Christian truth claims. Should we not, as ASA members, be more careful in emphasizing this point to the younger generation, and uphold in higher esteem the wonders of the Creator's work as seen in living systems, rather than in what Darwin claims?

3. I have been an applied physicist and a research engineer all my life. In my discussions with nonbelievers, I can question *any and all theories* in the physical sciences, whether it is the second law of thermodynamics or Einstein's theories of relativity, but if I raise a question regarding the problems inherent in the theory (dogma?) of macroevolution, I am quickly dismissed as an ignoramus. What seems ironic is that both the second law and the laws of general relativity have been *demonstrated to be accurate* to 10+ decimal places, and yet the problem of biogenesis, which is the very starting point of Darwinian evolution, has evaded all explanations for over 150 years.

4. Do we, as ASA members who adhere to our Statement of Faith, have a responsibility to be more careful in mediating grace to our ID members instead of belittling their valiant efforts to integrate the Creator more directly into his creation? At present, we face virulent and persistent attacks from neo-atheists (I would rather call them *miso-theists)* such as Dawkins, Harris, Hitchens, Dennett, and Stenger. To this we should add the increasing hostility, both subtle and open, exhibited by academe toward any and all practicing Christians, no matter what their professional credentials are. In fact, *I have yet to see an ontological naturalist take seriously the best BioLogos position, in spite of how well argued the effort might be.*

Again, should not we, as members of ASA, help strengthen the faith of our younger colleagues in the face of relentless opposition from academe, by uncritically defending a theory that is the *sine qua non* of the nonbeliever? I wonder if it is time to have a more balanced approach to how God weaves in his creation the *supernatural with the natural in a seamless manner, without gaps,* which *he* has done throughout history, an observation that is cogently argued by C. S. Lewis in his book *Miracles.*

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## Biological Information and Carbon

In "Information, Intelligence, and the Origins of Life," (*PSCF* 63, no. 4 [2011]: 219–30), Randy Isaac wrote, "Without a clear understanding of all possible historical paths, no credible probability of occurrence can be determined,"[1] and "… probabilities and improbabilities cannot be reliably assessed unless all historical pathways and processes are well understood."[2] These statements exemplify fiat science, for which no supporting data are needed. They trump all scientific data, logic, and sound reason. Because they cannot be falsified, they are scientifically meaningless but very dangerous.

Isaac does not consider that biological information is inextricably linked to carbon. Only carbon-based information units explore sequence space, and the information is not prescient. Carbon is the ink of life, and it is finite. The upper 35 kilometers of Earth's crust contains about $10^{46}$ carbon atoms. For any given number of carbon atoms, enzymes are more information dense than DNA or RNA. The $10^{46}$ carbon atoms can assemble into fewer than $10^{43}$ units of information composed of 400 amino acid residues.

Each family of proteins has a unique protein-folding motif containing amino acids, which are specific in type and sequence. A selector cannot select for an enzyme until it is functional, and an enzyme is not functional until each specific amino acid is properly sequenced. The rules of probability are in play during their initial sequencing, because they have no history. The protein-folding motif of an average-sized family of proteins contains between 54 and 108 amino acids that are specific. The probability of their proper sequencing would range between 1 chance in $10^{70}$ and 1 chance in $10^{140}$ per try for L-isomer biological amino acids that are independent and identically distributed. So, are carbon-based information units potent in the exploration of this sequence space?

If each of the $10^{43}$ units of information were to alter its structure, and therefore its information, once per second for 3 billion years, fewer than $10^{60}$ unique units of information would have been existent. These units fall short in the exploration of the sequence space for one average-sized, protein-folding motif by a factor ranging between $10^{10}$ and $10^{80}$.

The primordial soup contained a mixed bag of amino acids including nonbiological amino acids and D- and L-isomers. Sparking experiments produce nine biological amino acids but add 26 nonbiological amino acids to the mix. Meteorites transport 60 nonbiological amino acids to the mix. Eleven biological amino acids are not produced in sparking experiments or transported to Earth by meteorites and are "rare." If 10% of the amino acid residuals are glycine, the probability that an average-sized, carbon-based information unit would be composed of only L-isomers is about 1 chance in $2^{360}$ or less than 1 chance in $10^{108}$ per try. The integrity of the information contained within such units would be highly corrupted through the addition of nonbiological amino acids and D-isomers and through the infrequent insertion of "rare" biological amino acids. Several might escape corruption, but the probability is that these few would be written as gibberish. Unplanned carbon-based information is impotent in assembling the protein-folding motif of average-sized proteins.

The protein-folding motifs of 500 average-sized or larger protein families have a total of far more than 27,000 amino acids specific in type and sequence.[3] The probability of their correct sequencing would be far less than 1 chance in $10^{35,000}$ per try. A single alteration would remove an entire protein family from existence. The carbon-based information units from $10^{500}$ universes would be inadequate to investigate this sequence space.[4] The unplanned origin of life and the unplanned assembly of the first cell are highly speculative scientific hypotheses masquerading as scientific theories. *Scientific American* labels them "mysteries."[5] They do not belong in a natural science curriculum.

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

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

[2]Ibid.

[3]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.

[4]$10^{60}$ 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.

[5]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.[1] 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."[2]

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

[1]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.

[2]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
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July 19–22, 2013: Belmont University
                  Nashville, Tennessee