house is on fire!" The first sequence is repetitive and ordered, but not complex or informative. The second sequence is not ordered, in the sense of being repetitious, but it is complex and also informative. The second sequence is complex because its characters do not follow a rigidly repeating or predictable pattern—i.e, it is aperiodic and improbable. It is also informative because, unlike a *merely* complex sequence such as "rfsxdcnct<e%dwqj", the particular arrangement of characters is highly exact or "specified" so as to perform a (communication) function. Systems that are characterized by both specificity and complexity (what Bill Dembski calls "complex specified information") have "information content." Since such systems have the qualitative feature of complexity (aperiodicity), they are qualitatively distinguishable from systems characterized by simple periodic order. Thus, attempts to explain the origin of order have no relevance to discussions of the origin of information content. Significantly,

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[74] Dretske (1981) 12.

[75] Yockey (1981) 18.

[76] Orgel has drawn a similar distinction between order and/or the randomness that characterizes inanimate chemistry and what he calls the "specified complexity" of informational biomolecules. Orgel, (1973) 189ff. See also Thaxton, *et. al.* (192) 130ff.

the nucleotide sequences in the coding regions of DNA have, by all accounts, a high information content—that is, they are both highly specified and complex, just like meaningful English sentences.[77]

Conflating order and information has led many to attribute properties to brute matter that it does not possess. While energy in a system *can* create patterns of symmetric order such as whirling vortices, there is no evidence that energy alone can encode functionally specified sequences—whether biochemical or otherwise. As Yockey warns:

> Attempts to relate the idea of order . . . with biological organization or specificity must be regarded as a play on words which cannot stand careful scrutiny. Informational macromolecules can code genetic messages and therefore can carry information because the sequence of bases or residues is affected very little, if at all, by [self-organizing] physico-chemical factors.[78]

THE RETURN OF THE DESIGN HYPOTHESIS

The preceding discussion suggests that the properties of the material constituents of DNA—like those of any information-bearing medium—are not responsible for the information conveyed by the molecule. Indeed, in all informational systems, the information content or message is neither deducible from the properties of the material medium nor attributable to them. The properties of matter do not explain the origin of the information.

To amplify this point consider, first, that many different materials can express the same message. The headline of this morning's *New York Times* was written with ink on paper. Nevertheless, many other materials could have been used to convey the same message. The information in the headline could have been written with chalk on a board, with neon-filled tubes in a series of signs, or by a sky-writer over New York harbor. Clearly, the peculiar chemical properties of ink are not necessary to convey the message. Neither are the physical properties (i.e., the geometric shapes) of the letters necessary to transmit the information. The same message could have been expressed in Hebrew or Greek using entirely different alphabetic characters.[79]

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[77] Thaxton and Bradley (1994) 173-210. Thaxton, *et. al.* (1992) 127-166. Yockey (1992) 242-293.

[78] Yockey (1977) 380.

[79] Carl Wieland has illustrated this principle as follows: "Let's say Alphonse in Alsace wants to send a message, "Ned, the war is over. Al." He dictates it to a friend; the message has begun as patterns of air compression (spoken words). His friend puts it down as ink on paper and mails it to another, who puts it in a fax machine. The machine

Conversely, the same material medium (and alphabetic characters) can express many different messages—i.e. the medium is not sufficient to determine the message. Last November the *Times* used ink and English characters to tell the reading public that a Democrat, William Jefferson Clinton won the Presidential election. Yet the properties of the ink and the 26 letters available to the type-setter did not determine the content of the headline. Instead, the ink and English characters permitted the transmission of whatever headline that the election result required, as well as a vast ensemble of other possible arrangements of text, some meaningful, and many more not. Neither the chemistry of the ink nor the shapes of the letters determine the meaning of the text. In short, the message transcends the properties of the medium.

The information in DNA also transcends the properties of its material medium. Because chemical bonds do not determine the arrangement of nucleotide bases, the nucleotides can assume a vast array of possible sequences and thereby express many different messages. (Conversely, various materials can express the same messages, as happens in variant versions of the genetic code or when laboratory chemists use English instructions to direct the synthesis of naturally occurring proteins). Thus, again, the properties of the constituents do not determine the function—the information transmitted—by the whole. As Michael Polanyi has said: "As the arrangement of a printed page is extraneous to the chemistry of the printed page, so is the base sequence in a DNA molecule extraneous to the chemical forces at work in the DNA molecule."[80]

If the properties of matter (i.e., the medium) do not suffice to explain the origin of information, what does? Blind chance is, of course, a possibility but *not*, as we have seen in the case of DNA and proteins, where the amount of information (or the improbability of arrangement) gets too immense. The random selection and sequencing of Scrabble pieces out of a grab bag might occasionally produce a few meaningful words such as "cat" or "ran." Nevertheless, undirected selection will inevitably fail as the numbers of letters required to make a text increases. Fairly soon, chance

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transfers the message into a coded pattern of electrical impulses, which are sent down a phone line and received at a remote Indian outpost, where it is printed out in letters once again. Here the person who reads the fax lights a campfire and sends the same message as smoke signals. Old Ned in Nevada, miles away looks up and gets the exact message that was meant for him. Nothing physical has actually been transmitted; not a single atom or molecule travelled from Alsace to Nevada, yet it is obvious that something travelled all the way. This elusive something is called information." Wieland (1995) 11.

[80]Polanyi (1968) 1309.

becomes clearly inadequate as origin-of-life biologists have almost universally acknowledged.

Some have suggested that the discovery of some new scientific laws might explain the origin of biological information. As Manfred Eigen has argued, "our task is to find an algorithim, a natural law, that leads to the origin of information."[81]   But this suggestion betrays confusion on two counts.   First, scientific laws don't generally explain or cause natural phenomena, they describe them. For example, Newton's law of gravitation described, but did not explain, the attraction between planetary bodies. Second, scientific laws describe (almost by definition) highly regular phenomena—i.e., order.   Thus, to say that any scientific law can describe, or generate, an informational sequence, is essentially a contradiction in terms. The patterns that laws describe are necessarily highly ordered, not complex. Thus, like crystals, all law-like patterns have an extremelylimited capacity to convey information. One might, perhaps, find a complex set of material conditions capable of generating high information content on a regular basis, but everything we know suggests that the complexity and information content of such conditions would have to equal or exceed that of any system produced, thus again begging the question about the ultimate origin of information.

For example, the chemist J. C. Walton has argued (echoing earlier articles by Mora) that even the self-organization produced in Prigogine-style convection currents does not exceed the organization or information represented by the the experimental apparatus used to create the currents.[82] Similarly, Maynard-Smith[83], Dyson[84], Speigelman[85] have shown that Manfred Eigen's so-called hypercycle model for generating information naturalistically is subject to the same law of information loss, or what might be termed "the law of conservation of information."[86]   They show, first, that Eigen's hypercycles presuppose a large initial contribution of information in the form of a long RNA molecule and some forty specific proteins. More significantly, they show that because hypercycles lack an error-free mechanism of self-replication, they become susceptible to various

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[81] Eigen, M. (1992) 12.

[82] Walton (1977) 16-35. Mora (1965) 41.

[83] See Maynard Smith (1979) 445-46.

[84] Dyson (1985) 9-11, 35-9, 65-6,78.

[85] See discussion in Shapiro (1986) 161.

[86] Bill Dembski has given a formal expression to this law in his NTSE conference paper "Intelligent Design as a Theory of Information."

"error-catastrophes" that ultimately diminish, not increase, the information content of the system over time.

Stuart Kauffman's self-organizational theory also subtly acknowledges this difficulty. In his *The Origins of Order*, Kauffman suggests that large ensembles of molecules in solution (in a so-called "chemical minestrone") may have "auto-catalytic" properties that can explain the origin of the integrated complexity of living cells.[87] He acknowledges, however, that such autocatalysis would not occur unless the ensemble of molecules in obtained very specific spatial-temporal relationships to one another. In other words, for the direct autocatalysis of biological complexity to occur, a system of molecules must first achieve a very specific molecular configuration, or a low configurational entropy state. Yet this claim is isomorphic with the claim that the system must start with a high information content. Thus, to explain the origin of biological complexity at the systems-level, Kauffman's must presuppose the existence of highly specific and complex—i.e., an information-rich—arrangement of matter at the molecular level.[88] Therefore, his work—if it has relevance to the actual behavior of molecules—does not provide a naturalistic explanation for the origin of information.

Instead, our experience with information-intensive[89] systems (especially codes and languages) indicates that such systems always come from an intelligent source—i.e., from mental or personal agents. This generalization holds not only for the information present in languages and codes but also for the non-grammatical information (also describable as specified complexity) inherent in machines or expressed in works of art. Like the text of a newspaper, the parts of a supercomputer and the faces on Mount Rushmore require many instructions to specify their shape or arrangement[90]

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[87] Kauffman (1993) 285-341.

[88] See Thaxton, *et. al.* (1992) 127-143

[89] This qualification means to acknowledge that chance can produce low levels of information.

[90] Defining information as the number of instructions required to specify a structure or sequence allows scientists to distinguish sequences that are merely mathematically improbable from functional sequences or meaningful text. [Chaitan (1966) 547-569.] [Kolmogorov [1965] 3-11.] Classical information theory as developed in the 1940s by Claude Shannon could not distinguish merely improbable sequences from those that conveyed a message (e.g. "we hold these truths to be self-evident. . ." v. "ntnyhiznlhteqkhgdsjh"). Shannon's theory could measure the "information carrying capacity" of a given sequence of symbols, but not the "information content." This is significant because random (natural) processes might produce an improbable but unspecified system. Nevertheless, recent reformulations of the design argument based on the presence of information in DNA, have been based upon evaluations of information

and consequently, have a high information content. Each of these systems are also, not coincidentally, the result of intelligent design, not chance or material forces.

Our generalization about the cause of information has, ironically, received confirmation from origin-of-life research itself. During the last forty years, every naturalistic[91] model proposed has failed to explain the origin of information. Thus, mind or intelligence or what philosophers call "agent causation," now stands as the only known cause known to be capable of creating high information content (or what Dembski calls complex specified information).

Because mind or intelligent design is a necessary cause of an information-rich system, one can detect (or, logically, retrodict) the past action of an intelligent cause from the presence of an information-intensive effect, even if the cause itself cannot be directly observed.[92] Since information requires an intelligent source, the flowers spelling "Welcome to Victoria" in the gardens of Victoria harbor, lead visitors to infer the activity of intelligent agents even if they did not see the flowers planted and arranged. Similarly, the specifically arranged nucleotide sequences—the encoded information—in DNA imply the past action of an intelligent mind, even if such mental agency cannot be directly observed.

Moreover, the logical calculus underlying such inferences follows a valid and well-established method used in all historical and forensic sciences. In historical sciences, knowledge of the present causal powers of various entities and processes enables scientists to make inferences about possible causes in the past. When a thorough study of various possible causes turns up just a single adequate cause for a given effect, historical or forensic scientists can make fairly definitive inferences about the past.[93]

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content, or what Dembski has called "specified information," not carrying capacity. As such, they do not commit the fallacy of equivocation. The argument asserts that the presence of high information content (in whatever context, semantic, structural or computational) implicates a prior intelligent cause. It does not claim that information carrying capacity (i.e., unspecified information or complexity) does. Moreover, Dembski has recently given a formal and generalized account of specification. His treatment makes makes it possible to distinguish specified and unspecified information and makes the notion of specification applicable beyond its original computational (Kolmogorov [1965] 3-11.) context. See Dembski (1996) 115-152. Thaxton and Bradley (1994) 200-210. Thaxton, *et. al.* (1992) 127-166.

[91] For good summary and critique of different approaches see especially, Dose (1988) 348-56. Yockey (1992) 259-93, Thaxton, *et. al.* (1992), Shapiro (1986). For a contradictory hypothesis see Kauffman (1993) 287-341.

[92] Meyer (1990) 79-99.

[93] Meyer (1990) 79-99. Sober (1988) 4-5. Scriven (1966) 249-50.

Several years ago, for example, one of the forensic pathologists from the original Warren Commission that investigated the assassination of President Kennedy spoke out to quash rumors about a second gunman firing from in front of the motorcade. Apparently, the bullet hole in the back of President Kennedy's skull evidenced a distinctive beveling pattern that clearly indicated its direction of entry. In this case, it revealed that the bullet had entered from the rear. The pathologist called the beveling pattern a "distinctive diagnostic"[94] to indicate a necessary causal relationship between the direction of entry and the presence of the beveling. Inferences based on knowledge of necessary causes ("distinctive diagnostics") are quite common in historical and forensic sciences, and often lead to the detection of intelligent, as well as, natural causes. Since Criminal X's fingers are the only known cause of Criminal X's fingerprints, X's prints on the murder weapon incriminate him with a high degree of certainty. In the same way, since intelligent design is the only known cause of information-rich systems—high information content—implies an intelligent source.

Scientists in many fields recognize the connection between intelligence and information and make inferences accordingly. Archaeologists assume a mind produced the inscriptions on the Rosetta Stone. Evolutionary anthropologists try to demonstrate the intelligence of early hominids by arguing that certain chipped flints are too improbably specified to have been produced by natural causes. N.A.S.A.'s search for extra-terrestrial intelligence (S.E.T.I.)[95] presupposed that information imbedded in electromagnetic signals from space would indicate an intelligent source.[96] As yet, however, radio-astronomers have not found information-bearing signals coming from space. But closer to home, molecular biologists have identified sequences possessing high information content in the cell. Consequently, a growing number of scientists[97] now suggest that the information in DNA justifies making a "design inference."[98]

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[94] See transcript of the McNeil-Lehrer News Hour, May 19, 1992.

[95] Less exotic (and more successful) design detection occurs routinely in both science and industry. Fraud detection, forensic science and cryptography all depend upon the application of probabilistic or information theoretic criteria of intelligent design. Wilford (1994) A 10. Edwards, A.W.F. (1986) 295-312. Hilts, Philip J. (1992) section C, pp. 9. Patterson, W. (1987).

[96] McDonough (1987).

[97] Behe (1996). Kenyon and Mills (1996) 9-16 Ayoub (1996) 19-22. Dembski (1996). Moreland, *et. al.*, (1994). Bradley, (1988) 72-83. Augros, R. and Stanciu, G. (1987). Denton, M. (1986) 326-343. Thaxton, *et. al.* (1992). Ambrose, E.J. (1982). Thaxton, *et. al.* (1992). Walton (1977) 16-35.

[98] Dembski (1996). Behe (1993).

AN ARGUMENT FROM INGNORANCE?

Against all that has been said, many have maintained that this argument from information content to design constitutes nothing more than an argument from ignorance. Since we don't yet know how biological information could have arisen we invoke the mysterious notion of intelligent design. Thus, say objectors, intelligent design functions, not as an explanation, but as a kind of place holder for ignorance.

And yet, as Dembski has demonstrated[99], we often infer the causal activity of intelligent agents as the best explanation for many events and phenomena. Moreover, we do so rationally, according to objectifiable, if often tacit, complexity theoretic criteria. His examples of design inferences—from archeology to cryptography to fraud detection and criminal forensics—show that we make design inferences all the time and we often do so for a very good reason.[100] Intelligent agents have unique causal powers that nature does not. When we observe effects that we know only agents can produce, we rightly infer the antecedent presence of a prior intelligence even if we did not observe the action of the particular agent responsible. In other words, Dembski has shown that designed events leave a complexity, and information theoretic signature, that allows us to detect design reliably.[101] When these criteria are present, scenarios involving design, constitute better explanations than those that rely exclusively on chance and/or deterministic natural processes.

While admittedly, the design inference does not constitute a proof (nothing based upon empirical observation can), it most emphatically does not constitute an argument from ignorance. Instead, the design inference from biological information constitutes an "inference to the best explanation."

Recent work on the method of "inference to the best explanation"[102] suggests that determining which among a set of competing of possible explanations constitutes the best depends upon assessments of the causal powers of competing explanatory entities. Causes that have the capability to produce the evidence in question constitute better explanations of that

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[99]Dembski (1996) 1-25.

[100]*Ibid.*

[101]Dembski (1996).

[102]Lipton (1991). Meyer (1994). Sober (1993). Meyer (1991).

evidence than those that do not. This essay has evaluated and compared the causal efficacy of three broad categories of explanation—chance, necessity, (and chance and necessity combined) and design—*with respect to their ability to produce high information content.* As we have seen, neither chance nor necessity (nor their combination) seems to possess the ability to produce biological information in a prebiotic context. This result comports with our ordinary uniform human experience. Brute matter—whether acting randomly or by necessity—does not seem to possess the capability to produce high information content.

Yet it is not correct to say that we do not know how information arises. Indeed, we know from our own experience that intelligent agents create information all the time. Thus, our inference to design does not depend upon ignorance, but upon our knowledge of the demonstrated causal powers of nature and agency, respectively. The law of conservation of information developed in Dembski's conference paper formalizes this knowledge, helping us to make inferences about the causal histories of various artifacts, entities or events based upon the information theoretic signatures they exhibit. It implies that whenever high information content (or in his terminology, complex specified information) is present in an artifact or entity whose causal story is known, invariably creative intelligence—design—has played a causal role in the origin of that entity. Thus, our knowledge of causal powers, not our ignorance, leads to the acceptance of design as the best explanation for the origin of biological information in a prebiotic context.

Objectors complain, of course, that future inquiry may uncover other natural entities possessing as yet unknown causal powers. They object that the design inference presented here depends upon a negative generalization—naturalcauses cannot produce high information content— that future discoveries may well later falsify. We should 'never say never,' they say. Yet science often says never, even if it can't say so for sure. Indeed, negative generalizations play an important role in science. As many historians and philosophers of science have pointed out, scientific laws often tell us not only what does happen, but also what does not happen. The conservation laws in thermodynamics, for example, proscribe certain outcomes. The first law tells us that matter is never created or destroyed. The second tells us that the entropy of a closed system will never increase over time. Those who claim that such "proscriptive laws" do not constitute knowledge simply because they are based upon past, but not future, experience will not get very far at the National Science Foundation, especially if they want to use their skepticism to justify funding for, say, research on perpetual motion machines.

Moreover, without proscriptive generalizations, without knowledge about what possible cause can and cannot produce, historical scientists could never make any determinations about the past. As work on the method of the historical sciences has shown,[103] reconstructing the past requires making inferences from present effects back to past causal events. Yet historical scientists judge the plausibility of such inferences against our knowledge of the causal powers of the competing possible causes. Making inferences about the best historical explanation requires a progressive elimination of competing causal hypotheses. Deciding which causes can be eliminated from consideration requires knowing what effects a given cause can, and especially cannot, produce. If we can never say that certain entities do not possess certain causal powers, then we can never eliminate them— even provisionally—from consideration. And thus, we could never make historical inferences. Yet we do so all the time.

Recently, those investigating the cause of the TWA plane that crashed over Long Island eliminated a Navy missile as the cause of the crash because none of the Navy ships within missile range had missile launching capability. We may later learn otherwise, or we may later learn that ships without missile launching capability can launch them after all, but for now other explanations seem better. Indeed, to determine the best explanation we do not need to say 'never, for sure.' We only need to say that a given postulated cause is best given all the we know about the demonstrated causal powers of competing entities or agencies at present. That cause C can produce effect E, makes it a better explanation of E than some other cause D that has never produced E and which seems incapable of doing so on theoretical grounds, even if D may later demonstrate causal powers of which we are presently ignorant.

Thus, the objection that the design inference constitutes an argument from ignorance reduces in essence to a restatement of the problem of induction. Yet one can make this objection against any scientific law or explanation, or any historical inference that takes our knowledge of scientific generalizations about laws and causal powers into account. As Barrow and Tipler have noted, to criticize design arguments, as Hume did, simply because they assume the uniformity and (normative character) of natural law cuts just as deeply against "the rational basis of any form of scientific inquiry."[104] Our knowledge of what can and cannot produce high information content may later have to be revised, but so might the laws of thermodynamics. Inferences to design may also later prove incorrect, but

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[103]Meyer (1991). Sober (1988). Scriven (1966).

[104]Barrow, J. and Tipler, F. (1986) 69.

so may inferences that implicate various natural causes. Such a possibility does not stop scientists from making generalizations about the causal powers of various entities or using these generalizations to identify probable causes in particular cases. Inferences based upon past and present experience constitute knowledge (albeit provisional), not ignorance. Those who object to such inferences object to *science* as much as they object to a particular science of design.

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