

Avoiding Unsubstantiated Claims in Evolutionary Science

(This paper was rejected for inclusion in UNCW's Journal of Effective Teaching: Special Issue on Teaching Evolution, even though no other paper addressed the issues raised herein. You be the judge if these issues warrant the warnings presented in this paper. It has been reformatted to remove all JET-supplied formats.)

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Abstract

Evolutionary claims are often not substantiated by known science. Many of the claims previously purported are shown to be discredited by currently known science. Claims concerning the origin of life are shown not to be part of science. Claims concerning the origin of species are shown to require much more information before uncritically accepting the standard Darwinian scenario. Summaries of findings from both physical and informational science research are presented. Although not elaborated explicitly, these findings have implications in fields beyond science, such as in politics, religion, philosophy, and most fields of study.

Keywords: Origin of life, Macroevolution, Science speculation

Introduction

Making "scientific" claims that can't be substantiated by known science can cause a multitude of problems. Obviously, if such a claim is later shown to be false, the reputation of all science suffers, with all the ramifications of that reputation decline in such areas as funding and other support. Since many disciplines use Darwinian speculations thought to be scientific, the material in this paper is meaningful beyond the natural and informational sciences (my personal fields of expertise, with earned doctorates in each). The reputation with students is also significant, as they may ask "what else that I'm being taught is false?", or simply dismiss verifiable science with the unsubstantiated claim. Making such claims can also be a source of embarrassment to the teacher making such claims if confronted by a student to justify the claim with known science. This paper will highlight areas connected to evolution that are rife with unsubstantiated claims so that a prepared teacher can avoid making such claims. Some of the issues were presented (Johnson, 2004) at the 2004 International Conference on Bioinformatics, where I pointed out: "The incredibly complicated digital information that is the focus of Bioinformatics will raise doubts as to the role of chance in evolutionary biology... Does Bioinformatics support traditional biological views, or will it point in new directions, perhaps proposing other mechanisms for possible testing? Bioinformatics has much to say about the exquisite information in the macromolecules that form life, the repeated patterns, homologues, and gene sequences. What, if anything, does it have to say in regard to biology's unanswered questions?" Many references are included that highlight areas that have so much unknown that one must be very cautious when tempted to make pronouncements in those areas.

Origin of Life

It is significant that nearly everything presented (and which I accepted) as origin of life "Truth" during my education through my first Ph. D. in Chemistry by the American Chemical Society's program "From Molecules to Man" has been discredited by more recent discoveries in science. The basics of this program included chance amino acid formation, from which proteins

were formed, which produced DNA, which eventually became encased in a cell like that of known life. The now-famous Miller-Urey (Miller, 1953) implementation of the “prebiotic soup theory” (Oparin, 1952) usually is credited as the first production of amino acids from inorganic sources. They formed some organic monomers from an oxygen-free highly reduced mixture of methane, ammonia, and hydrogen gases with a spark generator designed to simulate lightening. The products included a racemic (no polarized light rotation) mixture of simple amino acids that were immediately removed from the reaction to prevent rapid decomposition (Cairns-Smith, 1993, p. 44-45). Although it was stated “We believe that there must have been a period when the earth's atmosphere was reducing, because the synthesis of compounds of biological interest takes place only under reducing conditions,” (Miller & Orgel, 1974, p. 33) “many researchers now hold that the ancient Earth's atmosphere, compared with the earlier view, had more oxygen and less hydrogen – as the atmosphere does today. Amino acids don't form as readily under that condition as they did in the 1953 experiment, and when they do form, they tend to break apart.” (Gorman, 2001) It is also recognized that “functionally effective proteins have a vanishingly small chance of arising spontaneously in a prebiotic environment.” (Jimenez-Montano, 2004) Yockey (2005) has pointed out that “all speculation on the origin of life on Earth by chance can not survive the first criterion of life: proteins are left-handed, sugars in DNA and RNA are right-handed,” (p. 119) and “unfortunately, the interpretations of the corpus of publications on the origin of life is false. Those experiments are based on a belief that life is just complicated chemistry and that the origin of life, if it could be found, is emergent from organic chemistry.” (p. 147)

Research on known life has resulted in an intractable problem. “The work of Watson and Crick and others has shown that proteins are formed according to the instructions coded in DNA. But there is a hitch. DNA cannot do its work, including forming more DNA, without the help of catalytic proteins, or enzymes. In short, proteins cannot form without DNA, but neither can DNA form without proteins. To those pondering the origin of life, it is a classic chicken-and-egg problem: Which came first, proteins or DNA?” (Horgan, 1991) “Anyone trying to solve this puzzle immediately encounters a paradox. Nowadays nucleic acids are synthesized only with the help of proteins, and proteins are synthesized only if their corresponding nucleotide sequence is present. It is extremely improbable that proteins and nucleic acids, both of which are structurally complex, arose spontaneously in the same place at the same time. Yet it also seems impossible to have one without the other. And so, at first glance, one might have to conclude that life could never, in fact, have originated by chemical means.” (Orgel, 1994)

The “RNA world” (Woese, 1967 & Crick, 1968) has been proposed to circumvent the difficulty of accounting for the DNA/RNA/protein origination, and currently is the most widely accepted undirected natural scenario for life's origin. In this scenario, RNA functions as both an enzyme and as a replicator. (Kruger, Grabowski, Zaug, Sands, & Cech, 1982) The 1989 Nobel Prize winning discovery of ribozymes, RNA that can function as an enzyme, has spurred much research and speculation for the RNA world. “The problem of the origin of life is the problem of the origin of the RNA World, and that everything that followed is in the domain of natural selection.” (Orgel, 2004) The “Molecular Biologists Dream” (Joyce & Orgel, 1999, p. 49–77) for the origin of the RNA World “can be strung together from optimistic extrapolations of the various achievements of prebiotic chemistry and directed RNA evolution.” (Orgel, 2004)

Orgel points out several remaining problems including the nonenzymatic synthesis, polymerization, and replication of nucleotides to produce RNA capable of exponential growth in the prebiotic environment, and that “difficulties remain so severe that alternatives to the de novo appearance of RNA on the primitive Earth deserve serious consideration.” (Orgel, 2004) “But where the first RNA came from is a mystery; it's hard to see how the chemicals on early Earth could have combined to form the complicated nucleotides that make up RNA.” (Davenport, 2000) “Numerous problems exist with the current thinking of RNA as the first genetic material. No plausible prebiotic processes have yet been demonstrated to produce the nucleosides or nucleotides or for efficient two-way nonenzymatic replication.” (Nelson, Levy, & Miller, 2000)

“The prebiotic synthesis of nucleotides in a sufficiently pure state to support RNA synthesis cannot be achieved using presently known chemistry.” (Orgel, 2004) It’s important to realize “ribosome creation requires many RNA-modification enzymes that are still unknown.” (Barry, 2008) “There is no evidence that transcription or RNA replication involve ribozyme catalysis... One must recognize that, despite considerable progress, the problem of the origin of the RNA World is far from being solved.” (Orgel, 2004)

“Nobody knows how it happened but, somehow, without violating the laws of physics and chemistry, a molecule arose that just happened to have the property of self-copying – a replicator.” (Dawkins, 1996C, p. 282-3) The question “How did life begin?” is one of the “biggest unanswered questions” in biology. (New Scientist, 2004) “What creates life out of the inanimate compounds that make up living things? No one knows. How were the first organisms assembled? Nature hasn't given us the slightest hint. If anything, the mystery has deepened over time.” (Easterbrook, 2007) “We once thought that the cell, the basic unit of life, was a simple bag of protoplasm. Then we learned that each cell in any life form is a teeming micro-universe of compartments, structures, and chemical agents—and each human being has billions of cells.” (Lester & Hefley, 1998, p. 30-31) “The unexpected levels of complexity revealed at the molecular level have further strained the concept of the random assembly of a self-replicating system.” (Swee-Eng, 1996) “When discussing organic evolution the only point of agreement seems to be: ‘It happened.’ Thereafter, there is little consensus, which at first sight must seem rather odd.” (Morris, 2000)

The above discussion from the physical science perspective should be sufficient to avoid any presentation of life's origin as science. The information content and processing makes it currently impossible (zero probability) to present any scenario as science. “The question ‘How did life originate?’ which interests us all, is inseparably linked to the question ‘Where did the information come from?’ Since the findings of James D. Watson and Francis H. C. Crick, it was increasingly realized by contemporary researchers that the information residing in the cells is of crucial importance for the existence of life. Anybody who wants to make meaningful statements about the origin of life would be forced to explain how the information originated. All evolutionary views are fundamentally unable to answer this crucial question.” (Gitt, 1997, p. 99) “There are no chemical bonds between the bases. Thus, there are no chemical rules to determine the order in which the bases will be attached to the background.” (Davis & Poe, 2002) Carl Sagan (1997) wrote: “The information content of a simple cell has been established as around 10^{12} bits, comparable to about a hundred million pages of the Encyclopaedia Britannica.” “Due to the abstract character of function and sign systems, life is not a subsystem of natural laws. This suggests that our reason is limited in respect to solving the problem of the origin of life and that we are left accepting life as an axiom... Life expresses both function and sign systems, which indicates that it is not a subsystem of the universe, since chance and necessity cannot explain sign systems, meaning, purpose, and goals.” (Voie, 2006) Evolutionary biologist George Williams (1995, p. 42-43) observed: “Evolutionary biologists have failed to realize that they work with two more or less incommensurable domains: that of information and that of matter... These two domains will never be brought together in any kind of the sense usually implied by the term ‘reductionism.’ ... Information doesn't have mass or charge or length in millimeters. Likewise, matter doesn't have bytes... This dearth of shared descriptors makes matter and information two separate domains of existence, which have to be discussed separately, in their own terms.”

“One cell division lasts from 20 to 80 minutes, and during this time the entire molecular library, equivalent to one thousand books, is copied correctly.” (Gitt, 1997, p. 90) “Crick expounded and enshrined what he called the ‘Central Dogma’ of molecular biology. The Central Dogma shows that influence can flow from the arrangement of the nucleotides on the DNA molecule to the arrangement of amino acids in proteins, but not from proteins to DNA. Like a sheet of paper or a series of magnetic points on a computer’s hard disk or the electrical domains in a random-access memory – or indeed all the undulations of the electromagnetic spectrum that

bear information through air or wires in telecommunications – DNA is a neutral carrier of information, independent of its chemistry and physics... As the Central Dogma ordains and information theory dictates, the DNA program is discrete and digital, and its information is transferred through chemical carriers – but it is not specified by chemical forces. Each unit of biological information is passed on according to a digital program – a biological code – that is transcribed and translated into amino acids.” (Gilder, 2006) Bill Gates, founder of Microsoft, writes (1996, p. 228): “Human DNA is like a computer program but far, far more advanced than any software we've ever created.”

“Information” has two significant meanings, “functional” (traditional) and “Shannon” (Shannon 1948), and both are important when considering the information of life. Information is literally attributing form or shape to something, which rules out other possible forms. Functional information principles may be used to quantify traditional information by calculating a value which “represents the probability that an arbitrary configuration of a system will achieve a specific function to a specified degree.” (Hazen, Griffin, Carothers, & Szostak, 2007) Shannon (1948) information theory deals with the reduction of possibilities or uncertainty. The amount of information in a string of symbols is inversely related to the probability of the occurrence of that string. The more improbable the string, the more uncertainty it reduces and the more information it conveys. Shannon information provides only a mathematical measure of improbability or complexity, not whether a symbol string is meaningful or significant. Information theory is concerned with storing and transmitting data in a manner that ensures the integrity of the data, regardless of the meaning attached to that data. It is important not only to transmit the messages reliably (a Shannon criterion) from the DNA, but the enzymes must already know how to interpret that coded information in order for proteins (including enzymes), RNA, and replicated DNA to be manufactured appropriately (a functional criterion). In other words, the data transmitted may have an effective Shannon information content that exceeds the number of raw data bits transmitted if one includes all of the information already known by the receiver. If a DNA molecule were placed into a pool of amino acids, the information in the DNA would be useless unless the needed receiver proteins (enzymes) are present.

The genetic information system is analogous to a computer’s algorithmic language, since both are segregated, linear, and digital. (Bennet, 1973) In bioinformatics, segregated means each codon (set of three bases from ACGT) is a distinct symbol, linear means these symbols are in a distinct meaningful sequence in the DNA/RNA, and digital means there’s no blending of characteristics of symbols and no lowering of fidelity during copying (as we all know from TV’s “Big Switch” – digital is better). “It seems that the two-pronged fundamental question: ‘Why is the genetic code the way it is and how did it come to be?’, that was asked over 50 years ago, at the dawn of molecular biology, might remain pertinent even in another 50 years. Our consolation is that we cannot think of a more fundamental problem in biology.” (Koonin & Novozhilov, 2008) “Peer-reviewed life-origin literature presupposes that, given enough time, genetic instructions arose via natural events. Thus far, no paper has provided a plausible mechanism for natural-process algorithm-writing... Both the semantics and syntax of codonic language must translate into appropriate semantics and syntax of protein language. That symbolization must then translate into the ‘language’ of three-dimensional conformation via minimum-free-energy folding. No combination of the four known forces of physics can account for such conceptual relationships. Symbolism and encryption/decryption are employed. Codons represent functional meaning only when the individual amino acids they prescribe are linked together in a certain order using a different language. Yet the individual amino acids do not directly react physicochemically with each triplet codon. Even after a linear digital sequence is created in a new language, ‘meaning’ is realized at the destination only upon folding and lock-and-key binding.” (Trevorsa & Abel, 2004)

Computer/electronic engineers have designed the hardware to read the computer’s native language instructions (non-physical machine language) and execute the operations specified by each instruction. A higher-level computer language (such as BASIC, C, or FORTRAN) may be

used to translate a desired algorithm (sequence of logical operations to solve a problem) into the computer's native language. A computer's operating system (OS), such as Linux or Windows, is a set of programs that allow other programs (applications) to execute on the computer's hardware (allowing access to storage and input/output devices), but to the computer hardware an OS is just another program (unless built into the hardware). To an application program, typically only the OS (not the hardware) is visible.

From the information perspective, the genetic system is a preexisting operating system (of unknown origin) that supports the storage and execution of a wide variety of specific genetic programs (the applications). Each program is stored in DNA (DNA is a storage medium, not a computer) and specifies all information needed to support the growth, metabolism, parts manufacturing, etc. for a specific organism via gene subprograms. DNA is an example of shared memory in a distributed heterogeneous multiprocessor system with Flynn classification multiple input streams and multiple output streams (Flynn, 1972). The native language includes a coding system (codon-based encryption) whose codes are read by enzyme "computers" (over 2000 in each cell, which have their own OS and don't know the codon meanings). The enzyme's output is to another OS in a ribosome (which has its own RNA program) where codes are decrypted. The needed output signals are then transmitted to the tRNA so that the amino acid specified by the codon is transported to the construction site to be added to the protein being built. For any functional communication to occur, a prerequisite is that both sender and receiver know the communication protocol and message meaning. There are multiple OSs, multiple programming languages, encoding/decoding hardware and software, specialized communications systems, error detection and correction mechanisms, specialized input/output channels for organelle control and feedback, and variety of specialized "devices" to accomplish the tasks of life. The author can attest that these concepts are not trivial since many were fundamental in his second Ph.D. thesis research (Johnson, 1997) in Computer and Information Sciences as well as in several courses taught on multiprocessing systems. If undirected origin of such a complex interacting "computer" system is to be viable, there is a need to demonstrate that the rules, laws, and theories that govern electronic computing systems and information don't apply to the even more complex information systems that are in living organisms. Laws of chemistry and physics, which follow exact statistical, thermodynamic, and spatial laws, are totally inadequate for generating complex specified information or those systems that process that information.

There are two topics that should not be included in science unless/until sufficient facts from known science demonstrate a feasible scenario: the origin of the mass and energy of the universe (which is scientifically unknowable, but is not covered in this paper – see Johnson 2009 for an analysis), and the origin of life. To pretend that a "scientific-sounding" scenario is actually science in these areas does a disservice to both science and the public, and diminishes the reputation of all science by anyone examining the evidence. It would be appropriate to teach why those areas are not science, and that science has no scientific answers to questions of origins.

Avoiding Pitfalls in Macroevolution

"We have seen that living things are too improbable and too beautifully 'designed' to have come into existence by chance. How, then, did they come into existence? The answer, Darwin's answer, is by gradual, step-by-step transformations from simple beginnings, from primordial entities sufficiently simple to have come into existence by chance. Each successive change in the gradual evolutionary process was simple enough, relative to its predecessor, to have arisen by chance. But the whole sequence of cumulative steps constitutes anything but a chance process, when you consider the complexity of the final end-product relative to the original starting point. The cumulative process is directed by nonrandom survival." (Dawkins, 1996B, p. 43) Neo-Darwinism breaks down the improbability of macroevolution into small changes (microevolution) that allow scaling up the backside of "Mount Improbable ... inch by million-year inch." (Dawkins, 1996C, p. 77) In this view, the changes can accumulate in the

DNA until a positive gene is formed (at that time, only genes that had physical manifestations were thought to contribute to a selective advantage), at which point that gene will be selected for continuation in the new organism's DNA. The non-coding part of DNA became known as "Junk DNA" which is "the remains of nature's experiments which failed." (Ohno, 1972) Dawkins popularized the idea that any DNA not actively trying to get to the next generation would slowly decay away through mutation and that genes are the basis of evolutionary selection. (Dawkins, 1976) Non-coding sections of DNA are seen as the result of mutations that haven't yet resulted in formation of useful genes so that they would provide a selective advantage. This theme was echoed in authoritative textbooks also. "Introns have accumulated mutations rapidly during evolution, and it is often possible to alter most of an intron's nucleotide sequence without greatly affecting gene function. This has led to the suggestion that intron sequences have no function at all and are largely genetic 'junk'." (Alberts, 1994, p. 533) "Much repetitive DNA serves no useful purpose whatever for its host. Rather, it is selfish or junk DNA, a molecular parasite that, over many generations, has disseminated itself throughout the genome." (Voet & Voet, 1995, p. 1138) Dawkins (1998) wrote "there's lots more DNA that doesn't even deserve the name pseudogene. It, too, is derived by duplication, but not duplication of functional genes. It consists of multiple copies of junk, 'tandem repeats', and other nonsense which may be useful for forensic detectives but which doesn't seem to be used in the body itself. Once again, creationists might spend some earnest time speculating on why the Creator should bother to litter genomes with untranslated pseudogenes and junk tandem repeat DNA."

While the mutation mechanism for gene formation makes an interesting story, there are a number of scientific difficulties with the scenario. Blind chance was the only known mechanism possible for such gene formation since a selective advantage was thought to require some manifestation that is genetically coded (such as making a particular protein). Since nothing prevents what would have become a mutated "correct" codon from mutating again to become useless (mutation is by chance), the probability for a useful mutated gene is that all required mutations take place in one organism before or during reproduction. A typical gene contains over 1,000 base-pairs, but if we speculate that an operative gene could have only the codons required for encoding a 50-amino acid protein, the minimum length of the gene would be at least 150 base-pairs. Since the Shannon information of such a hypothetical gene is unknown, the probability of forming such a gene can be estimated from $4^{-150} = 5 \times 10^{-91}$ (that's for one specific gene in one organism, which may decrease for larger gene size or increase if additional functional genes are considered). Since "useless" base-pairs have no advantage and since transferring the information requires at least 0.035 electron volts per bit for each step during replication (Yockey, 2005, p. 25) (there's no free lunch!), any mutation that eliminated those useless base-pairs would have a selective advantage so it would make sense that they would be removed from the genome long before they had a chance to form something with a selective advantage. Time is actually an enemy since entropy will tend to randomize genetic content unless directed energy prevents that from happening (there would be no advantage in directing energy to "useless" structures).

Recent studies have shown that non-coding DNA plays a role in embryonic development in such areas as the reproductive tract (Keplinger, Rabetoy, Cavener, 1996) and the central nervous system. (Kohler, Swchafer-Preuss, & Buttgerreit, 1996) "Geneticists have long focused on just the small part of DNA that contains blueprints for proteins. The remainder--in humans, 98 percent of the DNA--was often dismissed as junk. But the discovery of many hidden genes that work through RNA, rather than protein, has overturned that assumption. These RNA-only genes tend to be short and difficult to identify. But some of them play major roles in the health and development of plants and animals." (Gibbs, 2003) "Some scientists now suspect that much of what makes one person, and one species, different from the next are variations in the gems hidden within our 'junk' DNA." (Gibbs, 2003) At first, Darwinists thought that introns had no role in the production of proteins and regarded them as merely junk. However, research has proven that they play vitally important roles. "For years, more and more research has, in fact,

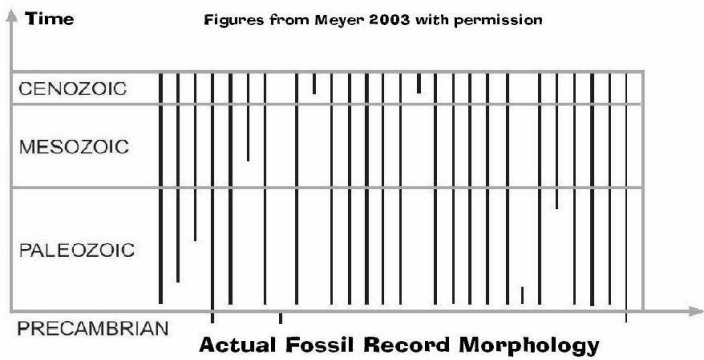
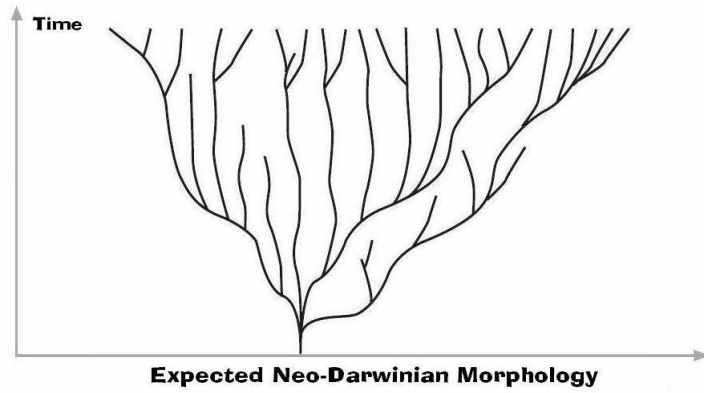
suggested that introns are not junk but influence how genes work... introns do have active roles.” (Ray, 2003) “Just when scientists thought they had DNA almost figured out, they are discovering in chromosomes two vast, but largely hidden, layers of information that affect inheritance, development, and disease.” (Gibbs, 2003) Genetic biologist Wojciech Makalowski states: “Now, more and more biologists regard repetitive elements as a genomic treasure... that repetitive elements are not useless junk DNA but rather are important, integral components of eukaryotic genomes.” (Makalowski, 2003) “Nonprotein coding RNA (ncRNA) refers to mRNA that is transcribed from DNA but not translated into protein. Rather than being 'junk' DNA (ie an evolutionary relic) some nonprotein coding transcripts may in fact play a critical role in regulating gene expression and so organizing the development and maintenance of complex life.” (Perkins, Jeffries, & Sullivan, 2005) “Scientists are puzzling over a collection of mystery DNA segments that seem to be essential to the survival of virtually all vertebrates. But their function is completely unknown. The segments, dubbed ‘ultraconserved elements’, lie in the large parts of the genome that do not code for any protein. Their presence adds to growing evidence that the importance of these areas, often dismissed as junk DNA, could be much more fundamental than anyone suspected.” (Pearson, 2004)

John Mattick, Director of the Centre for Molecular Biology and Biotechnology at the University of Queensland, writes (2003): “I think this will come to be a classic story of orthodoxy derailing objective analysis of the facts, in this case for a quarter of a century, the failure to recognize the full implications of this — particularly the possibility that the intervening noncoding sequences may be transmitting parallel information in the form of RNA molecules—may well go down as one of the biggest mistakes in the history of molecular biology... Indeed, what was damned as junk because it was not understood may, in fact, turn out to be the very basis of human complexity.”

Researchers are discovering that what had been dismissed as evolution relics are actually vital to life. What used to be considered evidence for neo-Darwinism gene-formation mechanism can no longer be used as such evidence. In this case, neo-Darwinism has been a proven science inhibitor as it postponed serious investigation of the non-coding DNA within the genome. This is reminiscent of the classification of 86 (later expanded to 180) human organs as "vestigial" that Robert Wiedersheim (1893) believed “lost their original physiological significance,” in that they were vestiges of evolution. (Wiedersheim, 1893) Functions have since been discovered for all 180 organs that were thought to be vestigial, including the wings of flightless birds, the appendix, and the ear muscles of humans. (Bergman, 1990)

“There is no evidence that genetic information can build up through a series of small steps of microevolution... Mutations reduce the information in the gene by making a protein less specific. They add no information, and they add no new molecular capability... None of them can serve as an example of a mutation that can lead to the large changes of macroevolution... The failure to observe even one mutation that adds information is more than just a failure to find support for the theory. It is evidence against the ... neo-Darwinian theory.” (Spetner, 1997, p. 159-160) Orr & Coyne (1992) write supporting punctuated equilibrium in some cases: “We conclude – unexpectedly – that there is little evidence for the neo-Darwinian view: its theoretical foundations and the experimental evidence supporting it are weak.” (p. 726) “We must concede there are presently no detailed Darwinian accounts of the evolution of any biochemical or cellular system, only a variety of wishful speculations.” (Harold, 2001, p. 205) Biologists Margulis & Sagan write (2003, p. 29): “We agree that very few potential offspring ever survive to reproduce and that populations do change through time, and that therefore natural selection is of critical importance to the evolutionary process. But this Darwinian claim to explain all of evolution is a popular half-truth whose lack of explicative power is compensated for only by the religious ferocity of its rhetoric. Although random mutations influenced the course of evolution, their influence was mainly by loss, alteration, and refinement. One mutation confers resistance to malaria but also makes happy blood cells into the deficient oxygen carriers of sickle cell anemics. Another converts a gorgeous newborn into a cystic fibrosis patient or a victim of early

onset diabetes. One mutation causes a flighty red-eyed fruit fly to fail to take wing. Never, however, did that one mutation make a wing, a fruit, a woody stem, or a claw appear. Mutations, in summary, tend to induce sickness, death, or deficiencies. No evidence in the vast literature of heredity changes shows unambiguous evidence that random mutation itself, even with geographical isolation of populations, leads to speciation. Then how do new species come into being?" "Yes, small-scale evolution is a fact, but there is no reason to think it is unbounded. In fact, all our data suggests that small-scale evolution cannot produce the sort of large-scale change Darwinism requires." (Hunter, 2003, p. 60) Anthropologist Roger Lewin, at the 1980 Conference on Macroevolution,



said: "The central question of the Chicago conference was whether the mechanisms underlying microevolution can be extrapolated to explain the phenomena of macroevolution. At the risk of doing violence to the position of some people at the meeting, the answer can be given as a clear, No." Although the fossil record is often assumed to support Darwinism, "Most of the animal phyla that are represented in the fossil record first appear, 'fully formed,' in the Cambrian some 550 million years ago... The fossil record is therefore of no help with respect to the origin and early diversification of the various animal phyla." (Barnes, Calow, & Olive, 2001, p. 9-10)

There have been a number of computer simulation that supposedly demonstrate the validity of Darwinism. These programs, like all computer programs, are designed and executed on designed platforms so that information, not chance data, caused solutions. "Based as it is on ideas, a computer is intrinsically an object of intelligent design. Every silicon chip holds as many as 700 layers of implanted chemicals in patterns defined with nanometer precision and then is integrated with scores of other chips by an elaborately patterned architecture of wires and switches all governed by layers of software programming written by human beings. Equally planned and programmed are all the computers running the models of evolution and 'artificial life' that are central to neo-Darwinian research. Everywhere on the apparatus and in the 'genetic algorithms' appear the scientist's fingerprints: the 'fitness functions' and 'target sequences.' These algorithms prove what they aim to refute: the need for intelligence and teleology [targets] in any creative process." (Gilder, 2006) "Neglect of key factors or unrealistic parameter settings permit conclusions to be claimed which merely reflect what the decision maker intended a priori... the computer experiments reported using the Avida framework so far have not demonstrated that neo-Darwinian processes could have produced the necessary coding information to produce the hundreds of molecular machines found in natural cells." (Truman, 2004)

The functional information increase moving up the biological tree of life has no scientific explanation as mutations never add information. The scenario that "selection" serves to increase information is equivalent to a shop owner who loses a little on each sale, but makes up for it in volume. With the human genome having a functional information of over 10^8 bits (6×10^9 bits of total information), and the simplest life only 267,000 bits, somehow over 10^7 bits of functional information has been injected into the genome. It is relatively easy to see how a genome can increase in length via insertion or replication, but such mutations would add no net

information. There is no known naturalistic mechanism for producing any increase in information, let alone information of the magnitude necessary to evolve from the root to the top of life's tree. The probabilities of forming the simplest organism's genome is $10^{30000000}$ more likely than forming that of a human (using the functional information formula).

The bottom line is use caution when extrapolating evolutionary changes that are known (all of which cause an information loss!) to presumed changes that require a net information increase. It is important to realize that chance cannot produce functional information (it can produce data or Shannon information), including that found in all living organisms. In case anyone doubts that Darwinism stretches reality, consider the case of Wells (2001) "I believed – took it as a given – that my science textbooks represented the best scientific knowledge available at that time. It was only when I was finishing my Ph.D. in cell and development biology, however, that I noticed what at first I took to be a strange anomaly. The textbook I was using prominently featured drawings of vertebrate embryos – fish, chickens, humans, etc. – where similarities were presented as evidence for descent from a common ancestor. Indeed, the drawings did appear very similar. But I'd been studying embryos for some time, looking at them under a microscope. And I knew that the drawings were just plain wrong. I re-checked all my other textbooks. They all had similar drawings, and they were all obviously wrong."

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