Evolutionary Design in Biology

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Much progress has been achieved in recent years in molecular biology and genetics. The sheer volume of data in the form of biological sequences has been enormous and efficient methods for dealing with these huge amounts of data are needed. In addition, the data alone does not provide information on the workings of biological systems; hence much research effort has focused on designing mathematical and computational models to address problems from molecular biology. Often, the terms bioinformatics and computational biology are used to refer to the research fields concerning themselves with designing solutions to molecular problems in biology. However, there is a slight distinction between bioinformatics and computational biology: the former is concerned with managing the enormous amounts of biological data and extracting information from it, while the latter is more concerned with the design and development of new algorithms to address problems such as protein or RNA folding. However, the boundary is blurry, and there is no consistent usage of the terms. We will use the term bioinformatics to encompass both fields. To cover all areas of research in bioinformatics is beyond the scope of this section and we refer the interested reader to [2] for a general introduction. A large part of what bioinformatics is concerned about is evolution and function of biological systems on a molecular level. Evolutionary computation and evolutionary design are concerned with developing computational systems that "mimic" certain aspects of natural evolution (mutation, crossover, selection, fitness). Much of the inner workings of natural evolutionary systems have been copied, sometimes in modified format into evolutionary computation systems. Artificial neural networks mimic the functioning of simple brain cell clusters. Fuzzy systems are concerned with the "fuzzyness" in decision making, similar to a human expert. These three computational paradigms fall into the category of computational intelligence (CI). While biological systems have helped to develop many of the computational paradigms in CI, CI is now returning the favor to help solve some of the most challenging biological mysteries itself. In many cases these probabilistic methods can produce biologically relevant results where exact deterministic methods fail. For an extensive overview of

successful applications of CI algorithms to problems in bioinformatics please refer to [1].

The work presented in this section covers four chapters.

The first chapter by Tom English and Garrison Greenwood covers a discussion of intelligent design (ID) and evolutionary computation. The proponents of intelligent design try to establish that the complexities inherent in many biological systems are such that there is no chance they may have "evolved". Rather, it is proposed that elements of design are evident, and hence these biological systems were designed, not evolved. The chapter investigates the general claims made by ID and shows the logical flaws in this reasoning on a number of examples. Also, it highlights how some of the mathematics and statistical reasoning is flawed. In addition, it provides examples of how evolutionary algorithms can evolve complex systems that according to ID would exhibit elements of design, but obviously this is not the case since the system evolved from a few very basic rules without human intelligence.

The second chapter by Jennifer Hallinan is a review chapter on the topic of synthetic biology. The differences and commonalities between genetic engineering and synthetic biology are explored. While genetic engineering is a reality today and involves the modification of genetic or biological systems, synthetic biology aims to construct an organism from first principles. A noteworthy example of a successful synthetic biology experiment is that of the creation of a poliovirus from the knowledge of its DNA sequence alone. After discussing some minimal requirements for the successful practice of synthetic biology the chapter explores the topic of biological networks and motifs. Understanding gene networks and gene expression is essential towards understanding how cellular systems work. The chapter advises us that a more data-driven approach to synthetic biology will prove useful and it explores the potential of evolutionary computation to inform the field of synthetic biology.

Chapter 3 by Shuhei Kimura discusses the inference of genetic networks with an evolutionary algorithm. Two inference methods, the problem decomposition approach and the cooperative co-evolution approach, are presented. Both of these methods are evaluated and it is demonstrated that they can infer genetic networks of dozens of genes. The analysis of actual DNA microarray data usually requires genetic networks of hundreds of genes. To address this Kimura proposes a method to combine the cooperative co-evolution approach with a clustering technique.

Chapter 4 by Christian Jacob discusses examples of massively parallel, decentralized information processing systems and explores how swarm intelligence can be used to build and investigate complex systems. The examples studied include gene regulation inside a bacterial cell, bacteria and cell population simulations including chemotaxis, cellular orchestration and army ant raiding, herd behavior (predator prey), and human behavior (sales table rush). All of these examples are beautifully illustrated with graphics that show the evolution of the systems or the swarm behavior. This is very useful for understanding these complex, dynamic systems. Some insightful comments on

swarm intelligence, evolutionary computation, and the re-use of software libraries are provided as well.

These chapters provide an interesting mix of problems and methods to show the diversity of biological applications that can be solved with evolutionary techniques. While biological systems have inspired new computational paradigms such as evolutionary computation or swarm intelligence, these techniques can now be used to further our understanding of biological systems themselves. We hope that you will enjoy these chapters.

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References

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Intelligent Design and Evolutionary Computation

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> We ought, it seems to me, to consider it likely that the formation of elementary living organisms, and the evolution of those organisms, are also governed by elementary properties of matter that we do not understand perfectly but whose existence we ought nevertheless admit.
>
> Émile Borel, *Probability and Certainty*

1.1 Introduction

In the United States, a succession of lost legal battles forced opponents of public education in evolution to downgrade their goals repeatedly. By the 1980s, evolution was ensconced in the biology curricula of public schools, and references to the creator of life were illegal. The question of the day was whether instruction in creation, without reference to the creator, as an alternative explanation of life violated the constitutional separation of church and state. In 1987, the U.S. Supreme Court decided that it did, and intelligent design (ID) rose from the ashes of creation science. ID may be seen as a downgraded form of creation. While the creation science movement sought to have biology students introduced to the notion that *creation* is evident in the complexity of living things, the ID movement sought to have students introduced to the notion that *design, intelligence*, and *purpose* are evident.[3] ID preserves everything in the notion of *creation* but the *making*.

Although intellectual endeavor is secondary to sociopolitical action in the ID movement, the objective here is to assess the intellectual component. Separating the two is not always possible. Sometimes ID advocates formulate their

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[3] The ID movement, led by the Discovery Institute, has downgraded its goals, and presently does not advocate teaching ID in public schools. The Discovery Institute continues, however, to advocate teaching the shortcomings of evolutionary theory. It bears mention also that the ID movement now distinguishes biological ID and cosmological ID. Here we focus on biological ID.

ideas in ways that make sense only in light of their sociopolitical objectives. The main intellectual offering of ID is the *design inference*, an ostensibly scientific adaptation of the classical argument from design. While the classical argument might indicate that a natural entity is too complex to have arisen unless created by an intelligent and purposive agent, and that the agent could only be God, a design inference eschews creation and declines to identify the agent, concluding that a non-natural and purposive intelligence designed the natural entity.

The sociopolitical ingenuity of the design inference is that, if taught as an alternative to evolution in public-school science classes, it would leave identification of the designer to schoolchildren. The faithful would conclude that science supports belief in God the Designer and disbelief in evolutionary theory. Whether ID's evasion of direct reference to God eventually will pass judicial scrutiny in the U.S. is unknown. The design inference has a legal vulnerability arising from the fact that *non-natural* intelligence is *supernatural*, and the supernatural is clearly linked with the religious in case law [24, p. 67]. In recent years, the ID movement has shifted to saying that intelligence is natural, but not material. (For an example of earlier usage, see [23].) Given that scientists conventionally regard nature to be material, the ID movement has changed the meaning of *natural* to suit itself, and for no apparent reason but to gain better legal footing. Similarly, many ID advocates call themselves evolutionists, falling back on a dictionary meaning of the term (a process of change in a given direction), rather than scientists' conventional interpretation (an undirected process of change deriving from random variation of offspring and natural selection). This chapter will use conventional scientific terminology.

There are two basic approaches to design inference: the argument from *irreducible complexity*, and the argument from *specified complexity*. The argument from irreducible complexity is a demonstration that a biological system with several or more parts could not serve any useful function if any of its parts were removed. This in effect shows that the system cannot have evolved directly. The argument from specified complexity demonstrates that an entity matches some pattern recognized by an intelligent agent, and that it is improbable that any match of the pattern would arise by natural (materialistic) causes in the history of the universe.

The ID movement has for some years considered evolutionary computation (EC) a threat. EC is the proving ground of ideas in evolutionary theory, according to William A. Dembski, billed by the ID movement as the "Isaac Newton of Information Theory" [13]. Positive results in EC apparently contradict Dembski's claims about "conservation of information" in chance-and-necessity processes. He and other ID advocates acknowledge this, and are at pains to show that the contradiction is only apparent [13]. Thus EC investigators have a potent means of challenging ID. In fact, the main biological claims of ID advocates such as Michael Behe [3] and Steven Meyer [28] are that evolution cannot account for certain biological innovations that occurred hundreds of millions of years ago, and it is easier to challenge the information-theoretic

claims of Dembski with simulation and analysis than it is to challenge the specific biological claims of other ID advocates with new data on ancient events.

Research in artificial life is closely related to that in EC, and in the present context the artificial life program Avida will be considered an example of EC. Research with Avida has been reported in *Nature* [25], and it apparently contradicts the central claim Behe makes in *Darwin's Black Box* [3], namely that gradual evolutionary processes cannot generate irreducible complexity (defined below). In a brief intended for submission to a federal judge, Dembski does not deny that Avida generated irreducible complexity, but instead argues that it lacks biological relevance [16, p. 19].

1.2 Historical Background

The current arguments in favor of ID follow a common theme. In one way or another they all state that the universe we observe is so complex that it simply could not have developed by mere chance; some intelligent agent had to have been responsible. Today ID is the primary opponent of Darwin's theories of evolution and disputes often become heated.

Is this controversy – some would call it a war – of competing ideas something new? Surprisingly, no. In fact, this war began centuries ago and the battles conducted today are not all that different from those waged in the past. It is therefore instructive to see exactly what the arguments were in favor of creationism then, and how they compare to the arguments being made by the ID community today. That is the purpose of this section.[4]

Darwin (1809–1882) was among the first to offer a plausible explanation of nature's development [9]. His theory was accompanied by a large amount of empirical evidence, which strongly contributed to its initial acceptance. In spite of its critics, Darwin's theory was largely responsible for the demise of creationism in the late 19th century. It therefore seems somewhat ironic that the tables have turned – today ID is the major threat to the teaching of evolution!

The earliest ID arguments were overtly religious with no attempts to hide the intelligent designer's identity. Archbishop James Ussher (1581–1656) is best known for declaring the world was created in late October 4004 BC. [43].

> In the beginning God created Heaven and Earth, Gen. I. V. I. Which beginning of time, according to our Chronologie, fell upon the entrance of the night proceeding the twenty third day of October, in the year of the Julian Calendar, 710 [4004 BC].

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[4] Some quotes appearing in this section have unusual grammar, spelling and punctuation. They were purposely kept that way to preserve the original wording of papers written in the 17th through 19th centuries.

Others interjected anatomy into the debate while still acknowledging God as the designer. John Ray (1627–1705) used the eye [37]:

> For first, Seeing, for instance, That the Eye is employed by Man and Animals for the sue of Vision, which, as they are framed, is so necessary for them, that they could not live without it; and God Almighty knew that it would be so; and seeing it is so admirably fitted and adapted this use, that all the Wit and Art of men and Angels could not have contrived it better is so well; it must needs be highly absurd and unreasonable to affirm, either that it was not designed at all for this use, or that it is impossible for man to know whether it was or not.

Of course early arguments were not restricted to just human anatomy. William Paley (1743–1805) compared the eye of a fish, which must process light refracted by water, with the eye of land animals, which must process light passing through air [35]. He believed such a subtle physical difference, while still performing the same function, was conclusive proof of a designer.

> Accordingly we find that the eye of a fish... is much rounder than the eye of terrestrial animals. What plainer manifestation of design can there be than this difference?

Remarkably the eye example is still used today, although the arguments are now more sophisticated with decades of biochemical research for support. Michael Behe attempts to discredit Darwin in the following way [4]:

> Neither of Darwin's black boxes – the origin of life or the origin of vision (or other complex biochemical systems) – has been accounted for by his theory.

Many early ID arguments were philosophical and had no real scientific content. This is not unexpected because science had made little progress by today's standards and the general populace had no background in it anyway. Perhaps the most famous argument made along this line is William Paley's story about finding a watch [35].

> In crossing a heath,[5] suppose I pitched my foot against a stone, and were asked how the stone came to be there; I might possibly answer that, for anything I knew to the contrary, it might have been there for ever: nor would it perhaps be very easy to show the absurdity of this answer. But suppose I had found a watch on the ground, and it should be inquired how the watch happened to be in that place; I should hardly think of the answer I had given before, that for anything I knew, the watch might have always been there. Yet why should not this answer serve for the watch as well as for the stone? ... when

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[5] A tract of open wasteland.

> we come to inspect the watch, we perceive ... that the watch must
> have had a maker: that there must have existed, at some time, and at
> some place or other, and artificer or artificers, who formed it for the
> purpose which we find it actually to answer; who comprehended its
> construction, and designed its use.

It should come as no surprise that such a widely referenced anecdote from the
past would be the basis for a philosophical counter-argument of today [10].

> All appearances to the contrary, the only watchmaker in nature is the
> blind forces of physics, albeit deployed in a very special way. A true
> watchmaker has foresight: he designs his cogs and springs, and plans
> their interconnections, with a future purpose in mind. Natural selec-
> tion, the blind, unconscious automatic process Darwin discovered. . .
> has no purpose in mind. It has no vision, no foresight, no sight at all.
> If it can be said to play the role of watchmaker in nature, it is the
> blind watchmaker.

Prior to the 20th century science had not progressed to a point where it could
provide much support to the proponents of evolution. Nevertheless, that did
not prevent some from disparaging scientific arguments anyway. For instance,
John Ray even went so far as to say scientific principles are meaningless with-
out belief in a designer [37].

> In particular I am difficult to believe, that the Bodies of Animals can
> be formed by Matter divided and moved by that Laws you will or can
> imagine, without the immediate Presidency, Direction and Regulation
> of some Intelligent Being.

The last quote from Ray also demonstrates a new and significant change
in the creationist's arguments. Up to this point there were no misgivings
about identifying who the intelligent designer was: it was God from the Old
Testament of the Bible. Notice in Ray's quote there was no specific reference
to a Judeo-Christian God. Instead, the designer's identity was purposely kept
vague. The ID community today is very careful to avoid any references to a
Judeo-Christian deity. William Dembski, one of the leaders in the present day
ID movement, recently put it this way [12]:

> Intelligent design is theologically minimalist. It detects intelligence
> without speculating about the nature of the intelligence.

Another change in tactics along this same line was to make secular arguments
based on what a reasonable man would (or at least should) believe. What gave
some of these new ID arguments credibility was highly respected scientists
were making them and not theologians. For instance, the renowned naturalist
Louis Agassiz (1807–1873) took believers of evolution to task [1].

The most advanced Darwinians seem reluctant to acknowledge the intervention of an intellectual power in the diversity which obtains in nature, under that plea that such an admission implies distinct creative acts for every species. What of it, if it were true?

The goal here was to put the Darwinist on the defensive. The argument went something like this: since there was no irrefutable proof that evolution can explain how the world developed, then any "reasonable person" should be open to alternative ideas – and of course creationism just happens to be one of those alternative ideas. These arguments were meant to intimidate, if not outright mock, those who wouldn't seriously consider creationist ideas. For example, in [1] Agassiz also said

Have those who object to repeated acts of creation ever considered that no progress can be made in knowledge without repeated acts of thinking? And what are thoughts but specific acts of the mind? Why should it then be unscientific to infer that the facts of nature are the result of a similar process, since there is no evidence of any other cause? The world has arisen in some way or other.

This tactic of mocking unbelievers is still used today. For example, in 1990 Phillip Johnson (who was a lawyer and not a scientist) wrote the following [23]:

What the science educators propose to teach as evolution and label as fact, is based not upon any incontrovertible empirical evidence, but upon a highly controversial philosophical presupposition. The controversy over evolution is therefore not going to go away as people become better educated on the subject.

Until the late 19th century science and religion were strongly intertwined. It is therefore not unexpected that creationist thought permeated early discussions about the origin of life. Even Darwin was not immune and recognized the role of a Creator. In his treatise *On the Origin of the Species* he stated

To my mind, it accords better with what we know of the laws impressed upon matter by the Creator, that the production and extinction of the past inhabitants of the world should have been due to secondary causes, like those determining the birth and death of the individual.

Nowadays science and religion are at odds with each other over the evolution issue. Without exaggeration, ID advocates seek to return science to the days of natural philosophy, when scientific beliefs were tested against higher religious truths. ID supporters talk about "design theory" as science while mainstream scientists counter that it is really no science at all. Unfortunately, this debate has moved to the public arena where emotions often trump objective dialog.

1.3 What Is Intelligent Design?

Advocates of ID use the term *intelligent design* to name both their field of inquiry and a putative cause of certain natural phenomena. They refer to their body of beliefs as *intelligent design theory*. Note that the sense of *theory* here is not *scientific theory*.

In ID theory, information is a physical primitive, like matter and energy, which may enter the natural universe from without.[6] An *intelligence* is a non-natural source of information – i.e., it changes probabilities of events in the natural universe. When an intelligence increases the probability of an event that is in some sense meaningful or functional, it is *goal-directed* or *telic*. The central thesis of ID is that some natural entities exhibit such complex organization that the processes giving rise to them cannot have been entirely natural, but instead must have been directed (informed) to some degree by telic intelligence. The type of organization of interest to ID theorists is known as *specified complexity* (or *complex specified information*). An entity with specified complexity higher than ID theory says could have arisen by purely natural processes is said to be *intelligently designed*. ID theorists consider irreducible complexity as an indicator of high specified complexity.

ID theory says something outside of nature may cause an event within nature. In contrast, mainstream scientists embrace *methodological naturalism*, the working assumption that all natural phenomena have natural causes. ID theory allows theists to associate the intelligent causation of humans with that of one or more deities. In particular, the Biblical notion that humans, as intelligent entities with free will, are created in the image of God, and thus stand apart from nature in some aspects, is supported by the philosophy of intelligent design.

Many ID sites on the Internet (e.g., [21]) offer the definition, attributed to Dembski, "Intelligent Design is the study of patterns in nature that are best explained as the result of intelligence." Although this is a casual definition, its shortcomings are worth examining. First, ID theory permits an event to be explained in terms of both non-natural intelligence and natural antecedents. Design is not all-or-nothing. Second, ID does not study the patterns per se, but *which* patterns indicate that intelligence has contributed information.

The following sections discuss the two main approaches to design inference: *argument from irreducible complexity* and *argument from specified complexity*.

1.4 Irreducible Complexity

The champion of irreducible complexity in the ID community is Michael Behe, a biochemist. He has given two definitions of the term. William Dembski, a

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[6] Recall that ID advocates say that intelligence is natural but not material, and that mainstream science holds that anything natural is material.

mathematician and philosopher, followed with a related definition. The artificial life program Avida has posed a challenge to the claim that evolution cannot give rise to irreducible complexity.

1.4.1 Behe's Definitions

In *The Origin of Species*, Charles Darwin wrote, "If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down" [9]. In *Darwin's Black Box*, biochemist and intelligent design advocate Michael Behe responds with the claim that some biological systems are irreducibly complex:

> By irreducibly complex I mean a single system which is composed of several interacting parts that contribute to the basic function, and where the removal of any one of the parts causes the system to effectively cease functioning. An irreducibly complex system cannot be produced directly (that is, by continuously improving the initial function, which continues to work by the same mechanism) by slight, successive modifications of a precursor system, because any precursor to an irreducibly complex system that is missing a part is by definition nonfunctional. [...] Even if a system is irreducibly complex (and thus cannot have been produced directly), however, one can not definitely rule out the possibility of an indirect, circuitous route. As the complexity of an interacting system increases, though, the likelihood of such an indirect route drops precipitously. [3, pp. 39–40].

Behe holds that irreducible complexity is evidence for intelligent design. There are two logical flaws here, however, both of which Behe has acknowledged [24]. First, to treat evidence against Darwinian gradualism as evidence for intelligent design is to set up a false dichotomy. For instance, there could be some biological structure for which both explanations are wrong. Second, a biological system that is irreducibly complex may have precursors that were not irreducibly complex.

To help understand this idea, think of an irreducibly complex biological structure as a stone arch. The argument from irreducible complexity is that all the stones could not have been put in place simultaneously by evolutionary processes, and that the arch must be the product of intelligent design. But this ignores the possibility that preexisting structures were used opportunistically as "scaffolding" in gradual assembly of the arch. If the scaffolding is removed by evolution after the arch is complete, then the arch is irreducibly complex, but arguments that it could not have emerged gradually are wrong.

Interestingly, H. J. Muller, a geneticist who went on to win a Nobel prize, held in 1918 that *interlocking complexity* (identical to irreducible complexity) arose through evolution:

> Most present-day animals are the result of a long process of evolution, in which at least thousands of mutations must have taken place. Each new mutant in turn must have derived its survival value from the effect which it produced upon the "reaction system" that had been brought into being by the many previously formed factors in cooperation; thus a complicated machine was gradually built up whose effective working was dependent upon the interlocking action of very numerous different elementary parts or factors, and many of the characters and factors which, when new, were originally merely an asset finally became necessary because other necessary characters and factors had subsequently become changed so as to be dependent on the former. It must result, in consequence, that a dropping out of, or even a slight change in any one of these parts is very likely to disturb fatally the whole machinery... [32]

Muller worked out interlocking complexity in more detail in a 1939 paper [33]. According to Orr [34], "Muller gives reasons for thinking that genes which at first improved function will routinely become essential parts of a pathway. So the gradual evolution of irreducibly complex systems is not only possible, it's expected."

Parts of the pathway may also arise from neutral mutations and gene duplication. A duplicate gene is available for mutation into a gene that serves a different function from the original. The mutated duplicate may serve a function similar to the original, and may come to be required by the organism. For instance, the genes for myoglobin, which stores oxygen in muscles, and hemoglobin, which stores oxygen in blood, are closely related, and there is strong evidence that one or both arose through duplication. Both are necessary to humans [34]. Another way in which parts of the pathway may arise is through *co-optation* (also known as cooption), the adaptation of an existing biological system to serve a new function. The role of neutral mutations, gene duplication, and co-optation in the evolution of systems deemed irreducibly complex by Behe will be discussed in the following.

Behe's examples of irreducible complexity have generally not stood up to scrutiny. He gives considerable attention to biochemical cascades – in particular, the blood-clotting cascade and the complementary cascade of the immune system. Here we focus on blood clotting. Behe says of cascades [3, p. 87]:

> Because of the nature of a cascade, a new protein would immediately have to be regulated. From the beginning, a new step in the cascade would require both a proenzyme and also an activating enzyme to switch on the proenzyme at the correct time and place. Since each step necessarily requires several parts, not only is the entire blood-clotting system irreducibly complex, but so is each step in the pathway.

To this Orr responds [34]:

> [Behe] even admits that some genes in his favorite pathway – blood clotting – are similar. But he refuses to draw the obvious conclusion: some genes are copies of others. [...] But this implies that such systems can arise step by step. Behe avoids this conclusion only by sheer evasion: he brands gene duplication a "hypothesis," leaves the similarity of his favorite genes unexplained...

Miller [30] argues that the gene for fibrinogen has as its ancestor a duplicate of a gene that had nothing to do with blood clotting. A genetic sequence similar to that of the fibrinogen gene has been identified in the sea cucumber, an echinoderm [45]. Furthermore, the blood clotting cascade is not irreducibly complex, because a major component, the Hageman factor, is missing in whales and dolphins [42], and three major components are missing in puffer fish [22].

Behe also introduced what has since become the most widely cited example of irreducible complexity, the bacterial flagellum. However, the base of the flagellum is structurally similar to the type-3 secretory system (TTSS) of some bacteria [6]. Furthermore, with 42 distinct proteins in the flagellum, and 25 in the TTSS, there are 10 homologous proteins in the two structures. This constitutes evidence that the TTSS was co-opted in evolution of the flagellum. But ID proponents contend "the other thirty proteins in the flagellar motor (that are not present in the TTSS) are unique to the motor and are not found in any other living system. From whence, then, were these protein parts co-opted?" [31]

A simple response to this challenge is that non-TTSS homologs have been identified for 17 of the 42 flagellar proteins, leaving only $42 - 10 - 17 = 15$ proteins without known homologs. A more subtle response is that only 20 proteins appear to be structurally indispensable to modern flagella (i.e., 22 are not), and only two of them have no known homologs [36]. Thus most proteins of the flagellum are not unique to the flagellum, and the notion that the structure arose through co-optation is at least plausible. That half of the flagellar proteins are not structurally necessary suggests the flagellum is not irreducibly complex, but this ignores issues in the evolution of regulation [36].

ID advocates insist that such indirect evidence of co-optation is insufficient. As Miller [29] has pointed out, demanding direct evidence of the evolution of biochemical systems has advantages for the ID movement:

Behe demands that evolutionary biologists should tell us exactly "how" evolution can produce a complex biochemical system. This is a good strategic choice on his part, because the systems he cites, being common to most eukaryotic cells, are literally hundreds of millions of years old. And, being biochemical, they leave no fossils.

In contrast, ID advocates might emphasize that the system of ossicles (small bones transmitting sound from the tympanic membrane to the cochlea) in the middle ear is irreducibly complex if not for direct fossil evidence of its evolution from a reptilian jawbone [39].

Responding to critics of *Darwin's Black Box*, Behe [5] points out limitations in his original definition of irreducible complexity:

> It focuses on already-completed systems, rather than on the process of trying to build a system, as natural selection would have to do. [...] What's more, the definition doesn't allow for degree of irreducible complexity [...] irreducible complexity could be better formulated in evolutionary terms by focusing on a proposed *pathway*, and on whether each step that would be necessary to build a certain system using that pathway was selected or unselected.

Here he acknowledges that neutral mutations (which he refers to as "unselected") can give rise to irreducible complexity. He observes "if a mutation is not selected, the probability of its being fixed in a population is independent of the probability of the next mutation." And this motivates his "evolutionary" definition of irreducible complexity: "An irreducibly complex evolutionary pathway is one that contains one or more unselected steps (that is, one or more necessary-but-unselected mutations). The degree of irreducible complexity is the number of unselected steps in the pathway" [5].

Behe relates the degree of irreducible complexity directly to the improbability that evolution followed the pathway. "If the improbability of the pathway exceeds the available probabilistic resources (roughly the number of organisms over the relevant time in the relevant phylogenetic branch) then Darwinism is deemed an unlikely explanation and intelligent design a likely one." There are two serious errors in logic here. First, there is the fallacy of the false dichotomy, with a forced choice between Darwinism and ID when a third alternative might explain the pathway. The improbability of one explanation in terms of natural causation does not lend credence to an explanation in terms of non-natural causation. Second, there is a mathematical fallacy long exploited by creationists. When an evolutionist specifies a particular evolutionary, Behe proceeds as though evolution could have taken no other path, and computes an absurdly low probability that the system arose by evolution [5]:

> To get a flavor of the difficulties [my adversary's] scenario faces, note that standard population genetics says that the rate at which neutral mutations become fixed in the population is equal to the mutation rate. Although the neutral mutation rate is usually stated as about 10^{-6} per gene per generation, that is for any random mutation in the gene. When one is looking at particular mutations such as the duplication of a certain gene or the mutation of one certain amino acid residue in the duplicated gene, the mutation rate is likely about 10^{-10}. Thus the fixation of just one step in the population for the scenario would be expected to occur only once every ten billion generations. Yet [my adversary's] scenario postulates multiple such events.

A quantity more relevant to falsifying evolutionary theory is the probability that *no* evolutionary pathway arrives at the system. (However, even this is

ad hoc.) Behe and others in the ID movement essentially take a divide-and-conquer approach, dispensing with evolutionary pathways individually rather than collectively to discredit evolutionary theory.

1.4.2 Dembski's Definition

William Dembski, better known in ID circles for his notion of specified complexity, claims to have generalized Behe's notion of irreducible complexity, but in fact has greatly restricted the class of irreducibly complex systems [15]. The salient point of his modification of Behe's definition of irreducible complexity is that "we need to establish that no simpler system achieves the same basic function." For instance, a three-legged stool is irreducibly complex for Behe, but not for Dembski, because a block serves the same function as the stool. The import of the "no simpler system" requirement is that evolution cannot obtain an irreducibly complex biological system through successive improvements of simpler precursors performing the "same basic function." That is, Dembski rules out *direct* evolution of irreducibly complex systems by definition. If a putatively irreducibly complex system turns out to have emerged by a direct evolutionary pathway, his ready response is that the system was not irreducibly complex in the first place.

Turning to *indirect* evolution of irreducibly complex systems, Dembski falls back on argument from ignorance [15]:

> Here the point at issue is no longer logical but empirical. The fact is that for irreducibly complex biochemical systems, no indirect Darwinian pathways are known. [...] What's needed is a seamless Darwinian account that's both detailed and testable of how subsystems undergoing coevolution could gradually transform into an irreducibly complex system. No such accounts are available or have so far been forthcoming.

Thus Dembski adopts Behe's tactic of limiting the domain of investigation to that of maximum biological ignorance, suggesting that evolutionary findings do not generalize to biochemical systems. Given that the biochemical systems of interest to ID advocates originated hundreds of millions of years ago and left no fossil traces, Dembski does not risk much in demanding seamless and detailed evolutionary accounts.

Why should our relative ignorance of the evolution of irreducibly complex biochemical systems lead us to believe something other than that we are ignorant? "[W]ithout the bias of speculative Darwinism coloring our conclusions, we are naturally inclined to see such irreducibly complex systems as the products of intelligent design." Dembski claims, in other words, that evolutionists have had their native perception of the truth educated out of them.

1.4.3 Evolution of Complexity in Avida

The artificial life program Avida has provided evidence that irreducible complexity can evolve [25]. In the Avida environment, a digital organism is a virtual computer with an assembly language program as its genotype. An organism must code to replicate itself in order to generate offspring. The only logical operation provided by the assembly language is NAND ("not and"). Multiple instructions are required to compute other logical functions. In [25], the fitness of an organism is the sum of fitness values for distinct logical functions it computes in its lifetime. Nine logical functions are associated with positive fitness – the greater the inherent "complexity" of computing the function, the greater the contribution to fitness. The logical function contributing the most to fitness is EQU ("equals"). In 50 runs with a population of 3600 organisms, 23 gave rise to EQU.

The focus of [25] is on the dominant genotype in the final population of a particular run giving rise to EQU. A step in the evolution of the genotype comes when an ancestor has a genotype different from that of its parent. The final dominant genotype, which computes all nine logical functions, has 83 instructions, and is 344 steps removed from its first ancestor, which had 50 instructions.

> The EQU function first appeared at step 111 (update 27,450). There were 103 single mutations, six double mutations, and two triple mutations among these steps. Forty-five of the steps increased overall fitness, 48 were neutral and 18 were deleterious relative to the immediate parent. [25]

The step giving rise to EQU was highly deleterious. Thus the "evolution of a complex feature, such as EQU, is not always an inexorably upward climb toward a fitness peak, but instead may involve sideways and even backward steps, some of which are important."

The evolved code includes a component that is irreducibly complex in the sense of Behe [3].

> The genome of the first EQU-performing organism had 60 instructions; eliminating any of 35 of them destroyed that function. Although the mutation of only one instruction produced this innovation when it originated, the EQU function evidently depends on many interacting components. [25]

The code is not irreducibly complex in the sense of Dembski [15], because it has been established that 19 Avida instructions suffice to compute EQU. However, in another run there was a genotype that computed EQU unless any of 17 instructions were eliminated. The researchers determined by inspection that there was redundant computation of some critical operations. Thus Dembski's stringent definition of irreducible complexity, which requires a near-minimalist implementation, appears to have been satisfied by one of the 50 runs.

Lenski et al. [25] realize that critics of the study will complain that they "'stacked the deck' by studying the evolution of a complex feature that could be built on simpler functions that were also useful." In fact, EQU did not emerge when all simpler logical functions were assigned zero fitness. They contend that this "is precisely what evolutionary theory requires." That is, evolutionary theory holds that complex features emerge through successive steps, not by saltation, and that intermediate forms persist in a population only if they imbue the individuals that possess them with some advantage.

1.5 Specified Complexity

For centuries, design advocates, though not the present-day ID advocates, have advanced the *argument from improbability* [40]. The approach is to show some event in nature is very unlikely to have occurred by chance, and to therefore conclude God caused it. But this argument is fallacious. For one thing, low probability does not necessarily justify rejection of chance. When numbers are drawn in a lottery, for instance, it is certain that the chance outcome will be one that was highly improbable *a priori* [40]. Another problem with the argument is that assigning an identity to the cause of the event is unwarranted [14].

William Dembski has developed an analogous *argument from specified complexity*, which concludes that a natural event reflects the intervention of intelligence [11, 13, 18]. That is, a natural event contains information that was introduced purposely by an unidentified source outside of nature. This statement is not quite the same thing as saying intelligence caused the event, because the event may have resulted from a combination of natural causes and intelligent intervention. For instance, one may argue that natural evolutionary mechanisms, while operating as claimed by mainstream scientists, do not account fully for life on earth, and that intelligence has guided (added information to) evolutionary processes. Note that information may have entered continually, and that there may have never have been a discrete design event.

To conclude that a natural event reflects intelligent design, one must demonstrate that the event is improbable. Dembski describes improbable events as *complex*. One must also demonstrate that the event is *specified* in the sense that it exhibits a pattern that exists independently of itself [11, 13]. To be more precise, there must exist some "semiotic agent" that describes the event with a sequence of signs [18]. Specified complexity, or *complex specified information* (CSI), is a quantity that "factors in" the improbability of the event and the cost of describing it. Dembski claims that when the CSI of an event exceeds a threshold value, inference that intelligence contributed to the event is warranted.

1.5.1 Design Inference as Statistical Hypothesis Testing

In unpublished work [18], Dembski has reduced the argument from specified complexity [11, 13] to statistical hypothesis testing. The approach is derived from that of Fisher, with a null (or *chance*) hypothesis possibly rejected in favor of an alternative hypothesis. The chance hypothesis says natural causes account entirely for an event in nature, and the alternative hypothesis says the event reflects design (contains information that could only have come from without nature). The Fisherian approach requires specification of the rejection region prior to sampling. But the argument from specified complexity entails selection of a past event and subsequent definition of a rejection region in terms of a pattern found in the event. Dembski claims to have corrected for "data dredging" and *a posteriori* fitting of the rejection region to the event by including *replicational resources* and *specificational resources* as penalty factors in a test statistic [18].

Dembski's argument goes something like this. Suppose $\mathbf{H}$ is the chance hypothesis, and let E be an event in the sample space of $\mathbf{H}$. For any pattern describable by semiotic agent S, there is a corresponding event T containing all matches of the pattern. Dembski uses T to denote both the event and the pattern [18]. The probability (under the chance hypothesis) of matching the pattern is

$$\mathbf{P}(T \mid \mathbf{H}).$$

T serves as a rejection region, and it is possible to make the probability low enough to ensure rejection by choosing a very specific pattern that matches few events, or perhaps no event but E. A penalty factor counters such a "rigged" selection of the pattern.

The *specificational resources* used by S in identifying pattern T are

$$\varphi_S(T),$$

which gives the rank-complexity of the semiotic agent's description of the pattern. In essence, the agent enumerates its pattern descriptions from less complex (e.g., shorter) to more complex (longer), looking for matches of E. The rank-complexity is the least index of a description of pattern T in the enumeration. It is a count of how many descriptions the agent processed to obtain the description of matching pattern T. Dembski [18] considers

$$\varphi_S(T) \cdot \mathbf{P}(T \mid \mathbf{H})$$

"an upper bound on the probability (with respect to the chance hypothesis H) for the chance occurrence of an event that matches any pattern whose descriptive complexity is no more than T and whose probability is no more than $\mathbf{P}(T \mid \mathbf{H})$" for a fixed agent S and a fixed event E. The negative logarithm of this quantity,

$$\sigma = -\log_2[\varphi_S(T) \cdot \mathbf{P}(T \mid \mathbf{H})] \text{ bits,}$$

is *specificity*, a type of information [18]. As the probability of matching the pattern goes down, specificity goes up. As the number of patterns "dredged" by the semiotic agent goes up, specificity goes down. Maximizing specificity – and ultimately inferring design in event E – is a matter of finding in the event a simple pattern that is matched with low probability under the chance hypothesis.

Not only is the pattern chosen to obtain high specificity, but the event E and the semiotic agent S, and another penalty is required. The number of *replicational resources* is bounded above by the product of the number of semiotic agents available and the number of events that might have been considered. In applications to biology, Dembski uses as an upper bound Seth Lloyd's estimate of the number of elementary logical operations in the history of the universe, 10^{120} [27]. Dembski claims that if

$$10^{120} \cdot \varphi_S(T) \cdot \mathbf{P}(T \mid \mathbf{H}) < 0.5,$$

then the chance hypothesis is less likely to account for event E than the alternative hypothesis of intelligent design [18]. The CSI of event E is the penalized specificity,

$$\chi = -\log_2[10^{120} \cdot \varphi_S(T) \cdot \mathbf{P}(T \mid \mathbf{H})] \approx \sigma - 399 \text{ bits.}$$

Intelligent design is inferred for event $\mathbf{H}$ if $\chi > 1$ or, equivalently, specificity in excess of 400 bits [18]. Note that Dembski sometimes invokes the argument from specified complexity to reject chance in favor of human intelligence, and in these cases he sets the number of replicational resources smaller [18].[7]

1.5.2 Some Criticisms of Specified Complexity

It seems that Dembski, as a mathematician and philosopher, thinks more analytically than algorithmically. Most of the following addresses aspects of computation of CSI. It is important to keep in mind the adversarial aspect of the argument from specified complexity. Chance hypotheses should come from mainstream scientists, not ID advocates. They often will be analytically intractable, and design inferences will require direct computation of CSI. Below are listed some major criticisms of Dembski's arguments.

A Model of Nature Is Conflated with Nature Itself

Recall that the chance hypothesis is essentially that natural causes account entirely for a natural event. The design inference is a claim that natural causes

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[7] ID advocates hold that human intelligence is not natural (materialistic). Thus humans can cause events with high levels of CSI.

alone do not suffice to explain the event. But in practice the chance hypothesis that is likely to be derived from a scientific model, and what is subject to rejection is not natural causation itself, but the model of natural causation. The distinction is of vital importance. If scientists do not understand some class of events, a chance hypothesis derived from their best model may be rejected in favor of design. The inability of the model to account for the event is treated as the inability of natural causation to account for the event. This constitutes a logically fallacious argument from ignorance. And as described above, ID advocates indeed focus on biological entities with histories that are very difficult to determine.

Key Aspects of CSI Are Not Explicit in Dembski's Treatment

In conventional mathematical terms, a "pattern" described by a semiotic agent is a *property*. A property T is a subset of some set U, and saying that $x \in U$ *has property* T is equivalent to saying that $x \in T$. Let D_S denote the set of all descriptions that semiotic agent S may emit. For all descriptions d in D_S, let $\varphi_S(d)$ be the rank-complexity of d described above. Let $D_S(E) \subseteq D_S$ be the set of all descriptions associated with event E by S. Finally, let

$$T_S(d) = \{\omega \in \Omega \mid \omega \text{ has the property } S \text{ describes with } d\},$$

where Ω is the sample space. This glosses over semantic interpretation of the descriptions in D_S. Nonetheless, it should convey that there is no way to determine the rejection region without knowing both its description and the semantics of the semiotic agent that generated the description. Then for all semiotic agents S and for all descriptions d in $D_S(E)$ the CSI is

$$\chi_S(d) = -\log_2[10^{120} \cdot \varphi_S(d) \cdot \mathbf{P}(T_S(d) \mid \mathbf{H})].$$

This appropriately indicates that CSI is associated with descriptions of event E. For completeness, one may define $\chi(E)$ as the maximum of $\chi_S(d)$ over all S and d, but maximization is infeasible in practice, and design inference requires only $\chi_S(d) > 1$ for some S and d.

"Divide-and-Conquer" Rejection of Disjunctive Hypotheses Is Permitted

When there are multiple chance hypotheses $\{\mathbf{H}_i\}$, they must be rejected jointly to infer intelligent design. Dembski fails to point out that the semiotic agent S and the description d in $D_S(E)$ must be held constant while rejecting all hypotheses [18]. This requirement is captured by generalizing the definition of χ_S to

$$\chi_S(d) = -\log_2[10^{120} \cdot \varphi_S(d) \cdot \max_i \mathbf{P}(T_S(d) \mid \mathbf{H}_i)].$$

CSI Is Not Computable

For Dembski, the physical (material) universe is discrete and finite, and so is Ω [11, 13, 18]. This would seem to bode well for computation of CSI, but problems arise from the fact that a semiotic agent may associate with event E a description of a property defined on an infinite set. Many finitely describable properties are not algorithmically decidable [26], irrespective of the nonexistence of infinite sets in the physical universe.

The value of $\mathbf{P}(T_S(d) \mid \mathbf{H})$ is the sum of $\mathbf{P}(\omega \mid \mathbf{H})$ over all points ω in rejection region $T_S(d)$. Its computation generally requires conversion of description d into an algorithm that decides which points in Ω have the described property. But if the described property is not decidable, $\mathbf{P}(T_S(d) \mid \mathbf{H})$ is computable only under special circumstances. This holds even if the initial "translation" of d into an algorithm is non-algorithmic.

Incomputable properties are especially likely to arise in the important case that Ω is a set of entities that describe or compute partial (not always total) recursive functions. An example is the set of all LISP programs of length not exceeding some large bound. A semiotic agent's description of program E will commonly refer to a nontrivial property of the function computed by E. But a key result in the theory of computation, Rice's theorem, implies that no algorithm decides whether other LISP programs compute functions with that property [26]. In other words, there is generally no algorithm to say whether programs in Ω belong to the rejection region. This indicates that for a wide range of computational entities CSI may be computed only for the form (e.g., the source code), and not the function. Note that some philosophers and scientists believe that brains compute partial (not total) recursive functions [19].

Some Design Hypotheses Call for Nonexistent Chance Hypotheses

In conventional statistical hypothesis testing, one begins with an alternative hypothesis and then selects a chance hypothesis. This does not carry over to the argument from specified complexity. An ID advocate may believe an event is designed, but mainstream scientists may not have provided an appropriate chance hypothesis to reject. The non-existence of the hypothesis (scientific model) may be due to scientific indifference or scientific ignorance.

As an example of scientific indifference, consider what is required to compute the CSI of the bacterial flagellum, which Dembski *qua* semiotic agent describes as a "bidirectional rotary motor-driven propeller" [18]. The sample space contains biological structures detached from whole phenotypes, and the chance hypothesis must associate probabilities of evolution with them. But nothing in evolutionary theory leads to such a hypothesis, and it is absurd to insist that scientists to supply one.

Ignorance is ubiquitous in science, and some phenomena (e.g., gravity) have resisted explanation for centuries. The inability of science to explain

a class of events does not constitute the least evidence for ID. To suggest otherwise is to engage in a logical fallacy known as argument from ignorance.

Computation of CSI May Be Infeasible When Theoretically Possible

If Ω is the set of all biological structures (begging the question of how to define "biological structure") that have existed (begging the question of how to determine all structures of entities that have ever lived) or might have existed (begging the question of how to determine what might have lived), how will an algorithm efficiently locate the points in the sample space with the property "bidirectional rotary motor-driven propeller"? No approach other than exhaustive exploration of the sample space for points with the property is evident. The time required for such a computation makes it infeasible. Furthermore, the practicality of defining the sample space for an algorithm to operate upon is highly dubious.

Another feasibility issue is the cost of computing $\mathbf{P}(\omega \mid \mathbf{H})$ for a single ω in Ω. Suppose $\mathbf{P}(\omega \mid \mathbf{H})$ is, loosely speaking, the probability of evolution of ω, and that $\mathbf{H}$ is derived from a simulation model supplied by a scientist. The results of a simulation run usually depend upon initial conditions and parameter settings. There will virtually always be uncertainty as to how to set these values, and the consequence is that many runs of the simulation model (with various settings) will be required to obtain $\mathbf{P}(\omega \mid \mathbf{H})$.

Putative Innovations in Statistical Hypothesis Testing Have Not Passed Peer Review

Dembski's approach to design inference [18] is correct only if he has made monumental contributions to statistical hypothesis testing. There is nothing precluding publication of his statistical work in a peer-reviewed journal of mathematics or statistics. At the time of this writing, Dembski has not published any of his work. Consequently, one must regard his statistical reasoning with skepticism.

1.5.3 The Law of Conservation of Information

In earlier work [13], Dembski argues informally for a *law of conservation of information*, which does not specify that complex specified information is strictly conserved in natural processes, but that gain of CSI is bounded above by 500 bits. That is, a closed physical system may go from a state of lower CSI to a state of higher CSI, but the increase cannot exceed 500 bits. The bound corresponds to a putative limit on the improbability of events in the physical universe, as described below. Dembski regards evolutionary computations (ECs) as closed systems, and if an EC produces an apparent gain of more than

500 bits of CSI in its population, he argues that humans have surreptitiously (perhaps haplessly) added CSI to the process [13].

The 500-bit bound on CSI gain is the negative logarithm of the *universal probability bound* Dembski advocates in earlier work, 10^{-150} [11,13]. He considers events with probability below the bound to be effectively impossible. Dembski [11] cites Émile Borel, who is quoted in the epigraph of this chapter, as a famous proponent of a universal probability bound. In fact Borel selects different bounds for different applications – they are hardly "universal" [7]. Some are much smaller, and some much larger, than Dembski's bound. In the work detailed above, Dembski indicates that "instead of a static universal probability bound of 10^{-150} we now have a dynamic one of $10^{-120}/\varphi_S(d)$" [18]. That is, the bound is adapted to the observer of an event and the observer's description of the event. This is in marked contrast with Borel's approach.

Dembski does not indicate in [18] how to rescue the law of "conservation" of information. He states, however, that $\varphi_S(d)$ should not exceed 10^{30} in practice, and observes that his old static bound of 10^{-150} is a lower bound on the dynamic bound. This suggests that Dembski may renew his claim that CSI gain cannot exceed 500 bits in a natural process. With the dependence of CSI upon observers and their descriptions of events, what it means to gain CSI is hardly obvious.

1.6 ID and Evolutionary Computation

Dembski has been at pains to argue, particularly in Chapter 4 of *No Free Lunch* [13], that the results of evolutionary computation violate his law of conservation of information, and that human investigators must be injecting their own intelligence into the EC programs under investigation. In particular, he has attacked Chellapilla and Fogel's study of co-evolution of checkers players [8], Ray's Tierra program for artificial life [38], Schneider's demonstration of gain of Shannon information in an evolutionary program [41], and Altshuler and Linden's evolutionary optimization of bent-wire antenna designs [2].

Dembski often cites the main "no free lunch" (NFL) theorem for optimization, which says in essence that if all objective functions are equally likely, then all optimizers that do not revisit points have identically distributed performance [44]. He takes this as an indication that performance is generally bad. Ironically, English [20] showed six years prior to the publication of Dembski's book that NFL arises as a consequence of (absolute) conservation of Shannon information in optimization, and that average performance is very good when test functions are uniformly distributed. In other words, NFL does not bode as poorly for EC as Dembski has thought.

Dembski has since responded [17] by analyzing search of "needles-in-a-haystack" functions, in which a few points in the domain are categorically good and the remainder are categorically bad [20]. He motivates the analysis by alluding to proteins as needles in the haystack of all sequences of amino

acids. For each function, it is highly improbable that an arbitrarily selected search algorithm locates a good solution in feasible time. Dembski holds that successful search requires a prior "search for a search" [17]. This amounts to *displacement* of the search problem from the original solution space to the space of search algorithms. He argues that a search problem cannot be solved more rapidly with displacement than in the original space. Thus from his perspective, if an EC finds a good solution in feasible time, the choice of the EC was necessarily informed by intelligence [17].

There is nothing novel in the notion that it is sometimes necessary to "align" the search algorithm with the problem [44], but there is in the idea that alignment requires search [17]. How does one search for a search algorithm? Dembski is very vague about this. All one can possibly do, in black-box optimization, is to examine the value of at least one point in the search space (domain) and use the information to select an algorithm. But then one has initiated a search of the function. It follows that any search for a search may be embedded in an algorithm for search of the original solution space.

"Displacement" is a construct that makes it appear that intelligence creates information by selecting an effective search algorithm to locate a solution. In reality, humans are able to tune an EC to a fitness function only when the fitness function is not a black box. Only when one knows some property or properties of the fitness function can one select an EC that is expected to outperform random sampling. And how does one recognize properties of a function? Does one's intelligence create information? No, it seems much more reasonable to say that one has learned (acquired information) about functions and algorithms in the past, and that one uses this repository of information to match algorithms to functions. There is a great deal of empirical research aimed at learning which forms of EC handle which classes of functions well.

1.7 Conclusion

We have criticized ID theory for its intrinsic faults. But in the end the only way to understand the theory is as a veiled apologetic. Jews, Christians, and Muslims agree that the God of Abraham created the diverse forms of life on earth, imbuing only humans with a capacity to create ex nihilo. Although some of the faithful accept that religion and science are different belief systems leading to different beliefs, others insist that science must never contradict religion. ID theorists begin with religious beliefs about life and humanity, and attempt to show that contradictory beliefs held by almost all mainstream scientists are wrong. They hide their religious motivation because they hope their theory will find its way into science classes of public schools.

Irreducible complexity is the weakest part of the apologetics. Behe has had to concede what Muller pointed out decades before he was born, namely that indirect evolutionary pathways may give rise to irreducible complexity.

And there is good fossil evidence that the interconnected bones of the mammalian middle ear evolved from a reptilian jawbone. The Avida simulation is reasonably interpreted as generating irreducibly complex programs. ID advocates continue, however, to focus on irreducibly complex biosystems for which there are few historical data (e.g., the flagellum). They argue that evolutionary theory fails to account for the emergence of these systems when in fact there are few hard data.

The argument from specified complexity rests on an approach to statistical hypothesis testing that has not passed peer review. Even if the statistical foundation is sound, the argument is logically flawed. When it claims to reject purely natural causation in favor of design, it actually rejects a model. That is, if there is no good model of a phenomenon, then the argument from specified complexity reduces to argument from ignorance. Even with an excellent model, specified complexity is in some cases impractical to compute, or even incomputable.

Dembski's claim that all entities with high specified complexity are intelligently designed seems to have been falsified by various evolutionary computations. But Dembski argues constantly that experimenters have smuggled intelligence into the computations. Accumulating further computational evidence should be valuable, but in the end formal mathematical analysis may be required to settle the dispute.

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