

**QUESTIONS AND ANSWERS ABOUT THE DISCOVERY INSTITUTE'S
BIBLIOGRAPHY OF SUPPLEMENTARY RESOURCES
FOR OHIO SCIENCE INSTRUCTION**

**The Discovery Institute
Seattle, Washington**

The National Center for Science Education (NCSE) recently accused the Discovery Institute of providing the Ohio Board of Education with a “misleading” bibliography that (1) “misrepresents the significance of the publications,” is (2) “inaccurate and tendentious,” and (3) “fails to provide any principled basis for the selection of the publications.” These charges are not only groundless, but severely distort the public record. The Supplementary Bibliography accurately describes the content of the articles it cites, as a careful reading of the articles themselves will demonstrate. Furthermore, the Bibliography accurately highlights the very points and arguments stressed by the authors themselves, as stated plainly in their abstracts, opening paragraphs, or conclusions. *Every case of misrepresentation claimed by the NCSE dissolves entirely on close inspection.*

We have organized our reply to the NCSE accusations into a series of questions and answers. Full documentation is provided in the Appendix.

First, a brief summary of the controversy. On Monday, March 11, 2002, philosopher of science Stephen Meyer and biologist Jonathan Wells, both of the Discovery Institute, debated biologist Kenneth Miller and physicist Lawrence Krauss before the Ohio Board of Education and a large public audience. At that debate, Meyer and Wells submitted a 22-page “Bibliography of Supplementary Resources for Ohio Science Instruction,” comprising journal articles, books, or monographs of relevance to the teaching of biology and evolution in public school classrooms. (The full original text is available at <http://www.discovery.org/viewDB/index.php3?program=CRSC%20Responses&command=view&id=1127>) On Friday, April 5, 2002, the NCSE released on its web page a 15-page critique of this bibliography, using information gathered from a questionnaire sent to a selected group of the scientists or authors cited in the Bibliography. (The full text is available at http://www.ncseweb.org/resources/articles/3878_analysis_of_the_discovery_inst_4_5_2002.asp) In that questionnaire, the NCSE asked the scientists (1) if they thought their work provided “scientific evidence for intelligent design” or “scientific evidence against evolution,” (2) if the Supplementary Bibliography accurately summarized their publications, and (3) if their publications were appropriate for use in high school science instruction.

The NCSE analysis, however, severely distorts both the content of the Supplementary Bibliography, and what was claimed for the Bibliography by Meyer and Wells.¹

1. Did the Supplementary Bibliography, or Meyer and Wells, say that the authors of the cited articles thought they were providing “scientific evidence for intelligent design?”

No. This statement is “spin” contrived by the NCSE for the purposes of their questionnaire. It is a complete fabrication.

Neither the Bibliography itself, nor Meyer and Wells, ever claimed that the articles were written to support intelligent design. In their public spoken comments, Meyer and Wells said that the Bibliography contained “some 40 peer-reviewed articles that question aspects or key tenets of Darwinian theory” (Meyer) or that are relevant to questions about “the adequacy of Darwinian evolution” (Wells). In an opinion column for the *Cincinnati Inquirer*, Meyer wrote that the articles in the Bibliography “raise significant challenges to key tenets of Darwinian evolution.”² We stand by these statements.

2. Did the Supplementary Bibliography, or Meyer and Wells, say that the cited articles “provide scientific evidence against evolution?”

No. Again, this statement was contrived by the NCSE. It’s another fabrication.

“Evolution”—used by itself—is a very broad term, which can mean anything from “change over time” (a fact accepted by intelligent design theorists as well as neo-Darwinian biologists) to the particular theory of neo-Darwinism described in biology textbooks. The Bibliography states that the articles it cites bear on *the theory of neo-Darwinism*, and Meyer and Wells consistently said this as well. “Evolution” is far too broad or imprecise a term in this context, which is why neither the Bibliography, nor Meyer and Wells, used the word without qualification.

3. Then what did the Supplementary Bibliography actually say about the articles?

Only this:

The publications represent dissenting viewpoints that challenge one or another aspect of neo-Darwinism (the prevailing theory of evolution taught in biology textbooks), discuss problems that evolutionary theory faces, or suggest important new lines of evidence that biology must consider when explaining origins.

Note again that there is no mention here either of “evidence for intelligent design” or of “evidence against evolution”—phrases spun from nothing by the NCSE. If the scientists who answered the NCSE questionnaire, therefore, said that their work neither provided evidence for intelligent design nor against evolution, they said no more or less than what the Supplementary Bibliography itself had already stated. The NCSE has erected a straw man.

Note also that the Bibliography’s introductory sentence is *disjunctive*. Its clauses describe three separate, although not necessarily exclusive, categories:

(1) “dissenting viewpoints that challenge one or another aspect of neo-Darwinism”

OR

(2) “problems that evolutionary theory faces”**OR****(3) “new lines of evidence that biology must consider when explaining origins”**

Saying that the pieces of fruit in a bowl are red, yellow, or green does not mean that any piece of fruit in the bowl must therefore be simultaneously red *and* yellow *and* green. We would have thought that the logic (and meaning) of a disjunctive proposition would be obvious. Indeed, it is obvious, to anyone who reads the sentence with ordinary charity. In fact, all the publications cited in the Supplementary Bibliography fall readily into at least one of the categories (1), (2), or (3).

Moreover, given that neither the Bibliography nor Meyer and Wells said that the publications were “evidence against evolution,” we should focus on what *was* the object of the Bibliography’s critical attention, namely, *neo-Darwinism*. Neo-Darwinism is a *particular theory* of evolution—not identical to “evolution” itself—according to which all living things have descended from a single common ancestor mainly through the process of natural selection acting on randomly-arising genetic variation. Unlike the vague term “evolution,” neo-Darwinism can be precisely defined, and has testable content. Key aspects or tenets of neo-Darwinism, as presented in biology textbooks, include such claims as:

- the sufficiency of small-scale random variation and natural selection to explain major changes in organismal form and function;
- the equivalence, given enough time, of the processes of micro- and macroevolution;
- the usefulness of “molecular clocks” to determine historical branching points between species;
- the existence of a single Tree of Life, with its roots in a Last Universal Common Ancestor (LUCA);
- the congruence or matching of evolutionary trees (i.e., phylogenies) derived from morphological and molecular evidence;
- the appearance, in embryology, of a conserved stage revealing the common ancestry of all vertebrates.

The publications cited in the Supplementary Bibliography, organized under the headings of “Questions of Pattern” and “Questions of Process,” do cast critical light on one or another of these aspects of neo-Darwinism. In most cases, in fact, as reading the articles themselves will demonstrate, these critical challenges are stated plainly by the authors in their abstracts, opening paragraphs, or conclusions.

4. Can you give an example of this?

Consider the article “Trees for bees,” by Peter Lockhart and Sydney Cameron, from the journal *Trends in Ecology and Evolution* (*TREE* 16 [2001]:84-88). This article describes the difficulty of constructing a consistent phylogeny (i.e., evolutionary history, or “family tree”) for the social bees. Here is that article’s abstract, in its entirety:

Controversy over the origins and evolution of social behavior in the major groups of social bees (the corbiculate bees) has fuelled arguments over different approaches for building evolutionary trees. However, the application of different analytical methodologies does not explain why molecular and morphological data suggest strikingly different hypotheses for the origin of eusociality in bees. Determining the phylogenetic root is expected to help resolve the question of the social evolution of corbiculate bees. However, this requires that the long branch attraction problem is overcome. This phenomenon affects both molecular and morphological data for corbiculate bees.

Here, in its entirety, is what the Supplementary Bibliography said about the same article:

The relationships of the four major groups of bees (the highly eusocial honey bees, the stingless bees, the bumble bees, and the solitary orchid bees) presents a classic challenge to evolutionary analysis. Lockhart (Massey University, New Zealand) and Cameron (the University of Arkansas) explain that “molecular and morphological data have suggested strikingly different phylogenetic relationships among corbiculate bee tribes” (pp. 84-85), an unresolved problem that they conclude does not stem from the different methods used by different investigators trying to reconstruct the history of the bees. “Disagreement exists because analyses of [DNA] sequences and morphology suggest different hypotheses, and not because researchers have used different criteria for building and testing evolutionary trees” (p. 87).

The adjective “classic,” employed in the Supplementary Bibliography, comes from Lockhart and Cameron themselves. Under the heading “Building trees for bees: a classic problem,” they wrote:

The corbiculate bee phylogeny represents a classic example of an evolutionary tree model in which the juxtaposition of long external branches and a short internal branch (Fig. 2a) makes it difficult to place outgroups correctly. With this tree shape, the root and direction of evolution are difficult to determine. (p. 84)

In short, the Supplementary Bibliography is entirely accurate in what it says about this article.

Nevertheless, in response to the NCSE questionnaire, Peter Lockhart wrote that “I don’t think [the summary] is a good representation of our work—our work does not present ‘a classic challenge to evolutionary analysis’.”

But this is nonsense. The Supplementary Bibliography did not pull the phrase “classic challenge” from thin air. Rather, “classic challenge” is a nearly identical restatement of Lockhart’s own phrases, “classic problem” and “classic example...in which it [is] difficult to place outgroups correctly.” Furthermore, in the context of the Bibliography summary, “evolutionary analysis” means the problem of finding a consistent evolutionary history for the social bees—again, exactly the research difficulty described in “Trees for bees.”

Thus, Lockhart’s objections to the Supplementary Bibliography summary carry no weight whatsoever, and boil down to parsing the delicate semantic differences between the words “problem” and “challenge.” In every respect, the language of the summary meticulously follows Lockhart’s own.

Indeed, every case of misrepresentation claimed by the NCSE dissolves on close inspection. (See the Appendix for a detailed, case-by-case analysis of the claims of misrepresentation.)

5. Then why are these scientists so upset about the Supplementary Bibliography?

In three words: fear, intimidation, and politics.

In 1995, computer scientist and theoretical biologist W. Daniel Hillis explained the risks of speaking too bluntly about Darwinian evolutionary theory in public. “There’s a feeling in biology,” he said, “that scientists should keep their dirty laundry hidden, because the religious right are always looking for any argument between evolutionists as support for their creationist theories. There’s a strong school of thought that one should never question Darwin in public.”³ Hillis’s remarks could easily be extended to the current intelligent design controversy in the United States. Some things are better left unsaid—or, if they are said, hedged about with design-unfriendly qualifiers—because the wrong people may be listening.

The scientific accuracy of the Supplementary Bibliography is not the real issue, as the Appendix demonstrates. Rather, the Bibliography was submitted to the Ohio Board of Education by Stephen Meyer and Jonathan Wells, senior fellows at the Discovery Institute, during a widely-publicized presentation on how to teach biology in Ohio public schools. As proponents of intelligent design and openness in scientific education, both Meyer and Wells (and the intelligent design community in general) have become focal points for loud criticism by the Darwinian evolutionary establishment.

One can understand how members of that establishment would prefer not to have their scientific publications cited by the Discovery Institute, or included in the Supplementary Bibliography. But the scientific literature belongs to no one—or, to put it another way, the scientific literature belongs to everyone: other scientists, teachers, students, interested laypeople. Philosophical opposition to the theory of intelligent design provides no grounds for censoring or limiting access to that literature.

So what *can* teachers and students discuss in their classrooms? One can see the issue of the Supplementary Bibliography as a test case about how the Darwinian establishment would like to run science education in Ohio. Is the scientific literature going to be locked away from teachers and students, to be dispensed in ideologically controlled packages unlikely to upset the status quo?

Or will teachers and students be able to explore the issues with real intellectual freedom?

The NCSE questionnaire was deliberately inflammatory, prefacing its presentation of the Supplementary Bibliography summaries with statements about the putative political goals of the Discovery Institute. Thus, the statements or capsule summaries in the Bibliography were never allowed to speak for themselves. Had the summaries been presented to the scientists cited in the Bibliography, however, without the surrounding material inserted by the NCSE, few would have objected to how their publications were being described. We will never know: The NCSE has seen to that.

Intelligent design has become a provocative idea in science, education, and public policy discussions. Those who consider the theory on its merits are often threatened with the pejorative label of “creationist” (or even stronger terms of disapprobation, such as “fundamentalist”). For any scientist whose career and funding depend in large measure on the approval of his colleagues, being seen as “soft on intelligent design” or “lending support to the anti-Darwinians” can be reputation-threatening. It is not hard to imagine how an e-mail message, such as that recently sent by the NCSE (telling scientists that their publications were being cited by the Discovery Institute), might be intimidating. No matter how accurate the Supplementary Bibliography was, under current circumstances many scientists would consider it unwise, both politically and professionally, to endorse its statements.

These are the unhappy realities of this debate. It takes a great deal of courage to consider intelligent design publicly as a possible scientific theory. It takes only the hint of a threat to one’s career, however, to shut down openness and intellectual freedom. The threat of guilt by association has long been an effective debate-stopper. But that does not make it right.

6. What about the charge of quote-mining?

Dissenters from Darwinian orthodoxy in biology, or dissenters in science generally, face a dilemma. If they do not cite the primary scientific literature, they may be accused of ignorance. If they do cite that literature, however, they may be accused of “quote-mining.”

It is wrong to quote scientists out of context, of course, and any reasonable person would condemn such a tactic. But the charge of “quote-mining” has become a thoughtlessly applied rejoinder, by critics, to *any* citation of the scientific literature—*no matter how accurate*—that the critics personally disapprove. “That’s quote-mining!” shuts down the

normal use of the scientific literature to support one's position or to encourage exploration of alternatives to current theories. The accusation turns the scientific literature and the knowledge it contains into the privileged province of the majority opinion. It creates a pejorative label for a legitimate, and indeed necessary, scholarly practice. Dissent becomes impossible.

Without evidence, a charge of quote-mining is hollow polemics. The best defense against the charge is to check the original publications, and this we do in the Appendix below.

APPENDIX

We have kept the original order of the Supplementary Bibliography for ease of reference. To focus on questions of accuracy, we have extracted the authors' replies from the NCSE press release. In some cases, the NCSE provided only fragments of the author's responses. We have reproduced those fragments, but await the fuller context of the scientist's comments. In other cases, the *substantive* part of the author's reply—i.e., that part actually giving an argument or evidence—was embedded in miscellaneous polemics or vituperation directed at the Discovery Institute. In those instances, we cite only the substantive portion of the author's response. We will add further data from the NCSE survey when it is made available to the press.

PUBLICATIONS LISTED UNDER THE HEADING “QUESTIONS OF PATTERN”

1. Ying Cao, Axel Janke, Peter J. Waddell, Michael Westerman, Osamu Takenaka, Shigenori Murata, Norihiro Okada, Svante Pääbo, and Masami Hasegawa, “Conflict Among Individual Mitochondrial Proteins in Resolving the Phylogeny of Eutherian Orders,” *Journal of Molecular Evolution* 47 (1998): 307-322.

Supplementary Bibliography summary:

It is widely believed that molecular data confirm morphological data when the history of groups such as the mammals is being reconstructed. Many cases exist, however, where molecules (such as proteins) give “false” or erroneous phylogenies. This paper, by a team of researchers from Japan, Germany, and Australia, demonstrates that different mitochondrial proteins can give different, and contradictory, groupings. In particular, the protein NADH dehydrogenase (ND1) places primates and rodents together as closest relatives, with ferungulates (artiodactyls + cetaceans + perisodactyls + carnivores) as more distantly related to primates—in contradiction to most other data, which places primates and ferungulates together as closest relatives. The authors conclude that this anomalous phylogenetic grouping “is not due to a stochastic error, but is due to convergent or parallel evolution” (p. 321), suggesting that molecular evidence is not free from the confounding (historically misleading) effects known to plague other types of systematic data, such as anatomical patterns.

Peter J. Waddell replied to the questionnaire, but the NCSE did not release his response.

2. Simon Conway Morris, “Evolution: Bringing Molecules into the Fold,” *Cell* 100 (2000):1-11.

Supplementary Bibliography summary:

In this article, Conway Morris (a paleontologist and professor in the Department of Earth Science, Cambridge University) argues that “when discussing organic evolution the only point of agreement seems to be ‘It happened.’ Thereafter, there is little consensus, which at first sight must seem rather odd.” Conway Morris goes on however to stress that “our understanding of evolutionary processes and mechanisms is incomplete” (p. 1), and “constructing phylogenies [evolutionary histories] is central to the evolutionary enterprise, yet rival schemes are often strongly contradictory. Can we yet recover the true history of life?” (p. 1). He concludes his review of current problems in evolutionary biology with a provocative thesis:

...if evolution is in some sense channeled, then this reopens the controversial prospect of a teleology; that is, the process is underpinned by a purpose. It is no coincidence that interest in the Anthropic Principle, which broadly seeks evidence for the boundary conditions of the Big Bang and the ensuing physics and chemistry uniquely favoring the emergence of life...is being extended to the fields of biochemistry and molecular biology (for one view, see Denton, 1998)

The book Conway Morris cites here—by the New Zealand geneticist Michael Denton—is entitled *Nature’s Destiny: How the Laws of Biology Reveal Purpose in the Universe*.

Simon Conway Morris did not reply to the questionnaire.

3. W. Ford Doolittle, “Tempo, Mode, the Progenote, and the Universal Root,” in W. Fitch and F. Ayala, eds., *Tempo and Mode in Evolution* (Washington, DC: National Academy Press, 1995), pp. 3-24.

Supplementary Bibliography summary:

A professor in the Department of Biochemistry and Molecular Biology of Dalhousie University (Canada), W. Ford Doolittle is one of the world’s leading molecular evolutionists. In these three [correction: five] related articles (the *Scientific American* piece is aimed at a general audience), Doolittle argues that recent discoveries in molecular biology have begun to fracture the root of Darwin’s single Tree of Life. “Thus, there is no more reason to imagine only a single first kind of cell as the progenitor of all contemporary life,” he argues (p. 356 of the *Current Opinion* article), “than there is to imagine only Adam and Eve as progenitors of the human species.” Doolittle contends that biology must rethink Darwin’s single Tree:

Some biologists find these notions confusing and discouraging. It is as if we have failed at the task that Darwin set for us: delineating the unique structure of the tree of life. But in fact, our science is working as it should. An attractive hypothesis or model (the single tree) suggested experiments, in this case the collection of gene sequences and their analysis with the methods of molecular phylogeny. The data

show the model to be too simple. Now new hypotheses, having final forms we cannot yet guess, are called for. (p. 95, *Scientific American* article)

W. Ford Doolittle replied to the questionnaire, but the NCSE did not release his response.

4. W. Ford Doolittle, “At the core of the Archaea,” *Proceedings of the National Academy of Sciences USA* 93 (1996): 8797-8799.

Supplementary Bibliography summary:

[summary the same as entry #3]

W. Ford Doolittle replied to the questionnaire. No data were released.

5. W. Ford Doolittle, “Uprooting the Tree of Life,” *Scientific American*, February 2000, pp. 90-95.

Supplementary Bibliography summary:

[summary the same as entry #3]

W. Ford Doolittle replied to the questionnaire. No data were released.

6. W. Ford Doolittle, “Phylogenetic Classification and the Universal Tree,” *Science* 284 (1999):2124-2128.

Supplementary Bibliography summary:

[summary the same as entry #3]

W. Ford Doolittle replied to the questionnaire. No data were released.

7. W. Ford Doolittle, “The nature of the universal ancestor and the evolution of the proteome,” *Current Opinion in Structural Biology* 10 (2000):355-358.

Supplementary Bibliography summary:

[summary the same as entry #3]

W. Ford Doolittle replied to the questionnaire. No data were released.

8. Douglas H. Erwin, “Early introduction of major morphological innovations,”
Acta Palaeontologica Polonica 38 (1994): 281-294.

Supplementary Bibliography Summary:

Is the puzzle of the Cambrian Explosion—the geologically sudden appearance of the major animal body plans—merely an artifact of taxonomic methods, a consequence of retrospectively classifying disparate groups that, at their origin, were not distinct? Douglas Erwin, a paleontologist at the Smithsonian Institution, says no. He argues that “the primary problem is the generation of the novel morphologies accorded high rank”—forms as distinctive as arthropods, mollusks, and chordates—“not higher taxa *per se*. ... The asymmetric pattern of morphological innovation [exhibited in the Cambrian Explosion] would be with us even if systematists eliminated ranks entirely” (p. 282, 284). In other words, the arthropod body plan by any other name would be as strange if it appeared suddenly in the Cambrian, as do actual arthropods. Given that the problem of the Cambrian Explosion is real, asks Erwin, how are we to solve it? In this article, he reviews several competing (albeit not necessarily exclusive) theories: empty ecospace (the idea that the animals radiated because they could, “ecospace”—i.e., specific niches—stood open and waiting to be occupied); genetic hypotheses, such as elevated mutation rates and novel genetic mechanisms; developmental hypotheses, which postulated that rapid morphological change was driven by the “discovery” of novel cell types and ontogenetic architectures; and lastly, complexity models, which regard initial bursts of innovation, followed by stabilization, “as an expected consequence of complex systems” (p. 289). Erwin does not decide in favor of any of these hypotheses, noting that although future work may alleviate the problem of testing, tests cannot “be conducted with much confidence today because of uncertainties in metazoan [animal] phylogeny” (p. 291).

Author’s comments on the summary’s accuracy:

“Citing a paper from 1994 is decidedly poor scholarship, however, given how fast this field has moved. The rapid advances in comparative developmental biology have rendered much of this pretty outdated. We now have a very well substantiated metazoan phylogeny, at least in general outline, allowing some of the tests suggested at the end of the cited passage. Moreover, comparative developmental studies have only served to emphasize the fundamental unity of bilaterian animals.”

REPLY:

Erwin does not challenge the accuracy of the summary. Rather, he says that his article is “pretty outdated.” Erwin’s colleagues, however, continue to cite this 1994 publication. In

a major review article published in 2000, for instance, paleontologist David Jablonski of the University of Chicago cited the article (D. Jablonski, “Micro- and macroevolution: scale and hierarchy in evolution biology and paleobiology,” *Deep Time* (Paleontological Society, 2000), pp. 15-52; see pages 23 and 44). Graham Budd, a paleontologist at the University of Uppsala, cited the paper in another major review published in 2000, “A critical reappraisal of the fossil record of the bilaterian phyla,” *Biological Reviews* 75 (2000): 253-295; see pages 257 and 290.

Jablonski and Budd say nothing about the paper being out of date. Both refer to the paper in the context of ongoing debates in paleontology.

9. Trisha Gura, “Bones, molecules...or both?” *Nature* 406 (2000):230-233.

Supplementary Bibliography summary:

This article from *Nature*, one of the top two science journals in the world (the other being *Science*), explores the conflicts that arise in biological systematics—the science that deals with the large-scale relationships of organisms—between anatomical lines of evidence, such as skeletal data, and newer sources of evidence, such as DNA or proteins: the molecular data:

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. (p. 230)

Science writer Gura explains how molecules and morphology in evolutionary systematics are frequently in conflict, giving different histories for groups of organisms, and the attempts that are being made to sort out the contradictions.

Trisha Gura replied to the questionnaire, but the NCSE did not release her response.

10. Michael S. Y. Lee, “Molecular Clock Calibrations and Metazoan Divergence Dates,” *Journal of Molecular Evolution* 49 (1999): 385-391.

Supplementary Bibliography summary:

Laypeople (and scientists from other fields) often assume that evolutionary biologists have successfully dated the historical divergence points of species using molecular data—and that such dates provide evidentially independent confirmation of evolutionary hypotheses. The so-called “molecular clock” thus conveys an aura of analytic precision in phylogenetic estimation. In this paper, however, Michael Lee (a molecular evolutionist at the University of Queensland, Australia) explains that molecular clocks in fact rest on paleontological assumptions for calibration, and thus that their reliability can be no better than the fossil data (and hypotheses) that they employ. As he explains,

Molecular clocks need to be calibrated, and this can be done only by direct recourse to (hopefully reliable) dates in the fossil record. Calibration of clocks indirectly through use of dates inferred from other molecular clock studies (which in turn are ultimately based on the fossil record) is less desirable, as it adds an extra layer of uncertainty, especially if these molecular inferences are highly controversial. (p. 386)

Reviewing several molecular clock studies, Lee is troubled that only a single fossil calibration point is used, and yet “it appears that none of these molecular studies have critically examined the reliability of this fossil dating by consulting the primary palaeontological literature, which is surprising in light of their conclusions that the fossil record is liable to be very misleading” (p. 386). In summary, Lee urges great caution in putting much weight on molecular clocks, given their reliance on palaeontological calibration:

Even if one makes the bold assumption that molecular clock models have little error, there seems little objective reason for accepting as sacrosanct a few fossil dates used in calibrations and rejecting as unreliable the much more numerous fossil dates that contradict the resultant molecular estimates. ... Unfortunately, molecular clock studies have yet to provide a set of rigorous criteria for justifying which fossil dates are to be used in calibrations and which are to be treated with skepticism. (p. 389)

Michael Lee did not reply to the questionnaire.

11. Michael S. Y. Lee, “Molecular phylogenies become functional,” *Trends in Ecology and Evolution* 14 (1999): 177-178.

Supplementary Bibliography summary:

It has been widely believed that “molecular convergence” is impossible: i.e., that gene and protein sequences could not evolve to the same sequence via natural selection. While morphological patterns may exhibit misleading functional similarities—misleading, that is, because the similarity in question would exist not for historical, but adaptive reasons—molecular data were thought to convey a reliable historical signal. If a high

enough degree of similarity were observed, the molecular data indicated true (evolutionary) history, or homology. In this report, however, Michael Lee of Queensland University explains that such “optimistic views of sequence data have now been challenged by recent studies that suggest that molecular data, like morphological traits, can exhibit concerted adaptive evolution”—meaning that molecular similarities may *not* always give reliable historical information. As Lee reports, of one such study,

...the mitochondrial cytochrome *b* gene implied...an absurd phylogeny of mammals, regardless of the method of tree construction. Cats and whales fell within primates, grouping with simians (monkeys and apes) and strepsirrhines (lemurs, bush-babies and lorises) to the exclusion of tarsiers. Cytochrome *b* is probably the most commonly sequenced gene in vertebrates, making this surprising result even more disconcerting. (p. 177)

Lee concludes that “morphological and molecular systematics might have more in common than previously assumed” (p. 178), meaning that misleading similarities, long the bane of classical evolutionary systematics, may also infect molecular data.

Michael Lee did not reply to the questionnaire.

12. Detlef D. Leipe, L. Aravind, and Eugene V. Koonin, “Did DNA replication evolve twice independently?” *Nucleic Acids Research* 27 (1999): 3389-3401.

Supplementary Bibliography summary:

Replicating one’s store of genetic information (DNA) is a basic process in all known organisms. While functional similarities exist among bacterial and eukaryotic (and archaeal) DNA replication systems, many of the component proteins of their respective replication machines are, surprisingly, *non-homologous*. As Detlef Leipe (of Department of Biology at Texas A & M University) and his co-workers explain,

DNA replication is an essential, central feature of cellular life....It is therefore surprising that the protein sequences of several central components of the DNA replication machinery, above all the principal replicative polymerases, show very little or no sequence similarity between bacteria and archaea/eukaryotes. (p. 3389)

Given these fundamental differences in basic cellular machinery, Leipe *et al.* suggest that the process of DNA replication may have evolved at least twice independently—a hypothesis quite unexpected on neo-Darwinian (common ancestry) assumptions. “The hypothesis of an independent evolution of DNA replication,” conclude Leipe *et al.*, “offers a parsimonious explanation for the strange assortment of apparently unrelated, homologous but not orthologous and orthologous components in the DNA replication machineries of bacteria and archaea/eukaryotes” (p. 3401).

Koonin’s comments on the summary’s accuracy:

“...the conclusion that this is ‘a hypothesis quite unexpected on neo- Darwinian (common ancestry) assumptions’ is (i) not taken from our paper and (ii) not at all compatible with the data or ideas presented in the paper.”

REPLY:

Although Koonin and co-authors did not explicitly claim that their hypothesis of the independent (polyphyletic) evolution of DNA replication was “unexpected on neo-Darwinian...assumptions,” almost any textbook diagram showing the history of DNA replication depicts a *single* (monophyletic) origin, in which DNA replication evolves *once*, and is then inherited by all organisms on earth.

This picture, which most biologists carry around in their heads, is fundamentally inconsistent with Koonin’s hypothesis “that the modern-type systems for dsDNA [double-stranded DNA] replication evolved independently in bacteria and the archaeal/eukaryotic lineage” (p. 3400). If Koonin’s hypothesis were the standard evolutionary view of monophyletic ancestry, then it would have been very odd for him to emphasize his new hypothesis by placing it in the title of his paper: “Did DNA replication evolve twice independently?” One asks a question such as that only if the usual view is something *else*, namely, that DNA replication evolved only once.

13. Peter J. Lockhart and Sydney A. Cameron, “Trees for bees,” *Trends in Ecology and Evolution* 16 (2001): 84-88.

Supplementary Bibliography summary:

The relationships of the four major groups of bees (the highly eusocial honey bees, the stingless bees, the bumble bees, and the solitary orchid bees) presents a classic challenge to evolutionary analysis. Lockhart (Massey University, New Zealand) and Cameron (the University of Arkansas) explain that “molecular and morphological data have suggested strikingly different phylogenetic relationships among corbiculate bee tribes” (pp. 84-85), an unresolved problem that they conclude does not stem from the different methods used by different investigators trying to reconstruct the history of the bees. “Disagreement exists because analyses of [DNA] sequences and morphology suggest different hypotheses, and not because researchers have used different criteria for building and testing evolutionary trees” (p. 87).

Author’s comments on the summary’s accuracy:

“I don’t think it is a good representation of our work — our work does not present ‘a classic challenge to evolutionary analysis’. In our paper we point out that technically it is a hard problem to reconstruct the phylogeny of corbiculate bees regardless of

whether you use morphological or molecular data (the reason for this concerns the pattern of radiation — four different lineages diverged in a short period of time a long time ago — given this pattern it is not surprising that different data types might suggest different phylogenies). In our article we do not say that interpretation of the molecular data is right and that interpretation of the morphological data is wrong (or vice versa). Instead we make some suggestions which we believe will help resolve why the different data types suggest different conclusions — we suggest that the bee morphologists relook at the interpretation of some of their data and we also encourage the molecular biologists to determine some additional data which would help test their hypotheses — we suggest that if these things are done then there should be a resolution to the controversy over which phylogeny is correct. We do not doubt that there is a phylogeny — in contrast, the statement by the Discovery Institute suggests that the bee controversy is *evidence for absence of phylogeny*. No scientist involved in the corbiculate bee debate has ever suggested this to my knowledge.”

REPLY:

Our full reply is given in the main text above. We note here only that the summary did not assert “the absence of phylogeny” for the bees (which, like all organisms, surely do have histories), but only the difficulty of finding out what that phylogeny actually was.

14. David P. Mindell, Michael D. Sorenson, and Derek E. Dimcheff, “Multiple independent origins of mitochondrial gene order in birds,” *Proceedings of the National Academy of Sciences USA* 95 (1998): 10693-10697.

Supplementary Bibliography summary:

The genetic information possessed by mitochondria, cell organelles with their own small complement of DNA (in a circular chromosome coding for 37 proteins, usually abbreviated as “mtDNA”), has been widely viewed as a good marker of phylogeny: the historical branching pattern that links organisms. In this study, however, David Mindell of the University of Michigan and his colleagues found that the specific order of mtDNA in birds “has had multiple independent originations...based on sampling of 137 species representing 13 traditionally recognized orders.” This suggests that—contrary to expectations—patterns such as gene order may be under functional constraints. If so, mtDNA may be subject to the same kind of historically misleading similarities that affect other types of systematic data. “Our finding of multiple independent origins for a particular mtDNA gene order among diverse birds,” conclude Mindell *et al.*, “and findings by others of convergent evolution for mt sequence duplications in snakes and lizards...suggests that some constraints on gene order mutation are in effect” (p. 10696). This may considerably complicate the use of mtDNA as a historical marker in evolutionary studies.

Author’s comments on the summary’s accuracy:

“The words enclosed in quotation marks are accurate. However, the quotes are entirely misinterpreted and taken out of context.”

REPLY:

Mindell does not explain how the summary misinterprets his publication or quotes it out of context. This is not surprising, however, as a closer look at the article in question provides additional support for the accuracy of the summary. The summary notes that Mindell *et al.*'s findings suggest that “mtDNA may be subject to the same kind of historically misleading similarities that affect other types of systematic data”—thus complicating “the use of mtDNA as a historical marker in evolutionary studies.”

And that is exactly what Mindell himself said. Again, this is hardly surprising, as the summary was simply a précis of the main points of his article. *Can convergent similarity affect molecular data (in this case, mitochondrial gene order) and be historically misleading? Yes; here is what Mindell et al. wrote in their “Results and Discussion”:*

Our discovery of multiple originations for a particular gene order in birds is analogous to the discovery of parallel inversions in chloroplast DNA (23) and points to the need for greater sampling of taxa in phylogenetic analyses based on gene order. Without such sampling, *convergent similarity among gene order characters will be more easily mistaken for similarity because of common descent, thereby confounding phylogenetic analyses.* (pp. 10694-10695; emphasis added)

We invite Professor Mindell to explain how this differs in any significant way from what the summary said.

15. Paul Morris and Emily Cobabe, “Cuvier meets Watson and Crick: the utility of molecules as classical homologies,” *Biological Journal of the Linnean Society* 44 (1991): 307-324.

Supplementary Bibliography summary:

Molecular data are widely employed in attempts to reconstruct the history of life—in large measure because such evidence is thought to be free from the interpretative difficulties that have plagued anatomical and other larger-scale data since Darwin’s time. This article by the evolutionary theorist Paul Morris of Harvard University (and his colleague Emily Cobabe, at the time of publication working at the University of Bristol) challenges this viewpoint, however, suggesting that “similar or even chemically identical molecules may be unrelated” (p. 307). If molecules (like morphology) is under strong functional constraints, similarities may indicate not history, but equivalent functional demands faced by diverse organisms. “As with anatomical data,” Morris and Cobabe

conclude, “structural identity in molecules is not always indicative of relatedness. Molecules can be highly structurally and functionally constrained. In proteins, this may require a demonstration of homology beyond sequence identity” (p. 322).

Author’s comments on the summary’s accuracy:

“The quotations are accurate; their assembly is a little misleading (the context of the first quote is a discussion of similar amino acids assembled by different synthesis pathways, where the evidence for homology lies in the synthesis pathways rather than in the amino acids, while the second quote is in the context of discussion of protein sequence similarity). The implications, particularly that molecular data are unable to reconstruct the history of life, are complete distortions of what we said.”

REPLY:

The summary never said or even implied that “molecular data are unable to reconstruct the history of life.” Rather, closely following Morris’s own arguments, the summary noted that his paper suggested *caution was needed in the use of molecular data*, because of its potential to mislead if not analyzed correctly.

In support of this, consider a long passage from the introduction to Morris’s paper, reproduced here exactly as it occurs in the original:

It has been recognized that the construction of phylogenies from the distribution of similar molecules is problematic. Numerous phylogenetic inferences have been drawn from the known occurrences of such molecules as chitin (Jeuniaux, 1963), creatine phosphate (Roche, Thoai & Robin, 1957; Rudull & Kechington, 1973) and respiratory pigments (Terwilliger, 1980). Kerkut (1960) noted that such biochemical phylogenies based upon presence/absence data in a few taxa are fraught with error, while Willmer (1990: 87), in a discussion of the disreputable status of comparative biochemistry, comments: “Scoring the presence of a molecule in a few sample from a few species from a phylum is never going to be good enough as grounds for comparisons between higher taxa, even without the problems of purification and uncertainties as to whether the molecules are endogenously synthesized or derived from food or environment. Some of the classic success stories of early comparative biochemistry appear to be untenable...Clearly there is a need to move on rapidly to a more sophisticated consideration of molecular history and interrelationships”. We agree that the construction of phylogenies from the distribution of similar molecules is an inadequate approach. In many cases, molecular structure alone can be misleading because molecules are structurally and functionally constrained. (p. 308)

Morris goes on to say that “other kinds of information, such as synthetic pathways and higher-level historical information, such as gene structure and chromosome placement, can be used as characters” (p. 308). The summary reflects this, by quoting Morris in its last sentence as saying that determining historical descent “may require a demonstration

of homology beyond sequence identity.” Morris’s charges of “complete distortion” are groundless.

16. Arcady R. Mushegian, James R. Garey, Jason Martin, and Leo X. Liu, “Large-Scale Taxonomic Profiling of Eukaryotic Model Organisms: A Comparison of Orthologous Proteins Encoded by the Human, Fly, Nematode, and Yeast Genomes,” *Genome Research* 8 (1998):590-598.

Supplementary Bibliography summary:

The authors of this article work in the growing field of bioinformatics, where large amounts of genetic data are analyzed (by computer) for patterns of similarity and difference. In this study, Mushegian and his colleagues found that “different proteins generate different phylogenetic tree topologies” (p. 591), meaning that some proteins may give an “incorrect” evolutionary history for the organisms from which they have been taken. Protein A, for instance, may indicate that humans and flies are more closely related, whereas Protein B may indicate that humans and nematodes are more closely related. Mushegian *et al.* advise that genetic and protein data should be treated with caution as markers of evolutionary history, because “different proteins can generate different apparent tree topologies [evolutionary histories], strongly suggesting that historical phylogenies should not be inferred based on a single protein-coding gene” (p. 596).

Arcady Mushegian replied to the questionnaire, but the NCSE did not release his response.

17. Gavin J. P. Naylor and Wesley M. Brown, “Amphioxus Mitochondrial DNA, Chordate Phylogeny, and the Limits of Inference Based on Comparisons of Sequences,” *Systematic Biology* 47 (1998): 61-76.

Supplementary Bibliography summary:

A popular perception (even among evolutionary biologists) is that molecular lines of evidence—in particular, DNA sequence data—strongly confirm more classical lines of evidence, such as fossils, and anatomical data drawn from extant species. In this study, however, by two molecular systematists Gavin Naylor (Zoology & Genetics, Iowa State University) and Wesley Brown (Biology, University of Michigan), mitochondrial DNA (mtDNA) drawn from 19 animal species failed “to yield the widely accepted phylogeny for chordates, and, within chordates, for vertebrates” (p. 61). This incorrect result was generated no matter what analytical method was used:

Given the breadth and the compelling nature of the data supporting [the expected] phylogeny, relationships supported by the mitochondrial sequence comparisons are almost certainly incorrect, despite their being supported by equally weighted parsimony, distance, and maximum-likelihood analyses. The incorrect groupings probably result in part from convergent base-compositional similarities among some of the taxa, similarities that are strong enough to overwhelm the historical signal. (p. 61)

If convergence afflicts molecular data in ways “strong enough to overwhelm the historical signal,” then analyzing DNA and protein similarities may not provide the royal road to the true history of life, any more than classical lines of comparative evidence could.

Gavin Naylor replied to the questionnaire, but the NCSE did not release his response.

18. Colin Patterson, David M. Williams, and Christopher J. Humphries, “Congruence Between Molecular and Morphological Phylogenies,” *Annual Review of Ecology and Systematics* 24 (1993): 153-188.

Supplementary Bibliography summary:

The authors, at the time of the publication of this paper all working at the British Museum of Natural History (Patterson is now deceased), argue that the widespread view that “molecules confirm morphology” in evolutionary studies is a myth: “...in practice, we find that incongruence between molecular trees (generated from different data sets or by different analytical methods) is as striking or pervasive as is incongruence between trees generated by morphologists” (p. 153). They conclude that “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.” (p. 179)

Author’s comments on the summary’s accuracy:

“The short answer to your question, ‘Do you consider this accurate?’ is no.”

“our review was written nearly 10 years ago and things have moved on since then. Many of the possible solutions to data incongruence we suggested then have now been acted upon and molecules and morphology agree in many more cases. In fact, many more examples using molecules and morphology together highlight and clarify topics relating directly to many evolutionary issues.”

REPLY:

It is impossible to know why Williams thinks the summary is inaccurate, as he has not provided, or at any rate the NCSE has not released, any argument supporting his judgment. The only word in the summary that is not either (1) a direct quote, (2) neutrally descriptive (e.g., saying where the authors worked), or (3) a connecting phrase (e.g., “they conclude”) is the noun “myth.” Perhaps this is too strong. Consider, however, Williams’s own statements in the Conclusions section of the original paper:

Partly because of morphology’s long history, congruence between morphological phylogenies is the exception rather than the rule. With molecular phylogenies, all generated within the last couple of decades, the situation is little better. Many cases of incongruence between molecular phylogenies are documented above; and when a consensus of all trees within 1% of the shortest in a parsimony analysis is published (e.g., 132, 152, 170), structure or resolution tends to evaporate. (p. 180)

Williams’s main objection is that he now thinks the paper is outdated. It is unfortunate that scientific publications do not carry expiration dates, like cartons of milk. A 1982 article on homology from the first author of this 1993 publication, Colin Patterson, is still widely cited in the literature, despite its relatively great age. We are undertaking a survey of the Science Citation Index and other sources to see how often, and how recently, this 1993 paper has been cited in the systematics literature. We will update this reply when those results are in hand.

19. Michael K. Richardson *et al.*, “There is no highly conserved stage in the vertebrates: implications for current theories of evolution and development,” *Anatomy and Embryology* 196 (1997): 91-106.

Supplementary Bibliography summary:

Biology textbooks for decades have featured drawings purporting to show that vertebrate embryos begin development looking essentially the same, and only later diverge to their characteristic morphologies. Michael Richardson, a British embryologist, and an international team of co-workers inspected actual vertebrate embryos and found that the textbooks diagrams (which trace to the 19th century German embryologist Ernst Haeckel) are false and misleading. There is no single stage of embryogenesis in vertebrates where all forms are similar: “The wide variation in morphology among vertebrate embryos is difficult to reconcile with the idea of a phylogenetically-conserved tailbud stage, and suggests that at least some developmental mechanisms are not highly constrained” (p. 91).

Author’s comments on the summary’s accuracy:

“Partly accurate and partly ambiguous. The creationists have taken a very complicated argument and extracted from it the bits and pieces that fit their world view. In particular, I have some problems with the following statement: ‘There is no single stage of

embryogenesis in vertebrates where all forms are similar.’ In fact, there *are* strong resemblances between vertebrate embryos at various times in development, but it is not possible to ascribe them to a single stage.”

REPLY:

Richardson rephrases the objectionable sentence from the summary—i.e., “there is no single stage of embryogenesis in vertebrates where all forms are similar”—as “In fact, there *are* strong resemblances between vertebrate embryos at various times in development, but it is not possible to ascribe them to a single stage.” This restatement, however, only rearranges what the summary itself said. The language of the summary was based on Richardson’s own abstract and conclusions, i.e., “modifications of embryonic development are difficult to reconcile with the idea that most or all vertebrates pass through an embryonic stage that is highly resistant to evolutionary change” (p. 105). Richardson’s objections are groundless.

20. Kensal E. van Holde, “Respiratory proteins of invertebrates: Structure, function and evolution,” *Zoology: Analysis of Complex Systems* 100 (1998): 287-297.

Supplementary Bibliography summary:

Oxygen carriers such as hemoglobin are vitally important proteins throughout the animals. But other oxygen-carrying molecules are utilized as well, such as hemocyanin (which uses a copper, not Fe-heme, binding site). The phylogenetic distribution of oxygen-carrying molecules is very puzzling, however, and cannot be easily fitted into current models of animal evolution. As Kensal van Holde (Biochemistry, Oregon State University) explains, “the phylogenetic distribution of the whole group of oxygen transport proteins cannot easily be reconciled with many current models of metazoan evolution.” After reviewing the contradictions between the distribution of oxygen carriers and hypotheses of animal evolution, van Holde concludes that “it seems likely that we need much more information before all parts of the puzzle can be fitted together” (p. 296).

Kensal van Holde replied to the questionnaire, but the NCSE did not release the response.

21. Kenneth Weiss, “We Hold These Truths to Be Self-Evident,” *Evolutionary Anthropology* 10 (2001):199-203.

Supplementary Bibliography summary:

Kenneth Weiss is the Evan Pugh Professor of Anthropology and Genetics at Penn State University. In this article, he argues that evolutionary biology relies far more on axioms—unprovable assumptions—than many biologists are willing to admit. He writes:

The prevailing cosmology that greeted Darwin’s *Origin of Species* in 1859 rested on the theologically based assumption that the universe was created at a single point in time by a purposive intelligence who selected a bestiary of species designed to be adapted to their environments. This was assumed to be given truth rather than something one had to infer from observation. By comparison, in biology we believe we are practicing a rigorous, objective, empirical method-of-knowing that does not rest on wishful thinking. Yet much of our work rests on axioms—conventional wisdom or laws of Nature, if you will—that we *assume* to be true, but cannot actually prove. (p. 199)

Weiss ends by saying “It is healthy to be skeptical even of truths we hold to be self-evident, and to ask: suppose it isn’t true—what would follow? Do we need a theory of evolutionary biology?” (Please note that in his footnotes, Weiss is highly skeptical of creationism, and endorses what he calls “the fact” of evolution.)

Author’s comments on the summary’s accuracy:

“This is misrepresenting the fuller context. For example, the last question that is quoted was followed by my asking what would be the minimal essential elements of such a theory that biologists would insist on.”

“The Discovery Institute does not give an honest sense of the clarity that I put in that disclaimer: ‘Given the spate of recent anti-evolutionary books, I feel compelled to make the statement here that nothing in this column in any way questions the *fact* of evolution, nor in any way supports creationist accounts (one cannot call them “explanations”) for the diversity of life.’”

REPLY:

Weiss argues that the Bibliography misrepresents the fuller context of his argument, by omitting the sentence that immediately followed his last question to the reader (“Do we need a theory of evolutionary biology?”). We are happy to provide the omitted sentence here, in bold, as it supports the accuracy of our summary. Weiss writes:

It is healthy to be skeptical even of truths we hold to be self-evident, and to ask: suppose it isn’t true—what would follow? Do we need a theory of evolutionary biology? **What beyond shared ancestry is inviolate?** (p. 203)

One of the key arguments of Weiss’s article was the axiomatic nature of the theory of common descent (“shared ancestry”). If common ancestry is “inviolable,” then it cannot be challenged by observation. In other words, the theory is simply not up for grabs. It is a genuine axiom, i.e., something assumed to be true, come what may.

Weiss also complains that we “did not give an honest sense of the clarity that I put in that disclaimer.” We regret understating the force of the endnote that Weiss attached to his provocative article. For the record: Kenneth Weiss feels compelled to state that nothing he has written questions evolution in any way, because he regards evolution as a *fact* which seems indubitably established. He does not support “creationist ‘explanations’” nor does he doubt evolution. He assumes common ancestry to be true axiomatically.

22. Carl Woese, “The universal ancestor,” *Proceedings of the National Academy of Sciences USA* 95 (1998): 6854-6859.

Supplementary Bibliography summary:

Probably no scientist has more influenced our current understanding of the base of the Tree of Life than the microbiologist Carl Woese of the University of Illinois. The widely-accepted tripartite division of life into the Archae, the Bacteria, and the Eukarya, is due to Woese’s work using ribosomal RNA (rRNA) patterns. In this provocative paper, Woese suggests that Darwin’s single Tree of Life, terminating in a single common ancestor (often abbreviated LUCA, for the Last Universal Common Ancestor), may never have existed. “It is time,” Woese argues, “to question underlying assumptions” (p. 6855). The problem stems from the failure of molecules to provide a consistent story for the early history of life. “No consistent organismal phylogeny has emerged from the many individual protein phylogenies so far produced,” Woese writes. “Phylogenetic incongruities 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” (p. 6854). Thus, if the LUCA existed, it was not an organism like any that we would recognize. “The universal ancestor is not an entity, not a thing. It is a process characteristic of a particular evolutionary stage” (p. 6858). The Tree of Life does not have a single root. Rather, stresses Woese, “we are left with no consistent and satisfactory picture of the universal ancestor” (p. 6855), and biology must come to grips with this.

Carl Woese did not reply to the questionnaire.

PUBLICATIONS LISTED UNDER THE HEADING “QUESTIONS OF PROCESS”

23. Robert L. Carroll, “Towards a new evolutionary synthesis,” *Trends in Ecology and Evolution* 15 (2000):27-32.

Supplementary Bibliography summary:

Robert Carroll is a professor in the Department of Biology and Curator of Vertebrate Paleontology at the Redpath Museum of McGill University (Montreal). In this article, Carroll argues that macroevolutionary changes cannot be derived from microevolutionary processes:

Increasing knowledge of the fossil record and the capacity for accurate geological dating demonstrate that large-scale patterns and rates of evolution are not compatible with those hypothesized by Darwin on the basis of extrapolation from modern populations and species....The most striking features of large-scale evolution are the extremely rapid divergence of lineages near the time of their origin, followed by long periods in which basic body plans and ways of life are retained. What is missing are the many intermediate forms hypothesized by Darwin, and the continual divergence of major lineages into the morphospace between distinct adaptive types. (p. 27)

Carroll concludes that a new evolutionary synthesis is needed, to explain such patterns as “the extreme speed of anatomical change and adaptive radiation” of the Cambrian Explosion, when “almost all of the advanced phyla [animal body plans] appeared” (p. 27).

Robert Carroll replied to the questionnaire, but the NCSE did not release his response.

24. Douglas Erwin, “Macroevolution is more than repeated rounds of microevolution,” *Evolution & Development* 2 (2000):78-84.

Supplementary Bibliography summary:

Douglas Erwin is a paleontologist on the staff of the National Museum of Natural History (at the Smithsonian), and one of the leading critics of claims that microevolutionary processes suffice to explain macroevolutionary patterns. In this article, Erwin challenges the standard view of evolution, and argues that other processes and mechanisms are needed:

Microevolution provides no satisfactory explanation for the extraordinary burst of novelty during the late Neoproterozoic-Cambrian radiation (Valentine et al. 1999; Knoll and Carroll 1999), nor the rapid production of novel plant architectures associated with the origin of land plants during the Devonian (Kendrick and Crane 1997), followed by the origination of most major insect groups (Labandeira and Sepkoski 1993). (p. 81)

The gap between microevolution and macroevolution, Erwin contends, is real: “These discontinuities impart a hierarchical structure to evolution, a structure which impedes,

obstructs, and even neutralizes the effects of microevolution” (p. 82). Much more work is needed, Erwin concludes, before we can claim to understand macroevolution.

Author’s comments on the summary’s accuracy:

“While the article considers the relationship between micro- and macro- evolution, the Discovery Institute is inaccurate in saying that I am challenging the standard view of evolution. The treatment of macroevolution in that paper is an extension, but by no means a challenge. Further, although more work may be needed to fully understand macroevolutionary events, there is no evidence that requires, or even suggests, a role for so-called ‘intelligent design’.”

REPLY:

Erwin wishes to tame his own arguments, by using the word “extension” instead of “challenge.” The inaccuracy of the summary turns on a single word, it seems.

But Erwin’s perception of evolution is *not* “the standard view,” or more precisely not the conventional neo-Darwinian view. In particular, Erwin has long argued that the modes of genetic and developmental change that led (for instance) to the Cambrian Explosion are no longer possible today. “Evolutionary biologists,” he wrote in 1993, “often implicitly assume that evolution is a uniformitarian, time-homogeneous process without strong temporal asymmetries in evolutionary mechanisms, rate or context” (“The origin of metazoan development: a palaeobiological perspective,” *Biological Journal of the Linnean Society* 50 [1993]:255-274; p. 255). Yet, he continues, “evolutionary patterns do exhibit such asymmetries.” The evolutionary events early in the history of life may simply have no modern analogue. “There is every indication,” Erwin wrote in 1999, “that the range of morphological innovation possible in the early Cambrian is simply not possible today” (“The Origin of Bodyplans,” *American Zoologist* 39:617-629; p. 626). If Erwin is right, neo-Darwinism may be unable to explain some of the most important events in the history of life, because time has wiped out forever the unique conditions under which those events occurred. “The possibility, even the likelihood,” writes Erwin in the paper cited in the Bibliography, “that there have been long-term changes in the nature of the process...further complicates the issue” (p. 82).

This is not how neo-Darwinians see their theory. If Erwin is “extending” neo-Darwinism, then “challenge” is a modest word indeed.

25. Scott F. Gilbert, Grace A. Loreda, Alla Brukman, and Ann C. Burke, “Morphogenesis of the turtle shell: the development of a novel structure in tetrapod evolution,” *Evolution & Development* 3 (2001): 47-58.

Supplementary Bibliography summary:

The origin of turtles, with their distinctive shells, has long been an evolutionary enigma. “The turtle shell,” write Scott Gilbert (Embryology, Swarthmore College) and his colleagues, “represents a classic evolutionary problem: the appearance of a major structural adaptation.” Could the characteristic features of turtles have arisen gradually, in a long series of Darwinian steps? “The problem for an evolutionary biologist,” comments systematist and reptile expert Olivier Rieppel of the Field Museum (Chicago), “is to explain these transformations in the context of a gradualistic process” (p. 990). But the first turtle in the fossil record appears abruptly, fully turtle: “The Chelonian Bauplan [turtle body plan] appears in the fossil record,” Gilbert *et al.* observe, “without intermediates, and the relationship of turtles to other amniote orders is not certain.” What inference should one draw from these patterns of evidence? “The absence of intermediates or transitional forms in the fossil record,” speculate Gilbert *et al.*—especially when the fossil record is coupled with the developmental and anatomical novelties exhibited by turtles—“could indicate that turtles arose saltationally” (p. 56). That is, turtles did not evolve by a gradual Darwinian process; as Rieppel describes this hypothesis, turtles may be “hopeful monsters.” (Neither Rieppel nor Gilbert and colleagues, however, provide a detailed model of this rapid evolutionary transition, but rather refer to the need for further research.)

Author’s comments on the summary’s accuracy:

“My research on turtles and my research into evolutionary developmental biology is fully within Darwinian parameters. My gripe has been that neo-Darwinism has supposed that *population* genetics was the only genetics needed to explain Darwinian evolution. I claim that *developmental* genetics is also needed. So my research has been to include developmental genetics into the Darwinian mix.”

REPLY:

While Gilbert argues that his research “is fully within Darwinian parameters,” he explicitly defines its significance by contrasting it with what he calls “gradualism and adaptationalistic explanations”—i.e., neo-Darwinism as ordinarily understood. Furthermore, Gilbert uses a term for rapid and discontinuous evolutionary change, “saltation,” that is certain to raise the hackles of any orthodox neo-Darwinian. He writes:

Regardless of the group chosen to include the ancestor of turtles, there is a dramatic evolutionary transition between the chelonian [turtle] and non-chelonian body plans. Mayr (1960) identified the origin of evolutionary novelties as a distinct and neglected problem, but the prevalence of gradualism and adaptationalistic explanations may have prevented its analysis until recently....The absence of intermediates or transitional forms in the fossil record could indicate that turtles arose saltationally. (p. 56)

We welcome further clarification from Gilbert on the meaning of “Darwinian parameters.” Until then, we stand by the accuracy of the summary.

26. Olivier Rieppel, “Turtles as Hopeful Monsters,” *BioEssays* 23 (2001): 987-991.

Supplementary Bibliography summary:

[the same as entry #25]

Olivier Rieppel did not reply to the questionnaire.

27. Scott F. Gilbert, John M. Opitz, and Rudolf A. Raff, “Resynthesizing Evolutionary and Developmental Biology,” *Developmental Biology* 173 (1996): 357-372.

Supplementary Bibliography summary:

In this major statement about the pressing need for a new theory of evolution, biologists Gilbert (Swarthmore), Opitz (Montana State), and Raff (Indiana University) argue that while the neo-Darwinian synthesis was a “remarkable achievement,” it fails to explain many of the most important phenomena of biology:

...starting in the 1970s, many biologists began questioning its adequacy in explaining evolution. Genetics might be adequate for explaining microevolution, but microevolutionary changes in gene frequency were not seen as able to turn a reptile into a mammal or to convert a fish into an amphibian. Microevolution looks at adaptations that concern the survival of the fittest, not the arrival of the fittest. As Goodwin (1995) points out, “the origin of species—Darwin’s problem—remains unsolved.” (p. 361)

Under the new synthesis that these authors propose, in which the processes of development are integrated into evolutionary understanding, “the role of natural selection...is seen to play less an important role. It is merely a filter for unsuccessful morphologies” (p. 368).

Author’s comments on the summary’s accuracy:

“My research on turtles and my research into evolutionary developmental biology is fully within Darwinian parameters. My gripe has been that neo- Darwinism has supposed that *population* genetics was the only genetics needed to explain Darwinian evolution. I claim that *developmental* genetics is also needed. So my research has been to include developmental genetics into the Darwinian mix.”

REPLY:

The summary and Gilbert's statement (above) say the same thing. Neo-Darwinism has neglected the processes of development, to its detriment. But Gilbert nevertheless wishes to have his writings described as "within Darwinian parameters," and that is hereby noted.

28. George L. Gabor Miklos, "Emergence of organizational complexities during metazoan evolution: perspectives from molecular biology, palaeontology and neo-Darwinism," *Mem. Ass. Australas. Palaeontols.* 15 (1993): 7-41.

Supplementary Bibliography summary:

George Miklos is an evolutionary geneticist at the Centre for Molecular Structure and Function of the Australian National University. In this article, Miklos levels a major, across-the-board indictment of neo-Darwinism. The flavor of the indictment can be gathered from the opening six sentence of the abstract:

The popular theory of evolution is the modern synthesis (neo-Darwinism), based on changes in populations underpinned by the mathematics of allelic variation and driven by natural selection. It accounts more for adaptive changes in the colouration of moths, than in explaining why there are moths at all. This theory does not predict why there were only 50 or so modal body plans, nor does it provide a basis for rapid, large scale innovations. It lacks significant connection with embryogenesis and hence there is no nexus to the evolution of form. It fails to address the question of why the anatomical gaps between phyla are no wider today than there were at their Cambrian appearance. It has no predictions about macromolecules and cellular evolution in the Archaean, about evolution via symbiogenesis, nor the manner in which cells and organisms alter and revise their genomic rules as they evolve. (p. 7)

Miklos's primary argument concerns the irrelevance—to the solution of the problem of macroevolution—of the scale of variation typically observed in neo-Darwinian studies, e.g., gene frequency (or allelic) shifts:

Allelic changes in natural populations are almost totally oblique to understanding the events that gave rise to the major metazoan body plans. Studies of speciation are targeting the evolutionary peripheries, and missing the significant metazoan issue—the origin of complex forms. (p. 29)

Neo-Darwinians, Miklos contends, have been unwilling to reevaluate their theory in the light of contrary evidence:

The modern synthesis moved evolution theory into a mathematical siding from which there has been no return. Here is a theory which, as I have shown in this essay, does not touch upon any level of detail or mechanism that impinges on

large scale evolutionary complexity or novelty. Whenever data have undermined its foundations, it is the data that have been considered inadequate. Thus the traditional gradualistic view is largely at variance with the fossil record, which is largely one of episodic change followed by stasis. (p. 29)

Evolutionary theory will need to break free of neo-Darwinism, Miklos concludes, to have any hope of explaining the deep puzzle that occupied Darwin, namely, how did animals (and plants) themselves come to be? Here is his final paragraph:

Finally, it is necessary to acknowledge that after over a century of the dominant paradigm, the evolution of major complexities in the history of life has had very little to do with the origin of species. The seamless moving footway of neo-Darwinism that was to have smoothly transported us from allelic variation in natural populations to understanding body plans in different phyla has led to a cul-de-sac. The origin of phyla is not via speciation 'writ large'. To understand what fuelled origins of phyla, the complexities that emerged long ago from macromolecular and supracellular complexes and from symbiogenic events will need to be understood via molecular embryology, where the quintessence of evolutionary truth is to be found. (p. 34)

George Miklos replied to the questionnaire, but the NCSE did not release his response.

29. Neil H. Shubin and Charles R. Marshall, "Fossils, genes, and the origin of novelty," in *Deep Time* (2000, The Paleontological Society), pp. 324-340.

Supplementary Bibliography summary:

Shubin (Paleontology, University of Chicago) and Marshall (Paleontology and Molecular Biology, UCLA) argue that the neo-Darwinian synthesis needs to come to grips with new evidence that the theory never anticipated and has difficulty explaining:

In the last 25 years, new data from genetics have dealt some profound surprises to the evolutionary biology community. Perhaps the most striking discovery is the extent to which major patterning genes and regulatory interactions are deeply conserved across vast expanses of time and phylogeny.... Indeed, in many cases, the developmental role of these homologous genes is also conserved in creatures with different body plans. Strikingly, many homologous genes appear to perform the same function in structures that share functional similarities but lack a common evolutionary origin. (p. 325)

Another puzzling problem is the Cambrian Explosion: "The disconnect between rates of genetic and morphological change," write Shubin and Marshall (p. 335), "is as vexing a problem for population geneticists as it is for paleontologists." They conclude that

evolutionists must bridge “the gap between microevolution and macroevolution,” by seeking “the mechanisms behind the production of morphological variation” (p. 338).

Neil Shubin and Charles Marshall did not reply to the questionnaire.

30. Keith Stewart Thomson, “Macroevolution: The Morphological Problem,” *American Zoologist* 32 (1992): 106-112.

Supplementary Bibliography summary:

Thomson (Oxford University) has long been disenchanted with the explanatory adequacy of neo-Darwinism. Macroevolution has resisted explanation, he argues:

While the origins of major morphological novelties remains unsolved, one can also view the stubborn persistence of macroevolutionary questioning, and particularly its revival in recent years, as a challenge to orthodoxy: resistance to the view that the synthetic theory tells us everything we need to know about evolutionary processes. (p. 106)

Although most evolutionary biologists, beginning with Darwin, saw evolutionary change as necessarily gradual, Thomson points out that “no one has satisfactorily demonstrated a *mechanism* at the population genetic level by which innumerable very small phenotypic changes could accumulate rapidly to produce large changes: a process for the origin of the magnificently improbable from the ineffably trivial” (p. 107, emphasis in original).

Author’s comments on the summary’s accuracy:

Keith Thomson replied to the questionnaire, but no data were released on his views of the summary’s accuracy. The NCSE quoted Thomson only on the educational suitability of his article.

31. Bärbel M.R. Stadler, Peter F. Stadler, Günther P. Wagner, and Walter Fontana, “The Topology of the Possible: Formal Spaces Underlying Patterns of Evolutionary Change,” *Journal of Theoretical Biology* 213 (2001):241-274.

32. Günther P. Wagner, “What is the Promise of Developmental Evolution? Part II: A Causal Explanation of Evolutionary Innovations May Be Impossible,” *Journal of Experimental Zoology (Mol Dev Evol)* 291 (2001): 305-309.

Supplementary Bibliography summary:

In these companion papers, theoretical biologist Günther Wagner (Yale University) and his colleagues argue that neo-Darwinism fails to explain many important biological phenomena, and that the relationship of these phenomena “to the mechanistic theory of evolutionary change, as represented by population genetics, remains unclear and tense” (*JTB*, p. 242). They suggest that this failure of explanation stems from the underlying assumptions of neo-Darwinism, such as that any evolutionary change is readily accessible to natural selection. Patterns of evidence, however, indicate that “this fluidity is largely a fiction and point at profound asymmetries in the accessibility of phenotypic and genetic states” (*JTB*, p. 242), meaning that many evolutionary transitions may be all but impossible. Going even further, Wagner contends that many important historical events in evolution may be forever inexplicable, because the conditions needed to understand those events—in particular, the genetic background to the changes in question—may be lost irretrievably. If this is the case, he writes, “*then it might be impossible to experimentally demonstrate exactly which genetic changes caused the evolutionary innovation*” (*JEZ*, p. 308, emphasis in original).

Author’s comments on the summary’s accuracy:

“In no way does my work represent an attack on the theory of descent with modification, i.e. the plain fact of evolution, or even the fundamental insights of the neo-Darwinian theory of evolution. It is intended as an attempt to extend the explanatory reach of Darwinian evolutionary thinking by eliminating some technical limitations that result from the mathematical language currently used to model evolutionary processes. All that work agrees with and is based on the fact that evolution proceeds by the spontaneous generation of genetic variation and the fixation of these variations by selection and/or drift. The points of my papers are narrow technical ones and in no way weaken the fundamental insights of Darwinian evolutionary thinking. They do, however, challenge some of the more speculative extensions of this theory, like the idea that everything is possible with more or less equal probability. But this does not affect the fundamentals of the neo-Darwinian theory of evolution.”

REPLY:

The Bibliography never claimed that Wagner’s work was “an attack on the theory of descent with modification”—this perception was mischievously created by the NCSE questionnaire. But it is hard to credit Wagner’s claim that his arguments do not threaten “the fundamental insights of the neo-Darwinian theory of evolution.” A cardinal tenet of neo-Darwinism hold that major adaptive changes—such as the origin of novel body plans—are caused by natural selection, and that selection is both necessary and sufficient to explain them. Wagner suggests that this may not be true.

If the theory outlined in his *Journal of Theoretical Biology* article is the case, he writes, then one consequence for “major evolutionary transitions is that natural selection does not provide a complete explanation for their occurrence” (p. 269). As he continues,

Natural selection is a sufficient explanation for the outcome of an evolutionary process, if the genetic variation contributing to the derived phenotype is easily

accessible. Whether a transition occurs, then only depends (to a first approximation) on the strength and direction of selection. If major transitions, however, require specially poised genotypic/developmental realizations of the ancestral phenotype, then the transition critically depends on factors not under the control of selection, since different genetic realizations of the same ancestral phenotype lie on a neutral network and are not distinguishable by selection on phenotypes. (p. 269)

In simpler language, unless the *right* (“specially poised”) mix of genes and development occurs, natural selection is powerless to cause evolutionary change, and thus cannot explain it.

While we respect Professor Wagner’s wish to interpret his ideas in a way least offensive to neo-Darwinian sensibilities, we fear that he soft-peddles their radical implications. He writes, for instance, that the problem of experimentally reconstructing *how* major evolutionary transitions occurred

is a real one that cannot be overcome by technical advances. It is a problem we must face, if the aforementioned model of phenotypic evolution applies to at least a significant subset of phenotypic transformations. It goes to the heart of what is knowable in developmental evolution. (*JEZ* article, p. 308)

Whether this is really a “narrow technical” point, we leave to the judgment of the reader.

PUBLICATIONS LISTED UNDER THE HEADING, “QUESTIONS ABOUT THE CENTRAL ISSUE: THE ORIGIN AND NATURE OF BIOLOGICAL COMPLEXITY”

33. Philip Ball, “Life’s lessons in design,” *Nature* 409 (2001): 413-416.

Supplementary Bibliography summary:

What might we learn from biological objects that could be applied to improving our own technologies? The research field of *biomimetics* tries to answer this question by looking closely at natural systems, and “reverse-engineering” them for solutions to similar technological problems faced by humanly-constructed artifacts. Questions of scale and complexity, of course, arise immediately, as Philip Ball (an editor at the journal *Nature*) notes:

One of the biggest obstacles to taking full advantage of what nature has to offer is that the living world has an awesomely elaborate means of construction. There is no assembly plant so delicate, versatile and adaptive as the cell. (p. 413)

The astonishing subtlety of biological designs beggars description; or, to put it another way, one cannot assume that every solution to a functional challenge will be intuitively obvious on first inspection. Consider, for instance, insect flight:

Specifically, insects are conjurors of the vortex. With deft flappings and rotations of their wings, they are able to manipulate the vortices shed from the edges to control their motion in ways that flight engineers can only dream of: taking off backwards, for example, or landing upside down. By such means, insects subvert the “conventional” aerofoil principles of flight, giving rise to the canard that the bee is aerodynamically impossible. In essence, the flight of the bumble-bee is a flight beyond the dynamic steady state: lift is generated at particular, exquisitely timed moments during the flap cycle. By rotating the wing so that it is parallel to the ground on the downstroke but perpendicular on the recovery stroke, an insect is able to recapture energy from the vortices shed from the wing edge. This reveals a new mechanism for flight that one could hardly have deduced from first principles, and which might be adopted for the development of miniaturized robotic flyers for remote sensing, surveying and planetary exploration. (p. 414)

Eventually, Ball argues, engineers seeking to learn from biology must turn to the realities of the microscopic realm. Synthetic silk, for instance, has yet to become a commercially successful product, not because we do not understand the biochemistry or genetics of silk production, but because real silk gains its strength from more than its protein structure:

It is the weaving of strands in the spinneret that gives them their strength. The details of this process are not understood; but it may be that not until we can build an artificial, miniaturized spinning mechanism will silk be an industrial material.

This is why biomimetics must reach down to the microscopic and ultimately the molecular scale. Some of nature’s best tricks are conceptually simple and easy to rationalize in physical or engineering terms; but realizing them requires machinery of exquisite delicacy. (p. 416)

Ball concludes that the horizon of knowledge opened by biomimetics is vast and continues to grow:

...fundamental research on the character of nature’s mechanisms, from the elephant to the protein, is sure to enrich the pool from which designers and engineers can draw ideas. The scope for deepening this pool is still tremendous. It is at the molecular scale, however, that we will surely see the greatest expansion of horizons, as structural studies and single-molecule experiments reveal the mechanics of biomolecules. If any reminder were still needed that nanotechnology should not seek to shrink mechanical engineering, cogs and all, to the molecular scale, it is found here. Nature’s wheel—the rotary motor of the bacterial flagellum—never got any larger than this, nor is it fashioned from hard, wear-resistant materials, nor is driven electromagnetically or by displacement of a

piston. But it is efficient, fast, linear and reversible. Somewhere there is a lesson in that. (p. 416)

Author's comments on the summary's accuracy:

“the effectiveness of evolution in fine-tuning the properties and features of natural systems.”

REPLY:

Without more information, it is impossible to say if Ball regards the Supplementary Bibliography summary as accurate or inaccurate. By our estimate, the discussion of evolution in the article is less than 1/30th of its total content.

34. Rodney Brooks, “The relationship between matter and life,” *Nature* 409 (2001): 409-411.

Supplementary Bibliography summary:

Rodney Brooks of the Artificial Intelligence Laboratory at MIT has long been a pathbreaking investigator in the construction of “AI” (artificial intelligence) and “Alife” (artificial life) systems. In this skeptical article, however, Brooks steps back from the bench to look critically at what AI and Alife research has actually demonstrated. He writes:

...both fields have been labelled as failures for not having lived up to grandiose promises. At the heart of this disappointment lies the fact that neither AI nor Alife has produced artefacts that could be confused with a living organism for more than an instant. AI just does not seem as present or aware as even a simple animal and Alife cannot match the complexities of the simplest forms of life. (p. 409)

The failures of these fields, Brooks argues, requires a diagnosis:

We build models to understand the biological systems better, but the models never work as well as biology. We have become very good at modelling fluids, materials, planetary dynamics, nuclear explosions and all manner of physical systems. Put some parameters into a program, let it crank, and out come accurate predictions of the physical character of the modelled system. But we are not good at modelling living systems, at small or large scales. Something is wrong. (p. 410)

After considering several modest “fixes” for AI and Alife (e.g., incorrect parameters, lack of computing power, lack of complexity in models), Brooks turns to a more challenging diagnosis: “we might be missing something fundamental and currently unimagined in our models of biology” (p. 410). He argues:

We would then need to find new ways of thinking about living systems to make any progress, and this will be much more disruptive to all biology. ... So what might be the nature of this unimagined feature of life? One possibility is that some aspect of living systems is invisible to us right now. The current scientific view of living things is that they are machines whose components are biomolecules. It is not completely impossible that we might discover some new properties of biomolecules or some new ingredient. One might imagine something on a par with the discovery of X-rays a century ago, which eventually led to our still-evolving understanding of quantum mechanics. Relativity was the other such discovery of the twentieth century, and had a similarly disruptive impact on the basic understanding of physics. Some similar discovery might rock our understanding of the basis of living systems. (p. 410)

Author's comments on the summary's accuracy:

“they have selectively quoted just parts of what I wrote in order to distort completely what I said in the article.”

REPLY:

Brooks does not explain how the summary distorts what he wrote. What follows is the abstract (in its entirety) of Brooks's article:

The disciplines of artificial intelligence and artificial life build computational systems inspired by various aspects of life. Despite the fact that living systems are composed only of non-living atoms there seems to be limits in the current levels of understanding within these disciplines in what is necessary to bridge the gap between non-living and living matter. (p. 409)

One wonders if Brooks regards *this* as a complete distortion. Given that nearly all of the Supplementary Bibliography summary reproduces Brooks's own words, with some neutral connecting language using his own terms (e.g, “failure”), we ask Brooks to give a hint about where the complete distortion is hiding. Copyright law forbids us from reproducing his entire article here, but if we could, the reader would be just as puzzled as we are.

The fact is, the summary is dead-on accurate, and Brooks's objections are groundless.

35. David W. Deamer, “The First Living Systems: a Bioenergetic Perspective,” *Microbiology and Molecular Biology Reviews* 61 (1997): 239-261.

Supplementary Bibliography summary:

Could living systems have arisen without a means of transferring energy from the environment to the primitive cell, in order to do the work characteristic of all organisms? Biochemist and origin-of-life researcher David W. Deamer, of the University of California-Santa Cruz, argues that current models for the evolution of life itself neglect this critical question. To bring the point home with clarity and force, Deamer suggests a thought experiment in which a prebiotic “soup” of non-living chemicals is gradually made more complex, “using what we know about the composition of a living cell” (p. 241). In no case, he argues, would a living system arise, without a means for capturing and transferring energy. He writes:

Imagine that on the early Earth, a complete system of catalytic and information-bearing molecules happened by chance to come together in a tide pool that was sufficiently concentrated to produce the equivalent of the contents of our flask. We could model this event in the laboratory by gently disrupting a live bacterial culture, subjecting it to a sterilizing filtration step, and adding the mixture to the flask of nutrient broth. No living cells are present, but entire bacterial genomes are available, together with ribosomes, membranous vesicles, ATP and other energy-containing substrates, and thousands of functional enzymes. Once again, would a living system arise under these conditions? Although Kauffman might be optimistic about the possibilities, most experimentalists would guess that little would happen other than slow, degradative reactions of hydrolysis, even though virtually the entire complement of molecules associated with the living state is present. The dispersion has lost the extreme level of order characteristic of cytoplasm in contemporary living cells. Equally important is that the ATP would be hydrolyzed in seconds, so that the system still lacks a continuous source of free energy to drive the metabolism and polymerization reactions associated with life. (p. 242)

Deamer suggests future directions of research to bring greater realism to origin-of-life theories, stressing that encapsulation (isolation from the environment) is a necessary condition for any plausible protobiont.

Author’s comments on the summary’s accuracy:

“No! The misleading (and loaded) words, of course, are ‘greater realism.’ Those were supplied gratis by the Discovery Institute folks. The correct words would be ‘increased understanding’.

REPLY:

Deamer may dislike the words “greater realism,” but that is unmistakably the theme of his article, and that is exactly how it has been cited by his colleagues.

In the recent book, *The Way of the Cell: Molecules, Organisms and the Order of Life* (Oxford University Press, 2001), for instance, cell biologist Franklin Harold—whose writings provide the opening epigraph to Deamer’s article—cites Deamer’s 1997 paper in

a discussion of the implausibility, *or lack of biological realism*, of “soup-first” (i.e., free solution) models for the origin of life. Harold writes:

The hypothesis, that life began with naked protogenes that replicated themselves in the primordial broth and then “learned” to encode proteins that promoted the protogenes’ multiplication, has been advocated with vary degrees of conviction and hesitancy by many of the leading lights in this field. It maintains almost a stranglehold on the minds of scientists and the general public alike, and fuels what is far and away the most intense research effort....But no one has yet grasped the prize: to generate RNA from a mixture of activated nucleosides in the absence of enzymes, and have it supply the template for its own replication. Even if the next issue of Nature heralds success, curmudgeonly physiologists will have questions to ask. Where, for instance, did the activated precursors come from on the primitive earth? What kept them and their products from diffusing away, or being degraded? Are the conditions for replication plausible in a geological setting? How can any self-replicating RNA molecule pick out the “correct” monomers from a broth that also contains chemically incorrect ones? Celebration will certainly be in order, but so will restraint and a soupçon of modesty.

Many of these misgivings would be allayed if the emergence of rudimentary metabolism, energetics, and heredity were conceived, not in free solution but in a compartment of some kind. In contemporary cells boundaries take the form of lipid bilayer membranes; and one can argue that lipids, too, were on hand in the prebiotic soup—perhaps not phospholipids, but short fatty acids. *In a provocative series of experiments, David Deamer and his colleagues prepared lipid extracts from a carbonaceous meteorite...*(pp. 242-243; emphasis added)

The publication cited here by Harold is the same 1997 paper cited by the Supplementary Bibliography—and *in precisely the same context*, namely, the need to strive for realism in abiogenesis simulations. If Deamer’s work yields “increased understanding,” therefore, to use the phrase he wishes we had used, it does so because of its greater biological realism. Deamer’s objections are groundless.

36. Michael J. Katz, *Templets and the explanation of complex patterns*, Cambridge: Cambridge University Press, 1986.

Supplementary Bibliography summary:

The first usage of the term “irreducibly complex” in the scientific literature was not due to Michael Behe of Lehigh University (although Behe certainly put his stamp on the term, and has given it wide currency). Ten years before *Darwin’s Black Box* was published, the theoretical biologist Michael J. Katz of Case Western Reserve University (Cleveland, Ohio) published an eight chapter scientific monograph with Cambridge University Press, entitled *Templets and the Explanation of Complex Patterns* (1986). In

that publication, “irreducible complexity” occurs as an index entry, and is explained in the text as follows:

In the natural world, there are many pattern-assembly systems for which there is no simple explanation. There are useful scientific explanations for these complex systems, but the final patterns that they produce are so heterogeneous that they cannot effectively be reduced to smaller or less intricate predecessor components. As I will argue in Chapters 7 and 8, these patterns are, in a fundamental sense, irreducibly complex... (pp. 26-27)

In context, it is abundantly clear that by “irreducible complexity,” Katz refers essentially to the same phenomena as does Behe. “For some natural phenomena,” he writes, “there simply is no reduction to smaller predecessors. In these cases, the companion rule to ‘order stems from order’ is that ‘complexity stems from complexity’” (p. 90). More fully:

...the unique characteristics of organisms are pattern characteristics. The first of these fundamental pattern characteristics is complexity. Cells and organisms are quite complex by all pattern criteria. They are built of heterogeneous elements arranged in heterogeneous configurations, and they do not self-assemble. One cannot stir together the parts of a cell or of an organism and spontaneously assemble a neuron or a walrus: to create a cell or an organisms one needs a preexisting cell or a preexisting organism, with its attendant complex templets. A fundamental characteristic of the biological realm is that organisms are complex patterns, and, for its creation, life requires extensive, and essentially maximal, templets. (p. 83)

Like Behe, Katz confronts the issue of the origin of life, and the dilemma raised for reductive or naturalistic explanation by the complexity of even the simplest organisms:

Today’s organisms are fabricated from preexisting templets—the templets of the genome and the remainder of the ovum [egg]—and these templets are, in turn, derived from other, parent organisms. The astronomical time scale of evolution, however, adds a dilemma to this chain-of-templets explanation: the evolutionary biologist presumes that once upon a time organisms appeared when there were no preexisting organisms. But, if all organisms must be templeted, then what were the primordial inanimate templets, and whence came those templets? (pp. 65-66)

The parallels between Katz’s argument, and those of design theorists such as Michael Behe, William Dembski, or Stephen Meyer, are so numerous and striking that if one did not know better, one might assume that a design theorist had written this (and dozens of other such passages in Katz’s book):

Self-assembly does not fully explain the organisms that we know; contemporary organisms are quite complex, they have a special and an intricate organization that would not occur spontaneously by chance. The ‘universal laws’ governing the assembly of biological materials are insufficient to explain our companion

organisms: one cannot stir together the appropriate raw materials and self-assemble a mouse. Complex organisms need further situational constraints and, specifically, they must come from preexisting organisms. This means that organisms—at least contemporary organisms—must be largely templated. (p. 65)

Michael Katz replied to the questionnaire, but the NCSE did not release his response.

37. Claire M. Fraser et al., “The Minimal Gene Complement of *Mycoplasma genitalium*,” *Science* 270 (1995): 397-403.

Supplementary Bibliography summary:

These related articles explore the concept of a “minimal genome,” and asks the question “What is the minimal number of genes necessary to support cellular life?” (p. 1). Peterson and Fraser, who work at The Institute for Genomic Research (TIGR), which led one of two international efforts to map the human genome, explain that research on the simplest known living thing, the parasitic bacterium *Mycoplasma genitalium*, has revealed unexpected complexity at the foundation of life:

The fact that an estimated one third of the essential set of genes in this minimal genome are of undefined function is an important result that has at least two potential interpretations. First, it draws dramatically into question a basic assumption held by many biologists that the fundamental mechanisms and functions underlying cellular life have for the most part been identified and well characterized. If approximately 100 genes in the simplest functioning cell are of unknown function and are essential to basic cellular processes, this assumption becomes quite dubious....we have much work to do before we can claim to have a clear understanding of even the simplest cell and its functions. (p. 6).

Peterson and Fraser end by pointing to what they call an “extremely interesting” possibility, namely, “that many gene functions have evolved independently more than once since the beginning of cellular life on the planet” (p. 7). Eugene Koonin, a leader in this field of research who works at the National Center for Biotechnology Information, explores the surprising discovery that only approximately 80 of the estimated 250 necessary genes are found “in all life forms” (p. 99), suggesting a much greater degree of genetic diversity among organisms, in their basic functions, than had been suspected.

Claire Fraser *et al.* did not reply to the questionnaire.

38. Clyde A. Hutchison et al., “Global Transposon Mutagenesis and a Minimal *Mycoplasma* Genome,” *Science* 286 (1999): 2165-2169.

Supplementary Bibliography summary:

[the same as entry #37]

Clyde Hutchison *et al.* did not reply to the questionnaire.

39. Eugene V. Koonin, “How Many Genes Can Make a Cell: The Minimal-Gene-Set Concept,” *Annual Review of Genomics and Human Genetics* 1 (2000):99-116.

Supplementary Bibliography summary:

[the same as entry #37]

Eugene Koonin replied to the questionnaire, but the NCSE did not release his response.

40. Jack Maniloff, “The minimal cell genome: ‘On being the right size,’” *Proceedings of the National Academy of Sciences USA* 93 (1996): 1004-1006.

Supplementary Bibliography summary:

[the same as entry #37]

Jack Maniloff did not reply to the questionnaire.

41. Arcady R. Mushegian and Eugene V. Koonin, “A minimal gene set for cellular life derived by comparison of complete bacterial genomes,” *Proceedings of the National Academy of Sciences USA* 93 (1996): 10268-10273.

Supplementary Bibliography summary:

[the same as entry #37]

Arcady Mushegian and Eugene V. Koonin replied to the questionnaire, but the NCSE did not release their response.

42. Scott N. Peterson and Claire M. Fraser, “The complexity of simplicity,” *Genome Biology* 2 (2001): 1-7.

Supplementary Bibliography summary:

[the same as entry #37]

Scott Peterson and Claire Fraser did not reply to the questionnaire.

43. Leslie E. Orgel, “Self-organizing biochemical cycles,” *Proceedings of the National Academy of Sciences* 97 (2000): 12503-12507.

Supplementary Bibliography summary:

How did basic metabolic pathways, such as the citric acid cycle, arise from non-biological precursors? Leslie Orgel of the Salk Institute for Biological Studies, one of the world’s leading origin-of-life researchers, notes that all scenarios for the spontaneous origin of metabolic cycles “have one feature in common: a self-organized cycle or network of chemical reactions that does not depend directly or indirectly on a genetic polymer” (p. 12503). In other words, starting with information-bearing molecules such as DNA or RNA is already too complex: the first metabolic system, then, must have originated in a much simpler state. Orgel is skeptical of such proposals, however:

Unfortunately, catalytic reactions of the required type in aqueous solution are virtually unknown; there is no reason to believe, for example, that any intermediate of the citric acid cycle would specifically catalyze any reaction of the citric acid cycle. The explanation of this is simple: noncovalent interactions between small molecules in aqueous solution are generally too weak to permit large and regiospecific catalytic accelerations [of the type required by living systems]. To postulate one fortuitously catalyzed reaction, perhaps catalyzed by a metal ion, might be reasonable, but to postulate a suite of them is to appeal to magic. (pp. 12504-12505)

Existing self-organization scenarios, therefore, appeal to a “near-miracle” (p. 12506), in which “one must postulate a series of remarkable coincidences to conclude that all of the reactions are catalyzed on the same mineral and that each intermediate product is formed in the correct position and orientation” (p. 12506). Orgel concludes:

The novel, potentially replicating polymers that have described up to now, like the nucleic acids, are formed by joining together relatively complex monomeric units. It is hard to see how any could have accumulated on the early earth. A plausible scenario for the origin of life must, therefore, await the discovery of a genetic polymer simpler than RNA and an efficient, potentially prebiotic, synthetic route to the component monomers. The suggestion that relatively pure, complex organic molecules might be made available in large amounts via a self-organizing, autocatalytic cycle might, in principle, help to explain the origin of the component monomers. I have emphasized the implausibility of the suggestion that

complicated cycles could self-organize, and the importance of learning more about the potential of surfaces to help organize simpler cycles. (p. 12507)

Author's comments on the summary's accuracy:

“The paper is intended to support a conventional Darwinian form of evolution based on reproduction, selection, and mutation of polymeric molecules and to argue against a different form of evolution based on self-organizing cycles of chemical reaction. Supporters of both sides of the argument take evolution for granted, as do all competent biologists, but they disagree about important details. ... it would be appropriate to point out that all scientists carrying out experimental work on the origins of life believe that one form or another of Darwinism can adequately explain the origin of life on the earth without any recourse to ‘intelligent design.’”

REPLY:

The summary did not claim that Orgel's paper supported intelligent design. Rather, closely following his own arguments, the Bibliography summarized Orgel's critique of self-organization models for the origin of metabolism. Orgel does not object to the accuracy of the summary (or the NCSE has not yet released the objection), but simply to its inclusion in the bibliography.

44. Eörs Szathmáry, “The evolution of replicators,” *Philosophical Transactions of the Royal Society of London B* 335 (2000): 1669-1676.

Supplementary Bibliography summary:

Any Darwinian scenario for the origin of biological complexity requires *replicators*: systems capable of storing and transmitting information with fidelity, yet also with some capacity for variation, to allow for adaptive change. In this theoretical analysis, Eörs Szathmáry (of the Institute for Advanced Study of the Collegium Budapest) argues that the problem of the origin of replicators is unsolved, mainly because of what he calls “the paradox of specificity” (p. 1669). In order for a self-organizing system (such as Stuart Kauffman's hypothetical autocatalytic protein nets) to exhibit more than very limited, and non-biological, heredity, it must contain a large number of different component types (i.e., molecules). But a large number of such types entails that harmful side reactions will follow: “This is due to the fact that in a simple medium there can always be side reactions, stoichiometric and catalytic, which compromise the functioning of the network as a whole—which might otherwise look good on paper” (p. 1672). As Szathmáry notes,

A rather large number (n) of different polypeptide sequences seems to be required for the imagined functioning of these autocatalytic protein nets (Kauffman 1986). A higher-level analogy of the side-reaction plague readily arises. Calculations of probabilities about such systems always assume that a protein may or may not

catalyse a given legitimate reaction in the system but that it would not catalyse harmful side reactions. This is obviously an error. Hence the paradox of specificity strikes again—the feasibility of autocatalytic attractor sets seems to require a large number of component types (high n), whereas the plague of side reactions calls for small systems (low n). No satisfactory solution of this problem has yet been given. (p. 1673)

Szathmáry summarizes numerous other difficulties for the origin of replicators, such as (a) the need for a highly specific set of building blocks, and (b) chemical difficulties confronting any system of template replication, in the absence of specific enzymes. Consider (a):

There is an important precondition for successful replication of all molecular replicators—the environment must contain the right raw materials. This sounds trivial, but in fact it is not. Consider the case of RNA replication. This needs activated ribonucleotides of the right conformation. One can imagine (and in fact synthesize) mirror images of the currently used nucleotides. An RNA molecule would not be able to replicate in a medium consisting of a mixture of the left and right mirror-image nucleotides. This obstacle to prebiotic replication is called “enantiomeric cross-inhibition” (Joyce *et al.* 1987). Replication needs the right raw materials in the environment of the replicator. For contemporary nucleic acids this environment is highly evolved—it is the cytoplasm of the cell, maintained to a large extent by the phenotypic effects of the genes themselves on the “vehicles” (Dawkins 1976) or “interactors” (Hull 1980) in which they are embedded and replicated. (p. 1673)

Or consider (b):

A common criterion for the replication process is that the two strands (template and copy) must spontaneously separate. Since they are held together by hydrogen bonds (also necessary for replication) the strands cannot be too long or otherwise they would stick together for too long a time. Long pieces of nucleic acids can be replicated in the cell because enzymes of the replicase complex also ensure the unwinding of the strands—this cannot be assumed in non-enzymatic [prebiotic] systems. (p. 1672)

Szathmáry’s review provides an excellent survey of the mechanistic difficulties facing the modelling of prebiotic systems during their transition to true biological states.

Author’s comments on the summary’s accuracy:

“This depends very much on how you define neo-Darwinism. First, like science in general, it is developing. Second, there are cutting- edge and pedestrian conceptualizations of neo-Darwinism. My coauthor on two books, John Maynard Smith, would be regarded by many as an arch neo-Darwinist. Yet, for those, *The Major Transitions in Evolution* [by Maynard Smith and Szathmáry] came as a bit of a shock...

But that's only because of an outdated idea of how a neo-Darwinist should approach evolution..."

REPLY:

We cannot discover from these comments whether Szathmáry thinks the summary is accurate. He refers to the reception of his book *The Major Transitions in Evolution*, and to "cutting-edge" versus "pedestrian conceptualizations" of neo-Darwinism, but the relevance of this to the summary is unclear.

¹The Discovery Institute is providing a complete set of the original articles to the Ohio Board of Education.

²Stephen C. Meyer, "Teach the controversy on origins," *Cincinnati Inquirer*, 30 March 2002.

³W. Daniel Hillis, as quoted in John Brockman, *The Third Culture: Beyond the Scientific Revolution* (New York: Simon & Schuster, 1995), p. 26.