

PROBABILITY, OPTIMIZATION THEORY AND EVOLUTION

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A Review of *No Free Lunch: Why Specified Complexity Cannot Be Purchased Without Intelligence* by William Dembski 2002. Rowman and Littlefield Publishers, Inc., Maryland. 404 pp. ISBN 0-7425-1297-5. \$35

Perhaps it is not surprising that mathematics has always been popular among anti-evolutionists. Math is unique in its ability to bamboozle a lay audience, making it well-suited to their purposes. William Dembski, of Baylor University, represents the cutting edge in anti-Darwinian mathematics. His bailiwick is probability and information theory, which he fashions into a formidable, but ultimately unsuccessful, weapon.

For years the Holy Grail of optimization theory was the production of an algorithm that would outperform blind search independent of the particular problem to be solved. The No Free Lunch (NFL) of Dembski's title refers to a collection of theorems establishing the nonexistence of such an algorithm (Wolpert and Macready, 1996). Specifically, the average performance of any algorithm over the class of all optimization problems is no better than blind search. It follows that an algorithm is assured of success only when information about the problem is in some way built into it.

Dembski presumes to use NFL as the foundation of an argument against the explanatory sufficiency of natural selection. In the first three chapters of the book he argues that complex specified information (CSI) is a reliable indicator of design. For Dembski this is a technical term in probability theory. Mathematically speaking, information content is something possessed by an event in a probability space. "Complex" then indicates an event of low probability, while "specified" notes the event's conformity to some independently describable pattern. He then argues that biological systems are replete with CSI and that NFL precludes selection's ability to create such information without preexisting CSI to act upon.

Dembski urges CSI as a tool for separating the products of intelligent design from those of chance and natural causes. He attempts to apply this tool to biological systems, believing he can thereby prove the intervention of an intelligent agent in the course of natural history. It is a drum he has been pounding for many years, through two earlier books and countless essays. His work devotes considerable effort to persuading the reader that his definition of CSI is both mathematically rigorous and practically applicable. Every aspect of this work has been strongly criticized by numerous philosophers and scientists (Fitelson et al 1999, Wilkins and Elsberry 2001, Godfrey-Smith 2001). Here I will address the primary flaws in his arguments as they apply specifically to evolutionary biology.

Assessing natural selection's creative abilities requires that we evaluate the efficacy of a particular algorithm acting on a given problem. NFL addresses only average performance over all possible problems. It therefore offers no reason to believe that selection can not construct complex adaptations. On the other hand, NFL does suggest that selection's ability to ascend the fitness landscapes it actually confronts implies its inability to scale the different landscapes that no doubt exist in some alternate reality. Mutation and recombination, viewed as algorithms for searching genotype space, will be effective only when the landscapes they confront obey certain properties. This makes it reasonable to ask why nature presents us with just the sorts of landscapes that are searched effectively by these mechanisms (Kauffman, 2000). The answer, at least in part, is that fitness landscapes coevolve with organisms. This is a bedrock principle of modern ecology.

Dembski draws a different conclusion, claiming that natural selection acts effectively only because CSI was front-loaded into the biosphere. This information is encoded in the fundamental constants of the universe. He writes:

For starters, [the collection of DNA-based self-replicating cellular organisms] had better be nonempty, and that presupposes raw materials like carbon, hydrogen, and oxygen. Such raw materials, however, presuppose star formation, and star formation in turn presupposes the fine-tuning of cosmological constants. Thus, for f to be the type of fitness function that allows Darwin's theory to flourish presupposes all the anthropic principles and cosmological fine-tuning that lead many physicists to see design in the universe. (210)

Most of us did not need difficult mathematical theorems to realize that Darwinism is viable only when nature satisfies certain axioms, and it is not a defect in evolutionary theory that it takes these axioms for granted. Determining why the universe has just the properties it does is hardly a problem within biology's domain. If Dembski wishes to claim that cosmological "fine-tuning" represents CSI then, following the requirements of his theory, he should perform a probability calculation to demonstrate that fact. Since there is no empirical basis for such a calculation, it is understandable that Dembski prefers simply to make assertions and be done with it.

And how are we to show the human genome possesses CSI? Within Dembski's framework, we must show that the probability of formation by natural selection of a particular gene sequence falls below some universal lower bound. Dembski offers 10^{-150} for this purpose, based on certain computations involving the Planck time and the number of fundamental particles in the observable universe. How do we measure this probability?

The classic creationist argument in this regard asserts that the chance formation of a gene sequence n bases long has probability 4^{-n} . The gene is modeled as an n -tuple in which each slot can be filled in any of four equiprobable ways. This argument is absurd for many reasons, its failure to consider selection's role in the process being the most prominent. Dembski attempts to circumvent this blunder while maintaining the computational tractability of the creationist version.

To do this he invokes the irreducible complexity (IC) of certain biochemical machines. This was the brainchild of biochemist Michael Behe, who introduced the idea in 1996. A machine composed of several well-matched, indispensable parts is IC. Such machines are said to pose an insurmountable challenge to Darwinian mechanisms because they entail some minimal complexity that could not emerge from a small change in a simpler, precursor system.

Dembski performs a breathtaking calculation that purports to measure the complexity of a bacterial flagellum. The flagellum is irreducibly complex, you see, implying it can be treated as a discrete combinatorial object. Dembski writes:

Such objects are invariably composed of building blocks. Moreover, these building blocks need to converge on some location. Finally, once at this location the building blocks need to be configured to form the object. It follows that the probability of obtaining an irreducibly complex system is [the product of these three probabilities]. (290)

The subsequent ten pages represent a valiant attempt to assign values to the terms of this product. The text soon becomes a dazzling congeries of binomial coefficients, perturbation probabilities, and sundry mathematical notation, all in the service of a computation that may as well have been written in Klingon for all the connection it has to reality. Modeling the formation of complex structures via a three part process of atomization, convergence and assembly is terribly unrealistic.

Further, IC machines cannot be treated as discrete combinatorial objects. Since the publication of Behe's book, numerous biologists have undertaken the thankless task of stating the obvious: irreducible complexity in the present tells us nothing about functional precursors in the past. This has been demonstrated in two ways: (1) By describing general schemata whereby an IC machine could arise gradually (Thornhill and Ussery, 2000). (2) By outlining hypothetical scenarios to explain specific biochemical machines. Structures so explained include the blood clotting cascade (Miller, 1999) and the flagellum (Rizzotti, 2000), among many others. The theoretical plausibility of such scenarios renders IC useless as a device for carrying out computations, and Dembski's argument is no improvement over the creationists.

Dembski's casual approach to probability calculations is fatal to his enterprise. His assertion that CSI reliably indicates design is moot given his inability to establish its presence in biological systems. For example, he accuses Manfred Eigen of making a category error for writing, in reference to understanding the origin of life, "Our task is to find an algorithm, a natural law that leads to the origin of information (Eigen 1992)." Dembski believes organisms possess CSI, which natural laws are fundamentally incapable of producing. But Eigen's whole point is that genetic information is not complex in the sense Dembski requires. It arises with high probability as soon as certain initial conditions are met.

The line between pure and applied mathematics is often blurry, but it is real. Dembski's arguments fail because the elaborate abstract models he constructs do not adequately capture the full richness of the natural world. Alas, such nuances will not deter the anti-evolution propagandists who will use Dembski's book as mathematical vindication for their arguments.

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