"Intelligent Design" as a Scientific Alternative to Evolution

Excerpted from the Expert Statement of Kenneth R. Miller. Submitted March 30, 2005 in the case *Kitzmiller v. Dover Area School District.*

"Intelligent Design Theory" is a new anti-evolution movement that has been presented as an alternative to an older formulation known as "creation science." It differs from the older movement in that it maintains a studied neutrality on the scientific evidence from geology and astronomy on the ages of the earth and the universe, and seems to accept the fossil record. It argues, however, that an unnamed "designer" must have been responsible for much of the process, although it presents no evidence for the actions of such a designer. This means that "intelligent design" is an entirely negative concept, since the case for "design" is made entirely by assembling a selection of arguments that call the validity of evolutionary mechanisms into question.

Joesph Levine and I did not include "design" theory in our textbook because it has not won acceptance from a significant portion of the scientific community. Indeed, ours is the same position taken by Dr. Bruce Gordon of Baylor University, one of the leaders of the design movement, and the first person to head a program devoted to intelligent design at a major American university. As Dr. Gordon writes, "In particular, the theory [of intelligent design] has been prematurely drawn into discussions of public science education, where it has no business making an appearance without broad recognition from the scientific community that it is making a worthwhile contribution to our understanding of the natural world" (Gordon, 2001). We agree. Until "design" passes scientific scrutiny, it has no place in science classrooms or textbooks.

"Intelligent design" advocates often cite the complexity of living cells as a reason to invoke the hypothesis of design. While this may seem to account for any unexplained problem in biology, it does so only by abandoning the scientific method and making "design" the solution to every such problem. An explanation of this sort, which can explain any conceivable evidence, in fact explains nothing. Since the "design" explanation is not testable, it falls outside the realm of science, and places it in the realm of theology, where non-natural explanations are an accepted part of the explanatory landscape. Theological explanations may be correct, of course (as when I believe that a loving God hears my prayers and acts in my life to answer them), but they cannot be tested by the methods of science — and therefore they are not science.

Dr. Bruce Alberts, President of the National Academy of Sciences, clearly had this in mind when he characterized his position on "intelligent design" in a letter to the New York Times:

> *In fact, the majestic chemistry of life should be astounding to everyone. But these facts should not be misrepresented as support for the idea that life's molecular complexity is a result of "intelligent design." To the contrary, modern scientific views of the molecular organization of life are entirely consistent with spontaneous variation and natural selection driving a powerful evolutionary process.*
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> *In evolution, as in all areas of science, our knowledge is incomplete. But the entire success of the scientific enterprise has depended on an*

> *insistence that these gaps be filled by natural explanations, logically derived from confirmable evidence. Because "intelligent design" theories are based on supernatural explanations, they can have nothing to do with science. (letter to NY Times, February 12, 2005)*

Alberts' position on "design" has recently been supported by John H. Marburger III, director of President Bush's Office of Science and Technology Policy:

> *Speaking at the annual conference of the National Association of Science Writers, Marburger fielded an audience question about "Intelligent Design" (ID), the latest supposedly scientific alternative to Charles Darwin's theory of descent with modification. The White House's chief scientist stated point blank, "Intelligent Design is not a scientific theory." And that's not all -- as if to ram the point home, Marburger soon continued, "I don't regard Intelligent Design as a scientific topic." (Chris Mooney, "Intelligent Denials", The American Prospect Online, Feb 22, 2005.)*

The Biochemical Challenge to Evolution

One of the principal claims made by adherents of intelligent design is that they can detect the presence of "design" in complex biological systems. As evidence, they cite a number of specific examples, including the vertebrate blood clotting cascade, the eukaryotic cilium, and most notably, the eubacterial flagellum (Behe 1996a, Behe 2002).

Of all these examples, the flagellum has been presented so often as a counter-example to evolution that it might well be considered the "poster child" of the modern anti-evolution movement. To anti-evolutionists, the high status of the flagellum reflects the supposed fact that it could not possibly have been produced by an evolutionary pathway.

There is, to be sure, nothing new or novel in pointing to a complex or intricate natural structure, and professing skepticism that it could have been produced by the "random" processes of mutation and natural selection. Nonetheless, the "argument from personal incredulity," as such sentiment has been appropriately described, has been a weapon of little value. Anyone can state at any time that *they* cannot imagine how evolutionary mechanisms might have produced a certain species, organ, structure. Such statements, obviously, are personal, and not scientific.

The hallmark of the intelligent design movement, however, is that it purports to rise about the level of personal skepticism. It claims to have found a *reason* why evolution could not have produced a structure like the bacterial flagellum, a reason purportedly based on sound, solid scientific evidence.

Why does the intelligent design movement regard the flagellum as unevolvable? Because it is said to possesses a quality known as "irreducible complexity." Irreducibly complex structures, we are told, could not have been produced by evolution, or, for that matter, by any natural process. They do exist, however, and therefore they must have been produced by something.

That something could only be an outside intelligent agency operating beyond the laws of nature — an intelligent designer. That, simply stated, is the core of the new argument from design, and the intellectual basis of the intelligent design movement.

The great irony of the flagellum's increasing acceptance as an icon of anti-evolution is the fact that research had demolished its status as an example of irreducible complexity almost at the very moment it was first proclaimed.

The flagellum was cited in *Darwin's Black Box* (Behe 1996a) a book by Michael Behe that employed it in a carefully-crafted anti-evolution argument. Building upon William Paley's well-known "argument from design," Behe sought to bring the argument two centuries forward into the realm of biochemistry. Like Paley, Behe appealed to his readers to appreciate the intricate complexity of living organisms as evidence for the work of a designer. Unlike Paley, however, he claimed to have discovered a scientific principle that could be used to prove that certain structures could not have been produced by evolution. That principle goes by the name of "irreducible complexity."

An irreducibly complex structure is defined as ". . . a single system composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning." (Behe 1996a, 39):

> *"An irreducibly complex system cannot be produced directly by numerous, successive, slight modifications of a precursor system, because any precursor to an irreducibly complex system that is missing a part is by definition nonfunctional. .... Since natural selection can only choose systems that are already working, then if a biological system cannot be produced gradually it would have to arise as an integrated unit, in one fell swoop, for natural selection to have anything to act on." (Behe 1996b)*

Living cells are filled, of course, with complex structures which have only recently become accessible to scientific observation and study, and whose detailed evolutionary origins are therefore not known. Therefore, in fashioning an argument against evolution one might pick nearly any cellular structure, the ribosome for example, and claim — correctly — that its origin has not been explained in detail by evolution.

The utility of the bacterial flagellum is that it seems to rise above this "argument from ignorance." By asserting that it is a structure "in which the removal of an element would cause the whole system to cease functioning" (Behe 2002), the flagellum is presented as a "molecular machine" whose individual parts must have been specifically crafted to work as a unified assembly. The existence of such a multipart machine, it is argued, provides genuine scientific proof of the actions of an intelligent designer.

In the case of the flagellum, the assertion of irreducible complexity means that a minimum number of protein components, perhaps 30, are required to produce a working biological function. By the logic of irreducible complexity, these individual components should have no function until all 30 are put into place, at which point the function of motility appears. What this

means, according to the argument, is that evolution could not have fashioned those components a few at a time, since they do not have functions that could be favored by natural selection. As Behe (2002) wrote: " . . . natural selection can only choose among systems that are already working," and an irreducibly complex system does not work unless all of its parts are in place. The flagellum is irreducibly complex, and therefore, it must have been designed.

The assertion that cellular machines are irreducibly complex, and therefore provide proof of design, has not gone unnoticed by the scientific community. A number of detailed rebuttals have appeared in the literature, and many have pointed out the poor reasoning of recasting the classic argument from design in the modern language of biochemistry (Coyne 1996; Miller 1996; Depew 1998; Thornhill and Ussery 2000). I have suggested elsewhere that the scientific literature contains counter-examples to any assertion that evolution cannot explain biochemical complexity (Miller 1999, p. 147), and other workers have addressed the issue of how evolutionary mechanisms allow biological systems to increase in information content (Schneider 2000; Adami, Ofria, & Collier 2000).

The most powerful rebuttals to the flagellum story, however, have emerged from the steady progress of scientific work on the genes and proteins associated with the flagellum and other cellular structures. Such studies have now established that the entire premise by which this molecular machine has been advanced as an argument against evolution is wrong — the bacterial flagellum is not irreducibly complex. As the evidence has shown, nature is filled with examples of "precursors" to the flagellum that are indeed "missing a part," and yet are fully-functional. Functional enough, in some cases, to pose a serious threat to human life.

Certain pathogenic bacteria attack human cells by means of specialized protein secretory systems that inject protein toxins into the cells of their hosts. The type III secretory system (TTSS) is such an example, allowing gram negative bacteria to translocate proteins directly into the cytoplasm of a host cell (Heuck 1998). The proteins transferred through the TTSS include a variety of truly dangerous molecules, some of which are known as "virulence factors," and are directly responsible for the pathogenic activity of some of the most deadly bacteria in existence (Büttner and Bonas 2002; Heuck 1998).

Molecular studies of proteins in the TTSS have revealed a surprising fact — the proteins of the TTSS are directly homologous to the proteins in the basal portion of the bacterial flagellum. As Heuck (1998) has pointed out, these homologies extend to a cluster of closely-associated proteins found in both of these molecular "machines." On the basis of these homologies, McNab (1999) has argued that the flagellum itself should be regarded as a type III secretory system. Extending such studies with a detailed comparison of the proteins associated with both systems, Aizawa has seconded this suggestion, noting that the two systems "consist of homologous component proteins with common physico-chemical properties" (Aizawa 2001). It is now clear, therefore, that a smaller subset of the full complement of proteins in the flagellum makes up the functional transmembrane portion of the TTSS.

Stated directly, the TTSS does its dirty work using a handful of proteins from the base of the flagellum. From the evolutionary point of view, this relationship is hardly surprising. In fact, it is to be expected that the opportunism of evolutionary processes would mix and match proteins

to produce new and novel functions. According to the doctrine of irreducible complexity, however, this should not be possible. If the flagellum is indeed irreducibly complex, then removing just one part, let alone 10 or 15, should render what remains "by definition nonfunctional." Yet the TTSS is indeed fully-functional, even though it is missing most of the parts of the flagellum. The TTSS may be bad news for us, but for the bacteria that possess it, it is a truly valuable biochemical machine.

The existence of the TTSS in a wide variety of bacteria demonstrates that a small portion of the "irreducibly complex" flagellum can indeed carry out an important biological function. Since such a function is clearly favored by natural selection, the contention that the flagellum must be fully-assembled before any of its component parts can be useful is obviously incorrect. As a result, the principal biochemical argument for intelligent design, the contention that the bacterial flagellum is irreducibly complex, has failed.

As I noted in an article for Natural History magazine (Miller 2002), similar analyses can be described for each of the other systems proposed as examples of intelligent design. The evolution of the vertebrate blood clotting cascade, for example, has been described in detail by Hanumanthaiah *et al* (2002), Davidson *et al* (2003) and Jiang and Doolittle (2003). The evolution of antibody-based adaptive immmunity, one of the most complex systems in the body, has been elucidated as well. This work has taken place in many laboratories, and representative reports have appeared in papers by Lewis and Wu (2000), Market and Papavasiliou (2003), DuPasquier *et al* (2004), Zhou *et al* (2004), and Klein and Nikolaidis (2005). In addition, Nonanka and Yoshizaki (2004) were able to show how evolution produced the complement system, a complex and important part of the body's defenses against infection.

More generally, Long *et al* (2003) have reviewed the origin of new genes with novel functions, and have described 22 examples of such genes. Krem and DiCera (2002) have described the ways in which evolution produces that complex cascade-like pathways that function in signaling pathways associated with functions from blood clotting to signal transduction in development. Intelligent design bases its critique of evolution on the claim that new information cannot be produced by Darwinian mechanisms, and yet this claim has been repeatedly disproved by observations of novel pathways and enzymes that have arisen in the recent past. Prijambada *et al* (1995) described the ways in which Darwinian mechanisms produced nylonase, a new enzyme that breaks down the synthetic polymer nylon. Despite the claims of "design" advocates to the contrary, the ability of living organisms to response to environmental change by evolution is truly remarkable. Bacteria have even been able to evolve new pathways to break down 2,4-dinitrotolulene, the explosive compound in TNT (Johnson *et al*, 2002).

The Informational Challenge to Evolution

At first glance, William Dembski's case for intelligent design seems to follow a distinctly different strategy in dealing with biological complexity. His recent book, *No Free Lunch* (Dembski 2002a), lays out this case, using information theory and mathematics to show that life is the result of intelligent design. Dembski makes the assertion that living organisms contain what he calls "complex specified information" (CSI), and claims to have shown that the

evolutionary mechanism of natural selection cannot produce CSI. Therefore, any instance of CSI in a living organism must be the result of intelligent design. And living organisms, according to Dembski, are chock-full of CSI.

Dembski's arguments, couched in the language of information theory, are highly technical and are defended, almost exclusively, by reference to their utility in detecting information produced by human beings. These include phone and credit card numbers, symphonies, and artistic woodcuts, to name just a few. One might then expect that Dembski, having shown how the presence of CSI can be demonstrated in man made objects, would then turn to a variety of biological objects. Instead, he turns to just one such object, the bacterial flagellum.

Dembski offers his readers a calculation showing that the flagellum could not have possibly have evolved. Significantly, he begins that calculation by linking his arguments to those of Behe, writing: "I want therefore in this section to show how irreducible complexity is a special case of specified complexity, and in particular I want to sketch how one calculates the relevant probabilities needed to eliminate chance and infer design for such systems" (Dembski 2002a, p. 289). Dembski then tells us that an irreducibly complex system, like the flagellum, is a "discrete combinatorial object." What this means, as he explains, is that the probability of assembling such an object can be calculated by determining the probabilities that each of its components might have originated by chance, that they might have been localized to the same region of the cell, and that they would be assembled in precisely the right order. Dembski refers to these three probabilities as **P**orig, **P**local, and **P**config, and he regards each of them as separate and independent (Dembski 2002a, p. 291).

This approach overlooks the fact that the last two probabilities are actually contained within the first. Localization and self-assembly of complex protein structures in prokaryotic cells are properties generally determined by signals built into the primary structures of the proteins themselves. The same is likely true for the amino acid sequences of the 30 or so protein components of the flagellum and the approximately 20 proteins involved in the flagellum's assembly (McNab 1999; Yonekura *et al* 2000). Therefore, if one gets the sequences of all the proteins right, localization and assembly will take care of themselves.

According to Dembski, evolution could still not construct the 30 proteins needed for the flagellum. His reason is that the probability of their assembly falls below what he terms the "universal probability bound." According to Dembski, the probability bound is a sensible allowance for the fact that highly improbable events do occur from time to time in nature. To allow for such events, he agrees that given enough time, any event with a probability larger than 10^{-150} might well take place. Therefore, if a sequence of events, such as a presumed evolutionary pathway, has a calculated probability less than 10^{-150}, we may conclude that the pathway is impossible. If the calculated probability is greater than 10^{-150}, it's possible (even if unlikely).

When Dembski turns his attention to the chances of evolving the 30 proteins of the bacterial flagellum, he makes what he regards as a generous assumption. Guessing that each of the proteins of the flagellum have about 300 amino acids, one might calculate that the chances of getting just one such protein to assemble from "random" evolutionary processes would be 20^{-300},

since there are 20 amino acids specified by the genetic code. Dembski, however, concedes that proteins need not get the *exact* amino acid sequence right in order to be functional, so he cuts the odds to just 20^{-30}, which he tells his readers is "on the order of 10^{-39}" (Dembski 2002a, p. 301). Since the flagellum requires 30 such proteins, he explains that 30 such probabilities "will all need to be multiplied to form the origination probability"(Dembski 2002a, p. 301). That would give us an origination probability for the flagellum of 10^{-1170}, far below the universal probability bound. This is presented as proof that flagellum couldn't have evolved, and therefore must be the product of design.

In contrast to this confident conclusion, a careful analysis of the way in which Dembski calculates the probability of an evolutionary origin for the flagellum shows how little biology actually stands behind those numbers. His computation calculates only the probability of spontaneous, random assembly for each of the proteins of the flagellum. Having come up with a probability value on the order of 10^{-1170}, he assures us that he has shown the flagellum to be unevolvable. This conclusion, of course, fits comfortably with his view that "The Darwinian mechanism is powerless to produce irreducibly complex systems..." (Dembski 2002a, p. 289).

However complex Dembski's analysis, the scientific problem with his calculations is almost too easy to spot. By treating the flagellum as a "discrete combinatorial object" he has shown only that it is unlikely that the parts of flagellum could assemble spontaneously. Unfortunately for his argument, no scientist has ever proposed that the flagellum or any other complex object evolved that way. Dembski, therefore, has constructed a classic "straw man" and addressed it away with an irrelevant calculation.

By treating the flagellum as a discrete combinatorial object he has assumed in his calculation that no subset of the 30 or so proteins of the flagellum could have biological activity. As we have already seen, this is wrong. Nearly a third of those proteins are closely related to components of the TTSS, which does indeed have biological activity. A calculation that ignores that fact has no scientific validity.

More importantly, Dembski's willingness to ignore the TTSS lays bare the underlying assumption of his entire approach towards the calculation of probabilities and the detection of "design." *He assumes what he is trying to prove.*

According to Dembski, the detection of "design" requires that an object display complexity that could not be produced by what he calls "natural causes." In order to do that, one must first examine all of the possibilities by which an object, like the flagellum, might have been generated naturally. Dembski and Behe, of course, come to the conclusion that there are no such natural causes. But how did they determine that? In fact, this "conclusion" is an unsupported assumption upon which all of his calculations depend. Suppose that there are such causes, but one simply happened not to think of them? Dembski actually seems to realize that this is a serious problem. He writes: "Now it can happen that we may not know enough to determine all the relevant chance hypotheses. Alternatively, we might think we know the relevant chance hypotheses, but later discover that we missed a crucial one. In the one case a design inference could not even get going; in the other, it would be mistaken" (Dembski 2002a, p. 123 (note 80)).

What Dembski is telling us is that in order to "detect" design in a biological object one must first come to the conclusion that the object *could not* have been produced by any "relevant chance hypotheses" (meaning evolution). Then, and only then, are Dembski's calculations brought into play. Stated more bluntly, what this really means is that the "method" first involves *assuming the absence* of an evolutionary pathway leading to the object, followed by a calculation "proving" the impossibility of spontaneous assembly. This faulty *a priori* reasoning is exactly the sort of logic upon which the new "science" of intelligent design has been constructed.

Not surprisingly, scientific reviewers have not missed this point — Dembski's arguments have been repeatedly criticized on this issue and on many others (Orr 2002; Charlesworth 2002; Padian 2002).

The Origin of Biological Information

Arguments in favor of "design" are often predicated on the statement that living organisms contain large quantities of biological information (which is true) and that no natural process can account for the presence of this information (which is false). They then conclude that the existence of such information is evidence for design.

Such arguments ignore a wealth of research and scholarship on the origins of biological information. In reality, evolutionary mechanisms that can generate increased complexity and biological information are very well understood, and are described in many research papers. Adami *et al* (2000) described a carefully-controlled model system in which increases in information are driven by repeated rounds of reproduction, mutation, and selection, the same forces that drive evolutionary change in nature. Adami's system mimics the evolutionary process in remarkable detail, as highlighted in a 2003 article in Nature (Lenski *et al* 2003). Thomas Schneider of the National Institutes of Health has come to similar conclusions with respect to information based in nucleic acids (Schneider 2000).

Specific experiments on a variety of living organisms have shown that information does indeed arise through distinctly Darwinian mechanisms. The supporting evidence includes a number of studies on gene duplication (Brown *et al*, 2003; Ohta, 2003; Lynch & Conery, 2000; Hughes & Freeman, 2003), as well as experiments in which organisms have responded to adverse environmental conditions by increasing the information content of their DNA (Lenski, 1995; Papadopoulos *et al*, 1999; Riehle *et al*, 2001).

The origin of biological information, as nearly all of these scientists have pointed out, is explained by the mechanism of evolution itself. Variation in the information content of living organisms arises by means of mutations, a few of which increase information content. Natural selection then chooses those variations best-suited to the environment, "fixing" the increased information in the genome. The energetic price that such increases in information entail is considerable, but is fully accounted by the great cost of unsuccessful variants in the struggle for existence. To pretend otherwise, as the intelligent design movement has, is unfortunate and misleading.