

Evolution and Probability
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Some of the most impressive-sounding criticisms of the conventional theory of biological evolution involve probability. Such arguments have been raised, not just by religious fundamentalists, but by numerous others who are reluctant to accept the prevailing scientific theory of the history of life on earth. On the basis of such arguments, some conclude that the currently accepted theories of naturalistic origin of life and evolution are seriously flawed. Others argue further that these arguments demonstrate that life on earth could only be the result of miraculous acts by a divine creator.

As a scientist of religious faith with training in probability theory, I have studied a number of these arguments in some detail. It is well known among mathematicians that probability arguments are treacherous — even experts can fool themselves. In the hands of those who are not expert both in probability *and* evolution, and especially in the hands of someone with an agenda to advance, the results are, in my experience, almost universally invalid. A few examples will illustrate how probability should and should not be used.

Looking at Hemoglobin

Anti-evolutionists have for many years advanced probability arguments in their efforts to “prove” the impossibility of scientific models in cosmology, astronomy, physics, and the origin of life. More recently, Michael Behe's concept of “irreducible complexity” in biochemical systems has fueled various arguments about the impossibility of a natural emergence of complex biological systems, such as blot clotting cascades, the bacterial flagellum, and hemoglobin. The basic approach used in these studies is to calculate the probability that some phenomenon could occur by a natural means, and then to claim that the extremely remote probabilities render the existing scientific theory invalid.

David Foster's *The Philosophical Scientists* (1993) uses such an approach, derived loosely from the earlier work of Hoyle and Wickramasinghe (1981; *see related article by Richard Carrier on p xxx*). The general argument goes something like this:

Consider the alpha chain of human hemoglobin — a key component of blood which serves as a transfer agent for oxygen. The alpha hemoglobin molecule is a protein chain based on a sequence of 141 amino acids, and the hemoglobin of virtually every human has the same sequence.

There are 20 different amino acids common in living systems. Thus the number of different chains [141 amino acids long] is 20^{141} , or roughly 10^{183} . If 5 billion years ago, as many as 10^{40} amino-acid–molecule generators, each producing a different randomly chosen 141–amino-acid sequence one billion times per second, began generating sequences, then at the present point in time only about 10^{66} sequences would have been generated. Thus the probability that human alpha hemoglobin

would have been produced is about $10^{66} \div 10^{183} = 10^{-117}$, a fantastically small number. Thus no conventional theory of molecular evolution can account for the origin of human alpha hemoglobin.

This is an intriguing line of reasoning, but it has serious flaws. One flaw, common to many arguments of this sort, is that it is an after-the-fact assessment of probability, which is unreliable without a very careful consideration of all possible alternate contingencies. This difficulty can be illustrated by examining discrepancy counts between the alpha hemoglobin chains of humans and other animal species (see examples in Hoyle and Wickramasinghe 1981: 17).

As one might expect from evolutionary models, the differences in the molecular structures of these hemoglobin chains are entirely consistent with the phylogenetic “family tree”. In particular, the human alpha chain is identical with that of chimpanzees and differs by only one amino acid from gorillas. In more distant vertebrate relatives, the alpha hemoglobin chain differs by 25 amino acids between humans and rabbits and by about 100 between humans and various fish species.

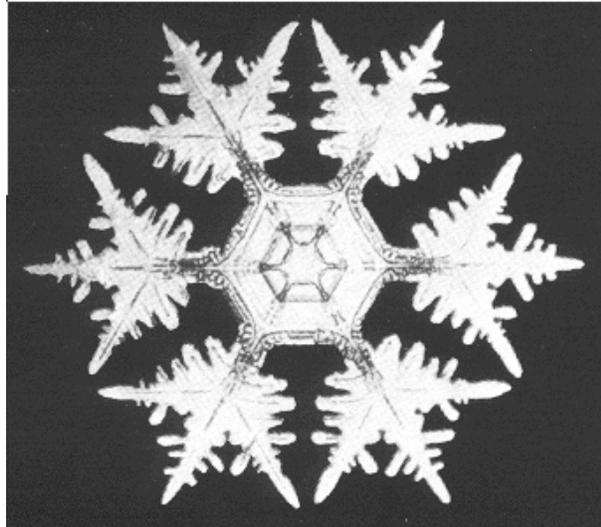
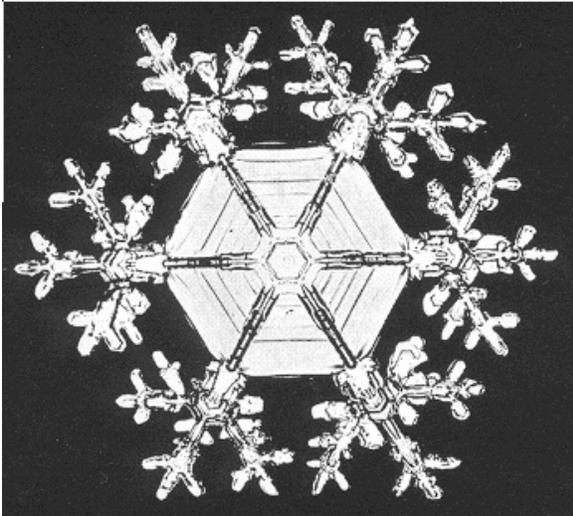
Thus there are countless variants of the alpha hemoglobin chain that perform the essential function of oxygen transport, since these variants successfully serve that function in various other animal species. Indeed, most of the 141 amino acids can be changed without altering this basic oxygen transport function. The process of evolution long ago settled on one particular sequence for humans, but many others *might* have been selected without loss of essential function.

Revising the probability calculations used by Hoyle and Wickramasinghe from this point of view — that only about 25 particular locations must be correct to enable the oxygen transport function — the probability that a chain 141 amino acids long would be a usable hemoglobin molecule can be calculated as 1 in 20^{25} , or roughly 1 in 10^{33} . This is still a very small probability, but it is vastly greater than 1 in 10^{183} — the probability calculated by Hoyle and Wickramasinghe. Given odds of 1 in 10^{33} , the hypothetical random molecular generators mentioned above could discover a usable hemoglobin molecule trillions of times per second (although no one suggests this is the way that hemoglobin actually arose). Furthermore, the probability calculations employed by anti-evolutionists assume that all 10^{183} amino acid chains of length 141 are equally likely to be produced. Instead, we know that some classes of molecules are much more likely than others to arise naturally.

In summary, modern biology has only a partial idea of the process through which human hemoglobin originated and how it has changed through the years. Thus it is highly premature to pretend that anyone understands the process well enough to compute accurate probabilities. Such calculations are inconclusive.

Learning From Snowflakes

Another way to better understand the difficulties with anti-evolution probability arguments is to consider snowflakes. Each individual flake is much less than a milligram in mass, yet snowflakes exhibit remarkably beautiful and symmetrical patterns. Bentley and Humphrey's book *Snow Crystals* (1962) includes over 2000 high-resolution black-and-white photos of real snowflakes. Many of these images are utterly fantastic, with wildly improbable yet astonishingly regular patterns. Each one occurred naturally and was collected and photographed by Bentley and his assistants.



What are the chances that one of these structures can form “at random”? To simplify the problem, let us consider only the phenomenon of 6-way symmetry, a characteristic of almost all snowflakes. Imagine laying out the snowflake on a small grid with 100 subdivisions on a side (so that the grid contains 10 000 cells) divided into 6 equal sectors (with about 1666 cells each). We can calculate the probability that the pattern in one sector will be identical with the five patterns in other sectors as follows: the probability that 2 sectors have identical patterns is approximately 2^{-1666} , or roughly 10^{-500} ; this value raised to the 5th power is 10^{-2500} . This probability is even more extreme than those I have seen in anti-evolution literature.

Even if we allow that snowflakes in nature are not perfectly symmetrical (so that perhaps some stretching might be required for the sectors to precisely overlap), a snowflake is an exceedingly improbable structure, by any reckoning. In particular, it is extremely unlikely that a random roll-of-the-dice assemblage of water molecules would assemble a single snowflake with a specific designated structure. And yet this phenomenon is repeated trillions of times in a typical snowstorm.

It is important to note that, in contrast to evolution, this process does not require billions of years to occur — most snowstorms last only a few minutes to hours at most. Further, there is no coding mechanism to specify the outcome, as there is in the intricate machinery of DNA-based genetics. Snowflakes just happen — a homogeneous, undifferentiated mass of water molecules cools and becomes a sea of beautiful snowflakes with highly specific and differentiated structures. One could almost convince oneself that snowflakes constitute a demonstration of supernatural power.

What is wrong with the above line of reasoning? It is the fundamental assumption that a snowflake forms all at once as a random roll-of-the-dice conglomeration of water molecules. It does not. It is the product of a long series of aggregations, each acting under known physical laws of atomic interactions, forming much as a crystal of salt forms. A snowflake's 6-way symmetry is in fact a reflection of an underlying 6-way symmetry inherent in the atomic structure of frozen water.

Arguing from Probability and Design

This same general criticism applies to many probability-based arguments against evolution. Such arguments usually assume an all-at-once, completely random assemblage with no pre-existing structure. But this is most assuredly not what has happened — the organism or amino-acid chain

we see today is the end product of countless generations over many millions of years, taking a small step each time. At each step, the existing structure is modified— added to, subtracted from, and so on. It is not “back to the drawing board” each time, but rather adjusting, fine-tuning, re-tooling existing plans. The evolutionary process is astonishing — one that we do not yet fully understand — but there is clearly nothing there that represents a violation of any of the fundamental the laws of probability.

Probability calculations should be a tool to help us calibrate the diversity of life and the extent to which various lineages may have diverged from common ancestors. Instead, they often are used as a tool to manipulate scientifically unsophisticated audiences. Further, probability-based arguments for a Creator are, as far as I can tell, merely another instance of the “God of the gaps” approach to theology — the shopworn philosophy that God can be found in the gaps of what currently remains unexplained in science. Those who have adopted this approach over the centuries have invariably been disappointed as scientific knowledge fills more and more of the remaining “gaps”.

Nowadays the catchphrase for this approach is “Intelligent Design Theory” (IDT). The idea is that such remote improbabilities can only be overcome by a designer. Many in the IDT movement see that designer as the God of the Bible, and design in nature as proof of the existence and direct involvement of God in minute details of everyday life. But it is wise to keep in mind the common experience of many religious believers, who have found that seeking “proofs” for the existence of God (scientific or otherwise) is an ineffective and often counter-productive route to faith. Jesus of Nazareth frequently commented on the dangers of seeking “signs” (Matthew 12:39, 16:4; Mark 8:12; Luke 11:29). Sounds like good advice to me.

References

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