

An Analysis of the Expert Testimony of Prof. David Hillis before the Texas State Board of Education on January 21, 2009

EXECUTIVE SUMMARY

At the January meeting of the Texas State Board of Education (TSBOE), University of Texas Austin professor David Hillis asserted that there are no legitimate scientific weaknesses in neo-Darwinian evolution. He stated that scientific weaknesses in evolution have “no scientific basis” and compared teaching these weaknesses to teaching “alchemy” or “astrology.”

Dr. Hillis’s assertions were false, and his comparisons were specious. Hundreds of Ph.D. scientists have expressed scientific skepticism of neo-Darwinian evolution.¹ Additionally, the TSBOE was presented with hundreds of scientific articles that discuss scientific weaknesses in key aspects of neo-Darwinian evolution. Additionally, much like his co-participant Ronald Wetherington, Hillis has bluffed about the facts of this debate, and his own arguments are controverted by the scientific record. Hillis’s testimony included multiple inaccurate statements. Hillis’s mistakes and misrepresentations included:

- Overselling the practical importance of evolution to agriculture and medicine.
- Failing to acknowledge scientific challenges to Darwin’s “tree of life” hypothesis and completely misrepresenting disagreements between molecule-based phylogenetic trees.
- Falsely claiming that there are high levels of congruence between anatomical and molecular phylogenies (leading experts acknowledge widespread disagreement between these two approaches).
- Overstating the length and understating the extent of the Cambrian explosion (again, leading experts disagree with Hillis’s claims).
- Invoking artificial selection as an explanation for biological information, even though it doesn’t accurately reflect the processes of unguided natural selection in the wild.
- Wrongly claiming that newly-discovered function for so-called “junk DNA” does not demonstrate a weakness of evolution, despite the fact that evolutionists themselves previously cited “junk DNA” as key evidence for evolution.
- Inaccurately portraying irreducible complexity as if it has been refuted by the scientific community (in reality, a variety of scientific papers show there is a vibrant scientific debate over irreducible complexity).
- **Downplaying natural** selection acting on mutations as the primary adaptive mechanism in orthodox evolutionary theory.

Dr. Hillis said he “wants the truth to be told.” That is commendable. Unfortunately, many of Dr. Hillis’s statements before the TSBOE were clearly false or misrepresentations of the truth. In that vein, what follows is a rebuttal to selected segments of Hillis’s testimony before the TSBOE.

A. Hillis Overstated the Practical Importance of Evolution

Dr. Hillis's testimony was brimming with praise for the alleged utility and power of modern evolutionary biology. He claimed that there are "a large number of modern agricultural practices that are now based upon evolutionary methods." But even some leading evolutionary biologists have conceded otherwise. University of Chicago evolutionary biologist Jerry Coyne admitted in the leading scientific journal *Nature*:

[I]f truth be told, evolution hasn't yielded many practical or commercial benefits. Yes, bacteria evolve drug resistance, and yes, we must take countermeasures, but beyond that there is not much to say. Evolution cannot help us predict what new vaccines to manufacture because microbes evolve unpredictably. But hasn't evolution helped guide animal and plant breeding? Not very much. Most improvement in crop plants and animals occurred long before we knew anything about evolution, and came about by people following the genetic principle of 'like begets like'. Even now, as its practitioners admit, the field of quantitative genetics has been of little value in helping improve varieties. Future advances will almost certainly come from transgenics, which is not based on evolution at all.²

To further show the alleged utility of evolution, Hillis discussed how mutations in one particular protein of the influenza virus allow it to escape detection by our immune system, stating "phylogenetic analysis ... is a critical tool for developing flu vaccines every year," and asserting that "knowledge of evolution helps millions of human lives be saved every year." While there is no doubt that influenza "evolution" is a real phenomenon, we must ask the crucial questions: *What degree of evolution is this? And can this sort of "evolution" be legitimately extrapolated to explain large-scale evolutionary changes?* In other words, if we were teaching students about this type of "evolution," should we teach them that it implies large scale macroevolutionary change that could explain the origin of complex biological features, such as new body plans?

The answer is clearly *no*. The truth is that the mutations in the hemagglutinin molecule testified about by Dr. Hillis represent small-scale neutral changes in a limited number of amino acids in one domain of the protein that do not change the virus's function for this protein (it resides on the surface of viruses and its function is to bind the flu virus to the infected cell).³ Nothing in Dr. Hillis's comments alters the fact that the flu virus remains a virtually identical virus after the microevolutionary changes he describes. Lives may be saved by studying functionally trivial amino acid changes in this protein, but it is not due to knowledge of any kind of evolution that can explain the origin of new species or body plans.

In fact, even when trying to fight diseases by combating anti-biotic resistance, neo-Darwinian theory provides little guidance. As State University of New York Professor of Neurosurgery Michael Egnor explains, "Darwinism tells us that ... bacteria survive antibiotics that they're not sensitive to, so non-killed bacteria will eventually outnumber killed bacteria. That's it."⁴ It is probably for this reason that, as noted, Jerry Coyne admitted in *Nature* that "if truth be told, evolution hasn't yielded many practical or commercial benefits. Yes, bacteria evolve drug

resistance, and yes, we must take countermeasures, but beyond that there is not much to say.”⁵ To actually create drugs that can outsmart evolving bacteria or cancer cells, biomedical researchers must rely upon drug cocktails that only work *because there are limits to the amount of evolution that microorganisms can undergo*.

Moreover, not all National Academy of Sciences (NAS) members feel as Hillis does about the utility of evolutionary biology. As NAS member Philip Skell wrote in *The Scientist* in 2005:

Darwinian evolution—whatever its other virtues—does not provide a fruitful heuristic in experimental biology. This becomes especially clear when we compare it with a heuristic framework such as the atomic model, which opens up structural chemistry and leads to advances in the synthesis of a multitude of new molecules of practical benefit. None of this demonstrates that Darwinism is false. It does, however, mean that the claim that it is the cornerstone of modern experimental biology will be met with quiet skepticism from a growing number of scientists in fields where theories actually do serve as cornerstones for tangible breakthroughs.⁶

Hillis has clearly overstated scientific opinions about the importance and utility of evolution.

B. Hillis Misled Board about Challenges to Darwin’s Tree of Life

Hillis cited himself as a “world’s leading exper[t] on the tree of life” and later told the TSBOE that there is “overwhelming agreement correspondence as you go from protein to protein, DNA sequence to DNA sequence” when reconstructing evolutionary history using biological molecules. Hillis’s self-proclaimed expertise makes it all the more egregious that he tried to mislead the TSBOE about the widespread prevalence of incongruencies between various molecular phylogenies within his field of systematics.

Indeed, the cover story of the journal *New Scientist*, published on the *very day* that Hillis testified before the TSBOE, was titled “Why Darwin was wrong about the tree of life.” Directly contradicting Hillis’s gross oversimplification of molecular systematics, the article reported that “The problem was that different genes told contradictory evolutionary stories.” The article observed that with the sequencing of the genes and proteins of various living organisms, the tree of life fell apart:

“For a long time the holy grail was to build a tree of life,” says Eric Baptiste, an evolutionary biologist at the Pierre and Marie Curie University in Paris, France. A few years ago it looked as though the grail was within reach. **But today the project lies in tatters, torn to pieces by an onslaught of negative evidence. Many biologists now argue that the tree concept is obsolete and needs to be discarded.** “We have no evidence at all that the tree of life is a reality,” says Baptiste. That bombshell has even persuaded some that our fundamental view of biology needs to change.⁷

To reiterate, the basic problem is that one gene or protein yields one version of the “tree of life,”

while another gene or protein yields an entirely different tree. As the *New Scientist* article stated:

The problems began in the early 1990s when it became possible to sequence actual bacterial and archaeal genes rather than just RNA. Everybody expected these DNA sequences to confirm the RNA tree, and sometimes they did but, crucially, sometimes they did not. RNA, for example, might suggest that species A was more closely related to species B than species C, but a tree made from DNA would suggest the reverse.⁸

Likewise, leading evolutionary bioinformatics specialist W. Ford Doolittle explains, “Molecular phylogenists will have failed to find the ‘true tree,’ not because their methods are inadequate or because they have chosen the wrong genes, but because the history of life cannot properly be represented as a tree.”⁹ Hillis (and others) may claim that this problem is only encountered when one tries to reconstruct the evolutionary relationships of microorganisms, such as bacteria, which can swap genes through a process called “horizontal gene transfer,” thereby muddying any phylogenetic signal. **But this objection holds no water, because the tree of life is challenged even among higher organisms where such gene-swapping does not take place.** As the article explains:

Syvanen recently compared 2000 genes that are common to humans, frogs, sea squirts, sea urchins, fruit flies and nematodes. In theory, he should have been able to use the gene sequences to construct an evolutionary tree showing the relationships between the six animals. He failed. The problem was that different genes told contradictory evolutionary stories. This was especially true of sea-squirt genes. Conventionally, sea squirts—also known as tunicates—are lumped together with frogs, humans and other vertebrates in the phylum Chordata, but the genes were sending mixed signals. Some genes did indeed cluster within the chordates, but others indicated that tunicates should be placed with sea urchins, which aren't chordates. “Roughly 50 per cent of its genes have one evolutionary history and 50 per cent another,” Syvanen says.¹⁰

To reiterate, even among higher organisms, the article explains that “The problem was that different genes told contradictory evolutionary stories,” therefore leading Syvanen to say regarding the relationships of these higher groups, “We’ve just annihilated the tree of life.” This directly contradicts the claims of Hillis.

Other scientists agree. Looking higher up the tree, a recent study published in *Science* tried to construct a phylogeny of animal relationships but concluded that “[d]espite the amount of data and breadth of taxa analyzed, relationships among most [animal] phyla remained unresolved.”¹¹ Likewise, Carl Woese, the father of evolutionary molecular systematics, observed that these problems extend well beyond the base of the tree of life: “Phylogenetic incongruities [conflicts] can be seen **everywhere in the universal tree, from its root to the major branchings within and among the various taxa to the makeup of the primary groupings themselves.**”¹²

Striking admissions of troubles in reconstructing the “tree of life” also came from a paper in the journal *PLOS Biology*, entitled “Bushes in the Tree of Life.” The authors acknowledge that “a

large fraction of single genes produce phylogenies of poor quality,” observing that one study “omitted 35% of single genes from their data matrix, because those genes produced phylogenies at odds with conventional wisdom.”¹³ The paper suggests that “certain critical parts of the [tree of life] may be difficult to resolve, regardless of the quantity of conventional data available.”¹⁴ The paper even contends that “[t]he recurring discovery of persistently unresolved clades (bushes) should force a re-evaluation of several widely held assumptions of molecular systematics.”¹⁵

Likewise, National Academy of Sciences biologist Lynn Margulis has had harsh words for the field of molecular systematics which Hillis studies. In her article, “The Phylogenetic Tree Topples” she explains that “many biologists claim they know for sure that *random mutation* (purposeless chance) is the source of inherited variation that generates new species of life and that life evolved in a single-common-trunk, dichotomously branching-phylogenetic-tree pattern!” But she dissents from that view and attacks the dogmatism of evolutionary systematists, noting that “[e]specially dogmatic are those molecular modelers of the ‘tree of life’ who, ignorant of alternative topologies (such as webs), don’t study ancestors.”¹⁶

Hillis may put up non-credible protests that none of this represents a “weakness” in neo-Darwinian evolution. He told the TSBOE that there is “overwhelming agreement correspondence as you go from protein to protein, DNA sequence to DNA sequence.” But should we believe him? As the *New Scientist* article admits, “Ever since Darwin the tree has been the unifying principle for understanding the history of life on Earth,” but since “different genes told contradictory evolutionary stories,” the notion of a tree of life is now quickly becoming a vision of the past—as the article stated, it’s being “annihilated.”

C. Hillis Misled the Board about the Congruence between Anatomical Phylogenies and Molecular Phylogenies

Despite the fact that he called himself a “tree of life expert,” David Hillis also made the grossly inaccurate claim that “there’s overwhelming correspondence between the basic structures we have about the tree of life from anatomical data, from biochemical data, molecular sequence data.” Yet many evolutionary scientists have recognized that evolutionary trees based upon morphology (physical characteristics of organisms) or fossils, commonly conflict with evolutionary trees based upon DNA or protein sequences (also called molecule-based trees).

For example, a review paper by Darwinian leaders in this field stated, “**As morphologists with high hopes of molecular systematics, we end this survey with our hopes dampened. Congruence between molecular phylogenies is as elusive as it is in morphology and as it is between molecules and morphology.**”¹⁷ Another set of pro-evolution experts wrote, “That molecular evidence typically squares with morphological patterns is a view held by many biologists, but interestingly, by relatively few systematists. Most of the latter know that the two lines of evidence **may often be incongruent.**”¹⁸

The widespread prevalence of disagreement and non-correspondence between molecule-based evolutionary trees and anatomy-based evolutionary trees led to a major article in *Nature* that reported that “disparities between molecular and morphological trees” lead to “evolution wars”

because “**Evolutionary trees constructed by studying biological molecules often don’t resemble those drawn up from morphology.**”¹⁹ The article’s revelation of the disparities between molecular and morphological phylogenies was striking:

When biologists talk of the ‘evolution wars’, they usually mean the ongoing battle for supremacy in American schoolrooms between Darwinists and their creationist opponents. But the phrase could also be applied to a debate that is raging within systematics. On one side stand traditionalists who have built evolutionary trees from decades of work on species’ morphological characteristics. On the other lie molecular systematists, who are convinced that comparisons of DNA and other biological molecules are the best way to unravel the secrets of evolutionary history.

[...]

So can the disparities between molecular and morphological trees ever be resolved? Some proponents of the molecular approach claim there is no need. The solution, they say, is to throw out morphology, and accept their version of the truth. “Our method provides the final conclusion about phylogeny,” claims Okada. Shared ancestry means a genetic relationship, the molecular camp argues, so it must be better to analyse DNA and the proteins it encodes, rather than morphological characters that can end up looking similar as a result of convergent evolution in unrelated groups, rather than through common descent. But morphologists respond that convergence can also happen at the molecular level, and note there is a long history of systematists making large claims based on one new form of evidence, only to be proved wrong at a later date.²⁰

Likewise, a review article in the journal *Bioessays* reported that despite a vast increase in the amount of data since Darwin’s time, “our ability to reconstruct accurately the tree of life may not have improved significantly over the last 100 years,” and that, “[d]espite increasing methodological sophistication, phylogenies derived from morphology, and those inferred from molecules, are not always converging on a consensus.”²¹ Strikingly, an article in *Trends in Ecology and Evolution* concluded, “the wealth of competing morphological, as well as molecular proposals [of] the prevailing phylogenies of the mammalian orders would reduce [the mammalian tree] to an unresolved bush, the only consistent clade probably being the grouping of elephants and sea cows.”²²

Hillis claimed there is “overwhelming correspondence” between anatomical and molecular phylogenies, but he seems to be inaccurately stating the facts on this matter. The truth is that there is great incongruence between these two different types of phylogenies, and that this incongruence is a huge issue within own his field of systematics. Why did Hillis misrepresent this information to the TSBOE?

D. Hillis Misrepresented the Timing and Extent of the Cambrian Explosion

Like anthropologist Ronald Wetherington, Hillis made glaring mistakes about the Cambrian

explosion, claiming that it occurred “over many tens or millions of years, not in the 5 million years that’s claimed by Discovery Institute,” and asserting that Stephen Meyer’s testimony was in “error.” But leading Cambrian explosion experts contradict Hillis’s claim and support Meyer’s account, as they have recognized that the Cambrian explosion represents only 5–10 million years of earth’s history:

- Robert Carroll stated in the leading journal *Trends in Ecology and Evolution* that it took less than ten million years: “The most conspicuous event in metazoan evolution was the dramatic origin of major new structures and body plans documented by the Cambrian explosion. Until 530 million years ago, multicellular animals consisted primarily of simple, soft-bodied forms, most of which have been identified from the fossil record as cnidarians and sponges. Then, within less than 10 million years, almost all of the advanced phyla appeared, including echinoderms, chordates, annelids, brachiopods, molluscs and a host of arthropods. The extreme speed of anatomical change and adaptive radiation during this brief time period requires explanations that go beyond those proposed for the evolution of species within the modern biota.”²³
- Likewise, an article in the journal *Development* by three Cambrian explosion experts explains that, “The Cambrian explosion is named for the geologically sudden appearance of numerous metazoan body plans (many of living phyla) between about 530 and 520 million years ago, only 1.7% of the duration of the fossil record of animals.”²⁴
- Another article a major evolution journal states that “recent geological investigations suggest that the Cambrian explosion may have occurred with a period of only 5-10 million years.”²⁵

At the very least, these contradictory opinions show evidence of a scientific debate, and that there are weaknesses in Hillis’s arguments regarding the Cambrian explosion that should not be withheld from students. At most, these expert opinions suggest that Dr. Hillis is incorrect.

Also like Wetherington, Hillis mistakenly stated that the Cambrian explosion was “very limited in scope” and that “most of the major phyla ... appear later than that.” But again, this is plainly incorrect.

One invertebrate biology textbook states that the Cambrian explosion “evidence tells us only that **all the major phyla appeared at about the same time**—500 to 600 million years ago. ... Many of the fossil members of these groups are similar to living counterparts today, and there is little indication, even within a phylum, of a steady progression of more and more complex forms. Moreover, few, if any, new phyla made their first appearance in the fossil record after about 500 million years ago.”²⁶ Likewise another invertebrate zoology textbook states, “**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.”²⁷

The truth is that nearly 70% (19 out of 28) of the known living animal phyla for which we have a fossil record make their first appearance in the Cambrian, as can be seen in the list below:

Phyla Known from the Precambrian: 3 Phyla (possibility of a fourth):

Cnidaria²⁸
Porifera²⁹
Gelatinosa (lower Cambrian)
Nuda

Phyla that Appear in the Cambrian: 19 Phyla

Annelida³⁰
Arthropoda³¹
Brachiopoda³²
Chaetognatha³³
Chordata³⁴
Coeloscleritophora³⁵
Ctenophora³⁶
Echinodermata³⁷
Halkieriida³⁸
Hemichordata³⁹
Hyolitha⁴⁰
Mollusca⁴¹
Nematoda⁴²
Onychophora⁴³
Phoronida⁴⁴
Pogonophora⁴⁵
Priapula⁴⁶
Tardigrada⁴⁷
Tardipolypoda⁴⁸

Phyla that Appear in Later Geologic Periods: 6 Phyla

Ordovician: Bryozoa/Ectoprocta⁴⁹
Devonian: Echiura⁵⁰
Pennsylvanian: Nemertina⁵¹
Jurassic: Entoprocta⁵²
Tertiary: Nematomorpha,⁵³ Rotifera.⁵⁴

Phyla With No Known Fossil Record: 12 Phyla

Acanthocephala,⁵⁵ Cycliophora,⁵⁶ Dicyemida, Gastrotricha,⁵⁷ Gnathostomulida,⁵⁸
Kinorhyncha,⁵⁹ Loricifera,⁶⁰ Orthonoectida, Pentastoma,⁶¹ Placozoa,⁶² Platyhelminthes,⁶³
Sipuncula.⁶⁴

Clearly Professor Hillis is misstating the fossil evidence regarding the Cambrian explosion.

Additionally, Hillis calls the Cambrian explosion “just one of many examples of adaptive radiation through time,” but an article in the journal *Science* recently observed that the empirical evidence showing exactly how adaptive radiations proceed is severely lacking.⁶⁵

Finally, Hillis also had the boldness to say that “there’s nothing about the Cambrian explosion that we could consider a weakness of evolution by any reasonable person.” Apparently Dr. Hillis must not consider Charles Darwin to be a “reasonable person.” In Darwin’s day, the Cambrian period was included in a period of a different name—the Silurian period. Regarding the explosion of new-life forms in the Silurian period, Darwin wrote in *Origin of Species* that “The case at present must remain inexplicable; and may be truly urged as a valid argument against the views here entertained.”⁶⁶ That was merely the punchline of Darwin’s chapter on the fossil record, but in the setup earlier in that chapter of his famous book, he remarked that the lack of fossil intermediate links “is the most obvious and gravest objection which can be urged against my theory.”⁶⁷

E. Hillis Inaccurately Tried to Explain the Origin of Information by Appealing to Artificial Selection

When asked about the origin of information that is encoded in DNA, Hillis first replied, “The origin of the information, I’m not sure if I have any idea what you’re talking about.” Apparently a few seconds later, Hillis felt it was not best to bluff that this was an unreasonable question, because he then acted as if he understood the question, claiming that *in vitro* laboratory experiments have produced functional information in RNAs through artificial selection. But these types of experiments have come under heavy criticism because they do not mimic natural processes and require intelligent intervention at every step. As mathematician and philosopher William Dembski and molecular biologist Jonathan Wells write:

Do SELEX experiments therefore demonstrate the power of purely materialistic forces to evolve biologically significant RNA structures under realistic prebiotic conditions? Not at all. Intelligent intervention by the experimenter is indispensable. In SELEX experiments, large pools of randomized RNA molecules are formed by intelligent synthesis and not by chance—there is no natural route to RNA (in fact, the chemical processes in nature that facilitate the formation of nucleotide bases undercut the formation of RNA’s sugar-phosphate backbone and vice versa). The artificially synthesized molecules are then sifted chemically by various means to select for catalytic function. What’s more, the catalytic function is specified by the investigator. Those molecules showing some activity are isolated and become templates for the next round of selection. And so on, round after round. At every step in SELEX and ribozyme (catalytic RNA) engineering experiments, the investigator is carefully arranging the outcome, even if he or she does not know the specific sequence that will emerge. It is simply irrelevant that the investigator learns the identity or structure of the evolved ribozyme only after the experiment is over. The investigator first had to specify a precise catalytic function. Next, the investigator had to specify a fitness measure gauging degree of catalytic function for a given polynucleotide. And finally, the investigator had to run an experiment to optimize the fitness measure. Only then does the investigator obtain a polynucleotide exhibiting the catalytic function of interest. In all such experiments the investigator is inserting crucial information at every step. Ribozyme engineering is engineering. Indeed, there is no evidence that natural

processes as found in nature can do their own ribozyme engineering without the aid of human intelligence.⁶⁸

Clearly SELEX experiments do not invoke natural causes that take place in the wild. Hillis also mentioned recombination and genetic drift as mechanisms that can produce the information in life, but these mechanisms are not said to be adaptive and they are not thought to produce adaptive complexity of life. The truth about the origin of biological information was perhaps best admitted by leading origin of life theorist at the University of Santa Cruz, David Deamer, who last year, when asked about the “origin of the gene,” replied, “I think genetic information more or less came out of nowhere by chance assemblages of short polymers.”⁶⁹ Such an answer does not inspire confidence in the ability of natural processes to generate new biological information.

F. Hillis’s Blunder Regarding “Junk DNA”

Hillis asserted that in four binders submitted to the TSBOE of 100+ articles documenting scientific weaknesses in evolution Discovery Institute was “arguing that because junk-DNA has function that that somehow conflicts with evolutionary theory.” He calls the binders a “misrepresentation of the facts.” But in fact it is Hillis who has misrepresented the facts. In the introduction to the section of the binder containing articles about “junk DNA,” it is stated:

The articles in this section do not specifically argue that neo-Darwinian evolution is flawed. However, there is an extensive record of evolutionary biologists asserting that non-functional “junk” DNA is evidence for Darwinian evolution, and these papers demonstrate function for such junk-DNA, contrary to the expectations and claims of many evolutionary scientists.

Because evolutionists view life as the result of an unguided and random process, they have long-stated and predicted that non-coding DNA would be functionless “junk.” As an article in *Scientific American* stated, “These regions have traditionally been regarded as useless accumulations of material from millions of years of evolution. ... In humans, about 97 percent of the genome is junk.”⁷⁰ Or as Richard Dawkins stated, “The simplest way to explain the surplus DNA is to suppose that it is a parasite or at best a harmless but useless passenger, hitching a ride in the survival machines created by the other DNA.”⁷¹ Indeed, one article in the journal *Science* explained that neo-Darwinian thinking has stifled and hindered research into junk-DNA:

Although catchy, the term ‘junk DNA’ for many years repelled mainstream researchers from studying noncoding DNA. Who, except a small number of genomic clochards, would like to dig through genomic garbage? However, in science as in normal life, there are some clochards who, at the risk of being ridiculed, explore unpopular territories. Because of them, the view of junk DNA, especially repetitive elements, began to change in the early 1990s. Now, more and more biologists regard repetitive elements as a genomic treasure.⁷²

There is in fact direct evidence from the mainstream scientific literature that modern neo-Darwinian biology has hindered scientific progress and research into junk-DNA. A 2003 article

in *Scientific American* explained that non-coding DNA sequences, called *introns*, were “long ago written off as irrelevant because they yield no proteins” and quoted molecular biologist John S. Mattick observing that introns “were immediately assumed to be evolutionary junk.”⁷³ However, in a stark admission, the article calls that Darwinian assumption “too hasty” and Mattick acknowledges that “The failure to recognize the importance of introns ‘may well go down as one of the biggest mistakes in the history of molecular biology.’”⁷⁴

Similarly, a paper from the *Annals of the New York Academy of Sciences* writes that “neo-Darwinian ‘narratives’ have been the primary obstacle to elucidating the effects of these enigmatic components of chromosomes,” and therefore, “a new conceptual framework is needed.”⁷⁵ The article concludes that “the selfish DNA narrative and allied frameworks must join the other ‘icons’ of neo-Darwinian evolutionary theory that, despite their variance with empirical evidence, nevertheless persist in the literature.”⁷⁶

These junk-DNA articles show that neo-Darwinism led many biologists to have false expectations about noncoding “junk” DNA. Perhaps evolutionary theory can accommodate the finding that junk DNA is not junk. But the evidence shows that evolution led scientists to have expectations that were wrong—a grave weakness in evolutionary theory.

G. Hillis Wrongly Claimed Irreducible Complexity Has Been Refuted

Hillis claims that “irreducible complexity has been refuted in the peer-reviewed research papers and rejected by the scientific community at large,” but in fact there are peer-reviewed research scientific publications and other mainstream scientific publications that support the idea of irreducible complexity and have discussed and elaborated upon this concept in a positive manner. Some of these publications include:

- W.-E. Lönnig, “Dynamic genomes, morphological stasis and the origin of irreducible complexity,” *Dynamical Genetics*, Pp. 101-119.
- W.-E. Lönnig & H. Saedler, “Chromosome Rearrangements and Transposable Elements,” *Annual Review of Genetics*, Vol. 36:389-410 (2002).
- Richard A. Watson, *Compositional Evolution* (MIT Press, 2006).
- Michael J. Behe and David W. Snoke, “Simulating Evolution by Gene Duplication of Protein Features That Require Multiple Amino Acid Residues,” *Protein Science*, Vol. 13: 2651-2664 (2004).
- Michael J. Behe, “Reply to My Critics: A Response to Reviews of Darwin’s Black Box: The Biochemical Challenge to Evolution,” *Biology and Philosophy*, Vol. 16: 685–709, (2001).
- Michael J. Behe, “Self-Organization and Irreducibly Complex Systems: A Reply to Shanks and Joplin,” *Philosophy of Science*, Vol. 67:155-162 (March 2000).
- Michael J. Behe and David W. Snoke, “A response to Michael Lynch,” *Protein Science*, Vol. 14:2226-2227 (2005).
- Michael J. Behe, “*Irreducible complexity: obstacle to Darwinian evolution*,” *Debating Design: From Darwin to DNA*, Pp. 352-370 (Cambridge University Press, 2004)

- Wolf-Ekkehard Lönnig, Kurt Stüber, Heinz Saedler, Jeong Hee Kim, "Biodiversity and Dollo's Law: To What Extent can the Phenotypic Differences between *Misopates orontium* and *Antirrhinum majus* be Bridged by Mutagenesis?," *Bioremediation, Biodiversity and Bioavailability*, Vol. 1:1-30 (2007).
- Stephen C. Meyer, "The origin of biological information and the higher taxonomic categories," *Proceedings of the Biological Society of Washington*, Vol. 117(2):213-239 (2004).
- Granville Sewell, "A Mathematician's View of Evolution," *The Mathematical Intelligencer*, Vol. 22 (4) (2000).
- Kirk K. Durston, David K. Y. Chiu, David L. Abel, Jack T. Trevors, "Measuring the functional sequence complexity of proteins," *Theoretical Biology and Medical Modelling*, Vol. 4:47 (2007).
- David L. Abel & Jack T. Trevors, "Self-organization vs. self-ordering events in life-origin models," *Physics of Life Reviews*, Vol. 3:211–228 (2006).
- Scott A. Minnich & Stephen C. Meyer, *Genetic Analysis of Coordinate Flagellar and Type III Regulatory Circuits in Pathogenic Bacteria*, in *Proceedings of the Second International Conference on Design & Nature, Rhodes Greece*.
- Ø. A. Voie, "Biological function and the genetic code are interdependent," *Chaos, Solitons and Fractals*, Vol. 28(4) (2006): 1000-1004.
- Michael J. Katz, *Templets and the Explanation of Complex Patterns* (Cambridge U. Press 1986).
- J.T. Trevors & D.L. Abel, "Chance and necessity do not explain the origin of life," *Cell Biology International*, Vol. 28:729-739 (2004).
- Evelyn Fox Keller, "Developmental Robustness," *Annals of the New York Academy of Sciences*, Vol. 981:189 (2002).

Indeed, scientists in recent months have debated Behe's arguments in leading scientific journals. A recent paper in the journal *Genetics* attempted to rebut Behe's arguments with regards to lower animals like fruit flies,⁷⁷ but ended up validating some of his core arguments regarding more slowly reproducing organisms such as humans. The article stated:

Our previous work has shown that, in humans, a new transcription factor binding site can be created by a single mutation in an average of 60,000 years, but, as our new results show, a coordinated pair of mutations that first inactivates a binding site and then creates a new one is very unlikely to occur on a reasonable timescale.⁷⁸

The mathematical study found that the amount of time to simply generate a new binding site via evolutionary processes "for humans with a much smaller effective population size, this type of change would take > 100 million years." Since humans have existed at most for a few million years, it would seem that Darwinian evolution has an unmovable obstacle in its way. As molecular biologist Douglas Axe observed when commenting on this article the recent *Genetics* paper:

Do you see the problem? On the one hand we're supposed to believe that the Darwinian mechanism converted a proto-insect into a stunning array of radically different life forms (termites, beetles, ants, wasps, bees, dragonflies, stick insects, aphids, fleas, flies, mantises, cockroaches, moths, butterflies, etc., each group with its own diversity) well within the space of 400 million years. But on the other hand, when we actually do the math we find that a single insignificant conversion of binding sites would reasonably be expected to consume all of that time. The contrast could hardly be more stark: The Darwinian story hopes to explain all the remarkable transformations within 400 million years, but the math shows that it actually explains no remarkable transformation in that time. If that doesn't call for a serious rethink, it's hard to imagine what would.⁷⁹

Behe directly responded to his critics in the journal *Genetics*, observing that his critics misunderstood his argument, stating, "Their criticism compares apples to oranges. My figure of 10^{20} is an empirical statistic from the literature; it is not, as their calculation is, a theoretical estimate from a population genetics model."⁸⁰

This is, of course, not the first time that Behe and his defenders and his critics have debated his ideas in scientific journals.⁸¹ If anything, this shows evidence of a scientific debate—not one that has been fully settled within the scientific community. Professor Hillis has every right to his view that irreducible complexity is incorrect. But he does not have the right to state that the scientific community has wholesale rejected irreducible complexity view nor can he claim that this debate is finished.

H. Hillis Misrepresented the Importance of Natural Selection to Neo-Darwinian Evolution

Hillis claimed that because biology textbooks appeal to processes other than natural selection, critics of neo-Darwinism are wrong to point out that natural selection and random mutation are incapable of producing the complexity of life. He specifically stated that "no one is arguing that natural selection is the only thing that accounts for all of life's diversity." **What Hillis failed to tell the Board, however, is that while there are other mechanisms of evolution, they are not purported to be the primary *adaptive* mechanisms, i.e. they are not claimed to have the ability to build new complex biological features that bring some advantage or increase in fitness to an organism.** Thus, criticisms of the selection-mutation mechanism represent a fundamental challenge to orthodox evolutionary theory as it is espoused by mainstream evolutionary biologists.

To show that natural selection is indeed invoked to account for the adaptive complexity of life, consider these examples which refute Hillis's misrepresentation of biological thinking:

- The U.S. National Academy of Sciences states in its booklet *Science, Evolution, and Creationism* that "The differential reproductive success of organisms with advantageous traits is known as natural selection, because nature 'selects' traits that enhance the ability of organisms to survive and reproduce,"⁸² and gives unqualified praise to Darwin's discovery of "natural selection as the driving force behind evolution."⁸³ The book

expressly claims natural selection acting upon random mutations is the process by which species obtain adaptations: “The process by which organisms with advantageous variations have greater reproductive success than other organisms within a population is known as ‘natural selection.’ Over multiple generations, some populations of organisms subjected to natural selection may change in ways that make them better able to survive and reproduce in a given environment. Others may be unable to adapt to a changing environment and will become extinct.”⁸⁴

- In the journal *Nucleic Acids Research*, influential evolutionary biologist Eugene V. Koonin recently summarized neo-Darwinian evolution, the Modern Synthesis (which is the model of evolution taught in most textbooks), as holding that “Evolution proceeds by fixation of the rare beneficial variations and elimination of deleterious variations: this is the process of natural selection that, along with random variation, is the principal driving force of evolution according to Darwin and the Modern Synthesis.”⁸⁵
- Sandra Alters textbook *Biology*, states that “The driving force of change—natural selection—is often referred to as *survival of the fittest*.”⁸⁶
- The leading textbook, *Genetics*, by Daniel L. Hartl and Elizabeth W. Jones states that “The driving force of adaptive evolution is natural selection, which is a consequence of hereditary differences among organisms in their ability to survive and reproduce in the prevailing environment.”⁸⁷
- In their chapter “Adaptation” of their book *How and why species multiply*, famous field evolutionary biologists Peter and Rosemary Grant state that, “In the cycle of speciation events modeled in Figure 3.1, natural selection is the main driving force in the differentiation of a population in allopatry.”⁸⁸
- In the volume *Creative Evolution*, a compendium of essays by leading evolutionary scientists, UCLA evolutionary biologist John H. Campbell observes that “Mutation with natural selection is the basic driving force for evolution.”⁸⁹
- Acclaimed evolution historian Peter J. Bowler observes, after Darwin many biologists “became convinced that natural selection was the driving force of evolution.”⁹⁰
- Harvard evolutionary biologist E.O. Wilson has observed that, “Evolution in a pure Darwinian world has no goal or purpose: the exclusive driving force is random mutations sorted out by natural selection from one generation to the next.”⁹¹

Of course there are other mechanisms that can cause evolution besides natural selection and random mutation. But after recognizing that “[t]he known evolutionary mechanisms include mutation, gene flow, genetic drift, nonrandom mating, and natural selection,”⁹² **even Hillis’s own textbook admits that natural selection is the evolutionary mechanism that results in adaptation!** In the words of Hillis and his co-authors:

What Evolutionary Mechanisms Result in Adaptation? Adaptation occurs

when some individuals in a population contribute more offspring to the next generation than others, such that *allele frequencies in the population change in a way that adapts individuals to the environment that influenced such reproductive success*. This is the mechanism that Darwin called ‘natural selection.’⁹³

Clearly natural selection is stated to be the primary adaptive force under neo-Darwinian evolution. Scientists who doubt the ability of natural selection acting on random mutation to generate the adaptive complexity of life are thus challenging a central dogma of modern evolutionary theory, not a straw man. That is why it is so significant that, as mainstream science journalist Susan Mazur reports, “hundreds of... evolutionary scientists (non-Creationists)... contend that natural selection is politics, not science, and that we are in a quagmire because of staggering commercial investment in a Darwinian industry built on an inadequate theory.”⁹⁴ One of those scientists is evolutionary biologist Stanley Salthe, who is highly critical of neo-Darwinian evolution. According to Salthe:

Oh sure natural selection’s been demonstrated . . . the interesting point, however, is that it has rarely if ever been demonstrated to have anything to do with evolution in the sense of long-term changes in populations. . . . Summing up we can see that the import of the Darwinian theory of evolution is just unexplainable caprice from top to bottom. What evolves is just what happened to happen.⁹⁵

Likewise, National Academy of Sciences member biologist Lynn Margulis (2003) has argued that “new mutations don’t create new species; they create offspring that are impaired.”⁹⁶ Margulis explained that mutations do not provide any useful raw materials because they tend to destroy function, introducing sickness and death:

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.⁹⁷

Contrary to Hillis’s bluffs, there are significant scientists who doubt the adequacy of the primary adaptive mechanism within modern neo-Darwinian evolutionary biology to account for the adaptive complexity of life. Should this fact be withheld from students?

I. Hillis Misrepresented Scientific Articles Documenting Weaknesses in Neo-Darwinism

Hillis made numerous misrepresentations when he talked about the four binders presented to the Board containing over 100 mainstream scientific articles discussing weaknesses in modern evolutionary biology.

Hillis charged that these articles do not represent weaknesses because the authors are allegedly “all ardent evolutionary biologists. Every single one of them,” except, he stated, for Dr. Stephen Meyer. Even if Hillis’s claim happened to be correct (it wasn’t), his reasoning was utterly nonsensical. As the introduction to the binders pointed out, the fact that prominent evolutionists themselves concede there are unresolved problems in modern evolutionary theory provides a telling confirmation that the scientific weaknesses of neo-Darwinism are real.⁹⁸

Furthermore, Hillis’s sweeping assertion that the article’s authors are “all ardent evolutionary biologists” was false. Even though many of the articles were authored by supporters of neo-Darwinian evolution, a significant number of the authors are well-credentialed scientific skeptics of neo-Darwinism. Some of these authors include:

- Philip L. Skell, member of the U.S. National Academy of Sciences, who is a vocal skeptic of neo-Darwinian evolution.
- Michael Behe, Professor of Biochemistry at Lehigh University who has published multiple articles in mainstream scientific venues challenging the sufficiency of the neo-Darwinian mechanism to account for biological complexity.
- D. W. Snoke, Associate Professor of Physics & Astronomy University of Pittsburgh, who has published peer-reviewed research with a mathematical basis challenging the sufficiency of Darwinian evolutionary processes to create new enzyme-substrate interactions.
- Wolf-Ekkehard Lönig, Senior Scientist in the Department of Molecular Plant Genetics at the Max-Planck-Institute for Plant Breeding Research, who has published multiple peer-reviewed articles skeptical of neo-Darwinian evolution and supporting notions of irreducible complexity.
- Øyvind A. Voie, Ph.D. Biology from the University of Oslo in Norway who has published peer-reviewed research challenging chemical evolutionary explanations for the origin of the language-based system underlying all of life.
- Jonathan Wells, who holds a Ph.D. in molecular biology from the University of California Berkeley and has published in mainstream scientific journals about scientific errors in how many biology textbooks have used embryology to support evolution.
- John A. Davison, Emeritus Associate Professor of Biology University of Vermont, who has published peer-reviewed research challenging the fundamentals of standard neo-Darwinian evolutionary explanations.
- Scott A. Minnich, Professor in the Dept of Microbiology and Molecular Biology & Biochemistry at University of Idaho, whose published research challenges the sufficiency of natural selection and random mutation to account for microbiological machines such as the flagellum.
- Granville Sewell, Professor of Mathematics at University of Texas, El Paso, who has published peer-reviewed work showing the insufficiency of natural selection to account

for some complex biological features.

- Douglas D. Axe, who holds a Ph.D. in Chemical Engineering from the California Institute of Technology, and whose work published in the *Journal of Molecular Biology* challenges evolutionary accounts of the origin of proteins.
- Richard Sternberg, former Smithsonian researcher who holds 2 Ph.D.s in evolutionary biology who has published research attacking core tenets of modern evolutionary biology, especially criticizing neo-Darwinism for leading scientists in the wrong direction with respect to non-coding DNA.

Contrary to Hillis's bluffs, Stephen C. Meyer is by no means the only scientist who is a scientific skeptic of neo-Darwinian evolution who authored a paper included in the binders.

It should be noted that although Hillis claimed that the weaknesses raised in the binders “have no scientific basis,” he did not take the time to offer the Board a single rebuttal to a single specific article. Hillis's objection to the articles that they don't show legitimate scientific weaknesses in evolution was specious: each article came with a description of why that article challenged some key aspect of biological or chemical evolution. Some of the many articles left un rebutted by Hillis included the following:

P. L. Skell, “Why do we invoke Darwin?” *The Scientist*, Vol. 19(16):10 (August 29, 2005).

National Academy of Sciences member Philip Skell discusses how Darwinian evolution is largely irrelevant to much biology research, and how biologists for the most part do not depend on Darwin's ideas to conduct their work. Skell concludes: “Darwinian evolution—whatever its other virtues—does not provide a fruitful heuristic in experimental biology. This becomes especially clear when we compare it with a heuristic framework such as the atomic model, which opens up structural chemistry and leads to advances in the synthesis of a multitude of new molecules of practical benefit. None of this demonstrates that Darwinism is false. It does, however, mean that the claim that it is the cornerstone of modern experimental biology will be met with quiet skepticism from a growing number of scientists in fields where theories actually do serve as cornerstones for tangible breakthroughs.”

M. Behe and D. W. Snoke, “Simulating evolution by gene duplication of protein features that require multiple amino acid residues,” *Protein Science*, Vol. 13 (2004).

This paper in the journal *Protein Science* describes how proteins interact with other proteins in a lock and key fit. Using computer simulations, they show that it is very difficult to evolve this special lock-and-key fit using mere random mutations and unguided natural selection alone.

W.-E. Lönnig and H. Saedler, “Chromosome Rearrangement and Transposable Elements,” *Annual Review of Genetics*, Vol. 36:389–410 (2002).

This article in a leading biology journal, *Annual Review of Genetics*, acknowledges that some biological systems are “irreducibly complex,” which poses a strong challenge to neo-Darwinian evolution.

W.-E. Lönnig, “Dynamic genomes, morphological stasis, and the origin of irreducible complexity,” in Valerio Parisi, Valeria De Fonzo, and Filippo Aluffi-Pentini eds., *Dynamical Genetics* (2004).

This chapter in the scientific book *Dynamical Genetics* explores hypotheses and data (such as irreducible complexity) that pose explicit challenges to biological evolution.

C. Patterson *et al.*, “Congruence Between Molecular and Morphological Phylogenies,” *Annual Review of Ecology and Systematics*, Vol. 24: 153-188 (1993).

This review article, lead-authored by the influential biologist Colin Patterson, compares phylogenetic trees based upon morphology to those based upon molecules and finds that there is very little congruence between the two types of trees, implying that Darwinian evolution has made poor predictions regarding expected confirmations of common descent from molecular biology. The authors express disappointment at their findings, stating: "As morphologists with high hopes of molecular systematics, we end this survey with our hopes dampened. Congruence between molecular phylogenies is as elusive as it is in morphology and as it is between molecules and morphology."

S. J. Gould, “Evolution’s Erratic Pace,” *Natural History* (May, 1977).

This article discusses the fact that transitional forms are commonly missing in the fossil record, stating “The extreme rarity of transitional forms in the fossil record persists as the trade secret of paleontology. The evolutionary trees that adorn our textbooks have data only at the tips and nodes of their branches; the rest is inference, however reasonable, not the evidence of fossils.”

S. J. Gould, “Is a new and general theory of evolution emerging?,” *Paleobiology*, Vol. 6(1):119-130 (January, 1980).

This article shows how evolutionists admit the fact that functional intermediates are hard to both imagine and find in the fossil record, as it states, "The absence of fossil evidence for intermediary stages between major transitions in organic design, indeed our inability, even in our imagination, to construct functional intermediates in many cases, has been a persistent and nagging problem for gradualistic accounts of evolution."

L. E. Orgel, “The Implausibility of Metabolic Cycles on the Prebiotic Earth,” *PLOS Biology*, Vol. 6(1) (January, 2008).

This article provides strong criticisms of theories stating that life originated through evolving metabolic pathways. The author critiques metabolic origin of life hypotheses because such metabolic pathways are too complex to arise by naturalistic processes.

J.T. Trevors and D.L. Abel, “Chance and necessity do not explain the origin of life,” *Cell Biology International*, Vol. 28:729-739 (2004).

This article argues that the language-dependent nature of the basic cell makes it highly improbable that such a system could arise through chance and necessity. As the article explains, “New approaches to investigating the origin of the genetic code are required. The constraints of historical science are such that the origin of life may never be understood. Selection pressure cannot select nucleotides at the digital programming level where primary structures form. Genomes predetermine the phenotypes which natural

selection only secondarily favors. Contentions that offer nothing more than long periods of time offer no mechanism of explanation for the derivation of genetic programming. No new information is provided by such tautologies. The argument simply says it happened. As such, it is nothing more than blind belief.”

These are just a few of many dozens of examples of articles that Hillis completely failed to rebut, even though he claimed they did not show legitimate weaknesses in evolution. Dr. Hillis does not seem capable of addressing the actual evidence of scientific weaknesses in modern evolutionary theory in a direct and accurate fashion. Those who rely on his testimony to censor scientific evidence that challenges evolution will be basing their decision upon false information, and doing a great disservice to students.

J. Conclusion

At the January experts hearing, Prof. Hillis insinuated that those who support retaining the “strengths and weaknesses” language want “students who do not learn about evolution in high school.” Yet none of expert reviewers who support the “strengths and weaknesses” language favor eliminating the teaching of evolution. **Rather, they want students to learn more about evolution, not less.** It is David Hillis and his colleagues who wish to dumb down the teaching of evolution so that students uncritically accept Darwinian evolution as the force underlying all of biology. Proponents of the existing TEKS language want students to be able to learn about *both* the scientific evidence for and against evolution, without censorship.

¹ See A Scientific Dissent from Darwinism at <http://www.dissentfromdarwin.org>

² Jerry Coyne, "Selling Darwin: Does it matter whether evolution has any commercial applications?," reviewing *The Evolving World: Evolution in Everyday Life* by David P. Mindell, in *Nature*, Vol 442:983-984 (August 31, 2006).

³ Arthur Chun-Chieh Shih, Tzu-Chang Hsiao, Mei-Shang Ho, and Wen-Hsiung Li, "Simultaneous amino acid substitutions at antigenic sites drive influenza A hemagglutinin evolution," *Proceedings of the National Academy of Sciences USA*, Vol. 104: 6283–6288 (April 10, 2007).

⁴ Michael Egnor, "Quick, Nurse, Give the Patient a Tautology!," http://www.evolutionnews.org/2007/03/quick_nurse_give_the_patient_a.html

⁵ Jerry Coyne, "Selling Darwin: Does it matter whether evolution has any commercial applications?," reviewing *The Evolving World: Evolution in Everyday Life* by David P. Mindell, in *Nature*, Vol 442:983-984 (August 31, 2006).

⁶ Philip Skell, "Why Do We Invoke Darwin? Evolutionary theory contributes little to experimental biology," *The Scientist* (August 29, 2005).

⁷ Graham Lawton, "Why Darwin was wrong about the tree of life," *New Scientist* (January 21, 2009) (emphasis added).

⁸ Graham Lawton, "Why Darwin was wrong about the tree of life," *New Scientist* (January 21, 2009).

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- ²¹ Matthew A. Wills, "The tree of life and the rock of ages: are we getting better at estimating phylogeny" in *BioEssays* 24: 203-207 (2002), reporting on the findings of Michael J. Benton, "Finding the tree of life: matching phylogenetic trees to the fossil record through the 20th century" *Proceedings of the Royal Society of London B*, Vol. 268: 2123-2130 (2001).
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- ⁹⁷ Lynn Margulis, Dorion Sagan, *Acquiring Genomes: A Theory of the Origins of the Species*, pg. 29 (Basic Books, 2003).
- ⁹⁸ The binders contained a footnote explaining why it is a strong argument to quote one's opponent: "For example, the American legal system has long acknowledged that citing an admission from one's opponent about a weakness in their own case is not considered to be a weak argument, but rather is strong and highly reliable evidence."