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Evolution: The Blind Watchmaker?

DR BRUCE WATTS

THE PROBABILITY OF COMPLEXITY

Isaac Asimov in **The Genetic Code**[1] talks about the 'haemoglobin number', which is a large number associated with the low chance of getting this common animal protein by the random combining of suitable organic molecules. Haemoglobin is a four chain protein consisting of 146 amino acids. There is one particular combination generally used by the human body, although some 30–50 variants causing disease (but not necessarily death) are known***** Since there are 20 different amino acids commonly found in living things, the number of combinations of 146 amino acids possible is 20^{146} which is approximately 10^{190}, that is, a 1 with 190 zeros after it. If there were 10^{100} different combinations produced every second (actually this is impossible as there are only around 10^{78} atoms in the observable universe) it would take ten trillion trillion (10^{25}) years, with no repetitions, to produce all the possibilities. Thus it is difficult to see how this molecule could occur by chance, let alone the cellular machinery to reproduce it. This sort of problem applies not only to probability associated with the origin of life but also to the probability of accidentally getting an advantageous mutation or chance improvement to a pre-existing biological structure (for example, a gene or protein).

AN EVOLUTIONIST RESPONDS

How does an evolutionist answer this problem? One author who has made an attempt is Richard Dawkins, a lecturer in zoology at Oxford University and a well-known anti-creationist. In a parody of William Paley's original argument for design, where Paley suggested the existence of a watch implies the work of a watchmaker (and the existence of complex life implies an intelligent creator), Dawkins wrote a book which he titled **The Blind Watchmaker**.[2] The book aims to dispose of the argument for God the designer and to demonstrate the ability of natural selection to achieve complexity.

In this book Dawkins sets out to defend the view that all life arose gradually by a process of mutation and natural selection from simpler forms, and ultimately from an inorganic chemical soup. Dawkins goes to some lengths to demonstrate that the punctuationists, who insist rapid evolution has occurred at irregular intervals, and the saltationists, who suggest single large jumps in complexity could occur in a one step mutation, are both proposing mechanisms that are well outside the realms of probability. He then attempts to tame the probability question by means of a computer model that is supposed to show how cumulative selection can operate in a non-random way to make complexity appear by chance. It is a key point in his argument that although the process can be non-random it must be non-directed, meaning that selection does not lead to any particular target. This watchmaker is meant to be truly blind: he must have no idea what a watch is or looks like so that the process of selecting does not work on the basis that it chooses 'mutations' that look or function like a watch.

Dawkins begins his thesis by using the phrase *'Methinks it is like a weasel'* and showing that a 'monkey' typing nonstop on a typewriter would have approximately 10^{40} different 28 letter phrases available by random choice. The monkey would thus have a 1 in 10^{40} chance of typing the correct phrase on any given attempt. However, the alleged age of the universe is a negligible time in comparison with how long it would take a million monkeys typing a different 28 letter version every second to make 10^{40} tries and come up with all the possible combinations. However, if 'cumulative selection' is used the odds change drastically. In this case the monkey retains his 28 letter phrase if it more closely resembles the target phrase, and then his next

*** FOOTNOTE**

A handful of abnormal haemoglobins are known which do not appear to cause disease, suggesting that not all single amino acid substitutions are functionally detrimental. That is, there are minor variations to the sequence which also 'work'.

Furthermore, amino acid coupling to produce peptide chains may not be entirely random — that is, certain 'letters' of this chemical alphabet are slightly more likely to follow some others. The work which has suggested this indicates that it is a very weak effect, however.

These two caveats together do affect the mathematical argument in this paragraph, but to a very small degree, and are mentioned merely for completeness.

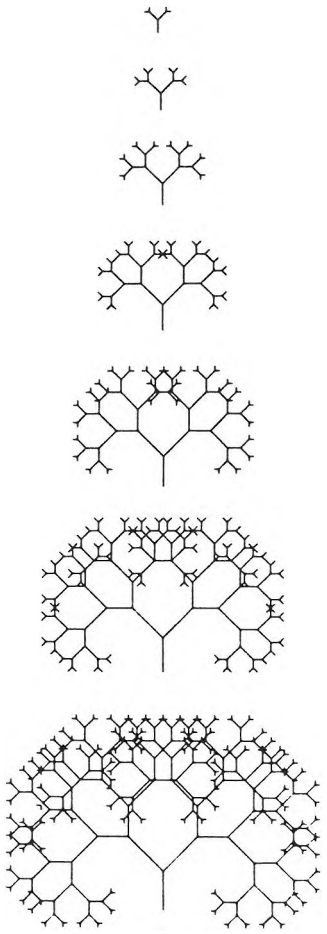

Figure 1. *Some of the branching line structures that Dawkins generated with his computer program (after Dawkins[3]).*

attempt builds on this by mutating it rather than starting again. Mutations in this calculation only affect letters in the phrase that are different to the target phrase *'Methinks it is like a weasel'*. If the new version contains new letters that are now like the target phrase, then these are also retained and the process is repeated. On average the monkey will now take some 40–60 tries before reaching its target phrase correctly.

The problem with this analogy, when applied to evolution, is that it is cumulative selection on the basis of knowing what the final product should be. Dawkins' 'watchmaker' is choosing mutations without being blind; prior knowledge is used to make intelligent choices. The selection is directed to a target.

COMPUTER 'BIOMORPHS'

Dawkins attempts to overcome this objection with another analogy, using what he calls computer biomorphs. A computer program generates branching line structures and then builds on the structures that are favoured by his own eye (see Figure 1). The computer program has nine variables which control the appearance of the branching structure, including length of the line before branching, number of branches, angle at which new branches are drawn, etc. By altering these variables the computer is able to generate a large number of interesting shapes, some of which bear a resemblance to insects, spiders, candelabras or spitfires (see Figure 2). The selection criterion is the computer operator's decision: if the shape resembles something vaguely familiar it is retained and then causes another mutation to occur to that branching structure.

At one point Dawkins lost his 'genetic formula' for an insect-like shape and then attempted to find it again by trial and error from scratch. This proved extremely difficult even knowing the target shape. He then, rather boldly I feel, claims that this showed that his selection was non-directed in originally coming up with the interesting shapes. He writes :-

> 'I *programmed EVOLUTION* (the name he gave his biomorph program) *into the computer, but I did not plan "my" insects, nor the scorpion, nor the spitfire, nor the lunar lander. I had not the slightest inkling that they would emerge, which is why "emerge" is the right word. True, my eyes did the selecting that guided their evolution, but at every stage I was limited to a small clutch of progeny offered up by random mutation, and my selection "strategy" such as it was, was*

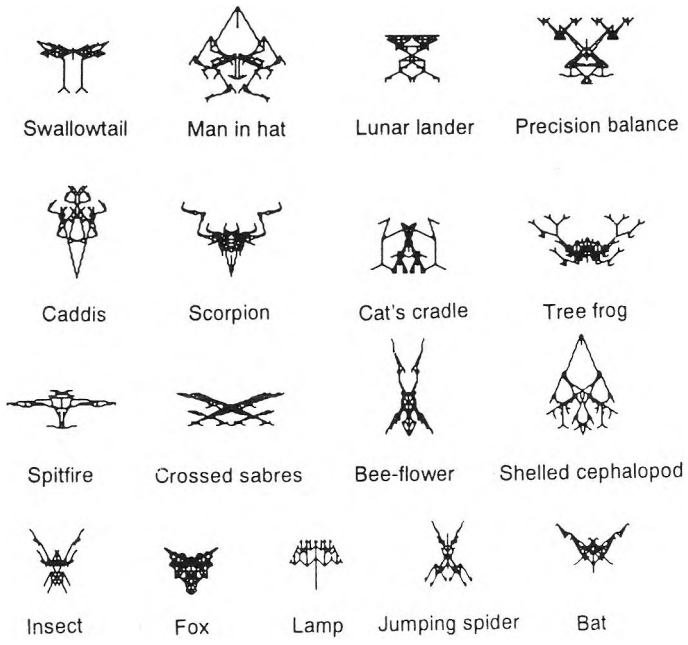

Figure 2. *Some of the large number of interesting shapes, generated by Dawkins' computer program EVOLUTION, which he called 'computer biomorphs' and gave names to because of their similarities to known objects or animals (after Dawkins[4]).*

opportunistic, capricious and short term. I was not aiming for any distant target and nor does natural selection.'[5]

However, despite this bold statement, the selection process **was** directed towards targets. The targets are 'objects of familiarity', which is a criterion that requires a knowledge of these objects and a (large) computer (the human brain) and an organ of sight (the human eye) in order to make non-random selections. If this model were truly non-directed Dawkins should in fact have worn a blindfold whilst choosing shapes! It is likely that using a blindfold and making selections over 40–60 generations the shapes would mostly resemble branching scribbles. The problem still remains how to cut down the amount of non-useful results from this computer simulation in order to arrive at anything useful (or at least anything giving an appearance of usefulness). True blinded selection leaves one with vast numbers of branching lines resembling nothing.

This critical lapse in logic seems to crop up regularly in evolutionary thought. The concept of convergent evolution is a euphemism for this type of thinking. Convergence is the term used to explain how organs or organisms with totally different 'ancestry' can evolve separately and wind up being extremely similar. For instance, the octopus eye and human eye are quite similar but have supposedly evolved separately; the marsupial thylacine (Tasmanian tiger) and the wolf are very similar in appearance but have evolved separately. The 'explanation' lies in the idea that similar habitats have brought forth similar phenotypes. But how is evolution to know in advance what a habitat requires? How is it within reason that by accident the same design would occur twice (or more in the case of the vertebrate eye) without any selection occurring on the basis of 'does it look like the target organ?'? Remember, we couldn't even get 'Methinks it is like a weasel' without intelligent directed input. Yet here 'evolution' has been granted the ability to see where it is going and choose selections that make another eye just like the one that has already evolved or another animal just like the kind that already exists. The watchmaker has his blindfold off again.

MAJOR HURDLES

There are several other major hurdles for the evolutionist who chooses a model like this to try to explain away the argument from design. Firstly, the term biomorph gives you a sense that there is some real order in the computer drawings. In fact, all that has been arrived at is a group of lines. The biomorph that resembles an insect has no intrinsic complexity, no design, no order and no value in itself that distinguishes it from a scribble that resembles nothing at all. Its only value is that it strikes a chord with the operator's human experience. Because it is a directed process rather than a mere survival of the fittest it is a video game that cannot be a model for natural selection in biology. 'Resembling an insect' is a criterion that assumes eyesight, human experience, knowledge of insects and the ability to compare drawings to real objects. This is hardly random when such a large input of intelligence is required to 'work' the model. It seems Dawkins is attempting to compare tennis balls with oranges when equating his biomorphs with biological organisation.

Interestingly, proteins in biology do have some similarities to Dawkins' biomorphs: they are molecules that usually depend on specific 3D shapes at their active sites for their function, and they are structures that are built in chains with repetitive peptide bonds between amino acids. This could be equated with branch points in a biomorph and thus be the closest that this computer model comes to having an analogy in living systems. Don't forget that hundreds of specific proteins are required for even the simplest cellular function, and possibly 10,000 or so for a fully functioning cell, so we are talking about the most basic level of order when discussing proteins.

Of course this brings us back to the impossible 'haemoglobin number' since haemoglobin is itself a protein, and we are thus left with the original dilemma of how to accidentally 'strike' something useful. Whereas the computer needs 40–60 tries to reach a 'biomorph', our universe hasn't enough atoms to begin trying to get a combination like haemoglobin. It should not be forgotten too that peptide bonds are equilibrium bonds and are thus reversible (the odds generally favouring dissociation in a chemical soup environment). To be truly analogous here the biomorph model ought to be arranged such that any branch that does form should be capable of disappearing at the next touch of the computer keyboard. In fact, it should be 100 times more likely to disappear than to add another branch each time the keyboard is used. As Arthur Wilder-Smith has calculated, the odds of getting **any** order of 10 amino acids joined in a chain in a chemical broth of amino acids is 1 in 10^{20} (that is, one chain 10 amino acids long per 10^{20} amino acid molecules in the broth) because of the rate of dissociation. The 10 amino acid polypeptide is then likely to dissociate very quickly anyway![6] It is thus difficult to see how a *specific* sequence of, say, 10 amino acids will occur randomly when the probability of any chain of this length forming, in any sequence at all, is so low in the first place. The odds deteriorate rapidly, as we have seen, when we attempt to get specific sequences longer than this.

Secondly, the biomorph model ignores the amount of information required to reach a point in biology where an organism can reproduce. That initial jump from nothing to the simplest living thing requires a single step selection rather than cumulative selection to use Dawkins' terminology. In chapter 6 of his book there is an example of a hypothetical intermediate step between a chemical soup and self-replication involving DNA. The particular concept is that of Graham Cairns-Smith, a Scottish chemist who has suggested that layers of clay crystals may align adjacent molecules in an identical arrangement thus replicating themselves in minute detail. It is then suggested that

this process becomes a means of transmitting information through generations of crystals. Furthermore, reactive clays may have catalysed organic reactions and been thus associated, albeit in a vague way, with the origin of RNA (or DNA). The RNA finally proves to be a better replicator and causes the extinction of its less fit clay predecessor.[7] Unfortunately for this model there are no known clay replicators and there is no conceivable way that a clay crystal could translate its information into the language of RNA. The RNA, if it did occur, then has only limited means of replication without the cellular machinery and metabolism of a living cell. Thus it remains merely to calculate the odds of a single lucky event that would arrive at the minimum amount of information required for the simplest living thing. In the case of the simplest known viruses (which cannot actually reproduce without borrowing the chemical machinery of a living cell) the length of the DNA sequence is approximately 2500 bases. This calculates out to a probability of the order of 1 in 10^{1500} of randomly selecting the right sequence from a pool containing only the 4 bases used in DNA (remember there are only 10^{78} atoms in the known universe). In other words, a living cell with the ability to replicate itself must of necessity be much more complex than this simplest of viruses.

SKIN TO EYE

Thirdly, the biomorph model attempts to explain how a complex organ like the eye could form by successive steps. Dawkins rightly rejects Lamarckism and large jump mutations, holding strictly to the view that there must have been very gradual slight changes between skin and its myriad intermediates leading up to the eye. He suggests that one needs only to think of a structure just one minute step backwards from the eye and it will then be conceivable that a mutation may change it to an eye, given that there is but a slight difference in the two. This logic/process can then be repeated for a further step backwards and *ad infinitum* a series can be constructed with slight gradual changes from eye to skin (or skin to eye).

Dawkins carefully avoids any mathematical analysis of this concept in his book. For instance, if the 'organ' one step back from the eye has some vision in order to be useful, then it will carry a DNA sequence coding for its structure that may be 10^8 bases long (especially since it must not be too different from the DNA sequence for an actual eye). Let's say for argument's sake the sequence is 10^6 codons long, then we have approximately 20 (20 amino acids to choose from) to the power of 1 million possible single point mutations that could occur. Perhaps 100 of these, in the extreme optimist's view, might improve the vision, leaving us with a likelihood of around 1 in $10^{100,000}$ that we will strike one of those mutations that will lead us closer to a complete eye. The probability of getting a mutation that improves an organ is thus on the same scale as that of getting a living cell from nothing. As Michael Denton puts it in his book **Evolution: A Theory in Crisis,** this whole issue of extreme improbability '*comes very close to a formal disproof of the whole Darwinian paradigm of nature.*'[8]

Fourthly, the biomorph model lacks the crucial ingredient of embryology. The computer has a set of guidelines for drawing branching structures ('genes' as Dawkins calls them) which directly give rise to his structures (biomorphs). In biology, however, the DNA sequence is a recipe that mixes up the right ingredients in the right way which then come together to form a structure. Our bodies are not built of DNA Lego; we are built of protein (among other things) which forms under the control of the information in the DNA. For example, the information for the construction of the eye comes from DNA in a variety of chromosomes. These influence distinct areas of the embryo (for example, ectoderm and neuroectoderm) to form the different layers of the eye's structure, which are then 'woven' together to complete a functioning complex organ. Thus any mutation to the DNA doesn't change the eye structure directly; it changes the recipe for the construction of an eye. Understanding this helps us see why a single point mutation can ruin an entire structure — the DNA is altered by one base and the recipe is altered at a critical point. If there were no embryological step it may be slightly easier to conceive of a successful mutation improving a structure. It also helps us see why it may not in fact even be possible to have a large series of very slight changes to the DNA leading up to a complex organ like the eye.

If the eye's structure were in fact a building made of DNA blocks, then it is conceivable that mutations may actually add to the structure and make it more complex. However, if there were say 10,000 theoretical intermediate versions of the DNA sequence between skin and eye, then we have 10,000 different recipes for eye construction. Unfortunately for evolution it is highly likely that nearly all these recipes won't work, and even though the proposed intermediate DNA sequence may be half way between 'skin' and 'eye' DNA sequences, it is unlikely to construct anything useful. Thus embryology makes it likely that a sequence of intermediate steps between 'skin' and 'eye' is an impossibility using the DNA-RNA-protein mechanism of all known animals. No such sequence may be feasible at all, let alone probable.

CONCLUSION

In closing, one can only be reminded of the Scriptures' view that *'their thinking became futile in association with their foolish hearts being darkened'* (Romans 1:21). The argument that design reflects purpose and intelligence holds good in the face of the pseudo-logic in **The Blind Watchmaker.** Richard Dawkins is brutal in his treatment of creationists in his book — he calls them feeble-minded, pathetic, selective, intellectual cavemen. However, he is short on substance when it comes to the 'nuts and bolts' of how complexity is achieved against logic and probability,

without an intelligent creator.

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Dr Bruce Watts is a medical doctor with an M.B., B.S. from The University of Sydney. He works in general practice at Woolgoolga on the New South Wales North Coast, Australia.