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WORD GAMES

DNA, Design, and Intelligence

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> Einstein said, "God does not play dice."
> He was right. God plays scrabble.
>
> Philip Gold

Since the late nineteenth century most biologists have rejected the idea that living organisms display evidence of intelligent design. While many acknowledge the *appearance* of design in biological systems, they insist that Darwinism, or neo-Darwinism, explains how this appearance arose naturalistically—that is, without invoking a directing intelligence or agency. Following Darwin, modern neo-Darwinists generally accept that natural selection acting on random variation can explain the appearance of design in living organisms.

As evolutionary biologist Francisco Ayala has explained, "The functional design of organisms and their features would ... seem to argue for the existence of a designer. It was Darwin's greatest accomplishment [however] to show that the directive organization of living beings can be explained as the result of a natural process, natural selection, without any need to resort to a Creator or other external agent."

Yet, however one assesses the explanatory power of Darwinism (or modern neo-Darwinism), the appearance of design in at least one important domain of biology cannot be so easily dismissed. During the last half of the twentieth century, advances in molecular biology and biochemistry have revolutionized our understanding of the miniature world within the cell. Research has revealed that cells—the fundamental units of life—store, transmit, and edit information and use that information to regulate their most fundamental metabolic processes. Far from characterizing cells as simple "homogeneous globules of plasm" as did Ernst Haeckel and other nineteenth-century biologists, biologists now describe cells as, among other things, "distributive real time computers" or complex information-processing systems. Recently, for example, a special issue of the prestigious journal *Cell*[6] was dedicated entirely to the topic of "macromolecular machines."

Darwin, of course, neither knew about these intricacies nor sought to explain their origin. Instead, his theory of biological evolution sought to explain how life could have grown gradually more complex *starting* from "one or a few simple forms." Strictly speaking, therefore, those who insist that the purely naturalistic Darwinian mechanism can explain the appearance of design in biology overstate their case. The complexities within the microcosm of the cell beg for some kind of explanation. Yet they lie beyond the purview of strictly biological evolutionary theory, which assumes, rather than explains, the existence of the first life and the information it required.

Explaining Life's Origin in Materialistic Terms

During the 1870s and 1880s scientists 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. Early theories of life's origin reflected this view. Haeckel likened cell "autogeny," as he called it, to the process of inorganic crystallization. Haeckel's English counterpart, T. H. Huxley, proposed a simple two-step method of chemical recombination to explain the origin of the first cell. Just as salt could be produced spontaneously by adding sodium to chloride, so, thought Haeckel and Huxley, could a living cell be produced by adding several chemical constituents together and then allowing spontaneous chemical reactions to produce the simple protoplasmic substance that they assumed to be the essence of life.

During the 1920s and 1930s a more sophisticated version of this so-called chemical evolutionary theory was proposed by a Russian biochemist named Alexander I. Oparin. Oparin had a much more accurate understanding of the complexity of cellular metabolism, but neither he, nor anyone 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 transformations and reactions, and many hundreds of millions (or even billions) of years.

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 circulated a gaseous mixture of methane, ammonia, water vapor, and hydrogen through a glass vessel containing an electrical discharge chamber. 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 percent) yield of amino acids in the U-shaped water trap he used to collect reaction products at the bottom of the vessel.

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 experimental results also received widespread press coverage in popular publications such as *Time* magazine and gave Oparin's model the status of textbook orthodoxy almost overnight. Thanks largely to Miller's experimental work, chemical evolution is now routinely presented in both high school and college biology textbooks 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 living cells—actually could have arisen on the early Earth.

To understand today's growing crisis in chemical evolutionary theory, this chapter will focus on the two most severe difficulties confronting it: the problem of hostile prebiotic conditions and the problem posed by the complexity of the cell and its components.

Hostile Prebiotic Conditions

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, ammonia, and hydrogen. He also assumed that the Earth's atmosphere contained virtually no free oxygen. 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—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.

In a chemically neutral atmosphere, reactions among atmospheric gases will not take place readily. Moreover, even a small amount of atmospheric oxygen will quench the production of biological building blocks and cause any biomolecules otherwise present to degrade rapidly.

As had been well known even before Miller's experiment, amino acids will form readily in an appropriate mixture of reducing gases.

What made Miller's experiment significant was not the production of amino acids *per se,* but the production of amino acids from presumably plausible prebiotic conditions. As Miller himself stated, "In this apparatus an attempt was made to duplicate a primitive atmosphere of the earth, and not to obtain the optimum conditions for the formation of amino acids." Now, however, the situation has changed. The only reason to continue assuming the existence of a chemically reducing, prebiotic atmosphere is that chemical evolutionary theory requires it.

Ironically, even if we assume for the moment that the reducing gases used by Stanley Miller do actually simulate conditions on the early Earth, his experiments inadvertently demonstrated the necessity of intelligent agency. Even successful simulation experiments require the intervention of the experimenters to prevent what are known as "interfering cross-reactions" and other chemically destructive processes. Without human intervention, Miller-type experiments invariably produce nonbiological substances that degrade amino acids into nonbiologically relevant compounds.

Experimenters prevent this by removing chemical products that induce undesirable cross-reactions. They employ other "unnatural" interventions as well. Simulation experimenters have typically used only short wavelength light, rather than both short and long wavelength ultraviolet light, which would be present in any realistic atmosphere. Why? The presence of the long-wavelength UV light quickly degrades amino acids.

Such manipulations constitute what chemist Michael Polanyi called a "profoundly informative intervention." They seem to "simulate," if anything, the need for an intelligent agent to overcome the randomizing influences of natural chemical processes.

Sequence Specificity in Proteins

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.

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. 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, 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 determine a complex three-dimensional shape or topography that the amino acid chain adopts. This usually highly complex 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 complex molecules in the cell, enabling it to catalyze specific chemical reactions or to build specific structures within the cell.

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.

Sequence Specificity in DNA

During the 1950s and 1960s, 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, 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 the DNA's helical strands. Chemists represent the four nucleotides with the letters A, T, G, and C (for adenine, thymine, guanine, and cytosine).

As it turns out, specific regions of the DNA molecule called coding regions have the same property of "sequence specificity" or "specified complexity" that characterizes written codes, linguistic texts, and protein molecules. Just as the letters in the alphabet of a written language may convey a particular message depending on their arrangement, so too do the sequences of nucleotide bases (the As, Ts, Gs, and Cs) inscribed along the spine of a DNA molecule convey a precise set of instructions for building proteins within the cell. The nucleotide bases in DNA function in much the same way as symbols in a machine code or alphabetic characters in a book.

In each case, the arrangement of the characters determines the function of the sequence as a whole. As Richard Dawkins has noted, "The machine code of the genes is uncannily computer-like." Or as Bill Gates has noted, "DNA is like a computer program, but far, far more advanced than any software we've ever created." In the case of a computer code, the specific arrangement of just two symbols (0 and 1) suffices to carry information. In the case of an English text, the twenty-six letters of the alphabet do the job. In the case of DNA, the complex but precise sequencing of the four nucleotide bases (A, T, G, and C) stores and transmits the information necessary to build proteins. Thus, the sequence specificity of proteins derives from a prior sequence specificity—from the *information*—encoded in DNA.

The elucidation of DNA's information-bearing properties raised the question of the ultimate origin of the information in both DNA and proteins. Indeed, many scientists now refer to the information problem as the "Holy Grail" of origin-of-life biology. As Bernd-Olaf Küppers recently stated, "the problem of the origin of life is clearly basically equivalent to the problem of the origin of biological information." Since the 1950s, three broad types of naturalistic explanation have been proposed by scientists to explain the origin of information: chance, prebiotic natural selection, and chemical necessity.

Beyond the Reach of Chance

While many outside origin-of-life biology may still invoke chance as a causal explanation for the origin of biological information, few serious researchers 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. Even assuming extremely favorable prebiotic conditions (whether realistic or not) and theoretically maximal reaction rates, such calculations have invariably shown that the probability of obtaining functionally sequenced biomacromolecules at random is, in Ilya Prigogine's words, "vanishingly small . . . even on the scale of . . . billions of years." As A. Graham Cairns-Smith wrote:

> Blind chance . . . is very limited. [Blind chance can produce] low levels of cooperation . . . exceedingly easily (the equivalent of letters and small words), but it becomes very quickly incompetent as the amount of organization increases. Very soon indeed long waiting periods and massive material resources become irrelevant.[7]

Consider the probabilistic hurdles that must be overcome to construct even one short protein molecule of about 100 amino acids in length. 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. The probability of building a chain of 100 amino acids in which all linkages involve peptide bonds is 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 occur 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 $(\frac{1}{2})^{100}$ or again roughly 1 chance in 10^{30}.

Third and most important of all, functioning proteins must have amino acids that link up in a specific sequential arrangement, just

like the letters in a meaningful sentence. Because there are 20 biologically occurring amino acids, the probability of getting a specific amino acid at a given site is 1/20. Even if we assume that some sites along the chain will tolerate several amino acids (using the variances determined by biochemist Robert Sauer of MIT), we find that the probability of achieving a functional sequence of amino acids in several functioning proteins at random is still "vanishingly small," roughly 1 chance in 10^{65}—an astronomically large number—for a protein only one hundred amino acids in length. (Actually the probability is even lower because there are many nonproteinous amino acids in nature that we have not accounted for in this calculation.)

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 (no more than 1 chance in 10^{125}), even given our multi-billion-year-old universe. Consider further that equally severe probabilistic difficulties attend the random assembly of functional DNA. Moreover, a minimally complex cell requires not 1, but at least 100 complex proteins (and many other biomolecular components such as DNA and RNA) all functioning in close coordination. For this reason, quantitative assessments of cellular complexity have simply reinforced an opinion that has prevailed since the mid-1960s within origin-of-life biology: chance is not an adequate explanation for the origin of biological complexity and specificity.

Natural Selection a Dead End

At nearly the same time that many researchers became disenchanted with chance explanations, theories of prebiotic natural selection also fell out of favor. Such theories allegedly overcame the difficulties of pure chance by providing a mechanism by which complexity-increasing events in the cell might be preserved and selected. Yet these theories shared many of the difficulties that afflict purely chance-based theories.

Natural selection presupposes a preexisting mechanism of self-replication. Yet, self-replication in all extant cells depends upon functional (and, therefore, to a high degree sequence-specific) proteins and nucleic acids. The origin of these molecules is precisely what

Oparin needed to explain. Thus, many rejected his postulation of prebiotic natural selection as begging the question. As the evolutionary biologist Dobzhansky would insist, "prebiological natural selection is a contradiction in terms."

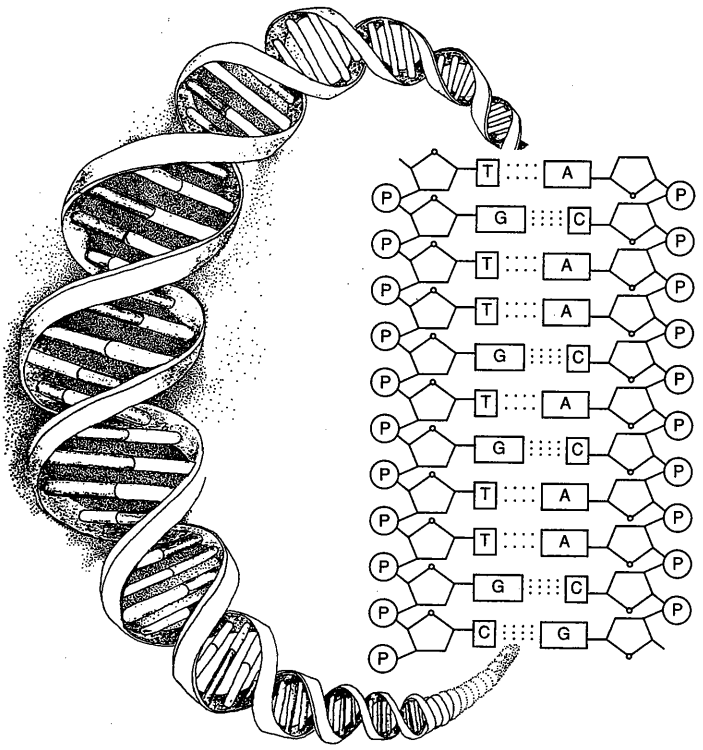
Further, natural selection can only select what chance has first produced, and chance, at least in a prebiotic setting, seems an implausible agent for producing the information present in even a single functioning protein or DNA molecule. As Christian de Duve has explained, theories of prebiotic natural selection "need information which implies they have to presuppose what is to be explained in the first place." For this reason, most scientists now dismiss appeals to prebiotic natural selection as essentially indistinguishable from appeals to chance.

Self-Organization

Because of these difficulties, many origin-of-life theorists after the mid-1960s attempted to address the problem of the origin of biological information in a completely new way. Rather than invoking prebiotic natural selection or "frozen accidents," many theorists suggested that the laws of nature and chemical attraction may themselves be responsible for the information in DNA and proteins. Some have 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. Just as electrostatic forces draw sodium (Na+) and chloride ions (Cl-) together into a highly ordered pattern within a crystal of salt (NaCl), so too might amino acids with special affinities for each other arrange themselves to form proteins. Kenyon and Steinman developed this idea in a book entitled *Biochemical Predestination*[8] in 1969.

In 1977, Prigogine and Nicolis proposed another theory of self-organization based on their observation 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, and thermal energy flowing through a heat sink will generate distinctive convection currents or "spiral wave activity."

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-



The bonding relationships between the chemical constituents of the DNA molecule. Sugars (designated by the pentagons) and phosphates (designated by the circled Ps) are chemically linked. Nucleotide bases (the As, Ts, Gs, and Cs) are bonded to the sugar-phosphate backbones. Nucleotide bases are linked by hydrogen bonds (designated by dotted double or triple lines) across the double helix. But no chemical bonds exist between the nucleotide bases along the message-bearing spine of the helix, demonstrating that physical and chemical forces are not responsible for the specific sequencing in the molecule.

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

The empirical difficulties attendant on self-organizational scenarios can be illustrated by examining a DNA molecule. The diagram above shows that 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. Yet 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.

Further, just as magnetic letters can be combined and recombined in any way to form various sequences on a metal surface, 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). The same type of chemical bond occurs between the bases and the backbone regardless of which base attaches. All four bases are acceptable; none is preferred. In other words, *differential* bonding affinities do not account for the sequencing of the bases. Because these same facts hold for RNA molecules, researchers who speculate that life began in an "RNA world" have also failed to solve the sequencing problem—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 it clear that the forces of attraction between the constituents in DNA, RNA, and protein do not explain the sequence specificity of these large information-bearing biomolecules.

Significantly, information theorists insist 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. Consider what would happen if the individual nucleotides (A, T, G, and 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. Every time cytosine (C) appeared, guanine (G) would follow. As a result, the DNA message text would be peppered with repeating sequences of As followed by Ts and Cs followed by Gs.

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—similar to what 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 repetitive and highly ordered, 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.

Bonding affinities, to the extent they exist, undercut the maximization of information. They cannot, therefore, be used to explain the origin of information. Affinities create mantras, not messages.

The tendency to confuse 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. Self-organizational theorists explain well what doesn't need explaining. What needs explaining is not the origin of order (whether in the form of crystals, swirling tornadoes, or the eyes of hurricanes), but the origin of *information*—the highly improbable, aperiodic, and yet specified sequences that make biological function possible.

Information, Design, and Intelligence

To see 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. Systems that are characterized by both specificity and complexity (what information theorists call specified complexity) have information content. Since such systems have the qualitative feature of aperiodicity or complexity, 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, 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 or functional lines of code in computer software. Yet the information contained in an English sentence or computer software does not derive from the chemistry of the ink or the physics of magnetism, but from a source extrinsic to physics and chemistry altogether. Indeed, in both cases, 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 biochemical messages.

If the properties of matter (i.e., the medium) do not suffice to explain the origin of information, what does? Our experience with information-intensive systems (especially codes and languages) indicates that such systems always come from an intelligent source—i.e., from mental or personal agents, not chance or material necessity.

This generalization about the cause of information has, ironically, received confirmation from origin-of-life research itself. During the last forty years, every naturalistic model proposed has failed to explain the origin of information—the great stumbling block for materialistic scenarios. Thus, mind or intelligence or what philosophers call "agent causation" now stands as the only cause known to be capable of creating an information-rich system, including the coding regions of DNA, functional proteins, and the cell as a whole.

Because mind or intelligent design is a necessary cause of an informative system, one can detect the past action of an intelligent cause from the presence of an information-intensive effect, even if the cause itself cannot be directly observed. Since information requires an intelligent source, the flowers spelling "Welcome to Victoria" in the gardens of Victoria Harbor in Canada lead visitors to infer the activity of intelligent agents even if they did not see the flowers planted and arranged.

Scientists in many fields now recognize the connection between intelligence and information and make inferences accordingly. Archaeologists assume a mind produced the inscriptions on the Rosetta Stone. SETI's search for extraterrestrial intelligence presupposes that the presence of information imbedded in electromagnetic signals from space would indicate an intelligent source. As yet, radio astronomers have not found information-bearing signals coming from space. But molecular biologists, looking closer to home,

have discovered information in the cell. Consequently, DNA justifies making what probability theorist William Dembski calls "the design inference."

God of the Gaps?

Of course, many scientists have argued that to infer design gives up on science. They say that inferring design constitutes an argument from scientific ignorance—a "God of the gaps" fallacy. Since science doesn't yet know how biological information could have arisen, design theorists invoke a mysterious notion—intelligent design—to fill a gap in scientific knowledge.

Yet design theorists do not infer design just because natural processes cannot explain the origin of biological systems, but because these systems manifest the distinctive hallmarks of intelligently designed systems—that is, they possess features that in any other realm of experience would trigger the recognition of an intelligent cause. For example, Michael Behe has inferred design not only because the gradualistic mechanism of natural selection cannot produce irreducibly complex systems, but also because in our experience irreducible complexity is a feature of systems known to have been intelligently designed. That is, whenever we see systems that have the feature of irreducible complexity and we know the causal story about how such systems originated, invariably intelligent design played a role in the origin of such systems. Thus, Behe infers intelligent design as the best explanation for the origin of irreducible complexity in cellular molecular motors, for example, based upon what we *know*, not what we do not know, about the causal powers of nature and intelligent agents, respectively.

Similarly, the specified complexity or information content of DNA and proteins implicates a prior intelligent cause, because specified complexity and high information content constitute a distinctive hallmark (or signature) of intelligence. Indeed, in all cases where we know the causal origin of high information content or specified complexity, experience has shown that intelligent design played a causal role. Thus, when we encounter such information in the biomacromolecules necessary to life, we may infer—based upon our *knowledge* of established cause-and-effect relationships—that an

intelligent cause operated in the past to produce the information necessary for the origin of life.

Design theorists infer a prior intelligent cause based upon present knowledge of cause-and-effect relationships. Inferences to design thus employ the standard uniformitarian method of reasoning used in all historical sciences, many of which routinely detect intelligent causes. We would not say, for example, that an archeologist had committed a "scribe of the gaps" fallacy simply because he inferred that an intelligent agent had produced an ancient hieroglyphic inscription. Instead, we recognize that the archeologist has made an inference based upon the *presence* of a feature (namely, high information content) that invariably implicates an intelligent cause, not (solely) upon the *absence* of evidence for a suitably efficacious natural cause.

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 presence of a prior intelligence even if we did not observe the action of the particular agent responsible. Since DNA displays an effect (namely, information content) that in our experience only agents can produce, intelligent design (and not apparent design) stands as the best explanation for the information content in DNA.