

Intelligent Design Theory as a Tool for Analyzing Biochemical Systems

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WE ARE PRIVILEGED TO LIVE IN A TIME OF UNPRECEDENTED PROGRESS in biology. Plants and animals have been studied since antiquity, yet for the great majority of that time naturalists were completely in the dark about the way living things actually work. Only with the discovery of the molecular basis of life has science been able to address questions about life's basic mechanisms. Science has learned over the past four decades that the many cellular tasks required to sustain life are carried out by machines—literally, molecular machines. In *Darwin's Black Box* I discussed several such machines. I showed that they are irreducibly complex—that is, they require a number of closely matched components before they can function—and thus are mammoth barriers to gradualistic, Darwinian evolution. I further argued that such irreducibly complex systems are best interpreted as the result of deliberate intelligent design.

In this chapter I want to proceed from that point to consider the likelihood of design for other biochemical systems. That is, given that some cellular systems were in fact designed, what can be said about other biochemical systems in which design is less obvious? The focus will be on how a theory of intelligent design can illuminate the structure of biochemical systems and how it can usefully direct future research.

from *Darwin's Black Box*. Let me begin by discussing the reasoning by which I reach a conclusion of design, as well as two examples of biochemical design: the bacterial flagellum and intracellular transport.

Conceptual Tools

I want to start by discussing two concepts that I hope will not be controversial. They are the concept of irreducible complexity and that of minimal function. Both irreducible complexity and minimal function will be important in trying to distinguish what features of a biochemical system may have been designed and which may have arisen solely by natural mechanisms.

The concept of minimal function provides a way to recognize that a device in the real world has to work at a certain minimal level of efficiency to be of any practical use. As an example, suppose that the world's first outboard motor had been designed and was being marketed. The motor functioned smoothly—burning gasoline at a controlled rate, transmitting the force along an axle and turning the propeller. However, the propeller rotated at only one revolution per hour. This is an impressive technological feat; after all, burning gasoline in a can next to a propeller does not turn it at all. Nonetheless few people would purchase such a machine, because it fails to perform at a level suitable for its purpose.

Our second concept is irreducible complexity. An irreducibly complex system is one that requires several closely matched parts in order to function and where removal of one of the components effectively causes the system to cease functioning. A good example of such a system is a mechanical mousetrap. Mousetraps that you can buy in a grocery store consist of a number of distinguishable parts. There are a flat wooden platform to act as a base; a metal hammer, which pins the mouse against the base when the hammer is tripped, crushing the mouse; a spring with extended ends to press against the platform and the hammer when the trap is charged; a sensitive catch that releases when slight pressure is applied, and a metal bar that connects to the catch and holds the hammer back when the trap is charged. There are also assorted staples to hold the system together.

The mousetrap depends critically on the presence of all five of its components; if there were no spring, the mouse would not be pinned to the base; if there were no platform, the other pieces would fall apart; and so on. The function of the mousetrap requires all the pieces: you cannot catch a few mice with just a platform, add a spring and catch a few more mice, add a holding bar and catch a few more. All of the components have to be in place before any mice are caught. Thus the mousetrap is irreducibly complex. Furthermore, the components of the mousetrap are closely matched to each other: if the holding bar were too short, it would not reach the catch, and

the system would be utterly useless. If the ends of the spring did not wrap around in the precise manner they do, the trap could not be loaded. If the catch were too big or too rounded, it would not be tripped when a mouse grabbed a piece of cheese (probably half of the time I set a trap the mouse steals the cheese without tripping it).

Let me interject a note of caution: some systems require several pieces but not ones that need to be closely matched. For example, suppose you were walking in the woods and came across an old log where the wind had blown a tree branch onto it, and the branch was perpendicular to the log. Here you have an irreducibly complex system—a lever and fulcrum. If there were a boulder nearby, you possibly could use the lever and fulcrum to move it. So some systems require several parts but not closely matched ones.

Closely matched, irreducibly complex systems are huge stumbling blocks for Darwinian evolution because they cannot be put together directly by improving a given function over many steps, as Darwinian gradualism would have it, where the function works by the same mechanism as the completed structure. The only possible recourse to a gradualist is to speculate that an irreducibly complex system might have come together through an indirect route—perhaps the mousetrap started out as a washing board, was changed into an orange crate, and somehow ended up as a mousetrap. One can never completely rule out such an indirect scenario, which is tantamount to trying to prove a negative. However, the more complex a system, the more difficult it becomes to envision such indirect scenarios, and the more examples of irreducible complexity we meet, the less and less persuasive such indirect scenarios become. It cannot be that everything in life started out as something else.

Closely matched, irreducibly complex systems not only are tall problems for Darwinism but also are the hallmarks of intelligent design. What is design? In my definition, design is simply the purposeful arrangement of parts. You cannot tell just by looking at something that it has not been designed—anything might have been designed. The coats on a rack in a restaurant may have been arranged just so by the owner before you came in. The trash and tin cans along the edge of a highway may have been placed by an artist trying to make an environmental statement. Apparently chance meetings between people might be the result of a grand design (conspiracy theorists thrive on postulating such designs). On the campus of my university there are sculptures which, if I saw them lying beside the road, I would guess were the result of chance blows to a piece of scrap metal, but they were designed.

The upshot of this conclusion—that anything could have been purposely arranged—is that we cannot know that something has not been designed.

The scientific problem then becomes, How do we confidently detect design? When is it reasonable to conclude, in the absence of firsthand knowledge or eyewitness accounts, that something has been designed?

For discrete physical systems—if there is not a gradual route to their production—design is evident when a number of separate, interacting components are ordered in such a way as to accomplish a function beyond the individual components. The greater the specificity of the interacting components required to produce the function, the greater is our confidence in the conclusion of design. A mousetrap is an obvious result of design. Any person, even someone who had not seen such a device before, would quickly conclude that a mousetrap was designed because of the way its parts interact to perform a function.

Irreducible Complexity in Biochemistry

Let us now switch our focus from the everyday world to the biochemical world of the cell. To understand how life works you have to descend from the level of the whole organism to the level of the cell and subcellular systems. Biochemistry is the basis of life—it is the study of the molecules that make up living tissues and cells. Within the past four decades science has advanced to the point where it has been able to isolate many of the components of the cell and understand in some detail how they work. With the background discussion in place we must now ask whether any biochemical systems are irreducibly complex. It turns out that many are. I will describe just two such systems. For more examples consult *Darwin's Black Box* or any undergraduate biochemistry textbook.

The first system I will consider is the familiar bacterial flagellum. The flagellum is an organelle that allows many bacteria to swim. It was shown about twenty-five years ago that, remarkably, the flagellum is a propeller that is rotated by a motor. The mechanical requirements of such a system are quite complex. Instead of describing this fantastic apparatus in my own words, I will quote a recent review of the flagellum written by Lucy Shapiro (1995) of the Department of Developmental Biology at Stanford University.

A rotating propeller at the cell surface, driven by a transmembrane proton gradient, provides many bacteria with the ability to move and thus respond to environmental signals. To acquire this powerful capability, the bacterial cell is faced with the challenge of building a tiny rotary engine at the base of the propeller. Although the motor is anchored in the cytoplasmic membrane, a significant portion of the entire mechanism extends into the cytoplasm and, at the other end, out into the environment. At least 20 individual proteins are used as parts for this complex structure and another 30 are used for its construction, function, and maintenance (525).

To carry out the feat of coordinating the ordered expression of about 50 genes, delivering the protein products of these genes to the construction site, and moving the correct parts to the upper floors while adhering to the design specifications with a high degree of accuracy, the cell requires impressive organizational skills. The construction scheme must deal with fundamental questions in structural and developmental biology: How does the cell measure the length of a component made up of polymerized subunits? When the appropriate length is reached, how does the cell turn off the assembly of one part of the structure and switch on the assembly of the next part? Are there checkpoint mechanisms that determine whether one flagellum component has been completed and that it is okay to start construction of the next component? How is this information conveyed to the expression of the flagellar genes? Because the assembly of the flagellum proceeds in large measure by the passage of structural proteins through a central channel to its distal tip, what is the export mechanism and how does it choose the proteins that are allowed entry into the pipeline?

As you can see from Shapiro's review, many discrete parts have to be in place to produce a functioning flagellum. Clearly the necessary pieces of the flagellum itself have to be in place. If there is no whip protein, the bacterium cannot swim. If there is no rotary motor, then the flagellum lies in rigor mortis. If there is no base, then the flagellum has nothing to hang on to when it tries to turn. Furthermore, the parts themselves are multifunctional. The rotary motor uses a flow of acid to power it, like a hydroelectric dam uses a flow of water to power its turbines. Several models have been proposed to explain how the motor works; none of them are simple.

Thus the flagellum itself is irreducibly complex. However, a simple examination of the flagellum shows only a portion of the components required for a functioning organelle. As Shapiro's review made clear, the assembly of this bulky machine is a significant logistical task. We must remember that the cell is essentially a completely automated factory, so all assembly has to be done by highly sophisticated robots, not by magic.

My second example of an irreducibly complex biochemical system is the one that targets proteins for delivery to subcellular compartments (Alberts et al. 1994, 551-650). The eukaryotic cell contains a number of membrane-enclosed areas that perform specialized tasks. These include lysosomes for digestion, Golgi vesicles for export, and others. Unfortunately the machinery for making proteins is outside these compartments, so how do the proteins that perform tasks in subcellular compartments find their way to their destination? It turns out that proteins that will wind up in subcellular compartments contain a special amino acid sequence near the beginning

called a signal sequence. As the proteins are being synthesized, a complex molecular assemblage called the signal recognition particle, or SRP, binds to the signal sequence. This causes synthesis of the protein to halt temporarily. During the pause in protein synthesis the SRP binds the transmembrane SRP receptor, which causes protein synthesis to resume and which allows passage of the protein into the interior of the endoplasmic reticulum (ER). As the protein passes into the ER the signal sequence is cut off.

For many proteins the ER is just a waystation on their travels to their final destinations. Proteins that will end up in a lysosome are enzymatically tagged with a carbohydrate residue called mannose-6-phosphate while still in the ER. An area of the ER membrane then begins to concentrate several proteins; one protein, clathrin, forms a sort of geodesic dome called a coated vesicle, which buds off from the ER. In the dome there is also a receptor protein that binds to both the clathrin and to the mannose-6-phosphate group of the protein that is being transported. The coated vesicle then leaves the ER, travels through the cytoplasm and binds to the lysosome through another specific receptor protein. Finally, in a maneuver involving several more proteins, the vesicle fuses with the lysosome, and the protein is at its destination.

During its travels our protein interacted with dozens of macromolecules to achieve one purpose: its arrival in the lysosome. Virtually all components of the transport system are necessary for the system to operate, and therefore the system is irreducible. The consequences of even a single gap in the transport chain can be seen in the hereditary defect known as I-cell disease. It results from a deficiency of the enzyme that places the mannose-6-phosphate on proteins to be targeted to the lysosomes. I-cell disease is characterized by progressive retardation, skeletal deformities and early death.

The Professional Literature

What has science had to say so far about these stunningly complex biochemical systems? A good place to look for an answer is the *Journal of Molecular Evolution*. *JME* was begun specifically to deal with the topic of how evolution occurs on the molecular level. It has high scientific standards and is edited by prominent figures in the field. In the February 1996 issue of *JME* there were published fourteen articles; of these, all fourteen were concerned simply with the comparison of protein or DNA sequences. A sequence comparison is an amino acid-by-amino acid comparison of two different proteins or a nucleotide-by-nucleotide comparison of two different pieces of DNA, noting the positions at which they are identical or similar and the places where they are not. Although it is useful for determining possible lines of descent, which is an interesting question in its own right, comparing

sequences cannot show how a complex biochemical system achieved its function—the question that most concerns us. By way of analogy, the instruction manuals for two different models of computer put out by the same company might have many identical words, sentences and even paragraphs, suggesting a common ancestry (perhaps the same author wrote both manuals), but comparing the sequences of letters in the instruction manual will never tell us if a computer can be produced step by step starting from a typewriter.

None of the papers discussed detailed models for intermediates in the development of complex biomolecular structures. In the past ten years *JME* has published more than a thousand papers. Of these, about one hundred discussed the chemical synthesis of molecules thought to be necessary for the origin of life, about fifty proposed mathematical models to improve sequence analysis, and about eight hundred were analyses of sequence. There were zero papers discussing detailed models for intermediates in the development of complex biomolecular structures. This is not a peculiarity of *JME*. No papers are to be found that discuss detailed models for intermediates in the development of complex biomolecular structures, whether in the *Proceedings of the National Academy of Science*, *Nature*, *Science*, the *Journal of Molecular Biology* or, to my knowledge, any science journal.

The idea of Darwinian molecular evolution is not based on science. The is no publication in the scientific literature—in journals or books—th describes how molecular evolution of any real, complex, biochemical system either did occur or even might have occurred. There are assertions that such evolution occurred, but absolutely none are supported by pertinent experiments or calculations. Since there is no authority on which to base claims knowledge, it can truly be said that the assertion of Darwinian molecular evolution is merely bluster.

Foundation

These are the facts that I offer to reach a conclusion of intelligent design: the irreducible complexity of the bacterial flagellum and the intermolecular transport system, as well as the utter sterility of Darwinian theory in explaining their origins. Although many scientists entertain hopes about the future prospects of explaining these biochemical systems within a Darwinian framework, at the very least I have established that preferring a theory of intelligent design to explain those systems is not unreasonable. If in the future other researchers demonstrate experimentally that the flagellum or vesicular transport can arise by a nondirected process, then I shall admit intelligent design theory is wrong. But I am not overly worried about that prospect, as in the meantime I do not want to sit on my hands waiting for laboratories

make good on their promissory notes.

I shall therefore use the conclusion of intelligent design as a jumping-off point. Specifically I want to explore the following question: Given that some biochemical systems were designed by an intelligent agent, and given the tools by which we came to that conclusion, how do we analyze other biochemical systems that may be more complicated and less discrete than the ones we have so far discussed? To give an idea of the general direction that I think intelligent design theory should head in biochemistry, I would like to describe the process by which DNA is replicated in modern cells and suggest some questions and approaches that a design theorist could explore. But first let me give some background information about the structure of DNA.

Nucleic Acid Structure

Nucleic acids are polymers of a small number of building blocks, called nucleotides (Voet and Voet 1995, 849-69). A nucleotide itself has several parts. The first part is a carbohydrate, either ribose (in RNA) or deoxyribose (in DNA). To deoxyribose is attached one of four bases, either adenine (A), cytosine (C), guanine (G) or thymine (T). Attached to a different part of the carbohydrate ring (to the 5'-OH group, which is pronounced the "five-prime hydroxyl" group) is a phosphate group. The sugar-phosphate portion of a nucleotide is analogous to the backbone portion of an amino acid, and the base is analogous to an amino acid side chain. It is only in its base that one nucleotide differs from another.

Two nucleotides can be joined chemically by reacting the phosphate of one nucleotide with the 3'-OH group of the carbohydrate portion of the second nucleotide. This still leaves a free phosphate group on one end and a free 3'-OH group on the other end, which can be further reacted with other nucleotides. Repetition of this process can generate very long polynucleotides. One single molecule of DNA can range from several thousand to about a billion nucleotides. The sequence of a polynucleotide is conventionally written starting from the 5' end to the 3' end.

Cellular DNA is found as an association of two separate strands (the famous double helix) that are strongly held together by an electrostatic force called hydrogen bonding. If A and T are correctly oriented they can form two hydrogen bonds with each other, and G can form three hydrogen bonds with C. In cells, wherever there is a G in one strand of DNA there is a C in the second strand and vice versa; and wherever there is an A in one strand there is a T in the second strand and vice versa. Thus the two strands are called complementary to each other. To be correctly oriented for hydrogen bonding the two strands must be pointed in different directions, with one

running 5' to 3' from left to right and the other going 5' to 3' from right to left.

The amount of DNA in a cell varies roughly with the complexity of the organism. Bacteria have about several million nucleotides of DNA. The amount of eukaryotic DNA ranges from a low of several tens of millions of nucleotides in fungi to a high of several hundred billion in some flowering plants. Humans come in at around three billion nucleotides.

Analysis of Replication

There comes a time in the life of every cell when it turns to thoughts of division. One major consideration in cell division is ensuring that the genetic information be copied and handed down uncorrupted; a great deal of effort is invested in that task (Voet and Voet 1995, 1020-45).

DNA replication is an enormously complex process with many different components that interact to ensure the faithful passing down of genetic information to the next generation. A large number of parts have to work together to that end. In the absence of one or more of a number of the components, DNA replication is either halted completely or significantly compromised, and the cell either dies or becomes quite sick.

However, DNA replication is not irreducibly complex in its entirety; in the same way that the biochemical systems I spoke of previously (the flagellum and intracellular transport) are irreducibly complex, I think those systems many components had to work together to produce a single function. In DNA replication, however, only one of the components actually performs the task of making a new DNA molecule—the polymerase enzyme. Furthermore, many of the additional components of the replication machinery form conceptually discrete subassemblies with conceptually discrete functions. The task of intelligent design theory in analyzing a system like DNA replication is to tease apart the components, determine the extent of their integration, and come to a tentative conclusion about what parts of the system are irreducibly complex, and what level of performance for each part is needed for minimal function. Whether discrete subassemblies have any useful function by themselves or whether they are necessarily parts of larger systems. Additional intelligent design theory wants to probe the plasticity of designed systems can closely related systems have been produced by natural processes such as drift or natural selection, or is there reason to believe that they also were designed?

In the remainder of this chapter I am going to point out what strike me as interesting aspects of DNA replication for future investigation, as well as suggest a few questions and some possible lines of research.

DNA Polymerase I

The simplest system that can replicate DNA in a test tube consists of a single enzyme called a DNA polymerase. The polymerase that Arthur Kornberg isolated in the 1950s (known as PolI) was able to take nearly any DNA that he threw into the test tube and, when supplied with activated nucleotides, replicate the DNA (Kornberg and Baker 1992, 101-5). However, there were problems with PolI: the DNA that it made contained some unusual features. When viewed by electron microscopy the product of DNA synthesis was frequently branched; it was not the linear molecule that Kornberg and others started with. After some work it was determined that the branching was due to the polymerase copying one strand and displacing the other. Occasionally during the displacement the protein would hop over to the displaced strand and begin to use that as a template instead of the strand it started with. Thus, although replication could proceed, the product of replication was not the same as the starting material—sequences of DNA got scrambled in the process.

The question that arises to a design theorist is whether the first cell might have contained only one simple polymerase. The considerations are that the polymerase would have been prone to just the errors that Kornberg came across when studying DNA polymerase I in isolation. Such a primitive polymerase would not be able to copy long DNA faithfully. It may, however, have copied shorter DNA reasonably well. For example, Kornberg showed that PolI could replicate the circular, single-stranded DNA bacteriophage ϕ X174 and produce circular DNA that was capable of infecting bacterial cells. (I should add that not all DNA polymerases can do this. For example, PolIII, which does the bulk of the replicating job in bacterial cells, has never been seen to replicate any DNA to completion without the aid of other proteins. It always gets stuck. Apparently some common DNA structures cause the enzyme to stall irrecoverably.) This shows that a simple polymerase can produce biologically active DNA, but the DNA must be rather short. The bacteriophage ϕ X174 can code for only ten genes. The simplest free-living organism we know of, the mycoplasma, contains hundreds of genes. To be certain that a simple polymerase is enough to replicate the genome of a self-sufficient cell, we must determine the probable length of the simplest cell's DNA—not an easy task, but perhaps doable with some effort.

A second consideration is that DNA polymerase I is not a simple enzyme. Rather, in Kornberg's phrase, it is "three enzymes in one." Besides the polymerizing activity, PolI can also degrade DNA in two different ways: it can degrade the DNA starting from a 3'-end and working back toward the 5'-end; and it can degrade starting at the 5'-end and working back toward the 3'-end. These different activities (polymerizing, 5', and 3'-nuclease) are done by

three different, discrete regions of the molecule. It is kind of like having a key chain that has a key, a lighter and a pocket knife attached.

The 3' 5' exonuclease activity plays a critical role in replication: it allows the enzyme to proofread the new DNA and cut out any mistakes it has made. Although the polymerase reads the sequence of the old DNA to produce new DNA, it turns out that simple base pairing allows about one mistake per thousand base pairs copied. Proofreading reduces errors to about one in a million base pairs. The question for design theorists is whether a proofreading exonuclease had to be present in the very first cell. That is, could the first cell, with its required complement of genes coded for by DNA, have successfully reproduced for a significant number of generations without proofreading function? In order to answer this question again the minimum number of genes in the first cell and the minimum length of DNA have to be known. Then it can be calculated how fast the information would be degraded in the absence of proofreading. Bacterial mutants that are missing PolI can grow in minimal media but not rich media. In other words, they can grow slowly but not quickly. Evidently the strain put on the system of reproducing DNA rapidly exceeds the ability of the mutant to correct or repair new DNA. Variations on this experimental system may allow intelligent design theorists to probe these questions.

The third activity of DNA polymerase I, the 5' 3' exonuclease activity only indirectly involved in DNA replication. It is responsible for removing the short pieces of RNA that the cell uses to prime replication, allowing the polymerase function to fill in the gaps. This is clearly an advanced function and would not have been expected to be part of a simple polymerase (if a system much simpler than present cells is possible.) However, a question for intelligent design theorists is whether a simpler system, one with a simple polymerase, could switch over to a more complex system. That is, if a primitive cell was using just the polymerase activity (and maybe the proofreading activity) of PolI to replicate its DNA, is it even possible or likely that such a polymerase could be switched in midstream, so to speak, to an enzyme that degrades RNA and fills in gaps? A possible experimental approach to this question is to take mutants in which the 5' 3' activity has been deleted (such mutants are viable) and determine if the activity can be reestablished. (There may be difficulties with this approach, but it is a place to start.)

Clamp Protein and Loader

Let us now look at another feature of the modern DNA replication machinery (Marians 1992). Most enzymes work by randomly colliding with the substrate (the chemical that they are going to transform), catalyzing a reaction and dissociating from the product. If that were the case with DN

polymerase, then it would bind to DNA, add a nucleotide to the new chain that was being made and then fall off the chain. In order to put the next nucleotide onto the growing chain, the enzyme would again have to find its way back to the growing end, bind, bind a nucleotide and catalyze the addition. This same cycle would have to repeat itself a very large number of times to complete the new DNA chain. Modern polymerases do not do this, however. They catalyze the addition of a nucleotide but do not then fall off the DNA. Rather they stay bound to it until the next nucleotide comes in, and then they catalyze its addition to the chain, and they again stay bound. The ability of an enzyme to stay stuck to the DNA chain for multiple rounds of catalysis is called "processivity." The processivity of different modern DNA polymerases ranges from about 10 to about 100. That is, they stay stuck for an average of 10-100 nucleotide additions, and then they fall off and have to find their way back again. If this happened in the cell it would slow replication enormously. In the cell polymerases stay on the DNA until their job is completed, which might be only after millions of nucleotides have been joined. Their processivity in the cell is at least a hundred thousand times greater than it is in a test tube.

It turns out that in all cells there are things called clamp proteins. It was shown a few years ago that several copies of clamp protein join together to form a doughnut shape, where the hole in the middle is big enough to accommodate DNA. When the clamp is on DNA, it binds to the DNA polymerase and keeps it held bound until it reaches the end of its polymerizing job. However, clamp protein alone cannot bind to DNA. It has to be loaded onto the DNA by several other proteins that are part of the replication complex. The sequence goes this way: DNA polymerase III binds to DNA, the other proteins bind to DNA polymerase, and clamp protein binds to the other proteins. In a process that requires the expenditure of energy, the other proteins then place the clamp onto the DNA where it stabilizes the DNA, increasing its processivity to very high levels.

Such a system raises a number of questions for the design theorist. The first question is whether or not the clamp/clamp-loader system is irreducibly complex. This is not as straightforward a question as for the bacterial flagellum or intracellular transport. First of all, we have to define a function for the subsystem. Is the function to load a clamp, or to increase polymerase processivity, or to simply bind DNA? Depending on what we think is the function, we might decide that the system is or is not irreducibly complex. The next question is what are all the parts of the system. The roles of several of the proteins in the clamp-loader system are not known, and the mechanism of the process is still unclear. Questions about this will have to be informed by continuing investigation of the workings of the replication

apparatus. Even when these questions are answered, however, many others will remain. For example, even if the system is somehow not irreducibly complex, could it nonetheless have developed incrementally? If the clamp first acquired the ability to bind to DNA, would it have been disallowed because it would be a roadblock to the polymerase? If the loading protein first attached themselves to the polymerase, why would they have done so? Would they have interfered with its function of making DNA? If the clamp loader were first attached to the polymerase, and then a clamp protein acquired the ability to bind to the loader, and then the system first began loading the clamp, would the dramatic increase in processivity have been a help or a hindrance? If a cell were somehow used to making DNA slowly would the ability to make it rapidly tax the control systems of the cell or the metabolic pathways that provide activated nucleotides?

Topological Problems

Let us turn to another aspect of replication (Lohman and Ferrari 1994 Lohman and Bjornson 1996; Wang 1996). DNA is a double helix. In order to read the information in DNA the cell has to pull apart the two strands so that the new strand it is synthesizing can physically interact with the template DNA. Pulling apart the strands creates a number of problems. First of all the two strands like to be together—they stick to each other just as if they had tiny magnets up and down their length. In order to pull apart the DNA you have to tug on it; you have to put energy into the system. In modern cell a protein binds to a specific spot along the DNA, and the protein proceeds to open up the double strand. A second protein, called a helicase, now comes along. Helicase is like a snowplow; it is a molecular machine that plows down the middle of the double helix, pushing apart the two strands. This allows the polymerase and associated proteins to travel along behind it in ease and comfort.

There is a problem, though, with this setup. If you push apart two DNA strands they generally do not float around separately. If they are close to one another they will rapidly snap back and form a double strand again almost as soon as the helicase passes. Even if the strands are not near each other, a single strand will usually fold up and form hydrogen bonds with itself—in other words, a tangled mess. So it is not enough to push apart the two strands of DNA; there must also be a way to keep the strands apart once they have been separated.

In modern cells this job is done by single-strand binding protein, or SSB. As the helicase separates the strands of DNA, SSB coats them. The binding of SSB prevents the strands from rejoining until the new DNA strand has been made.

There is another difficulty in being a double helix. It can be illustrated with a simple example. Take two intertwined shoe laces and ask a friend to hold them together at each end. Now take a pencil, insert it between the strands near one end, and start pushing it down toward the other end. As you can see, shoestrings behind the pencil become melted, in the jargon of biochemistry. The shoestrings ahead of the pencil become more and more tangled. It becomes harder and harder to push the pencil forward.

Helicase and polymerase encounter the same problem with DNA. It does not matter whether you are talking about intertwined strings or intertwined DNA strands; the problem of tangling is the result of the topological interconnectedness of the two strands. If this problem persisted for very long in a modern cell, DNA replication would grind to a halt. However, the cell contains several enzymes, called topoisomerases, to take care of the difficulty. The way in which they do so can be illustrated with an enzyme called gyrase. Gyrase binds to DNA by wrapping the DNA around itself. It then makes a cut in both strands of the DNA, pulls them apart and allows a separate portion of the DNA to pass through the cut. It then reseals the cut and lets go of the DNA. This action decreases the number of twists in DNA.

In modern organisms helicase, SSB and gyrase all are required at the replication fork. Mutants in which any of them are missing are not viable—they die. The questions for intelligent design theory are subtle. All of these parts interact but not directly. They do not necessarily even have to touch each other. All can be isolated and work by themselves, but in doing so they do not replicate DNA. Could a primitive cell have existed without these components? Could they each have been added individually, or must they all have been added together? One possible way for replication to proceed without any of these components is to do so very slowly. In that way the replication complex might be able to rotate as it proceeded down the DNA. How slowly would it have to go to do so? How small would the replication machinery have to be to avoid the frictional problems inherent in rotating once every turn of the double helix? If a cell already had a functioning replication system, could these other components be added without upsetting it? For example, if a cell were used to replicating its DNA without SSB, would the binding of a proto-SSB to the replicating DNA be a help or a roadblock? If the cell were used to going slowly to prevent the build up of torsional forces, would the presence of a new gyrase—decreasing that force—be useful or not?

The answers are not obvious. The questions may be able to be approached experimentally, but the exact approaches will require some clever thinking.

The Replication Fork

When DNA polymerase I—the Kornberg enzyme—is thrown into a test tube

with DNA and activated nucleotides, it will replicate the DNA. However, Pol replicates just one strand at a time and displaces the other strand of the helix as it moves along. Another enzyme then has to start at the opposite end of the displaced strand and replicate it. Some viruses replicate their DNA in much the same way. The viral polymerase replicates one strand, displacing the second strand; and then the second strand is replicated later.

Modern cells, however, do not replicate DNA one strand at a time. They do both strands at once. Electron micrographs of replicating DNA show that the double strand is opened up and that the replication machinery proceeds in one direction (this is called the replication fork). But new DNA is made using both strands as templates. This creates a problem. All known polymerases must make new DNA in the 5' to 3' direction. However, since the two strands of DNA run in opposite directions, then as the replication fork proceeds in one direction it would have to, it seems, make one new strand in the 5' to 3' direction, but the opposite new strand must be made in the 3' to 5' direction, contradicting what we know about polymerases.

It turns out, however, that the deduction is wrong. Both new strands are made in the 5' to 3' direction. This is done in a remarkably convoluted way. The replication fork one strand is made continuously in the 5' to 3' direction; this is called the leading strand. The other strand, called the lagging strand, is made discontinuously, in relatively small pieces called Okazaki fragments. A piece is made beginning at the replication fork and proceeding for a while backward away from the fork. As the replication fork proceeds further away the polymerase making the lagging strand hops back to the new location again makes a new DNA chain proceeding away from the fork and continues until it bumps into the beginning of the last Okazaki fragment made.

When the end of the newly made fragment bumps into the beginning of the last-made fragment, several jobs have to be done to hook the two fragments together. The first job is that the primer that begins every Okazaki fragment and is made of RNA (not DNA) must be removed. This is the job of Pol I 5' to 3' nuclease activity. The gap then has to be filled in, which Pol I does with its polymerizing activity. Finally the two ends of the fragment have to be joined together; this is the job of an enzyme called DNA ligase.

After the completion of one Okazaki fragment, the equipment has to be recycled to the beginning of the replication fork again. Pol III has to be released, the clamp has to let go, and a new clamp has to be loaded at the beginning of the next fragment.

Clearly the formation and control of the replication fork is an enormous complex process. An intelligent design theorist would have many questions about the origin of this system. Supposing that a simple polymerase like Pol I replicating each strand separately was the starting point, is it feasible that

replication fork could develop step by step? The PolIII activity is present as a dimer at the modern replication fork; suppose a primitive polymerase were duplicated and somehow started to replicate the second strand in the opposite direction while remaining attached to the first strand—would that have been an improvement? Or would the change slow down replication and clog things with short fragments that could not be used?

Associated Problems and Viruses

The problems I have brought up about DNA replication so far are only questions about the development of direct pieces of the replication machine itself—the parts that do the primary job. But many other factors have to be integrated into this picture. For example, replication of DNA has to be coordinated with cell division. If the two were unconnected, then many copies of genomic DNA might be present in a cell as it started to divide, which might make the mechanical process of division very difficult or downright impossible. If cell division were more rapid than DNA replication, the genetic information might be divided and lost. At the least the cell would be wasting resources making other cell structures that, when they were divided off from the parent cell, would carry no genetic instructions to continue. A second example of problems of control is seen in the effect in modern cells of an unbalanced nucleotide pool. If the four nucleotides that are the activated precursors to cellular DNA are not kept in a fairly even ratio with each other, many more mutations are introduced as the DNA is copied, launching the cell on the pathway to self-destruction.

If I may be permitted a homely analogy, throughout this chapter we have been wondering how a car could be put together step by step. We have concentrated mostly on getting the mechanical parts together and have not concerned ourselves with whether the oil was the right grade or whether the gasoline had been sufficiently refined. Nonetheless these other parts are also critical and require an intelligent design theorist's attention.

The final point I wish to mention about DNA replication brings up not only scientific problems that confront design theorists but also philosophical problems. Many viruses take over the cell's replication machinery when they invade and turn it to replicating viral DNA exclusively. However, viral replication frequently differs in a number of details from cellular replication. Let us look at just one of them.

Cellular DNA replication has to be primed by the prying apart of the DNA strands and the synthesis of a short piece of RNA, to which DNA is then attached. DNA synthesis cannot be started *de novo*. In adenoviruses (which cause cancer in certain animals), however, a piece of RNA does not have to be made, but DNA synthesis still must be primed. The priming is done by a

protein that is covalently attached to each 5' end of each viral strand (Kornberg and Baker 1992, 303-5). To the protein is covalently attached a cytidine. The cytidine attached to the protein acts as the primer for the synthesis of the complementary strand.

A question that looms large over design theory is this: Could this variation on the cellular replication mechanism have come about step by step, in a Darwinian fashion? And could other viral replication mechanisms, which differ from cellular mechanisms and from that of adenovirus, have come about in a Darwinian fashion? The conundrum is this: either the replication mechanisms could have come about at random, and thus there is a fair amount of plasticity in the replication process; or else the viral replication mechanisms were designed, and the philosophical problem of evil raises its head. Understanding the development of viral replication mechanisms may have large implications not only for science but for philosophy as well.

I should emphasize that design theorists have an absolutely clear field in all the areas of DNA replication that I have discussed. No one has ever published a paper in the professional science literature that explains in detailed fashion how DNA replication in toto or any of its parts might have been produced in a Darwinian, step-by-step fashion. If you search the electronic databases for papers that have the words *evolution* and *replication* in their title, you come up completely empty. In 1992 Arthur Kornberg published the second edition of his well-known text, entitled *DNA Replication*. In the six thousand entries in the index to the text, there is only one evolution. The referenced section talks mostly about origin-of-life issues which are riddled with difficulties and in any event cannot explain the development of replication. Thus this area is wide open for analysis of intelligent design theory.

The Job of Science

Since many readers do not enjoy lengthy articles about the details of biochemical systems, why have I gone on and on about DNA replication? I think my delving into details is necessary to remind us that the job of science is a difficult one and does not come to a standstill when we discover some aspects of life were designed. The job of science is to describe, as close as it can, the way the physical world works and, to the extent it can, the way it came to be. This cannot be shrugged off. As I have tried to show, DNA replication is an enormously complex process, but it can be broken down into conceptually and physically discrete subparts. Before we investigate, it may be the case that all of the subparts were explicitly designed, or that some parts were designed and others arose by natural mechanisms, or that all the parts arose by natural mechanisms. It is the job of science to determine

Big Bang Model Refined by Fire

HUGH ROSS

NOT SINCE THE COPERNICAN REVOLUTION HAVE SCIENTISTS AND theologians battled so ferociously over an astronomical theory as they have in the twentieth century over the big bang. The only casualties in this protracted conflict have been falsehoods and fears, though some remain slow to die. The protracted fighting has not been futile. Rather it has solidified and amplified the scientist's understanding of the cosmos and the Christian's case for faith in the biblical Creator.

In *The Fingerprint of God* I gave some background on this big bang battle, especially how and why it began. Two key players were Immanuel Kant and Albert Einstein. Kant turned the philosophical and scientific tide toward belief in an infinite universe, thereby attempting to make God irrelevant. Einstein surprised himself and the world with brilliant theoretical work that was observationally supported, that contradicted an infinite universe and that demanded a beginning (and a relatively recent one at that). The scientific community, even Einstein himself, went through contortions to escape the creation event, which came to be known as the big bang. They understood its implication—the necessity of an Initiator, someone who initiated and carefully controlled the progress of that event.

discredit the religious and therefore repugnant idea of a beginning. Cosmologists proposed one bizarre hypothesis after another—some ancient, some science fiction—in attempting to counter the growing conviction that the universe had a beginning. Ironically all their efforts only highlighted the beauty and accuracy of the big bang model.

Only with difficulty did Christian theology make sense of these developments. Perhaps still staggered by the weight of Darwinism and the Scopes debacle, some Christians mistook Einstein's theory of relativity for relativism and reacted against it. Others, remembering that Kant gave lip service to God's existence, saw themselves as defending God by opposing Einstein. Still others, thinking a creation date of several billion years back would certainly support atheistic evolution, resisted the big bang to defend biblical truth.

In *The Creator and the Cosmos* and *Creation and Time I* treated the challenges to the big bang model stemming respectively from science and theology. *The Creator and the Cosmos* marshaled the scientific evidence supporting the big bang, evidence augmented by the search for alternate models. It also described how this evidence revealed divine design more graphically and irrefutably than anyone might have imagined. In *Creation and Time I* showed how a reexamination of the biblical text, especially the Hebrew manuscripts and the writings of early church scholars, more clearly and consistently support the big bang model—namely, an old-universe, old-earth interpretation of the text—than they do any recent-creation scenario (i.e., one in which the universe is only a few thousand years old).

My latest book, *Beyond the Cosmos*, addresses the fear that advancing scientific knowledge may contradict biblical truths and undercut the Christian understanding of God as Creator-Redeemer. Thus in *Beyond the Cosmos* I show how recent developments in string theory support Christianity's foundational, and too often divisive, doctrines. Understanding string theory also gives us a renewed and enlarged sense of awe for the indescribably magnificent capacities of the Creator.

As the empirical support for big bang cosmology mounts and as the model becomes increasingly well understood, signs of a personal, transcendent, loving Creator become increasingly evident. Despite the skepticism of our age, we find the Creator revealed in clear and exciting ways. Many new discoveries are continually enlarging and enhancing the list of features that signal design behind the universe, our solar system, the earth and living things. The aim of this chapter is to present some of these key features that signal design. I begin with a brief review of how astronomy and astronomers work.

Astronomy's Unique Perspective

Unlike other scientific disciplines, astronomy directly observes and measures the past. Because light travels at a fixed, finite velocity, we see and measure the conditions of astronomical objects as they were when the objects began radiating light toward us. When we look at the sun, for example, we see its conditions eight minutes ago, when the visible light and other radiation we now detect left the sun. When we map the Orion Nebula, we see it as it was 1,200 years ago. When we examine the center of our galaxy, we discover what was happening there 30,000 years ago. When we study the core of the Andromeda Galaxy, we observe what took place 2 million years ago.

Astronomers witness the past. To see how the creation was taking shape a certain number of years ago, we need only focus our instruments on objects the appropriate distance away. With recent technological advances, we can actually see all the way back to a split second after the cosmic explosion with which all the universe's time, space, matter and energy began.

In 1992 the Cosmic Background Explorer (COBE) satellite brought us the first image of the moment when light separated from darkness, an event that occurred when the cosmos was just one ten-thousandth of a percent of its current age. Heralded by Stephen Hawking as "the discovery of the century, if not of all time" (quoted in Hawkes 1992, 1), this finding made front-page headlines around the world for days. It was widely acknowledged by scientists as the strongest proof yet for a hot big bang and thus for the existence of a transcendent Initiator (Ross 1995a, 19-20).

The COBE image made such a splash because it solved one of the puzzling anomalies of the big bang model—the mystery of the clumpy, rather than smooth, distribution of matter throughout the universe. COBE research as well as subsequent research (Ross 1995a, 31-47; 1995b, 5; 1996c, 3-4) indicates that exotic matter (i.e., matter that does not strongly interact with radiation) is about four to eight times more abundant in the universe than ordinary matter. This constitution of matter explains why it would clump and gives credence to the big bang model. Most recently astronomers have identified at least three distinct kinds of exotic matter.

A later, less widely publicized set of COBE measurements provided even more direct and dramatic proof of the hot big bang (creation) model. These measurements showed that the cosmic background radiation (the radiation remaining from the creation event) fits the spectral profile of a perfect radiator to better than 0.03 percent precision over the entire range of wavelengths. In other words, the universe is a half-billion times more entropic (i.e., more efficient in radiating heat and light) than a burning candle. Only one scientific explanation accounts for this extreme entropy measure: The universe must have started from a nearly infinitely hot and infinitely compact volume.

The Latest Observations

With the dual 400-inch Keck telescopes, astronomers have been able to verify the cooling down of the big bang by measuring the effects of the cosmic background radiation in extremely distant gas clouds. According to the big bang, at such great distances we are seeing the universe in a much younger and more compact state than today. Hence the radiation from the creation event should be hotter than it is now. The cooling curve astronomers observe precisely matches what the big bang model predicts.

In addition to measuring the cosmic cool-off, astronomers can now observe the maturation of galaxies from infancy to middle age (their current developmental stage). By sending us images of different types of galaxies at distances ranging from 50 million to 14 billion light years (Flam 1994, 1806; Goldsmith 1996, 450), the Hubble space telescope has given us a stop-action view of galaxy development, like a photo album of our life from babyhood until today. One of the latest sets of photo images shows us an epoch before galaxies existed, like a photo of your parents just before you were born. Only the building blocks—small clumps of hot young stars—of galaxies are visible in these shots (Glanz 1996a, 756). Such images of the prehistories and life histories of various galaxies give the most visually convincing testimony yet that the cosmos arose from a powerful creation event.

Additional convincing evidence for the hot big bang creation event has come from research into the relative abundances of various elements throughout the cosmos. Since stars can synthesize only some of these elements, an independent nuclear furnace must have generated the remainder. The only plausible candidate for this quantity and quality of nuclear fusion is the big bang itself, and only when the cosmos was between three and four minutes old. The combined effects of the big bang and 15 billion years of stellar burning result in exactly the abundance of elements we find in the universe. No other model comes close.

In 1995 a space shuttle telescope measured an abundance of helium in some distant intergalactic clouds. These clouds predate stars, galaxies and all other compact astronomical bodies. Whatever helium exists there could only have come from the first four minutes of the big bang. This measurement then gives us a reality check on the big bang model. We know that helium comprises 26 percent of all ordinary matter in the universe and that only 2 percent of the helium comes from stellar burning. If the universe did indeed arise from a hot big bang, the quantity of helium in these ancient clouds should amount to 24 percent. That is exactly the proportion measured by the shuttle. This finding ranks as one of the most direct and unambiguous confirmations of the hot big bang creation event (Ross 1995b, 5).

Resolution of Expansion Rate "Crisis"

For more than a decade two groups of astronomers, using different measuring techniques, have been producing discordant values for the universe's expansion rate. One group claimed a value of 80 km/sec/megaparsec (one parsec = 3.26 light years) while the other group stood by a value of 55 km/sec/megaparsec. The higher value yields a creation date of 8.4 to 12.5 billion years ago (the difference depends on the universe's mass density). The lower yields a creation date between 12.2 and 18.2 billion years ago. These dates were at odds with those indicated by the oldest stars and by the abundances of radiometric elements (17 and 16 billion years, respectively).

To help clear up this discrepancy (along with the resulting feud among astronomers), measuring the cosmic expansion rate became the Hubble space telescope's (HST's) top priority. One of the first such measurements to come from the HST suggested a value of 877 km/sec/mpc. Assuming a mass density for the universe large enough (though clearly improbable) to eventually halt its expansion, the research team made a bold announcement to the press: "The universe is only about half as old as scientists formerly thought—about 8 billion years old." Because of the huge discrepancy with the dating of the oldest stars and other age indicators, the big bang model was declared "in crisis."

The public heard nothing about two earlier sets of HST measurements indicating expansion rate values of 7311 and 529 km/sec/mpc. Few if any newspapers reported that the universe's mass density measures to be only about one-fifth the value that would be needed to eventually halt the universe's expansion.

Since that controversial announcement appeared, seven more sets of expansion rate measurements have been published, all with smaller error bars (Cowen 1996a, 292; Saha et al. 1995, 8-26; Sandage et al. 1996, L15-L18; Sandage and Tammann 1995, pp. 1-11; Schaefer, 1996, pp. L19-L23; Tammann and Sandage 1995, 16-24; Tanvir et al. 1995, 27-31). The methods used as well as the expansion values are given in table 15.1. The creation-date calculations are based on the mean of five recent, independent mass density measures (Coles and Ellis 1994, 609-13; Cowen 1996b, 246; Glanz 1996c, 1590; Hogan 1994, 374-75; Peebles 1993, 475-83).

Meanwhile, research dating the oldest stars, which are contained in globular clusters, has advanced significantly. Four American and Canadian astronomers have just completed exhaustive calculations of stellar burning rates in the seventeen oldest globular clusters associated with our galaxy (Chaboyer et al. 1996, 957-61). The mean age the team derived for such stars was 14.6 ± 1.3 billion years. The best determinations for the time

interval between the creation event and the formation of these early stars range from 0.1 to 1.0 billion years. Therefore the so-called discrepancy between the age of the universe and the ages of the oldest stars has been completely removed. As table 15.2 indicates, all the methods for measuring the date of the universe's creation are tending toward the same answer, giving us yet more support for the big bang creation event.

method	expansion rate	creation date
cepheid stars in NGC 4639	57 ± 4 km/s/mpc	16 Gyr
cepheid stars in NGC 4496	62 ± 5 km/s/mpc	15 Gyr
cepheid stars in NGC 5253	52 ± 8 km/s/mpc	18 Gyr
globulars in Virgo Cluster	55 ± 7 km/s/mpc	17 Gyr
supernovae recalibration	57 ± 4 km/s/mpc	16 Gyr
cepheids in M96	69 ± 8 km/s/mpc	14 Gyr
cepheids in NGC 1365	73 ± 8 km/s/mpc	13 Gyr

mean date for creation: 15.31 ± 1.6 Gyr

Table 15.1 Best Measurements of the Expansion of the Universe up to 1996.8

method	creation date
expansion rate of the universe	15.3 ± 1.6 Gyr
burning and formation times of the oldest stars	15.1 ± 1.6 Gyr
decay of the radiometric elements	16.0 ± 4.0 Gyr
time interval when intelligent physical life is possible	17.0 ± 7.0 Gyr

mean date for creation: 15.4 ± 1.6 Gyr

Table 15.2 Four Independent Measures of the Date for the Cosmos's Creation Method

Loopholes Tighten

The preponderance of evidence has all but eliminated secular opposition to the hot big bang model. Five astronomers who still resist the evidence admit that they do so for nonscientific reasons, disliking the theistic implications. When the five recently collaborated on an article for *Nature*, the famed British journal printed a black frame around each page, boldly imprinted with the warning "hypothesis"—an unprecedented editorial decision.

For these holdouts one of the despised implications of the hot big bang model issues from the work of Stephen Hawking, George Ellis and Roger Penrose. In 1970 these three proved that if the equations of general relativity are valid and if the universe contains any measurable mass, then space and time must have originated concurrently with matter and energy. In other words, time itself is finite and had a beginning outside of the universe's boundaries.

Obviously the universe contains mass. But in 1970 a small shadow of doubt still hovered over general relativity, leaving room for speculation. Ten years later, however, a NASA rocket experiment all but erased that shadow, shrinking it to less than a hundredth of a percent. In 1994 a team led by radio astronomer Joseph Taylor used 21 years of measurements on the orbital periods of binary pulsar PSR 1913+16 (two neutron stars orbiting one another) to confirm general relativity to a precision of 99,999,999,999,999 parts in a hundred trillion. In Penrose's words, this finding made Einstein's theory of general relativity "the most accurately tested theory known to science" (Penrose 1994, 230).

The origin of matter, energy, space and time in a singular hot big bang establishes that the source of the universe is independent of its space-time dimensions. Indeed its source is a Creator who exhibits both personality and complete transcendence.

Extradimensional Creation

The Creator's transcendence has been dramatically confirmed and extended. The breakthroughs came as physicists and astronomers tackled two previously intractable problems facing the big bang models. The first dilemma was this: treating fundamental particles as point entities (the traditional view) made unifying any of the four forces of physics impossible. Since we have both theoretical and experimental proof that this unification can and did occur for the weak nuclear force and the electromagnetic force, a new approach to fundamental particles was required. That new approach introduced lines or loops of energy, called strings. When theoreticians treated fundamental particles as highly stretched, vibrating, rotating elastic bands undergoing the extreme heat of the first

split second of creation, the dilemma disappeared. Strings behave as points under subsequent cooler conditions but not in the crucial beginning moment. Counterintuitively strings require more than three spatial dimensions. To operate they need more room than three dimensions have to offer; they need several dimensions beyond the ones of ordinary experience.

The second dilemma was that in the current space-time dimensions of the universe, all gravitational theories imply that quantum mechanics is impossible, and all quantum mechanical theories imply that gravity is impossible. Andrew Strominger hypothesized a brilliant resolution in the form of "extremal" (i.e., very small) black holes, which become massless at critical moments (Breckenridge et al. 1996, 423-26; Callan and Maldacena 1996, 591-608; Maldacena and Strominger 1996, 428-29; Strominger and Vafa 1996, 99-104; Taubes 1995, 1699). At first, however, he seemed merely to have traded one dilemma for another. Black holes are massive objects so highly collapsed that their gravity attracts anything within proximity. How can a black hole be massless without violating the definition of a black hole or without violating the principles of gravity? Simply put, how can there be gravity without mass?

The answer lay once again in extradimensionality. Strominger discovered that in six spatial dimensions the mass of an extremal black hole is proportional to its surface area. As the surface shrinks, the mass eventually becomes zero. The resolution works given the existence of at least six extra spatial dimensions.

String theory therefore solves the two troubling dilemmas (Ross 1996a, 21-33). Accordingly the theory tells us that the universe was created with ten rapidly expanding space-time dimensions. When the universe was just 10^{-43} seconds old, the moment when gravity separated from the strong-electroweak force, six of these ten dimensions ceased to expand. Today these six dimensions still remain as a component of the universe, but they are as tightly curled up as when the universe was only 10^{-43} seconds old, having a diameter of 10^{33} centimeters, so small as to be virtually undetectable.

Four lines of evidence indicate that this theory is correct (Ross 1996a, 28-30). Perhaps the most convincing is that string theory produces as a bonus all of the equations of special and general relativity. In other words, if we knew nothing at all about relativity, this ten-dimensional string theory would have revealed relativity theory in complete form. Such profound, precise corroboration is both rare and wonderful in scientific research. Moreover, it has important implications for Christian theology, helping to explain certain mysteries and paradoxes that have puzzled biblical scholars for centuries.

1. God existed before the universe. God exists totally apart from the universe and yet can be everywhere within it (Gen 1:1; Col 1:16-17).
2. Time has a beginning. God's existence and cause-and-effect activities precede time (2 Tim 1:9; Tit 1:2).
3. Jesus Christ created the universe. He has no beginning and was not created (Jn 1:3; Col 1:16-17).
4. God created the universe from what cannot be detected with the five senses (Heb 11:3).
5. After his resurrection Jesus could pass through walls in his physical body, an evidence of his extradimensionality (Lk 24:36-43; Jn 20:26-28).
6. God is very near, yet we cannot see him—a further suggestion of his extradimensionality (Ex 33:20; Deut 30:11-14; Jn 6:46).
7. God designed the universe in such a way that it would support human beings (Gen 1—2; Neh 9:6; Job 38; Ps 8:3; Is 45:18).

Table 15.3 Biblical Cosmology Confirmed via Extradimensionality

Design Parameters

As helpful as big bang cosmology has been in attesting to the Creator's existence and transcendence, it has provided even greater service in attesting to the Creator's personality. The more we learn about the physics of the universe, the more clearly we see reflected not only the awesome power but also the mind and heart of the One who planned and initiated and sustains all things, inanimate and animate. Big bang cosmology is elucidating the universe and in so doing rendering the design of the universe irrefutable. Astronomers and physicists widely acknowledge that the only reasonable explanation for the intricately harmonious features of the universe, our solar system, our planet—all ingeniously focused on the requirements for life—is the action and ongoing involvement of a personal, intelligent Creator.

In 1961 Robert Dicke was the first to suggest that gravity required fine-tuning if life—any conceivable kind of life—were to be possible anywhere and at any time in the universe. In 1963 Carl Sagan calculated two more characteristics requiring fine-tuning, namely, the mass of a star and the distance of a planet from its star. In the first printing of *The Fingerprint of God* (1989), I listed sixteen characteristics of the universe and another nineteen of the solar system that must be fine-tuned to make life possible and sustainable. In the most recent edition of *The Creator and the Cosmos* (1995), those lists had grown to twenty-six characteristics for the universe and forty-one for the solar system. The pace of new discoveries demonstrating design in the universe and solar system has escalated dramatically, so much so that I now publish a quarterly update. The most recent of these updates

describes thirty-two characteristics for the universe and seventy-five for the solar system.

A summary of the twenty-nine characteristics of the universe that must be fine-tuned for any kind of physical life to be possible appears in table 15.4. Table 15.5 describes the fine-tuning necessary in forty-five characteristics of the solar system. Table 15.6 gives a conservative calculation of the probability that all these (and more) characteristics of the solar system, acknowledged as fine-tuned for life, could be met without invoking design. References to the discoveries on which these tables and calculations are based but not published in my previous works are Burrows and Lumine 1995, 333; Editors 1996, 18, 21; Glanz 1996b, 449-50; Gonzalez 1997; Jayawardhana 1994, 1527; Kerr 1996, 814-15; Lieb, Loss, and Solowej 1995, 985-989; Mayor and Queloz 1995, 355-59; Muller and MacDonald 1995, 107-8; Ross 1995c, 1-3; 1996a, 32-33; 1996b, 1-3; 1997, in press; Rye, Kuo, and Holland 1995, 603-5; Snow and Witt 1995, 1455-57; Wetherell 1995, 470; White and Keel 1992, 129-30; White, Keel, and Corselice 1996; Zuckerman, Forveille, and Kastner 1995, 494-96.

1. strong nuclear force constant
 - if larger: no hydrogen; nuclei essential for life would be unstable
 - if smaller: no elements other than hydrogen
2. weak nuclear force constant
 - if larger: too much hydrogen converted to helium in big bang, hence too much heavy element material made by star burning; no expulsion of heavy elements from stars
 - if smaller: too little helium produced from big bang, hence too little heavy element material made by star burning; no expulsion of heavy elements from stars
3. gravitational force constant
 - if larger: stars would be too hot and would burn up quickly and unevenly
 - if smaller: stars would be so cool that nuclear fusion would not ignite, thus no heavy element production
4. electromagnetic force constant
 - if larger: insufficient chemical bonding; elements more massive than boron would be unstable to fission
 - if smaller: insufficient chemical bonding
5. ratio of electromagnetic force constant to gravitational force constant
 - if larger: no stars less than 1.4 solar masses, hence short and uneven stellar burning
 - if smaller: no stars more than 0.8 solar masses, hence no heavy element production

6. ratio of electron to proton mass
 - if larger: insufficient chemical bonding
 - if smaller: insufficient chemical bonding
7. ratio of number of protons to number of electrons
 - if larger: electromagnetism dominates gravity preventing galaxy, star and planet formation
 - if smaller: electromagnetism dominates gravity preventing galaxy, star and planet formation
8. expansion rate of the universe
 - if larger: no galaxy formation
 - if smaller: universe collapses prior to star formation
9. entropy level of the universe
 - if larger: no star condensation within the protogalaxies
 - if smaller: no protogalaxy formation
10. mass density of the universe
 - if larger: too much deuterium from big bang, hence stars burn too rapidly
 - if smaller: insufficient helium from big bang, hence too few heavy elements forming
11. velocity of light
 - if larger: stars would be too luminous
 - if smaller: stars would not be luminous enough
12. age of the universe
 - if older: no solar-type stars in a stable burning phase in the right part of the galaxy
 - if younger: solar-type stars in a stable burning phase would not yet have formed
13. initial uniformity of radiation
 - if smoother: stars, star clusters and galaxies would not have formed
 - if coarser: universe by now would be mostly black holes and empty space
14. average distance between galaxies
 - if larger: insufficient gas would be infused into our galaxy to sustain star formation for a long enough time
 - if smaller: the sun's orbit would be too radically disturbed
15. galaxy cluster type
 - if too rich: galaxy collisions and mergers would disrupt solar orbit
 - if too sparse: insufficient infusion of gas to sustain star formation for a long enough time
16. average distance between stars
 - if larger: heavy element density too thin for rocky planets to form

- if smaller: planetary orbits would become destabilized
17. fine structure constant (a number used to describe the fine structure splitting of spectral lines)
- if larger: no stars more than 0.7 solar masses
- if smaller: no stars less than 1.8 solar masses
- if larger than 0.06: matter is unstable in large magnetic fields
18. decay rate of the proton
- if greater: life would be exterminated by the release of radiation
- if smaller: insufficient matter in the universe for life
19. ^{12}C to ^{16}O nuclear energy level ratio
- if larger: insufficient oxygen
- if smaller: insufficient carbon
20. ground state energy level for ^4He
- if larger: insufficient carbon and oxygen
- if smaller: insufficient carbon and oxygen
21. decay rate of ^8Be
- if slower: heavy element fusion would generate catastrophic explosions in all the stars
- if faster: no element production beyond beryllium and hence no life chemistry possible
22. mass excess of the neutron over the proton
- if greater: neutron decay would leave too few neutrons to form the heavy elements essential for life
- if smaller: proton decay would cause all stars to rapidly collapse into neutron stars or black holes
23. initial excess of nucleons over antinucleons
- if greater: too much radiation for planets to form
- if smaller: not enough matter for galaxies or stars to form
24. polarity of the water molecule
- if greater: heat of fusion and vaporization would be too great for life to exist
- if smaller: heat of fusion and vaporization would be too small for life; liquid water would be too inferior of solvent for life chemistry to proceed; ice would not float, leading to a runaway freeze-up
25. supernovae eruptions
- if too close: radiation would exterminate life on the planet
- if too far: not enough heavy element ashes for the formation of rocky planets
- if too infrequent: not enough heavy element ashes for the formation of rocky planets
- if too frequent: life on the planet would be exterminated

- if too soon: not enough heavy element ashes for the formation of rocky planets
- if too late: life on the planet would be exterminated by radiation
26. white dwarf binaries
- if too few: insufficient fluorine produced for life chemistry to proceed
- if too many: disruption of planetary orbits from stellar density; life on the planet would be exterminated
- if too soon: not enough heavy elements made for efficient fluorine production
- if too late: fluorine made too late for incorporation in protoplanet
27. ratio of the mass of exotic matter to ordinary matter
- if smaller: galaxies would not form
- if larger: universe would collapse before solar type stars can form
28. number of effective dimensions in the early universe
- if smaller: quantum mechanics, gravity and relativity could not coexist, and life would be impossible
- if larger: quantum mechanics, gravity and relativity could not coexist, and life would be impossible
29. number of effective dimensions in the present universe
- if smaller: electron, planet, and star orbits would become unstable
- if larger: electron, planet, and star orbits would become unstable

Table 15.4 Evidence for the Fine-Tuning of the Universe

The following parameters of a planet, its moon, its star and its galaxy must have values falling within narrowly defined ranges for life of any kind to exist. Characteristics 4 and 5 are repeated from table 15.4 since they apply to both the universe and the galaxy.

1. galaxy size
 - if too large: infusion of gas and stars would disturb sun's orbit and ignite too many galactic eruptions
 - if too small: insufficient infusion of gas to sustain star formation for long enough time
2. galaxy type
 - if too elliptical: star formation would cease before sufficient heavy element buildup for life chemistry
 - if too irregular: radiation exposure on occasion would be too severe and heavy elements for life chemistry would not be available
3. galaxy location

- if shorter: surface temperature range necessary for life would not be sustained
23. age
if too young: planet would rotate too rapidly
if too old: planet would rotate too slowly
24. magnetic field
if stronger: electromagnetic storms would be too severe
if weaker: ozone shield would be inadequately protected from hard stellar and solar radiation
25. thickness of crust
if thicker: too much oxygen would be transferred from the atmosphere to the crust
if thinner: volcanic and tectonic activity would be too great
26. albedo (ratio of reflected light to total amount falling on surface)
if greater: runaway glaciation would develop
if less: runaway greenhouse effect would develop
27. asteroidal and cometary collision rate
if greater: too many species would become extinct
if less: crust would be too depleted of materials essential for life
28. mass of body colliding with primordial earth
if smaller: earth's atmosphere would be too thick; moon would be too small
if greater: earth's orbit and form would be too greatly disturbed
29. timing of body colliding with primordial earth
if earlier: earth's atmosphere would be too thick; moon would be too small
if later: sun would be too luminous at epoch for advanced life
30. oxygen-to-nitrogen ratio in atmosphere
if larger: advanced life functions would proceed too quickly
if smaller: advanced life functions would proceed too slowly
31. carbon dioxide level in atmosphere
if greater: runaway greenhouse effect would develop
if less: plants would be unable to maintain efficient photosynthesis
32. water vapor level in atmosphere
if greater: runaway greenhouse effect would develop
if less: rainfall would be too meager for advanced life on the land
33. atmospheric electric discharge rate
if greater: too much fire destruction would occur
if less: too little nitrogen would be fixed in the atmosphere
34. ozone level in atmosphere
if greater: surface temperatures would be too low

- if less: surface temperatures would be too high; there would be too much ultraviolet radiation at the surface
35. oxygen quantity in atmosphere
if greater: plants and hydrocarbons would burn up too easily
if less: advanced animals would have too little to breathe
36. seismic activity
if greater: too many life forms would be destroyed
if less: nutrients on ocean floors from river runoff would not be recycled to continents through tectonics; not enough carbon dioxide would be released from carbonates
37. volcanic activity
if greater: too many life forms would be destroyed
if less: not enough carbon dioxide and water would be released into the atmosphere
38. oceans-to-continents ratio
if greater: diversity and complexity of life forms would be limited
if smaller: diversity and complexity of life forms would be limited
39. global distribution of continents (for earth)
if too much in the southern hemisphere: seasonal differences would be too severe for advanced life
40. soil mineralization
if too nutrient-poor: diversity and complexity of life forms would be limited
if too nutrient-rich: diversity and complexity of life forms would be limited
41. quantity of forest and grass fires
if too many: too much destruction of plant and animal life
if too few: not enough charcoal returned to soil, limiting biomass and diversity of life
42. gravitational interaction with a moon
if greater: tidal effects on the oceans, atmosphere and rotational period would be too severe
if less: orbital obliquity changes would cause climatic instabilities; movement of nutrients and life from the oceans to the continents and vice versa would be insufficient; magnetic field would be too weak
43. Jupiter distance
if greater: too many asteroid and comet collisions would occur on earth
if less: earth's orbit would become unstable
44. Jupiter mass
if greater: earth's orbit would become unstable
if less: too many asteroid and comet collisions would occur on earth

45. drift in major planet distances
if greater: earth's orbit would become unstable
if less: too many asteroid and comet collisions would occur on earth

Table 15.5 Evidence for the Fine-Tuning of the Galaxy-Sun-Earth-Moon System for Life Support

Parameter	Probability of Galaxy, Star, Planet or Moon Falling in Required Range
galaxy size	.1
galaxy type	.1
galaxy location	.1
star location relative to galactic center	.2
star distance from closest spiral arm	.1
proximity of solar nebula to a supernova eruption	.01
timing of solar nebula formation relative to supernova eruption	.01
number of stars in system	.2
star birth date	.2
star age	.4
star mass	.001
star luminosity relative to speciation	.0001
star color	.4
star's long term distance from galactic plane	.1
supernovae rates and locations	.01
white dwarf binary types, rates and locations	.01
H ₃ ⁺ production in galaxy	.3
planetary distance from star	.001
inclination of planetary orbit	.8
axis tilt	.3
rotation period	.1
rate of change in rotation period	.05
orbit eccentricity	.3
surface gravity (escape velocity)	.001
tidal force	.1
magnetic field	.01
albedo	.1
density	.1
thickness of crust	.01
oceans to continents ratio	.2
rate of change in oceans to continents ratio	.1
global distribution of continents	.3
asteroidal and cometary collision rate	.1
mass of body colliding with primordial earth	.002
timing of body colliding with primordial earth	.05
rate of change in asteroidal and comet collision rate	.1
position and mass of Jupiter relative to earth	.01
eccentricity and regularity of Jupiter's and Saturn's orbits	.05

drift and rate of drift in major planet distances	.1
atmospheric transparency	.01
atmospheric pressure	.1
atmospheric electric discharge rate	.1
atmospheric temperature gradient	.01
carbon dioxide level in atmosphere	.01
oxygen quantity in atmosphere	.01
ozone quantity and location in atmosphere	.01
water vapor level in atmosphere	.01
oxygen to nitrogen ratio in atmosphere	.1
quantity of greenhouse gases in atmosphere	.01
soil mineralization	.1
quantity of forest and grass fires	.1
tectonic activity	.1
rate of decline in tectonics	.1
volcanic activity	.1
rate of decline in volcanic activity	.1
dependency factors	10,000,000,000
longevity requirements	.0001

Probability for occurrence of all 55 parameters = 10^{89}
Maximum possible number of planets in universe = 10^{92}

Much less than 1 chance in one hundred billion trillion trillion exists that even one such planet would occur anywhere in the universe.

Table 15.6 An Estimate of the Probability for Attaining the Necessary Parameters for Life Support

Thirty-five years of research on the anthropic principle (i.e., the principle that the universe tends to provide every necessity for human life) has steadily confirmed that the universe is designed. What we see is the exact opposite of the old God-of-the-gaps fallacy. As knowledge and understanding of the natural realm have advanced, it is those scientific explanations of the cosmos that avoid design that have run into trouble. Thirty-five years of research have moved so conclusively in the direction of design that astronomers who reject design no longer have a scientific basis for their position. As Ed Harrison remarks, any honest appraisal of the cosmos's finely tuned features leads to a moment of truth:

Here is the cosmological proof of the existence of God—the design argument of Paley—updated and refurbished. The fine tuning of the universe provides *prima facie* evidence of deistic design. Take your choice: blind chance that requires multitudes of universes, or design that requires only one. . . . Many scientists, when they admit their views, incline toward the teleological or design argument. (Harrison 1985, 252, 263)

To place one's confidence in blind chance and the unknowable existence of a virtually infinite number of universes is to commit a type of gambler's

fallacy. For consider someone who argues that a single coin flipped ten thousand times and coming up heads all ten thousand times provides no evidence that the coin is biased in favor of heads over tails—after all, there might be $2^{10,000}$ coins and $2^{10,000}$ different coin flippers producing $2^{10,000}$ outcomes different from the observed result of 10,000 consecutive heads. What is the problem here? With no evidence whatsoever for the existence of $2^{10,000}$ coins, $2^{10,000}$ coin flippers or $2^{10,000}$ distinct outcomes, one posits an extremely large sample size simply to ensure that the improbability of the event in question will not be too small. This is both tendentious and fallacious. All we have evidence for in the case of the coin flipper is a sample of size one. Given one coin and one coin flipper and a finite number of flips, the most reasonable interpretation is that someone rigged either the coin or the flips to land heads 10,000 times in a row.

There is only one universe for which we have any evidence, and ours is it. General relativity tells us that since the first split second of the universe's existence, the space-time manifold of the universe has been thermodynamically closed. This means the space-time envelope of our universe cannot overlap the space-time envelope of any other hypothetical universe(s). Therefore either we can place our bets on the only universe we can ever possibly know, or we can speculate about hypothetical universes that will forever remain beyond human knowing. To bet that our universe fell in place exactly as it did, precisely suited for life, because innumerable chance events were taking place in universes causally inaccessible to ours makes even less sense than to bet that on the 10,001st toss the same coin that has come up heads on the previous 10,000 observed tosses will come up tails.

Conclusion

Christian theology has no reason to fear and every reason to embrace scientific research into the origin and characteristics of the universe. The more cosmologists learn, the stronger the evidence for the existence of God and for his identity as revealed in the Bible. Those who fight hardest against the design of the universe often produce the most powerful new evidences for it. As technology improves our tools for measuring the universe and as the scope and power of our scientific theories increases, the more compelling becomes the case for God as Creator and Redeemer. Though not many scholars who write about the new developments in cosmology acknowledge Jesus as Lord and Savior, they do admit that the best and perhaps the only explanation for the universe we observe is a Designer beyond the space-time continuum of the universe. In this admission they testify eloquently to the God who made us and wants to be known by us.

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16 Design in Physics & Biology

Cosmological Principle & Cosmic Imperative?

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FOR MUCH OF THE HISTORY OF WESTERN THOUGHT, IT WAS NOT considered improper for natural philosophers—or what we now call scientists—to think about design in nature. With the rise of modern science in the seventeenth century, however, this began to change. As Hansen observes,

One example from the physics of harmony and resonance may clarify the transformation [of science]. In a world of essences and sympathies—the world of natural magic and medieval science—the qualitative differences between strings made of sheep gut and wolf gut sufficed to explain why the strings would be discordant, for there was natural antipathy between sheep and wolves. . . . [However,] by the 1630's the work of Galileo, Mersenne, and others established a mathematical relationship for the vibrating string, which came to be known as Mersenne's law. This scientific triumph epitomizes a transformation both of the terms of physical explanation and of the character of the fundamental units of nature. (Hansen 1986, 135-36)

Hansen concludes that the "new quantitative and mechanistic approach eventually established a new metaphysics that left no room" for design in nature and relegated anything that implied design to the realm of "something unreal, something supernatural in the modern sense" (Hansen 1986, 136).