



Was Darwin Wrong?

"Neo-Darwinian Evolution Really Can't Work!"



**Letter to Gert Korthof
From Lee M. Spetner**



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<p>LETTER OF DR SPETNER 31 Aug 2000</p>	<p>MY REPLY 7 Oct 2000</p>	<p>Spetner 24 Jan 2001</p>
<p><i>Dear Gert,</i></p> <p>I read your detailed review of my book <i>Not By Chance!</i> I commend you on the effort you put into it and the knowledge you exhibited. I think you are a better defender of evolution than Richard Dawkins. His prose may be better than yours (of course, English is his native tongue), but your substance is superior. I do, however, think your review deserves a critical answer. Let me offer you my detailed critique of the review, point by point.</p>	<p><i>Dear Lee,</i></p> <p>Thank You! I am very honoured to be compared favourably to Richard Dawkins! And I keep trying to improve my prose. But most off all I appreciate it very much that you took the trouble to write such a detailed reply. I posted it without hesitation on my site, because it is not hostile at all, despite the fact that you and I entertain fairly opposite opinions.</p>	<p><i>Dear Gert,</i></p> <p>You formatted your reply to me very well - putting your comments side by side with mine in two columns. I don't think I can extend that to 3 columns to include my second response to you, so I have adopted the format below to show the entire dialogue from the beginning, starting with my original response. I trust you would see fit to post this on your website to replace the dialogue you now have. I'm sure you will be able to choose a suitable format.</p>
<p>Before I enter into the critique itself, let me establish an important and necessary guideline. The word <i>evolution</i> is generally used in at least two different senses, and the distinction is important in discussing your review, and in almost any discussion of evolution. One meaning of <i>evolution</i> is the descent of all life from a putative single primitive source. I shall denote the word used in this sense as <i>Evolution A</i>. On the other hand, the word is also used to denote any kind of change of a population. The change can sometimes occur in response to environmental pressure (natural selection), and sometimes it can just be random (genetic drift). I shall denote the word used in this sense as <i>Evolution B</i>. Evolution B has been observed. Evolution A is an inference; it is not an observable.</p>	<p>I don't understand why you use <i>Evolution A</i>, <i>Evolution B</i>, because in your book starting on page 67 you use the well-known concepts 'micro-' and 'macro'-evolution. For this discussion:</p> <hr/> <p>Evolution A = macro evolution = Common Descent Evolution B = micro evolution = changes in populations</p> <hr/>	<p>I'll tell you why I'm using Evolution A and B instead of macro & micro evolution. I'm using Evolution A precisely because I want to distinguish it from macroevolution. I am using it precisely to avoid the confusion demonstrated in some of your remarks below. Thus, your equations, above, do not represent what I intended in the meaning of Evolution A. By Evolution A, I mean what I had earlier called "the grand sweep of evolution," the evolution of all life from some simple beginning. It is the same as common descent, but somehow the term common descent doesn't capture the drama of the grand sweep of evolution. Maybe Evolution A is too insipid a term, but I wanted something shorter than "the grand sweep of evolution." I thought I would gain some clarity with this terminology. Apparently, with you I only achieved confusion. Sorry about that. I'll try to do</p>

better if I ever treat this subject again. But for this discussion, let me continue to use it and beg your indulgence.

About inferred - observed:

The existence of your brain is **inferred**, not observed, because nobody including yourself has actually observed your brain. Further you did not observe your own **birth**, you can only **infer** your birth. Furthermore your **conception** isn't observed by anybody: it is just **inferred** based on naturalistic theories! So there is no imperative to account for it.

You miss the point here, Gert, and therefore your comparisons are not useful. We know brains exist; we have seen and handled them. Even though I did not observe my birth, there are others who have and can testify to it. Evolution A, on the other hand, is a phenomenon that may or may not have occurred. You assume it has; I am agnostic on the matter. Whether or not it has occurred is, in fact, a key point of divergence between evolutionists and creationists. There is no imperative to have a theory to explain Evolution A, because it was not observed and we don't even know that there is such a thing. If we had a theory that could account for Evolution A, there would be reason to give that concept some serious consideration. But there is no such theory. I have seen the argument stated often, that even if there are defects with neo-Darwinian theory, it's the best theory we have to explain the evolution of all life from a single simple ancestor. That's not a very compelling argument to one who questions Evolution A.

The distinction between these two meanings of *evolution* is often ignored by those defending neo-Darwinian evolution, but the distinction is critical. The claim is made for Evolution A, but proof is often limited to Evolution B. The implication is that the observation of Evolution B is a substantiation of Evolution A. But this is not so. Since Evolution A is not observable, it can be substantiated only by circumstantial evidence. And circumstantial evidence must be accompanied by a theory of how it relates to what is to be proved. Neo-Darwinian theory (NDT) is generally accepted to be that theory. The thesis of my book is that NDT cannot account for Evolution A. I shall do my best to untangle the thread of confusion in these two meanings of evolution as I proceed through this analysis of your review. The important claim of neo-Darwinism is that it can account for Evolution A. This claim is what the public perceives as the core of the controversy over evolution. This claim is the source of the contention that life is the result of purely natural processes, which ensue from well-known natural laws, a claim which I reject as never having been substantiated. This unsubstantiated claim is quite an important one, since it is frequently offered as a basis for a philosophy of life. In what follows, I shall note where these two meanings of evolution are confounded. In a

(1) The distinction is vague: you only mention the extremes of the scale. But the extremes are no problem. The question is: where does **micro** stop, where does **macro** start? How many species are allowed to be produced by **microevolution**? Are dog, wolf, coyote, fox the result of **microevolution**? Are all birds the result of **microevolution**? Or are all the birds of, say, Australia the result of **microevolution**?

(2) You forget to make that important distinction yourself where it matters: "NREH can account for observations of **evolution** better than can the NDT" (p210). If the distinction is so important to you, why don't you use **micro**, **macro**? It is relevant for you because "nonrandom variation could produce some large-scale evolution" (209). Is 'Large-scale' the same as 'Macro'? Why didn't you write so? By the way: does it mean that NREH accounts for **micro and macro**? But you did not have to account for macro-evolution? You must substantiate your distinction **micro/macro**. You need to be more precise in your claim about what supposedly is accounted for and what not by neo-Darwinism.

(3) Important: we **observe micro-** and **macro** differences in living organisms:

(1) The distinction is not vague precisely because I am dealing with the extremes, which you acknowledge is no problem. You are taking the discussion off track. We are not writing a treatise on macro- and micro- evolution. My objective here was to point out that because of the great difference between Evolution A and Evolution B, one cannot justifiably use the observation of the latter to confirm the former. Where micro starts and macro begins is not the issue here. It is irrelevant to the point I am making. Will you please try a little harder to tune in to what I am saying.

(2) Your comments here on my NREH are inappropriate. I think they result from your equating my Evolution A with macroevolution, which reflects a misunderstanding of what I wrote, as I noted above. Let me make something clear. I say that NDT cannot account for Evolution A, which is the grand sweep of evolution from the putative primitive organism (cell?) to all the life of today. I did not say that NDT could not account for some examples of macroevolution. I don't know of any examples for which it could account, but there may well be some, given the arbitrariness of the definitions of species and of macroevolution. But it cannot account for Evolution A, and here is where the distinction between Evolutions

discussion of whether NDT can account for evolution, it is Evolution A that must be accounted for.

subspecies, species, genera, families, etc.

A and B is important, the distinction you seem so eager to blur. But it won't blur easily because they are two opposite extremes and are disparate. Now why do I introduce Evolution B at all? I did that only because I wanted to show the logical error of using the observation of B to serve as proof of A, which is so often done. I also want to make clear just what the NREH can account for. It has the potential to account for some examples of macroevolution (not Evolution A). Whether it can indeed account for them is a question that requires further study. I do not want to follow in the footsteps of the Darwinians and make unsubstantiated claims. I said in my book that the NREH is speculative. But it is no more speculative than NDT. Yet, it does not suffer from the faults of NDT, which I have pointed out in my book. I think I have been quite precise in asserting that NDT is supposed to account for Evolution A, and it does not.

(3) Gert, please. This is irrelevant to our discussion.

2. Neo-Darwinism: Could it work?

In this section of your review, you tried to rescue neo-Darwinism from my attack by pointing out errors in my argument. In what follows, I show that you are mistaken in each of your points.

I did not set out "to rescue neo-Darwinism", but simply pointed out errors in your argument.

I withdraw my imputation of your intention "to rescue neo-Darwinism." My apologies. But you have not succeeded in pointing out any errors.

2.1 Richard Dawkins's Blind Watchmaker

The critical comments you made in this subsection are answered in the relevant sections below. I just want to point out here that I devoted a chapter in my book criticizing Dawkins book, because many lay readers got the impression that he made a convincing case for evolution. In particular, although his simulation is only a caricature of the evolutionary process and he may have intended it only for pedagogical purposes, many readers thought he was actually demonstrating evolution. I therefore felt it necessary to criticize it.

I enjoyed that part very much! It was an eye-opener for me. Don't apologise!

OK. Thank you.

2.2 Speciation Through Mutation

In my calculation of the probability of evolving a new species, I purposely chose horse evolution as my example because it is a celebrated one, and the fossil evidence for it is better than for most other organisms. The horse is also a well-known animal and many people can relate to it easily. But I chose it mainly because it is considered a good example of an important element of Evolution A, and it is Evolution A on which I have mounted the attack in my book. I have shown that NDT cannot account for Evolution A. Of all mammalian evolution, the horse has the best documentation in the fossil record.

Reasonable.

However there is one disadvantage of your choice: geneticists can't extract DNA from fossil horses.

Let me make something clear. Mainstream NDT claims that macroevolution occurs through a long series of small steps, each involving an adaptive mutation occurring at random, followed by natural selection. This claim has never, to my knowledge, been substantiated as plausible by any calculation. Clearly, it cannot be observed, so calculation (or simulation) is the only means at our disposal to substantiate it. The burden of substantiation should normally fall on the proposers of the theory. But as you know, NDT was accepted without such nice formalities. I have therefore taken it upon myself to make the calculation that evolutionists should have made, and I show that the theory is not supported by a reasonable model of the process. An antagonist can always pick holes in a model of any kind since no model is a perfect representation of the process being studied. Reasonable models are widely used in science and they play an important role in its progress. You cannot reject the model unless you are able to give a more reasonable one and calculate from it a result that supports NDT. You want DNA sequences, which we do not have. That lack of information is not sufficient to disqualify my model. The only proper way to attack my model is to present a better one that supports NDT. Consider the following. I suggested a minimum of 500 adaptive point mutations per speciation to evolve the horse. If a run through 60 species led from eohippus to the modern horse, then the DNA of the modern horse would differ from that of eohippus by 30,000 base pairs. That means that the fractional difference of the DNA of the modern horse and that of eohippus would be only 0.0005. (We don't know what it really is, and we never will unless we can find a DNA sample of an eohippus fossil. But we might some day be able to put some limits on the base-pair difference by getting DNA samples of a suitably related modern species.) Do you have any good reason to suppose that 60 million years of active evolution would produce a genetic result differing from the ancestor by a fraction much less than 0.0005? Note that the chimpanzee and the human (whose DNA's are considered to be surprisingly close together) have a fractional DNA difference of about 0.02, and that was supposed to have happened in less than 10 million years. Whereas I chose 500, taken from Stebbins, as a reasonable value for the number of point mutations to achieve a new species, a similar estimate has been made by Haldane (1957), as cited by Futuyama (1979), of 1,000. Haldane calculated that the replacement of this

many loci through natural selection would take some 300,000 years. If we use that for horse evolution, and let the generation time be about 4 years, then one speciation would take about a million years. My estimate of 60 species for horse evolution would then take about 60 million years, which fits the paleontological data. I think you are being picayune in objecting to my estimate of 500 without offering a better alternative.

Speciation can be a slippery subject in this discussion and I shall try making my meaning as clear as I can. You have tried to catch me by fabricating a contradiction between my citation of *Drosophila* speciation by a single chromosomal inversion and my requirement of 500 mutations for speciation in the horse. Speciation is usually defined as the splitting of a population of organisms into two sub populations that become reproductively isolated from each other. So, the example of the speciation in *Drosophila* through a single chromosomal inversion satisfies the definition. But I thought I made it clear that the purpose for which I brought the horse example was to examine a typical element of Evolution A. Gert, surely you aren't suggesting that chromosomal inversion is a typical step in Evolution A. You would surely not suggest that the speciations in horse evolution were effected mainly by chromosomal inversions!

We need chromosomal data of the horse family too. Since it is difficult for extinct species, all we can do is to study as many as possible of living horse species. See for a defence of the importance of chromosomal changes in speciation: D.R. Forsdyke [Two Levels of Information in DNA](#): "Over 90% (and probably over 98%) of all speciation events are accompanied by karyotic changes [chromosomal macromutations], and ... in the majority of cases the structural chromosomal rearrangements have played a primary role in initiating divergence". [M. White(1978): *Modes of Speciation*]. Surely, there is a controversy going on, but you cannot ignore chromosomal mutations as a mode of speciation. Even the origin of humans involved a chromosomal mutation: the human chromosome 2 equals in size and content the chimpanzee chromosomes 12+13. Humans have 2n=46 and chimps 2n=48 chromosomes.

Thank you for the reference to Forsdyke (which you sent me separately). I am actually of the opinion that many, if not all, speciations result from chromosomal rearrangements. This is the thesis I propose in my NREH. In my book, I pointed out that genetic rearrangements do not strictly fall under the category of random mutations. They are executed with great precision by a special genetic mechanism, which seems to have only that as its role. The references you cite to chromosomal rearrangements as the major cause of speciation supports my thesis. To the extent that such complex genetic changes make meaningful, and often adaptive, phenotypic changes, they would be highly improbable if they were indeed random. I also pointed out in my book that such complex genetic changes, if they were triggered by the environment, as they well might be, would be nonrandom and an example of the NREH. I treated the horse evolution assuming a long series of random point mutations, because the majority opinion among evolutionists is that it is the way speciation works. If you were to agree that most speciation results from chromosomal rearrangements (I am too timid to go that far, myself) then my treatment of the of the horse evolution was not for you. But your implication that most macroevolution occurs by chromosomal rearrangements agrees with of the NREH, for which I thank you.

For some reason, you don't like my model of speciation requiring 500 small genetic changes. But you don't suggest an alternative. How many genetic changes would you prefer? 400? 100? Or would you dare suggest only one? You don't say explicitly, but you imply that one would be enough. My choice of 500 was at least taken from the literature. Tell me what alternative you would suggest - with a reference to the literature, of course.

It is unreasonable to use an estimate to refute a scientific theory (neo-Darwinism). As if an estimate of a variable in Einstein's or Newton's theory would be good enough to refute his theory. Estimates are acceptable for a temporary result, but not if you want a definitive proof or disproof of a scientific theory. Estimates are no substitutes for data.
What number of steps would be acceptable for you? Is 1 step too much? 2 steps?

One always uses estimates. Estimates of parameters can certainly be used to refute the theory of Einstein or Newton, provided no one has a better estimate that substantiates the theory. Some estimates are better than others. No physical parameters are known with infinite precision. As I noted above, the proponents of NDT had the obligation of making the appropriate estimates and checking the theory. It is unreasonable for you to require my parameter estimates to be more precise than knowledge permits and satisfy more stringent requirements than those imposed on other model checks on a theory. It is particularly unreasonable in light of the

		<p>neglect of evolutionists to check their own theory. It is common practice to check a theory with the best parameter estimate one can make. If the theory does not pass that test, and if its proponents nevertheless wish to retain the theory, they must show that a better parameter estimate would vindicate it. It will not do just to make a vague statement that my parameters might be wrong.</p>
<p>You cite textbooks in saying, "the most important step in speciation is reproductive isolation and this is achieved by geographic isolation and other mechanisms. Not necessarily the accumulation of many small mutations." Well, of course geographic isolation is a good way to get reproductive isolation. But you are mistaken in thinking that it is the end of the story. It is not. It is only the beginning. Then there must be an accumulation of many genetic changes. Ernst Mayr said, "The proponents of the synthetic theory [of which he is one] maintain that all evolution is due to the accumulation of small genetic changes, guided by natural selection, and that transpecific evolution is nothing but an extrapolation and magnification of the events that take place within populations and species." (1). I'd say that's pretty authoritative.</p>	<p>All that being true, your choice of <i>speciation</i> as the point in time to measure is inadequate. A good case would be the absolute genetic distance between chimpanzee and human. As soon as we have sequenced the complete genomes of both species, we know the genetic distance and in combination with their time of divergence, one can verify or falsify the neo-Darwinian theory for the human-chimpanzee pair of species.</p>	<p>I disagree with you. A theory must pass every test. You cannot disqualify a test of the theory by saying that some day a better test will be available. When that time comes, the theory will have to pass that test too. But meanwhile, it must pass the tests that can be made now. And don't tell me about the possibility of falsifying NDT. One of the biggest complaints about it is that it cannot be falsified. No matter what objections have been raised against the theory, evolutionists weasel out of it with excuses and scenarios, much like you did above. Nevertheless, I think it really can be falsified</p>
<p>I didn't make up this model, and it's not a straw man. It is the closest thing there is to an official model of NDT. It is the model I attack, showing that it cannot work. There is no model so widely accepted among evolutionists other than this one. Mayr, in the above-cited reference does mention competing models by "a well informed minority", but he proceeds to note how these other models have been refuted by such authorities as Simpson (2) and Rensch (3). The speciation model I chose is the one most widely held by evolutionists still today.</p>	<p>You attack the model <i>including all the assumptions</i>. Furthermore: The logic of a falsification does not allow pointing to a single statement out of the collection of model + assumptions as being false. See: Del Ratzsch (2).</p> <p>Even if the model was generally accepted, using the model with wrong parameters generates worthless results.</p>	<p>It's just too easy for you to dismiss my model by claiming my choice of parameters is not perfect. If NDT is to be substantiated, which it has so far not been, it must be verified using the best model available. I am showing you that it is indeed refuted by the best available, and most widely accepted model. If you want to argue against that refutation, you must show that NDT is verified by a better model.</p>

Your picture represents a rather distorted view of this widely held model. It is true that reproductive isolation occurs first. But then, you go on to say, "genetic differences can and will accumulate" as if to imply that these subsequent genetic changes are unimportant. They may not have contributed to reproductive isolation, but they surely contribute to the interspecific phenotypic differences observed in the fossil record. And it is from the fossil record, and from that alone, that the evolution of the horse has been inferred. The product of reproductive isolation by itself, without subsequent phenotypic change, would not be recognized in the fossil record as a new species. Speciation in horse evolution, as observed in the fossil record, is widely and authoritatively held to be the result of many small genetic changes. These genetic changes are what I analyzed.

Of course morphological changes are the only ones visible in fossil record. However relating morphological and genetical changes is only provisory. We need details if we want a definitive confirmation or disconfirmation of neo-Darwinism applied to the horse evolution. And because of that the only way progress can be made is to measure genetic distances between living horse species.

I'm sorry, Gert, but if NDT is to be an acceptable theory, it has to stand up to analyses of all kinds - both morphological and genetic. It just won't do to say that we have to wait until the genetic evidence is all in before we can test the theory. That would be true if the theory were only under consideration and not yet accepted. But NDT is playing the role of an accepted theory. NDT and its predecessors have been around for almost a century and a half. Don't you agree that an analysis of its validity is long overdue? Or do you want to put it off for another few decades?

I picked the figure of 500 as a reasonable estimate of the number of steps (mutations) required for a new species to be recognized in the fossil record. If you don't like it, then give me a better estimate. I took this figure from Stebbins because it was the only one I could find in the literature. You say you don't agree that Stebbins was one of the "architects of neo-Darwinism. You may not agree, but he was. In my book, you will find that I say, "The scientists who participated in establishing the new theory included the geneticists G. Ledyard Stebbins and Theodosius Dobzhansky, the zoologists Ernst Mayr and Julian Huxley, the paleontologists George Gaylord Simpson, and Glen L. Jepson, and the mathematical geneticists Sir Ronald A. Fisher, and Sewall Wright." (4). What is known as neo-Darwinian theory was established in large part by a committee originally set up by the Geological Society of America in 1941, and lasted through the decade (5). The committee was called "The Committee on Common Problems of Genetics, Paleontology, and Systematics." G. Ledyard Stebbins was the vice chairman of the Western Group.

What worries me is: "it was the only one I could find". It means something!

The estimate could be used for a tentative result, but it is really a too small basis to "shatter the modern theory of evolution". From a logical point of view one cannot blame NDT. The input parameter 500 could be incorrect. Or any of the other parameters.

Well, I have given you another one by Haldane (above), and it agrees with the one I got from Stebbins.

No Gert. Either you must suggest better parameter values than the ones I chose and show they validate NDT, or else you must accept my analysis.

<p>You were also critical of my citing such an old book as Fisher (1958). You might be surprised to learn that the book was originally published in 1929! I just happened to have bought the 1958 reprint. What I cited from Fisher was a mathematical theorem. Once a theorem is proved, it remains proved forever. It doesn't get overturned by new experiments, and it doesn't go "out of style". Mathematics is not biology!</p>	<p>"Fisher's genetic models are also <i>linear</i> - they assume that the effect of an allele is proportional to the frequency with which it occurs, and that the effects of different alleles simply add up. Linear mathematics held sway in classical times because the calculations were simple enough to be done with pencil and paper. Today, most areas of science are adopting nonlinear models, with more complex, but far more realistic, dynamics." (1).</p> <p><i>Mathematical proof is not the issue, but its relevance for real-life.</i></p>	<p>You can't get away with making a vague generalization about the need for nonlinear analysis. If you think I had to make a nonlinear analysis, please show me where. I actually made the calculations myself of the probability of disappearance of an adaptive mutation. I credited Fisher with it because, to my knowledge, he made it first. If you want a more up-to-date reference, you will find it in Graur & Li (2000) in Chapter 2 in their section on Gene Substitution, where they make the same calculation and get the same result. Now that should be recent enough for you.</p>
<p>To continue, you say that, "Mutation rate is low but populations can be large." You don't carry this through to any kind of a conclusion, but you let it hang as if to imply that my calculations are therefore invalid. Not true. The present human population of 6 billion that you cite is an extreme example. No other vertebrate species approaches that population. In my calculation, I chose a breeding population of 100,000. My geneticist friends tell me that number is overly generous. Breeding populations of mammals are more typically just a few thousand, and often less.</p>	<p>It would be very helpful for assessing the validity of your calculation method to know what happens if applied it to insect populations (or rats or rabbits) using 1-500 steps. If your method forbids the generation of even <i>one</i> new insect species, than you would really doubt the validity of your method, wouldn't you? One would certainly doubt if no micro-evolution in bacteria happened in your simulation.</p> <hr/> <p>But I do not have that information. Would your model allow for <i>any</i> micro-evolution at all? For example the generation of species from your '365 basic species'?"</p>	<p>Not at all. Let's get something straight here. My calculation of horse evolution is not my method. I am simply applying a little mathematics to one most evolutionists claim is the way life evolves. I am questioning the validity of NDT. However, since the definition of species permits insect speciation to be achieved by a single point mutation, one cannot conclude with my method, or any other correct method, that a new insect species cannot arise. The same goes for bacterial evolution.</p> <hr/> <p>Of course the model allows for microevolution. I think you are here dealing with irrelevancies.</p>
<p>3. Nonrandom variation</p> <p>You also don't like my nonrandom evolutionary hypothesis. Your criticism makes me smile. You ask: "How does one guarantee that mutations are adaptive instead of harmful? ... How did this beautiful adaptation originate? Where does it come from? Assume that 'adaptive mutations' exist, are they adding information to the genome? Is this evidence enough 'to shatter the modern theory of evolution?'"</p>		
<p>Gert, I guess you didn't get it. You said, "Please note that Spetner produces an alternative <i>evolutionary</i> hypothesis (NREH). So Spetner is not against evolution in the sense that all organisms have common ancestry." Now that doesn't follow. There you go confounding Evolution A and Evolution B. The hypothesis I offered explains a lot of the changes that have been observed, which NDT is hard pressed to account for. I gave several of these examples, including birds and fish. But just because I can offer a hypothesis to account for change (Evolution B) does not mean that I hold a common ancestry of all life (Evolution A). I don't.</p>	<p>Lee, I am not "confounding" anything, you (and all creationists following Denton (1985)) use the ill-defined and arbitrary distinction micro - macro. The problem with that distinction is that its proponents never define it adequately, that is covering the complete system of life. You defined only the extremes of the micro and macro continuum. You skipped the most difficult task: the middle.</p>	<p>This is one of the reasons I chose not to use the macro/micro distinction in this discussion. This part of our discussion, Gert, stems from your misunderstanding of my argument. You insist that my Evolution A is equivalent to macroevolution. That is not so. My argument does not require me to deal with anything but Evolution A, to show that it cannot be achieved by random mutations.</p>

Let me take your last question first. You ask, "Is this evidence enough to 'shatter the modern theory of evolution'?" It's the right question, but you asked it in the wrong place. The NREH is a *hypothesis*; it is not by itself evidence. It is based on evidence. But that is not my basis for shattering NDT. That was done in Chapters 4 and 5 of my book. The NREH is introduced in Chapter 7 to provide an alternative for the theory I shattered. I know you won't like my claim of shattering. But Gert, that's what I did! In Chapter 4, I showed that the model of cumulative selection cannot work without contradicting the possibility of convergent evolution. In Chapter 5, I showed that no known mutations that could play the role assigned them in NDT have been observed to add any information to the union of all genomes in the living world. (I have elsewhere called this union the *biocosm*.) Either of these alone is sufficient to shatter NDT. I can elaborate on this further if you would care to question it.

The rest of your questions are versions of "How did it originate?" You noticed correctly that I did not offer an explanation of how the suggested adaptive ability, or indeed, how life itself, originated. You probably didn't read my short epilogue, maybe because it was "tainted" with a little religion, as opposed to the rest of my book, which was strictly science. In the epilogue, I anticipated your question of origin. I said (p. 211) "One cannot fault the NREH because it fails to account for the development of life from a single cell. Such a development has not been observed, so there is no imperative for a theory to account for it. The NREH accounts for what has been observed, and it does so better than the NDT. Those are adequate credentials for a theory of evolution." I hasten to add here, provided one is careful not to confound Evolution A and B.

"You probably didn't read my short epilogue": *I quoted from your epilogue in my review!*

Of course the "development of life from a single cell" has not been observed! That is a serious misunderstanding! No Darwinist claims that! But there is one overwhelming observation: there are millions of wildly different species on this earth! Darwinism has been designed to explain both those millions of species and adaptation. You say: "The NREH accounts for what has been observed", but in your epilogue(!) you state that "nonrandom variation could produce some large-scale evolution" (p209). If it is important not to confound Evo-A/B, why didn't you state that more clearly in your book to prevent misreading.

Well, what can I say? Then I guess you didn't absorb the message I intended.

The misunderstanding, Gert, is on your part. I know very well that Darwinists do not claim that they have observed the "development of life from a single cell". Now, please pay close attention to what I am saying and think about it. I say that NDT, insofar as it deals with Evolution A, is attempting to account for something that has not been observed, and it does not account for it. My NREH makes no attempt to account for Evolution A, which has not been observed, and may very well have not happened. My point here is that the NREH's not accounting for Evolution A is not a defect in it. Is that clear or not?

No, Gert, the mutations triggering the adaptive response do not add information. All the information was already in the genome. If you will, you might say that one bit was added to turn on the cryptic genes. But no more than that. Then a complicated array of genes can be turned on to exhibit a complex response.

So: where does all the information come from?

I do not account for where that information came from. A scientific understanding of living organisms does not have to include an understanding of their origin. That subject is outside the scope of NREH as a scientific theory. If you really want to know where the information came from, you may have to go outside the scope of Science. But I don't want to go into that, and I'm sure you don't want me to either. The evolutionist claims his theory accounts for origins. But NDT does not account for Evolution A. My complaint against NDT is its claim to account for origins. I make no such claim for NREH, which can account for evolutionary events, but not for Evolution A.

4. Can random variation build information?

Gert, I think that in this section of your review you are missing the point. Enzyme specificity is not, as you contend, my *definition* of information. Rather, I take enzyme specificity as an *example* in which information can be quantified. The information we must deal with in biology and evolution is not the same as the information Shannon defined and worked with. Shannon divorced messages from their meaning because a communication engineer's job is to transmit a message as faithfully as possible, regardless of the meaning that may be attached to it. Thus, the engineer deals with a string of symbols and measures the information by dealing only with the symbols. He can encode it as he pleases, so long as at the end he decodes it and delivers to the receiver the same symbol string sent by the transmitter. In biology, information lies in functionality, or meaning, rather than just in the symbol strings themselves. In biology, the amount of information in a DNA string is not generally determinable at the level of the symbols. In biology, *meaning* and *functionality* are important in determining information content. (That's why it's so hard to quantify this kind of information.) Thus, a functioning enzyme contains information, even though it may be difficult to quantify. Nevertheless, if a mutation causes that enzyme to lose its functionality, then information is lost. Not all the information is necessarily lost, because it could generally be recovered by a back mutation. But there is nevertheless a loss. But we need not quibble about quantifying information content. The important point I make is that Evolution A *cannot* be achieved only by mutations that degrade

Surprisingly I agree with everything in this paragraph!!!
Indeed Shannon's concept of information has its limitations when applied to DNA! (Please note that this is quite in contradiction with how creationists like William Dembski (3) and Hubert Yockey apply the concept of information to biology).
I noted in [Information Content, Compressibility and Meaning](#) that the mathematical concept of information is inadequate for human as well for the DNA language, because it abstracts from meaning.

I am pleased to see that we agree on something. Perhaps if we continue our dialogue, we may find that we agree on much more. In Biology, information is nothing if it is not meaning.

enzyme functionality. Although degrading the enzyme's function might be a useful step at some point in a long evolutionary process, the process cannot consist *only* of such mutations.

You said, "Spetner would be right about specificity only if all existing enzymes have maximum specificity for their catalytic tasks (because then every modification means loss of specificity) ... " Gert, I did not say that "every modification means a loss of specificity." I did not say that a mutation cannot add information. I shall emphasize again: *There is no theorem requiring mutations to lose information.* I can easily imagine mutations that gain information. The simplest example is what is known as a *back mutation*. A back mutation undoes the effect of a previous mutation. If the a single nucleotide change in the genome were to lose information, then a subsequent mutation back to the previous condition would regain the lost information. The back mutation clearly *adds* information. Since these mutations are known to occur, they form a counterexample to any conjecture that random mutations must lose information.

Thanks for your clarification.

You see, we are already beginning to expand the scope of our agreement!

An important point I make in my book, and which I shall make here, is that *no mutations observed so far qualify as examples of the kind of mutations required for Evolution A*. In discussing mutations in my book I noted in each case in which the molecular change was known, that it could not serve as a prototype for the mutations required by NDT. In all the cases I discussed, it was the loss of information that prevented the mutation from serving as a prototype of those required by NDT. The back mutation likewise cannot serve as a prototype of the NDT-required mutations. Here the reason is not that it loses information it actually gains information. But the information it gains is already in the biocosm and the mutation contributes nothing new. Evolution A cannot be accounted for if the only information gain was by back mutations. You say, "[a] loss of specificity *could be* the first step to a novel catalytic task in a new environment. [it could] have crucial survival value " [my emphasis]

"no mutations...": *This is nonsense.* For example **Lactate dehydrogenase** can be changed into **malate dehydrogenase** by replacing just one of its 317 amino acids (Wilks et al. 1988) (4). Furthermore since there are hardly any true novelties in evolution, every gene is a modification of an older gene. With the recent avalanche of DNA sequence data, a surprising number of unexpected similarities among proteins not previously known to be related to each other have been revealed (4).

Thank you for the reference to Wilks et al. I am delighted to add that piece of information to my collection. Yes, I agree with you that the mutation in this example does appear to add a lot of information to the genome, and I believe it really does (I have also found another, by the way). In describing NDT, I wrote in my book, "On the average, each step must then have added a little information" (p. 130). The emphasis here on little is not in the original, but that word is important, and perhaps it should have been emphasized. Again on p. 160, I wrote, "Not even one mutation has been observed that adds a little information to the genome." I'll tell you why I wrote that NDT must rely on adding a little information at each step. That's because the greater the information gain, the smaller the probability of achieving it through a single random point mutation. That means that if we should observe a lot of information being added to a genome by a point mutation, we must suspect that the genetic milieu into which that mutation fell was not random. For example, that mutation might have thrown a genetic switch that would turn on an already-present complex response adaptive to a specialized environment. On the other hand, and this may be the case with the mutation described by Wilks et al., the mutation might be the key needed to produce a new enzyme, much like a back

		<p>mutation can activate a gene that a previous mutation had disabled. The statement on p. 160 of my book still stands: "Not even one mutation has been observed that adds a little information to the genome." That doesn't mean it can't happen, but it hasn't happened, as far as I know. Thank you also for introducing me to the new book by Graur & Li (2000). It's a gold mine of information!</p>
<p>I agree, but your whole paragraph 4 is irrelevant to my argument. I emphasized the "could be" in the above quote, because your argument in this paragraph is sprinkled with "could-be"s. It is the argument from "just-so" stories so typical of evolutionists from Darwin on. You then say, "So it is a plausible scenario that a novel catalytic function evolves via less optimal steps.". When the facts are lacking, make up a scenario. Then, you say, "Theoretically there is no reason to suppose that novel enzymatic functions cannot evolve. The task is to find supporting evidence "</p>	<p>Just read chapter 6 <i>Gene Duplication, Exon Shuffling, and Concerted Evolution</i> of Graur & Li (4) and you find lots of hard data!</p>	<p>That chapter does not contain any "hard data" on evolution by mutation. Its demonstration of evolution through mutation relies, instead, on the same scenario approach that you have used, and what most evolutionists for years have been using in place of logical arguments. In that chapter I counted 124 instances of "scenario" words, such as "probably", "may be", "suggest", "may have", and so on. Hard data? Yes, but not for evolution by mutation! My point is that, although loss of specificity can have survival value, it cannot be typical of the mutations needed by NDT. Indeed, I show an example in my book (pp. 154-157) of a mutation that loses specificity of an enzyme that has survival value. There are several examples of point mutations that cause loss of information and yet have survival value in special environments. Mutations that only lose specificity cannot, by themselves, account for Evolution A.</p>
<p>As support for the first sentence above, you cite Kauffman (6). But that book does not support your broad statement. To support that statement you would have to calculate the probability of getting a typical enzyme to evolve by modifying some existing unused gene, one amino acid at a time. Kauffman does not make such a calculation. To make that calculation you would have to find a path from a gene encoding one good enzyme to another through an unbroken chain of single point mutations. (We're not even discussing the development of a new enzyme <i>ab initio</i>.) Since nobody knows if such a chain even exists, there is no real support for your statement.</p>	<p>Now you ask for a scenario!!! ("you would have to find a path ...").</p> <hr/> <p>Every gene can be converted into any other gene by point mutations, gene duplication, exon shuffling because all life uses the same genetic language. Therefore there is continuity at the genetic level for all life, despite the enormous diversity at the morphological level. You did not explain that to your readers. For practical reasons we cannot show the billions of paths for all the millions of genes of all of the millions of biological species, however <i>typical</i> paths are in the textbooks.</p>	<p>No, Gert, I'm not asking for the kind of qualitative scenario evolutionists have been offering for almost a century and a half. I'm asking for a calculation that would show your claim to be even possible!</p> <hr/> <p>You are wrong here, Gert, and if I succeed in getting this point across to you, I shall have made some headway in advancing mutual understanding between us. To show the continuity you mention you would at least have to demonstrate the existence of a sequence of point mutations in which each element has a selective advantage. There really have to be an enormous number of such sequences because the success of any one has a low probability. You just cavalierly assume "there is continuity," and you want me to "explain that to my readers"? Well, I did in Chapter 4, and explained that such "continuity" is highly improbable.</p>

But let me tell you why it is actually *unreasonable* to suppose that the information-and-complexity buildup required for Evolution A can arise according to NDT. If Evolution A really occurred, then there must be a great many potential sequences, each consisting of many mutational steps, that can contribute to the increase in the information and complexity required to achieve Evolution A. That is, there must be a huge number of possible point mutations that, on selection, can add information to the biocosm. If so many exist, then surely several should have been observed among all the experiments in all the genetics laboratories throughout the world. But *none* have been observed, *not a single one!* That is more than just a *lack* of evidence for the existence of long strings of these mutations *it is positive evidence against it!*

You will be flooded with examples if you read the literature! We are living in the age of genomics. Geneticists have learned how to sequence genomes fast! Nobody will bring it to your home (unless you have subscriptions). There is no lack of evidence, there is an abundance of evidence. Your point of view would have an empirical basis if there was a solid discontinuity between taxonomic groups at the genetic level. But there is nothing of the sort! On the contrary: there is continuity at the genetic level throughout the whole system of life.

There is no flood, and in fact, there are still no examples. There was one case, which I described in my book, that I had originally thought was an example. A point mutation not only produced what appeared to be a small increase, but there were three such mutations that were observed to occur in the laboratory in succession, each one enhancing the ability of a bacterium to metabolize an artificial sugar. But examination of these mutations showed that each was a decrease in information: the first disabled a repressor gene for an existing enzyme, the second flattened the activity profile of the enzyme over the three substrates for which its activity was measured, and the third disabled a gene encoding a transport protein. I repeat: There are no known (yet) examples of mutations that can serve as prototypes of the mutations required by NDT.

In the last paragraph of your section 4, you seem to confuse survival value with information buildup. The single random mutation that grants a microorganism resistance to streptomycin has survival value in the presence of the drug. But since it degrades the match between the microorganism and the drug, it *loses* information. If you object to calling this an information loss, then surely you will at least agree that mutations that only degrade a molecular match cannot be a major component of Evolution A. To me, such a change is a loss of information. Think of what a string of such mutations would accomplish. A steady degradation of specificity would not lead to any long-term buildup of information or complexity of the kind Evolution A had to achieve. Such a string is an evolutionary dead end.

I know the difference. I will clarify it in my review.

There is no "steady degradation of specificity". In organisms that possess two or more **carbamoylphosphate synthetases** following gene duplication, the enzymes are always specific - arginine-specific, urea-specific, or pyrimidine-specific - whereas in lineages in which gene duplication did not occur, the enzyme functions in a generalized or multifunctional manner. See: Graur & Li, p283.

I did not say there was a steady degradation of specificity. I said that a mutation producing a degradation of specificity, even though it may be beneficial in a particular special case, cannot serve as a prototype for the mutations required by NDT, because a string of such mutations would be an evolutionary dead end. Your citation from Graur & Li does not show an example of a mutation adding a small amount of information. It is instead a series of hypothesized scenarios of how evolution might have worked, without at all considering the probabilities of getting the right mutations at the right time.

5. Is Spetner a Creationist?

Here, as in your section 3, you demand an explanation of the "origin" of the potential that exists in the organism to account for my NREH. Gert, I don't play by your rules. As I wrote in my book, and as I repeated above, Evolution A has never been observed and there is therefore no pressing need to account for it.*

* This is the most serious conceptual error you make in your letter. Darwinism is designed to explain the whole system of life on earth. Common Descent is not an observation; Common Descent is the theory to explain the origin of all species on earth. You mix up theory and observation. Remarkably, at the same time you claim in your book that your NREH explains large-scale evolution! (p210)

You do not understand me. I am not mixing up anything. On the contrary, I am doing my best to keep matters straight in spite of your misunderstanding, which I am sure is not deliberate, because I am convinced of your honesty. Let me try once more to explain to you my position. Neo-Darwinian theory attempts, as you say, to explain the whole system of life on earth. In particular, it attempts to explain the origin of life in natural terms. It therefore assumes that life had a natural origin (as opposed to a supernatural origin). Now, I have no objection to that assumption as a working hypothesis. I start objecting, however, when naturalism is elevated from the role of a working assumption and presented as a fact. Personally, I prefer, instead of assuming a natural origin of life, to say, let's see how far back we can push the naturalism idea. If someone could

really push it all the way back to inert chemicals, that would be an astounding achievement. Now, I think we both agree that we should be discussing Science and not Theology. Consequently, there is no place for the supernatural in our discussion. We both further agree that Common Descent is an attempt to account for the natural origin of life. I think you will also agree that the attempt has not (yet?) succeeded. Whether it ever will is a matter only of conjecture, and not of Science. Now, in my book I have suggested a hypothesis (NREH) to account for observed changes in populations. These are the changes that are commonly referred to as "evolution". I offer a causative hypothesis that these changes occurred through the environmental triggering of latent information residing in the organism before the triggering. You are asking me to account also for the cause of the presence of that information. If I did, you would want me to continue on back to a first cause, which you a priori have assumed is a chance event. But I do not accept your assumption, although I do not invalidate your right to make it. I contend that your assumption may be wrong, and that the first cause may not have been a random event. But I shall not go further along these lines. To argue my case for not wanting to accept your assumption of a random first cause, I would have to leave Science and enter Theology. I refuse to do that here, and I am sure that if I were to, my theology would not interest you. It would be irrelevant to a Scientific discussion, which is what we are trying to have. Therefore, I contend that since I do not accept your assumption of a random first cause, and since there is no evidence for it, I cannot be required to account for a natural origin of the information in the organism. I apologize for having made this so long, but I hope I have, at least, made my position clear. I hope that I have made it sufficiently clear to remove this point from our scientific discussion.

Here, I think, is the crux of the practical and popular conflict between the evolutionist and the creationist. If we understand this clearly, and if there is good will on both sides, I think the conflict can be resolved. I do not object to research into evolution and into finding naturalistic explanations of as much as we can.**
Indeed, I applaud it. But I do object to the insistence that life had a purely natural origin when there is no evidence for it. I have no objection to research into trying to find a naturalistic origin. I think such research should be pushed as far as it can go. But naturalistic origin of life should not be advertised as a known fact.

** But *that* is what evolutionists are doing: "finding naturalistic explanations of as much as we can"!
However if we pursue this task we have to assume that there is a so-called 'naturalistic' explanation, otherwise searching would not make sense.

Science is methodologically atheistic.

If you agree that we should not stop searching, than you should agree we should not stop assuming there is a 'naturalistic' explanation for everything.

It does not logically follow that to search for natural explanations of as much as we can, we must assume there is a natural explanation of everything. Rather, we try to find a natural explanation of as much as we can. If you want to assume that life had a natural origin, that's your choice. But you cannot then conclude on the basis of that assumption that life had a natural origin. That is begging the question.

I don't know what what you mean by that.. It seems to me that Science, as practiced today, is agnostic, rather than atheistic. But you must agree that there may well be truths that cannot be reached by Science. Just as there are mathematical truths that cannot be reached by mathematics (1). In which case, evolutionists should be more humble and not insist that there is no Creator and that life formed by purely natural means. A little agnosticism would be very becoming. Evolutionists should just leave creation and origins out of their discussions.

Not at all, as I explained above.

When it comes to teaching evolution in science courses in the public schools, I object to teaching that a natural origin of life is a proven fact. Until and unless it is proven, let's not push it in the science class. I object to such propaganda just as I suppose you would object to teaching creation in the science class. I think that *neither* of these teachings belongs in a science class.

In science classes nothing else than scientific theories can be taught, including the origin of life, including tentative scientific hypotheses of the origin of life.

If anybody claims the origin of life has been solved, than I would love to hear it.

Luckily creationists don't need to prove God?

I agree. But they should not be led to believe that the assumption of naturalism is a fact.

Here are some examples from biology textbooks (high school and junior college) that convey to the student in no uncertain terms that the origin of life and its subsequent evolution is understood, and that it is a fact that it occurred by purely natural means. Miller & Levine Biology Prentice-Hall (1993), pp.342-348:

"From the jumbled mixture of molecules in the organic soup that formed in Earth's oceans, the highly organized structures of RNA and DNA must somehow have evolved."

"Although the origin of the first true cells is uncertain, we can identify several of their characteristics with certainty."

"At some point, an ancient form of photosynthesis evolved in early cells"

"Between 1.4 and 1.6 billion years ago, the first eukaryotic cells evolved, fully adapted to an aerobic world."

"A few hundred million years after the evolution of sexual reproduction, evolving life forms crossed another great threshold: the development of multicellular organisms from

single-celled organisms. In the blink of an evolutionary eye these first multicellular organisms experienced a great adaptive radiation. Earth's parade of life was well on its way."

The following quotes are from Camp & Arms, Exploring Biology (1984) Saunders College Publishing, which has been used as a textbook in junior colleges in California, and may still be used today:

"Most scientists today believed that chance chemical events, occurring over a time span of more than a billion years, built up increasingly complex and life-like clusters of chemicals; some of these eventually became cells." (293).

"So, unlikely as living systems are, they had so much time to evolve that their origin was probably inevitable!" (296).

"Slowly, over a long timespan, some aggregates evolved coordinated chemical pathways that could carry on the functions of life: metabolism, information transfer, and faithful reproduction." (305).

Don't you agree that, in light the present state of origin-of-life research, statements like these overstate the case? Don't you agree that statements like these are indoctrinational to an atheistic Weltanschauung? What would you say if corresponding statements about the divine creation of life appeared in biology textbooks? I think that indoctrinational statements on both sides of this issue are out of place in a science text.

And evolutionists do not have to disprove it. Yet, many of them gratuitously keep trying.

Well, does that make me a creationist?

Sincerely,

Lee Spetner

Is this a Hide-and-Seek-Game? (See for my answer section 5 of the updated review). Do you deny being a creationist? Don't you belief in Creation?

Sincerely,

Gert Korthof

My question was rhetorical. I thought the answer was obvious: I am a creationist: I believe life was created by a higher intelligence.

Notes

1. Mayr, E., (1963). *Animal Species and Evolution*, Belknap Press, Harvard University, p, 586.
2. Simpson, G. G., (1953). *The Major Features of Evolution*, New York: Columbia Univ. Press.
3. Rensch, B., (1954). *Neuere Probleme der Abstammungslehre*, Stuttgart: Enke. Also (1960). *Evolution Above The Species Level*, New York: Columbia University Press (2nd ed.).
4. Spetner, L. M., (1997). *Not By Chance!*, Brooklyn: Judaica Press.
5. Jepsen, G. L., G. G. Simpson, & E. Mayr, (1949). *Genetics, Paleontology, and Evolution*, Princeton UP.
6. Kauffman, S. A., (1993) *The Origins of Order*, New York: Oxford UP.

Notes

1. Ian Stewart(1998) *Life's Other Secret. The new mathematics of the living world.*, p109-110.
2. Del Ratzsch(1996) *The Battle of Beginnings*, p112-113.
3. "[On the origin of information by means of intelligent design](#)" on this site.
4. Dan Grauer and Wen-Hsiung Li (2000) *Fundamentals of Molecular Evolution*, p264. (Please note that Dan Graur is at Tel Aviv University).

Notes

1. Gödel, Kurt, *On Formally Undecidable Propositions of Principia Mathematica and Related Systems*. (1962) Translated into English from the German by B. Meltzer and R. B. Braithwaite. London: Oliver & Boyd. Originally published in German: *Über formal unentscheidbare Sätze der Principia Mathematica und verwandter Systeme I*, Monatshefte für Mathematik und Physik 38: 173-198 (1931). (I have not seen the original and it is difficult to obtain.)

Note: 7 May 2001: second letter of Lee Spetner added. My reply is on a [separate page](#) [23 May 01].

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