

# Letters

However, all this is irrelevant for Isaac, because, "... all possible historical paths ..." and "... all historical pathways ..." have not been investigated. He checkmates every reasoned objection. Isaac's fiat science undermines natural science and science education, and it allows adherents of an exclusive unplanned biological origin to get rid of God for all time.

## Notes

<sup>1</sup>Randy Isaac, "Information, Intelligence, and the Origins of Life," *Perspectives on Science and Christian Faith* 63, no. 4 (2011): 228.

<sup>2</sup>Ibid.

<sup>3</sup>Each of 500 average-sized or larger proteins would have a minimum of 54 amino acids specific in type and sequence.

500 proteins x 54 specific amino acids/protein = 27,000 specific amino acids.

<sup>4</sup> $10^{60}$  information units investigating sequence space/planet x 10 planets/star x  $10^{24}$  stars/universe x  $10^{500}$  universes =  $10^{585}$  information units investigating sequence space.

<sup>5</sup>Philip Ball, "10 Unsolved Mysteries," *Scientific American* 305, no. 4 (October 2011): 48-9.

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## Calculating Probabilities of Carbon-Based Biomolecules

The quotations from my article cited by Nelson are not statements of "fiat science" but of practical reality. If a calculation of a reaction rate fails to include all relevant reaction paths, the result of the calculation will be in error. Perhaps it would have been clearer if I had added the adjective "... all *relevant* historical pathways ..." to indicate that the omission of a plausible path would lead to an erroneous result. I did not mean to imply that everything must be known before anything can be said.

As Nelson points out, all known biological information is carbon-based. In principle, it may be possible for life to be based on other elements, but this is not yet our experience.

The probability calculations that Nelson provides for various proteins are reasonably accurate for the scenario he assumes. The path he considers is essentially a collection of amino acids, from 54 to 27,000 for various protein families, coalescing in a random single-step assembly into the proper sequence. As he concludes, this is virtually impossible. However, it is not relevant to any evolutionary theory, none of which postulates such a path. All evolutionary theories hypothesize some type of step-by-step approach rather than a single step.

A macroscopic analogy may help illustrate the difference. Two blocks from the ASA office in Ipswich, MA, is a dam on the Ipswich River. Fish from below the dam can be observed upstream from the dam even though the dam is significantly higher than any of these fish can jump. Before we infer that a fisherman is catching the fish and transporting them upstream from the dam, we need to ensure we have considered all possible paths. On the far side of the river, we find a fish ladder that enables the fish to proceed step-by-step to reach the upstream side of the dam. What was impossible has become a feasible journey for the fish.

Wilf and Ewens have shown mathematically that while the probability of a single-step random assembly of a collection of elements scales *exponentially* with the number of elements, a step-by-step random assembly of those elements scales *logarithmically* with the number of elements.<sup>1</sup> That is the difference between impossibility and feasibility.

Nelson is correct to point out that we have not discovered the "fish ladder" that would account for the formation of the earliest complexes of biomolecules that could reproduce themselves and begin the chain of continuity of what we call life. But there is no reason to conclude that such a step-by-step process does not exist. No law or principle from information theory or any other discipline precludes such a scenario.

In evolutionary biology, probability calculations may have some value in determining whether a particular path to an event was feasible, but they are of little value in determining whether that event happened. The set of possibilities is too large. The fundamental flaw in every argument based on irreducible complexity is that only one or a few possible paths are analyzed. Upon finding those paths to be virtually impossible, the conclusion is drawn that no path is possible. Darwin encouraged some of this thinking by insisting on fine gradualism as a necessary feature. He did not have the benefit of the genetic research of the last few decades that shows the rich palette of pathways by which nature can proceed. We now understand that the number of possible paths is far greater than can be reasonably assessed.

Nelson is concerned that the units of biological information "fall short in the exploration of the sequence space for one average-sized, protein-folding motif by a factor ranging between  $10^{10}$  and  $10^{80}$ ." However, a recent study by Burke and Elber suggests a finite number of networks of protein-folding configurations so that "a model of evolution with only a few sequences evolving to fill out sequence space is plausible. The sequence space is well connected and allows for sequence migration between folds."<sup>2</sup>

In summary, we must approach probability arguments with a great deal of humility. It must be acknowledged that we know too little of nature's options to derive a credible probability. The search for the pathway to life goes on.

## Notes

<sup>1</sup>Herbert S. Wilf and Warren J. Ewens, "There's Plenty of Time for Evolution," *Proceedings of the National Academy of Sciences* 107, no. 52 (2010): 22454-6.

<sup>2</sup>Sean Burke and Ron Elber, "Super Folds, Networks, and Barriers," *Proteins: Structure, Function, and Bioinformatics* (2011), doi:10.1002/prot.23212.

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## Upcoming ASA Conferences

July 20-23, 2012: Point Loma Nazarene University  
San Diego, California

July 19-22, 2013: Belmont University  
Nashville, Tennessee