Research

CENTER FOR SCIENCE & CULTURE
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LIST OF PEER-REVIEWED AND MAINSTREAM SCIENTIFIC PUBLICATIONS SUPPORTING INTELLIGENT DESIGN

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Part I: Introduction

While intelligent design (ID) is still a relatively new scientific field, it has seen significant growth in its research program and produced a strong record of over 200 peer-reviewed scientific publications — appearing in journals such as *Journal of Theoretical Biology*, *PLOS One*, *BIO-Complexity*, *Journal of Bacteriology*, *Journal of Molecular Biology*, *Journal of Mathematical Biology*, *Complexity*, *Theoretical Biology and Medical Modelling*, *Life*, *Entropy*, *Quarterly Review of Biology*, *Frontiers in Bioscience*, *Acta Biotheoretica*, *Biomimetics*, *Biomimetics and Bioinspiration, Systems Engineering*, *Journal of the Royal Statistical Society*, *Journal of BioSemiotics, Origins of Life and Evolution of Biospheres*, Rivista *di Biologia / Biology Forum*, *Frontiers in Robotics and AI*, *Perspectives in Biology and Medicine*, *Protein Science*, Physics Essays, *Physica Scripta, Encyclopedia of Life Sciences, Journal of Engineering Design*, *Proceedings of the Biological Society of Washington*, *Annual Review of Genetics*, and others. Collectively, this research is converging on a consensus: many complex features of life and the universe cannot arise by unguided processes (e.g., Darwinian evolution), but indicate an intelligent cause. **This body of work also shows that intelligent design is a legitimate scientific field worthy of consideration by the scientific community.** Many of these peer-reviewed pro-ID publications are listed and described below.

Despite ID's impressive publication record, critics have often claimed that pro-ID scientists don't do relevant research, don't publish it in peer-reviewed journals, don't contribute to the progress of scientific knowledge, or don't engage with the broader scientific community. **A guiding purpose behind this page is to show that those accusations are absolutely false.**

We must also note two important qualifications — qualifications which show that the accomplishments of ID listed here are understated.

First, recognition in peer-reviewed or mainstream literature is not an absolute requirement to demonstrate an idea's scientific merit. Darwin's own theory of evolution was first published in a book — *The Origin of Species* — intended for a general and scientific audience, not in a peer-reviewed paper. Moreover, because ID is a minority scientific field, its supporters often face what historian of science Thomas Kuhn called “intolerance” from “normal scientists” who protect the reigning paradigm of evolutionary biology. As a result, ID frequently does not receive fair consideration for publication in mainstream peer-reviewed scientific journals (or similar venues). This makes ID’s peer-reviewed scientific publication record all the more impressive: ID has generated many peer-reviewed scientific publications, despite the intolerance and unfair treatment that it regularly faces.

Second, an idea, theory, argument, concept, or claim need not be “science” in order to be true. A core tenet of ID thinking is the rejection of “scientism,” the view that science is the only valid pathway to true knowledge. ID proponents resoundingly reject scientism, recognizing that while science has provided many benefits to our world and is a wonderful “way of knowing” to find insights into nature, it is certainly not the only way to gain knowledge. Thus, while this page lists many pro-ID *scientific publications,* it also includes a section listing peer-reviewed *philosophical publications* that support design.

Despite these caveats, it’s undeniable that science is a highly influential and powerful force in the modern world, and that in many domains peer-review remains the gold standard for assessing whether a claim holds scientific merit. Thus, while something need not be scientific to be true, and something need not be published in peer-reviewed venues to have scientific merit, it’s also important to recognize that ID *has generated many peer-reviewed scientific publications*. This peer-reviewed publication record shows that ID is a serious scientific theory backed by a community of credible scientists, and that ID deserves — and is receiving — serious consideration by the scientific community.

Types of ID Research

Intelligent design research publications come in many forms. Some explicitly argue for “intelligent design” by name — and quite a few such publications exist. But a publication need not do this to be a fairly considered a pro-ID scientific paper. For example, many publications are developing or supporting core ID concepts such as “irreducible complexity” or “specified complexity,” assessing the potency of natural mechanisms to explain complexity, or refining and applying the methods by which we detect design. Still other publications are using the assumption of design as a heuristic to guide our investigations of the natural world and help us better understand how natural systems operate. This highlights the fact that ID research can be divided into two general categories — pure and applied:

- *Pure ID research* asks how we can detect design, and/or investigates natural systems to determine whether design is the best explanation. This kind of research might also involve critiquing naturalistic explanations as part of making a case for design.
- *Applied ID research* uses the assumption of design to guide our investigations of nature, further our scientific knowledge, and better elucidate how natural systems work.

This distinction between different types of ID research is important to appreciate because not all pro-ID publications look the same — yet both types of research publications warrant inclusion in this list.

Criteria for Inclusion on This Page

A publication qualifies for inclusion on the scientific sections of this page if it is both **(A) Scientifically Credible** and **(B) Supportive of Intelligent Design** — but its inclusion will not endanger the careers of the publication's authors. To elaborate on definitions of (A) and (B):

(A) Scientifically Credible is defined as:
(i) A peer-reviewed scientific paper, book, or book chapter published in a scientific venue *(these publications are listed in **Category 1**, below)*, OR
(ii) A publication in a mainstream scientific venue, though not necessarily peer-reviewed *(these publications are listed in **Category 2**, below).*

(B) Supportive of Intelligent Design is defined as:
(i) The publication is authored by at least one known ID proponent and the publication is doing pure ID research, OR
(ii) The publication is authored by at least one known ID proponent and the publication is doing applied ID research, OR
(iii) The publication is not authored by any known ID proponent, but it explicitly and affirmatively cites ID concepts or literature, and/or makes some point that is generally identified strictly as an ID concept or argument (e.g., irreducible complexity, specified complexity, etc.). Such publications show ID is making a positive impact upon researchers outside the ID research community.

As noted above, while many scientific arguments for design exist, not all ID arguments must be scientific. Thus, this page also includes a special third category of peer-reviewed humanities publications that are supportive of intelligent design appearing in philosophical, theological, historical, or other humanities publications *(these publications are listed in **Category 3**, below)*.

In the Table of Contents below, we provide a bibliographic list of selected publications supporting intelligent design, followed by an extensive annotated bibliography of these publications. Again, the publications are grouped into three categories:

- **Category 1**: Peer-Reviewed Scientific Publications Supportive of Intelligent Design
- **Category 2**: Further Mainstream Scientific Publications: Peer-Edited or Editor-Reviewed Publications Supportive of Intelligent Design Published in Mainstream Scientific Journals, Scientific Anthologies, Conference Proceedings, Publishers, Etc.
- **Category 3**: Humanities Publications: Peer-Reviewed Publications Supportive of Intelligent Design Published in Academic Journals, Books, or Conference Proceedings within Philosophy, Theology, History, or other Humanities Disciplines.

Please note that what follows below are not exhaustive lists. All of the lists in these categories are still incomplete, some highly incomplete. This is in part because a large portion of peer-reviewed and mainstream publications supportive of intelligent design cannot be listed due to threats of potential harm to the careers of the authors if it became publicly known that they were sympathetic to ID.

PART II: TABLE OF CONTENTS & BIBLIOGRAPHIC LIST OF PAPERS

PART III: ANNOTATED BIBLIOGRAPHY OF PEER-REVIEWED PUBLICATIONS

Category 1: Peer-Reviewed Scientific Publications Supportive of Intelligent Design

- **James Johansen, "Bacterial chemotaxis control process analysis with SysML," *Systems Engineering*, 2024: 1-23 (2024).**
  James Johansen is a design-friendly professor of engineering at Biola University who specializes in applying engineering principles and tools to biological research. His article demonstrates how applying the systems engineering modeling tool SysML to bacterial chemotaxis (i.e., navigation) yields valuable insights into its global design logic. The article further demonstrates how only a design-based framework reveals the higher-level organization of biological systems.

  SysML consists of nine diagrams that map a system's structure, behavior, requirements, and parameters. Each diagram highlights a different facet of a complex system; together they generate insights into a system's design logic and operations. Johansen incorporated SysML into a methodology he developed to reverse engineer biological systems, which he called Reverse-Engineering Object-Oriented Systems Engineering Method (RE-OOSEM). The methodology incudes six elements:

  > (1) Survey academic articles and textbook sources … (2) Capture the descriptive information … (3) Convert the descriptive information summary into prescriptive engineering information for architecture capture. … (4) Generate a high-level functional architecture that maps the prescriptive information to function. … (5) Capture the system architectural details into as many SysML diagrams as necessary … (6) Evaluate the system architecture and fuse information from various SysML diagrams.

  Johansen's application of RE-OOSEM to chemotaxis yielded several insights:

  > The results show the following engineering perspective observations. (1) Several control components are not dedicated but are available and utilized when needed. (2) Individual chemoreceptors act together as a sensor array. (3) Phosphate groups act as a signaling mechanism. (4) Methylation via CH 3 groups of the chemoreceptor results in sensitivity adaptation. (5) Closed-loop control collaboratively utilizes ligand bonding, phosphorylation, and methylation. (6) Timing relationships of the control subprocesses give insight into the system's architecture.

  Johansen described how future research could model chemotaxis in diverse species to extract the engineering principles behind the differences between different chemotactic systems. It could also incorporate additional mathematical modeling and simulations to "bring further realism to how the chemotaxis process operates and why." Johansen's methodology will prove a valuable tool for future research into other biological systems.
- **Olen R. Brown and David A. Hullender, "Darwinian evolution has become dogma; AI can rescue what is salvageable," *Progress in Biophysics and Molecular Biology*, 186: 53-56 (2024).**
  This peer-reviewed paper in an Elsevier journal notes that "The publication of scientific disagreements with elements of Darwinian evolution including its modern variants are increasing" and cites various examples from the literature:

> The publication of scientific disagreements with elements of Darwinian evolution including its modern variants are increasing. The view that "Evolution is both a fact and … the most important theory in biology. Evolution explains every situation" (Russo and André, 2019) is being challenged. Wray and Hoekstra in the Comment Does evolutionary theory need a rethink" published in Nature (Wray and Hoekstra, 2014) reported that Kevin Leland and seven colleagues responded "Yes, urgently", while Gregory Wray and five colleagues responded: "No, all is well". Typical of balanced questioning is Dennis Noble who wrote "Something has gone deeply wrong in biology" (Noble, 2021).

The paper thus argues that "that the theory of biological evolution, including its modern variants, suffers from several logical deficits, is absurdly improbable mathematically, and also biologically mechanism-deficient." However, as the paper's title suggests, the authors believe that "Darwinian evolution has become dogma" and some new method is needed to move past non-objective adherence to evolutionary models. They believe this method is artificial intelligence (AI).

The authors thus propose that "the new approach of AI … is required to move forward scientifically." They note that AI provides "powerful analytical tools" that can be used for evaluating the merits of scientific theories and ask "could a complex computer be programmed to evaluate the theory (many say the fact) of biological evolution? Or perhaps test particular postulates essential to the theory?" They believe AI is well suited for this task, noting that it has already been used to "rediscover fundamental equations" in fields like physics and chemistry, and has been highly successful at playing games and solving puzzles. They believe this makes AI applicable to studying evolution:

> Evolution, also, is a puzzle. It necessarily involves the absurdly improbable self-assembly of many complex biological machines using simpler parts (Brown and Hullender, 2023). Gartner et al. (2020) stated, "self-assembly of a large biological molecule from small building blocks is like finishing a puzzle of magnetic pieces by shaking the box." AI works well for chess; we propose that it would work well for assessing ideas about biological evolution, especially the problem of self-assembly. Initially, it should be applied to testing the limits of the usefulness of 'survival of the fittest' for microevolution and the highly-improbable self-assembly required for macroevolution.

However, they believe this will lead to a problem: evolution will be challenged, and some may not want AI applied in this manner. They write that this should not matter because dogmas should never prevent scientific questions from being asked:

> A perceived potential difficulty, which might, however, produce the first positive result of applying AI, is that focused discussion of the tenets, assumptions, and established facts of biological evolution would result. Consensus without criticism is not healthy for science. Biologists can learn from the field of Physics which is open to recognizing new ideas. It has shown itself receptive to change with concepts about gravity evolving from Newton to Einstein and the current interpretations, an example. The consequences of challenging the overall theory and subcomponents of biological evolution are monumentally significant for progress in this field and has ramifications for all of science including the freedom to challenge dogmas. "The scientist is free, and must be free to

> ask any question, to doubt any assertion, to seek for any evidence, to correct any errors" — J. Robert Oppenheimer.
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> […]
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> Problems with the Darwinian theory of evolution, including its modern variants, and origin of life theories are significant and require new approaches and a willingness of scientists to look for bold solutions. The application of AI has great promise both for assessing the problems and weaknesses and for providing innovative and significant solutions of great significance for science and humankind. AI can be the pathway to correcting the problems in evolutionary theory, but the human brain must create that pathway. There must be no barriers to freedom of inquiry. There is no place for dogma in science.

What would AI find if it were let loose to critically investigate biological evolution? Their main argument is that we need to apply it to such a task. But they predict that if AI were applied to questions of biological origins, it would find serious flaws in evolutionary models: "We conclude that AI has this potential and encourage its application immediately for evaluating theories of biological evolution. It seems remote that AI would conclude that it is 'turtles all the way down'."

- **Winston Ewert, "AminoGraph Analysis of the Auditory Protein Prestin From Bats and Whales Reveals a Dependency-Graph Signal That Is Missed by the Standard Convergence Model,"** ***BIO-Complexity*****, 2023: 1 (2023).**
  In this paper, Winston Ewert further develops his previous work on the dependency-graph model for accounting for the similarities and differences between organisms. Whereas his earlier work had focused on binary datasets that take account only of the presence or absence of a given gene family, this work advances his ideas to focus on datasets of amino acid alignments:

  > Here, we introduce a tool (*AminoGraph*) that infers dependency graphs from protein sequence alignments, and we apply this to prestin, a mammalian auditory protein that requires special modifications for ultrasonic hearing in species that use echolocation.

  Ewert's *AminoGraph* program generates, based upon an input of amino acid sequences, a graph representing module dependencies. The program identifies modules as modifications of the protein sequence from an archetypal version. If a protein possesses the alterations of another protein in addition to further changes, it is said to be dependent on the other protein.

  Ewert notes the problem of conflicting phylogenetic trees, which is typically explained, in evolutionary terms, by processes such as incomplete lineage sorting, horizontal gene transfer, and the duplication or extinction of genes, or, less frequently, by convergent evolution. He focuses on echolocation in mammals, where two groups of bats (Vespertilioniformes and Rhinolophoidea) and one group of whales (Odontoceti) can echolocate. According to evolutionary theory, echolocation arose independently in all three of those clades.

  The protein chiefly responsible for echolocation is prestin, a motor protein found in hair cells in the inner ear. Previous research has revealed that, when a phylogeny is constructed on the basis of prestin's amino acid sequence, the three echolocating groups are brought together. Ewert replicated this result using the program Clustal W. Nonetheless, he observes,

> There is only a weak signal bringing all of the echolocating species together. There are not many similarities which are common to all echolocating species. This is somewhat surprising because we saw in Figure 2 that all of the echolocating species are grouped together. This, however, does not indicate a common signal between all echolocating species. Rather, it reflects two signals, one linking Odontoceti and Rhinolophoidea, and the other linking Rhinolophoidea and Vespertilioniformes. The only way for a tree to reflect both signals is to bring all three groups together.

What should we conclude from this? Ewert notes:

> The conclusion to be drawn is that the problem of discordant phylogenies is not simply that some genes or proteins suggest different phylogenetic trees than the generally accepted species tree. Rather, we find that even within a single gene or protein, such as the prestin protein, phylogenetic trees are only capable of representing one signal, and thus, phylogenetic inference programs attempt to choose the signal with the greatest strength. This is not an accurate reflection of the data. Instead, we need a theory that can accommodate these conflicting signals.

Ewert argues that discordant signals like these are better explained on a dependency-graph model since, on this scenario, "different parts of the genome will show different patterns of similarities depending on which modules influenced that section of the genome."

Ewert ran his AminoGraph program on the prestin amino acid sequence from echolocating bats, bats lacking echolocation, echolocating whales, whales lacking echolocation, and other mammals lacking echolocation. The resultant dependency graph revealed important insights regarding how the prestin protein was modified in order to adequately detect the high sound frequencies that are produced during echolocation. In each mammal capable of echolocation, the results revealed that a combination of two modules (designated Echolocation A & B) was used. Ewert notes:

> Essentially, we can think of a module as a list of changes to the amino acid sequence. Each module merges together all of the changes from the modules it depends on before adding its own changes. For example, in Figure 3 , the Echolocation A module inherits all of the changes made in Chiroptera and passes these them on to Rhinolophoidea and Vespertilioniformes. Pteropodiformes also inherits the changes from Chiroptera, and so Rhinolophoidea inherits two copies of the Chiroptera changes. However, because these are the same changes they do not conflict, and there is no problem.

How can the predictions of a dependency graph model be distinguished from common descent? Ewert argues:

> Our evidence for the correctness of our model is the various sequences that AminoGraph detects as exhibiting the structure expected based on a dependency graph. This is akin to many arguments for common descent that identify hierarchical signals in various datasets. We are doing essentially the same thing by showing that there is a

> dependency graph signal in these datasets. … the dependency graph signal is a refinement of the hierarchical signal. That is, cases of sequences that exhibit dependency graph signals will also exhibit a hierarchical signal. However, almost all sequences that exhibit a hierarchical signal would not also exhibit a dependency graph signal. Even data that deviate from a hierarchical signal would not tend to exhibit a dependency graph signal because the dependency graph signal requires that a pattern of amino acid substitutions appear in distinct groups. Finding this pattern is a successful prediction of the dependency graph model.

In summary, Ewert's model proposes an alternative common-design-based model for explaining the distributions of similarities and differences at the level of amino acid sequence, though, as Ewert himself admits, the dependency graph "requires more development before it can be claimed as the best explanation over common descent."

- **Olen R. Brown and David A. Hullender, "Biological evolution requires an emergent, self-organizing principle,"** ***Progress in Biophysics and Molecular Biology*****, 182: 75-102 (2023).** This peer-reviewed paper in a journal published by Elsevier reviews "fundamental flaws in Darwinian evolution, including its modern versions." According to the paper, these flaws come down to the fact that too many mutations are needed to produce new species or many new complex features — more mutations than could be produced by Darwinian evolution. They explain:

> Fixed mutations 'explain' microevolution but not macroevolution including speciation events and the origination of all the major body plans of the Cambrian explosion. Complex, multifactorial change is required for speciation events and inevitably requires self-organization beyond what is accomplished by known mechanisms. The assembly of ribosomes and ATP synthase are specific examples. We propose their origin is a model for what is unexplained in biological evolution. Probability of evolution … values are absurdly improbable. Speciation and higher taxonomic changes become exponentially less probable as the number of required, genetically-based events increase. Also, the power required of the proposed selection mechanism (survival of the fittest) is nil for any biological advance requiring multiple changes, because they regularly occur in multiple generations (different genomes) and would not be selectively conserved by the concept survival of the fittest (a concept ultimately centered on the individual). Thus, survival of the fittest cannot 'explain' the origin of the millions of current and extinct species.

They note that "challenges to the theory (textbooks say the fact) of evolution are almost universally discouraged, even ridiculed and denied, by main-stream biology" and believe that "the doctrine of evolution by chance events is both sustained and taught from a privileged perspective, and this is harmful to the body of science." They argue that "the theory of evolution, including all modern additions, is fundamentally flawed" and the reason is "because of its inherent, fatal contradiction," which they summarize as follows:

> [T]he mechanisms postulated for evolutionary change become exponentially increasingly probable as change decreases in magnitude. Conversely, the probability that survival of the fittest selectively rescues any change decreases with the magnitude

> of the change and becomes insignificant for speciation because complex changes are multifactorial and multigenerational.

In other words, mutations that are likely to occur are small-scale and have trivial effects, whereas the mutations that are needed to produce the highly fit features we see in living organisms require "complex changes" that are unlikely to occur. They discuss various features which they argue are too complex to evolve. These include:

- **Spider Silk**: They argue that the evolutionary origin of spider spinnerets is essentially unknown: "The ability of spiders to produce the unique silk protein, to assemble the spinnerets, and to use silk so effectively in so many ways essential to the spider's existence is not rationally explained by theories of evolution. We state this, not because these processes cannot be individualized into small enough elements that could be envisioned to each have originated by a small biochemical step. The impossibility arises because the doctrine of evolution by chance events requires that each individual step in this complexification must have increased survival value."

- **Ribosomes**: In a section titled, "Ribosome assembly, a major problem for evolution," they say "This complexity and order, essential for assembly of ribosomes, is striking." Yet they note that the problem of the evolutionary origin of this vital cellular process of ribosome assembly has barely been investigated: "Does any discipline in physics, chemistry, or biology claim to be able to chart the journey, and all of the mechanisms underlying the assembly, of any of the organelles in even the simplest of cells? More significantly, why has so little importance been placed on this for evolution? The body of science is inadequately curious when it accepts that this bio-motor occurred via evolution by chance and natural selection."

- **Oxidative Phosphorylation**: ATP, the energy molecule that life uses to power biochemical reactions, is produced through a process called oxidative phosphorylation. The authors observe that the origin of this process poses a challenge to blind evolution: "For elucidating this bioenergetics process, oxidative phosphorylation, Peter Mitchell received the Nobel Prize. Its significance as a problem for evolution can hardly be overemphasized. We reiterate. Energy, its transformation and utilization, separates life from nonlife. The origin of the biological machinery governing bioenergetics is among the most daunting requirement for evolutionary mechanisms. … Energy is essential for life. How would life in Darwin's hopeful, warm, little pond get started? The complexity, rate and specificity in space, time, and function of energy conversion in living cells is astounding. The theory of evolution requires that it arose bit by bit over immense time; accumulating its parts, including those that are separately nonfunctional, by very small individual changes occurring by chance; and that survival of the fittest explains each step of complexification. The evolution of a Prokaryote and its capture as a slave in a Eukaryote is similar to the proposal that life itself arose on another planet and was brought to earth. Surely, 21st century evolutionary science requires more as a theory of everything about life." Citing the concept of irreducible complexity, they provide a striking commentary on whether such a system could evolve:

  > Even this greatly-abbreviated overview of the self-assembly required for, and the functioning of, bioenergetics via oxidative phosphorylation reveals the

> complexity of this process. The relevance to this perspective review is the obvious interdependent nature of the elements, many functional only when complete, and the large number of such elements required. Indeed, we submit that it has functionally irreducibly complex elements.

- **Enzymes:** The authors note that standard explanations for the origin of enzymes involve duplication and divergence of function, but known examples include only "trivial" changes in activity:

  > It is proposed, and of course it as possible, even logical, that a gene that codes for an essential enzyme could be duplicated and the duplicated gene could mutate. The protein coded by this duplicate gene might catalyze a slightly different reaction. Examples exist, but they involve only slight differences in substrate, product, or reaction mechanism because a mutation can introduce only very limited kinds of changes in a specific protein. This limits the scope of change to triviality compared to the scope required by evolution for the creation of the enormous number of enzymes required in all of life's biota. We are reminded of a poem. "There was a little girl, and she had a little curl, right in the middle of her forehead. When she was good, she was very, very good, and when she was bad she was horrid." The power of selection based on random, genetic mutation as a source of change for evolution is like the little girl in this poem, it is good (even very good) at explaining what it can explain - trivial (small) changes — but horrid at explaining all of the major changes needed for evolution of species. Compartmentalization into small changes that lack a functional advantage, is an insurmountable problem for this explanation.

  They conclude, "Even the 21st century forms of Darwinian evolution fail the daunting task of explaining how the first enzyme arose."

- **ATP Synthase:** The authors quote a paper by Nick Lane and William Martin which states: "Harnessing energy as ion gradients across membranes is as universal as the genetic code … yet its origins are obscure." After discussing the complexity of the ATP synthase molecular machine, they ask: "Could this complex process have had a simpler origin? Reasonably, some almost-complete forms could have some function that was selectable by 'survival of the fittest'; is it reasonable that all would have?" They then quote David Snoke writing in *BioCosmos*: "Many people have the experience of looking at a living system, or an ecological system, and concluding, 'This is all too amazing to just have happened by chance'". The authors then comment: "We have experienced that the 'many people' referred to are often attacked, dismissed, or responded to superficially. … Snoke's thinking (Snoke, 2022) is a good example of the rigorous approach we hope to promote."

In light of these criticisms they draw strong conclusions about the theory of evolution:

> The theory of biological evolution is a great pretender. It pretends to understand self-assembly in cells while enjoying a special, privileged place in science that is not enjoyed by even the physicists and cosmologists proposing the big bang who currently actively compete with theories of everything.

But if not evolutionary models, then what? The paper opens by quoting Max Planck saying, “We must assume behind this force the existence of a conscious and intelligent Mind. This Mind is the matrix of all matter.” They even note that the Nobel Laureate biologist George Wald said that "time performs the miracles". Of course, Wald was a materialist, but they note that Wald uses the term “miracles” in some sense. Indeed, they hint that there are larger implications from the scientific evidence:

> A typical example of the materialist’s response to probabilities is found in the SMR blog Modern science, philosophy and religion (Do probability arguments refute evolution, 2022) which concluded, in part: “In a larger context, one must question whether highly technical issues such as biomolecular structure or calculations of probabilities have any place in a discussion of modern philosophy or theology.” We do not concur with this opinion and our probabilities are appropriately constructed with clearly stated assumptions.

The paper even gives a nod to the possibility that “common design” could explain the similarities between different types of organisms:

> In this case, it must be assumed that the reason for quantifiable DNA similarities is based on the “common ancestor” idea. It is argued by main-stream biology that there is no other possibility based on science. Most specifically, it is declared that the idea of a “common designer” for the use of the same components for constructing similar body parts and similar internal components for self-assembly in cells, and the DNA and genetic code itself, is disallowed as unscientific.

The paper further notes that for many evolutionists, the implication of their theory is that there is “no design/purpose anywhere in nature” and “Thus, there is no design/purpose to be found in humans and no design/purpose in their existence. Life’s but a walking shadow … It is a tale Told by an idiot, full of sound and fury, Signifying nothing.” They note:

> The consequences of laws of science are broad and they necessarily extend influentially to natural philosophy, and more personally, to one’s world view. Acknowledging this does not make one a non-scientist.

While the paper does not explicitly argue for intelligent design, it expresses an openness to invoking non-mechanistic causes like an “intelligent Mind,” as the paper states.

- **Steinar Thorvaldsen and Ola Hössjer, “Estimating the information content of genetic sequence data,” *Journal of the Royal Statistical Society: Series C: Applied Statistics*, 2023: qlad062 (2023).**
  This peer-reviewed paper in the *Journal of the Royal Statistical Society: Series C: Applied Statistics*, by ID-friendly scientists Steinar Thorvaldsen and Ola Hössjer, explores how we can best measure biological information. It starts by noting that a proper metric of biological information must consider “meaning” and the “semantic aspect”:

  > Biology has approved the concept of information but has, to a certain extent, avoided the concept of meaning. In qualitative terms, genetic function is possibly the best

> depiction of the ‘meaning’ of a sequence. This biochemical function is determined by direct empirical experimentation and links information content to functionality (Adami & Nitash, 2022). De Mul (2021) distinguishes between the syntactic aspect of biological sequences and structures, and their semantic aspect. Shannon information is only about syntax, whereas it is life itself that gives meaning to sequences. Functional information is based on the probability that an arbitrary configuration of a system (letter sequence or protein) will obtain a specific function to a specified degree (Hazen et al., 2007). It can be considered as a bridge between Shannon information, which only includes probabilities but not function, and the concept of semantic information, which is very wide and therefore is difficult to quantify in terms of probabilities, although it includes function as a possibility.

They aim to provide means of measuring biological information which determine whether functional information is being gained or lost during evolution: “one should be able to quantify this change of information for a given population of organisms for a given number of generations and estimate the amount of self-information and genetic variation gained or lost during the evolution of that lineage (cf. Díaz-Pachón & Marks, 2020).” They are not the first to attempt providing improved metrics of biological information, noting:

> In 2003, Jack Szostak published a short paper in *Nature*, pointing out that the meaning or functionality of a message is vital in molecular biology (Szostak, 2003). Because classical information theory does not distinguish between functionality and nonfunctionality, Szostak introduced the need for a new measure of information, which he called functional information. Some years later, he and three other colleagues defined functional information in terms of a gene string as $-\log_2$ of the fraction of functional sequences that have fitness values (activity of a biopolymer) greater than a specified value (Hazen et al., 2007). This is the probability that a random sequence will encode a molecule ‘with greater fitness than any given degree of function’

They further note the difficulty of measuring functional biological information because of “the extreme scarcity of functional sequences in populations of random sequences”:

> It is difficult to experimentally determine the connection between functional information and activity because of the extreme scarcity of functional sequences in populations of random sequences. Since there are multiple sequences with a given expression, the corresponding functional information will always be lower than the measure of the information needed to specify any particular sequence. It is important to notice that functional information is not a property of any one molecule, but of the collection of all optional sequences classified by activity.

They also observe that it is important to try to find metrics of information that address both the “probabilistic and qualitative” dimensions:

> In biology, information has both a probabilistic and qualitative dimension over an observable dataset. Through the representation and use of information and its pragmatic assessment, there is substantial justification for considering biology within such an informational platform. In this article, we have presented some advances in terms of quantifying genetic information as a joint variable of function and sequence

> data, and to estimate the corresponding functional information through rejection sampling. Both structure-based and sequence-based domains, which are available in CATH and Pfam databases respectively, are promising representatives of functional regions within proteins with quantifiable information content. Information is a conceptual key to a proper understanding of reality that reveals itself as we do science. Despite the large amount of evidence that information plays a vital role in genetic systems, quantitative information processing does not yet feature much in the genetic principles at the centre of mainstream theories and textbooks. This absence is problematic and disconnects genetics from other scientific disciplines. Scientific and philosophical thinking and work should rather, with increasing confidence, place information 'as one of three elemental components of existence (along with space/time and energy/matter)' (Atmar 2001).

This paper shows that intelligent design is inspiring improved methods of measuring biological information and better ways to understand biological complexity in terms of not just its probability, but its meaning and function.

- **Douglas D. Axe, Jireh Gerry, Alisa D. Daniels, Sabrina Wilkerson, William Mitchell, Sarah Randall, "Fitness Decline Over Long-Term Evolution of a Small Population of Asexual Computational Organisms,"** ***BIO-Complexity*****, 2023: 2 (2023).**
  In this paper, Douglas Axe and colleagues simulate a long-term evolution experiment using a virtual population involving a thousand computational organisms. This work builds upon Axe's previously developed *Stylus* program, which simulates evolution in a population of organisms that have genes that specify drawings representing Chinese written characters. According to the paper:

> Following a population of 1,000 model organisms through 2,000,000 fixation events, we find that fitness declines approximately as a two-phase exponential decay. The long-term result is substantial loss of function for all 223 genes, seen both in a collapse of numerical scores and in loss of legibility. The cause of the collapse is an imbalance in the initial genome: the number of ways for mutations to produce a new worst gene is so much higher than the number of ways to improve the current worst that selection is unable to prevent decline. This result raises the question of genome decay in real organisms. It seems likely that the same imbalance exists there, though life may have ways of averting the decline we describe here.

The program uses a *weakest-link* model of fitness — meaning that the fitness of the computational organism is "limited by the poorest performing gene in the genome." This simplification is required for any computational model of population dynamics, but it is well suited to studying a minimally complex organism in which all genes are essential. Since all genes are essential, "any one of them would limit the rate of reproduction if it were to become disproportionately slow." On the other hand, "there would be no benefit in any one of the processes becoming disproportionately fast." Thus, on this scenario, "any gene will become rate limiting if it underperforms the others."

Another advantage of the *weakest-link* model of fitness is a gene is scored by *Stylus* for its correspondence of its coded product to the respective Chinese character. The program would thus not detect if a modification to the Chinese character caused it to resemble a different character. However, if the original gene codes for a core function (and is thus essential for viability), then “any such fortuitous appearance of a different function would be unhelpful in that it would be accompanied by loss of a necessary function.”

The authors ran the simulation using a population size of 1,000 and used 19 different values for the selection coefficient, *s*, for the introduced variant genotype. When the value of *s* was given as -0.008, the probability of fixation was seen to be vanishingly low — under one in a million. On the other hand, values that are greater than +0.008 are likely to be too infrequent to become fixed. The results indicated that throughout the course of two-million fixation events, there was “a consistent downward trend in fitness.” Although occasionally fitness would be enhanced by a fixation event, “these were well outnumbered by those that slightly decreased fitness.” They note:

> [S]election greatly slows the genomic decline, even though it is unable to prevent it. The dramatic difference between the distribution of s values for incident mutations (Figure 6A) and the distribution of s values for fixed mutations (Figure 6B) is entirely due to selection. Although the shapes of these distributions change somewhat over the course of the experiment, the strong drop in the likelihood of fixation caused by lower s values is consistent throughout.

They argue that such decline is inevitable (though its timescale is proportional to mutation rate). This is a consequence of the fact that slightly deleterious mutations vastly outnumber beneficial ones, together with the fact that selection cannot purge slightly deleterious mutations in modestly sized populations.

The problems uncovered by these simulation experiments are likely to be greatly exacerbated in real organisms with minimal genomes, since they have many more essential genes. They conclude with an important caveat:

> Considering the difficulty of direct confirmation, we judge this problem of genomic degradation to be less certain than the evolutionary problems that have been described before. It does, however, constitute a paradox that — because of what is at stake — should be given careful attention.

The paper thus raises significant questions about the efficacy of the mutation-selection mechanism in building complex systems beginning from a minimally complex organism.

- **Richard S. Gunasekera, Komal K. B. Raja, Suresh Hewapathirana, Emanuel Tundrea, Vinodh Gunasekera, Thushara Galbadage, and Paul A. Nelson, “ORFanID: A web-based search engine for the discovery and identification of orphan and taxonomically restricted genes,” *PLOS One*, 18 (10): e0291260 (2023).**
  Evolutionary explanations for the origin of new genes hold that genes often originate when some ancestral gene duplicates, and then those duplicates slowly diverge in sequence over time to form new gene sequences with new functions. This evolutionary “duplication and divergence model” therefore predicts the existence of “orthologous” genes — genes with similar sequences that represent close relatives descended from common ancestral genes. But what if a gene sequence is unique and shows no sequence similarity to any other gene? How would the duplication and divergence model explain the evolutionary origin of such a gene? Orphan or

“ORFan” genes represent precisely such genes which have amino acid sequences that resemble no other known gene. This paper, authored by a team of scientists including ID theorists Paul Nelson and Richard Gunasekera, reports an ID-funded project that is exploring the nature and origin of orphan genes:

> With the numerous genomes sequenced today, it has been revealed that a noteworthy percentage of genes in a given taxon of organisms in the phylogenetic tree of life do not have orthologous sequences in other taxa. These sequences are commonly referred to as “orphans” or “ORFans” if found as single occurrences in a single species or as “taxonomically restricted genes” (TRGs) when found at higher taxonomic levels. Quantitative and collective studies of these genes are necessary for understanding their biological origins.

The article explains that orphan genes are not rare, and in fact make up “large fractions” of the genomes of many species, meaning “TRGs represent important mediators of phenotypic novelty.” The prevalence of orphan genes has implications for evolutionary models of the origin of new genes, since these models predict “we should see a connection” between the gene sequences of related genes. The paper notes, however, that the study of orphan genes has largely been neglected because they were poorly understood — presumably also because they did not fit standard evolutionary models:

> The neglect of orphans has continued to some extent in the genomic era, as functional roles are mainly assigned to newly sequenced genes mainly via homology criteria (e.g., existing annotations in other species). However, it has been shown in some cases that orphan genes are uniquely involved in making one species distinct from another phenotypically.

The project announced in this paper aims to correct the neglect of orphan genes by presenting a new online tool, ORFanID, for searching genome databases to identify and catalogue orphan genes. Reflecting this neglect, the paper notes that existing bioinformatics tools “are not suited to identify orphans as ORFanID is designed to do.” ORFanID is distinct because it not only identifies orphan genes but connects to a database cataloguing orphan genes across many species which can be used by future researchers who wish to engage in large-scale investigations of orphan genes:

> ORFanID’s distinctiveness is in three aspects: (1) It processes not just protein/amino acid sequences but also DNA/nucleotide sequences. (2) With its built-in homology interpreter and classifier, this search engine provides the taxonomic rank of a gene either as an orphan gene or as a gene restricted to a taxonomic level in the tree of life; (3) As ORFans and TRGs are identified, ORFanID builds its own database with the results of the analysis and provides the researcher with the possibility to further explore the data.

Orphan genes / TRGs are of great interest to the design hypotheses. Evolutionary models require material templating from common ancestors whereas design allows for, and indeed predicts, the free use of all possible protein sequence space, as the immaterial designing intellect inferred by ID theory can move without limit to any point in that space and actualize it. In other words, minds are capable of producing the precise types of informational discontinuities that we see in orphan genes. The results of this project therefore have the potential for major positive implications for intelligent design.

The paper notes that “These findings can lead to the creation of databases of these clandestine genes that have been pre-identified at the various taxonomic levels by ORFanID, resulting in a deeper understanding of the purpose of orphan genes, their function in genomes, and their potential impact on life.” This project thus not only has the potential to provide powerful evidence for design but also to further our understanding of orphan genes and what makes species (or taxa) unique. This project shows that scientists in the are conducting research relevant to important biological questions of interest to all biological scientists.

- **Granville Sewell, “Human-Engineered Self-Replicating Machines,” *BioCosmos*, 3 (1): 12-15 (2023).**
  In this peer-reviewed article, mathematics professor Granville Sewell illustrates why engineers are nowhere close to designing a machine capable of true self-replication. He connects the challenges of our designing a self-replicating machine with the difficulty of explaining how undirected natural processes could have generated the first self-replicating cell. He begins by examining the challenge of creating a self-replicating car:

  > We know how to build a simple model T. Now let’s build a factory inside this car, so that it can produce model T cars automatically, and call the new car, with the model T factory inside, a ‘model U’. … Of course, the model U cars are not self-replicators, because they can only construct simple model T’s. So let’s add more technology to this car so that it can build model U’s, that is, model T’s with car-building factories inside. This new ‘model V’ car, with a fully automated factory inside capable of producing model U’s (which are themselves far beyond our current technology) would be unthinkably complex. But is this new model V now a self-replicator? No, because it only builds the much simpler model U.

  The problem poses an infinite regress where every component (e.g., model U car) that replicates a sub-component (e.g., model T car) must be more complex than what it replicates. Yet that component would need an ever more complex supra-component to replicate it (e.g., model V car). The continuous need for increasingly complex replicators seems unending.

  Sewell than describes attempts to create self-replicators including Cornell University’s self-replicating blocks, RepRap 3D printers, and the University of Vermont’s “living robots.” None of these entities performs true self-replication but at best “assisted” self-replication:

  > The *Robotica* article (6) by the designers of the RepRap 3D printer series includes a short summary [following the outline in the Freitas and Merkle book (10)] of efforts to design self-replicating machines. They cite Von Neumann (11) as the first to propose such a machine. But his theoretical machine had to reside in a stockroom with an unlimited supply of spare parts and is thus, like the real Cornell device, also not helpful in understanding how life began. The authors call their printers ‘assisted’ self-replicating machines and acknowledge that ‘an artificial autotrophic self-reproducer remains an unachieved Utopia for the subject.

A central challenge of self-replicators is mining raw materials from the environment and then manufacturing all required components. Nothing humans have created even comes close to performing these functions. Sewell notes that even the simplest of autonomous cells must also perform these functions, and no one has proposed a scenario for how such systems could have emerged on the early earth that appears even remotely plausible.

- **Jonathan Bartlett, "Random with Respect to Fitness or External Selection? An Important but Often Overlooked Distinction,"** ***Acta Biotheoretica,*** **71:2 (2023).**
  It is generally assumed that mutations occur more-or-less randomly with respect to an organism's fitness. Though there may be mutational bias (with certain mutations more likely to occur than others), it is thought that such biases do not favor the needs of the organism. In this paper, design theorist Jonathan Bartlett argues that "experiments used to establish randomness with respect to fitness are only capable of showing that mutations are random with respect to current external selection." However, the distribution of mutations may be skewed in favor of the organism's fitness. For example, if a particular mutational variant that causes lethality never (or hardly ever) arises, the distribution of mutations is shifted in a manner that is favorable to fitness – though this would not be detected by conventional experiments, such as those by Luria-Delbrück, which cannot consider harmful mutations that never or very rarely occur. Indeed, Bartlett cites papers which adduce evidence that the rate of mutations can often be significantly reduced in essential housekeeping genes relative to non-essential contingency genes.

  Another manner in which mutations may be biased in favor of fitness is through cyclical mutational mechanisms, whereby "reversions to a previous configuration is significantly more likely than for an arbitrary mutation." Bartlett notes that "A simple example of a cyclical mutation would be a site-specific, reversible DNA inversion. These are commonly found as a means of rapid adaptations in bacteria."

  If indeed there is a suppression of detrimental or lethal mutations, what are the implications? Bartlett argues that, if this is the case, "then studies of the effects of mutations in vitro cannot be used as a proxy for the distribution of the effects of mutations in vivo, since in vitro studies assume a random distribution of mutations. If that assumption is unfounded, then so are the results of such studies." He further notes that,

  > An example of this is Graur (2017), which uses the in vitro distribution data as a proxy for the distribution of in vivo mutations, and uses that as the basis of estimating parameters for population dynamics in humans. However, if there are mutational mechanisms which bias the fitness of mutations, even if it remains random with respect to external selection, then the in vitro data cannot properly serve as a proxy for in vivo outcomes.

  If mutations are non-random, as suggested by Bartlett, this undermines a fundamental tenet of neo-Darwinism. Moreover, this paper has implications for ID since it describes a way in which a designer might set up mutational constraints on certain sequences in order to bias the probabilistic space and influence evolutionary trajectories in a manner favorable to the organism.

- **Stuart Burgess, Alex Beeston, Joshua Carr, Kallia Siempou, Maya Simmonds, and Yasmin Zanker, "A Bio-Inspired Arched Foot with Individual Toe Joints and Plantar Fascia," *Biomimetics*, 8 (6): 455 (2023).**
  In this peer-reviewed article, ID-friendly engineer Stuart Burgess and his team demonstrate how the design of the human foot inspired the development of a new artificial foot that could be used for robotics and prosthetics. The development of a biologically inspired foot via biomimetics shows illustrates how biological systems are optimally designed. The authors summarize their work as follows:

  > This paper presents the design and testing of an arched foot with several biomimetic features, including five individual MTP (toe) joints, four individual midfoot joints, and plantar fascia. The creation of a triple-arched foot represents a step further in bio-inspired design compared to other published designs. The arched structure creates flexibility that is similar to human feet with a vertical deflection of up to 12 mm. The individual toe joints enable abduction–adduction in the forefoot and therefore a natural pronation motion.

  They also explain why the human foot appears optimally designed:

  > Flexible arches and MTP (toe) joints are known to have advantages such as enabling walking on uneven ground [1], shock absorption [2], and energy storage and release [3]. … The human foot has a multi-configurable system that allows it to have optimal stiffness at different stages of the gait cycle [27]. During landing phase, the foot needs to be flexible and shock-absorbing, but during the push-off phase, the foot needs to be a stiff lever. Fine-tuning of stiffness occurs due to active mechanisms such as intrinsic muscles [28] but also passive mechanisms.

  In their design for an artificial foot, the authors copying such features from the human foot as the three arches, the elastic tissue between bones, and the three-point contact of the heel to the ground. They explain why the highly optimized features of the human foot allow it to function effectively while walking, running, traversing uneven ground, and absorbing shocks.

  The authors tested their model and reported how it compared to a human foot in performance. In many ways, the human foot surpassed their design. They concluded by describing how they wish to better mimic the human foot in future designs to achieve improved performance.

- **Stuart Burgess, "Why the Ankle-Foot Complex Is a Masterpiece of Engineering and a Rebuttal of 'Bad Design' Arguments," *BIO-Complexity*, 2022: 3 (2022).**
  ID critics have argued that the human foot-ankle complex is sub-optimal because it reflects an unguided process where evolution attempted to convert a skeletal structure adapted for quadrupedal locomotion to bipedalism. In this peer-reviewed paper, ID-friendly engineering professor Stuart Burgess responds and shows that the ankle-foot complex "show a very high degree of complexity and fine-tuning" and "masterful engineering." Moreover, "Engineering insight reveals a close relationship between form and function in the ankle, a relationship seen in its multiple bones and the layout of those bones" and the "five midfoot bones are needed to form the optimal kinematic and structural interface between the hindfoot and forefoot."

Burgess observes that many who have studied the foot without a preconceived bias have recognized its "excellent design." He quotes Leonardo da Vinci who called the human foot "a masterpiece of engineering and a work of art," and more modern researchers who observe the "nearly effortless human gait" or who note that various foot structures "work in perfect synchronisation" because it is "superbly constructed for ambulation."

In contrast, "bad design" proponents believe that most of the seven anklebones are pointless, poorly coordinated, and fundamentally a bad design because a "fused structure" would work better than "a joint with so many separate parts." Burgess answers arguments that the ankle-foot performs poorly for bipedalism because it was originally evolved for quadrupedal locomotion by observing that such arguments "are based on circular reasoning and assumptions about what evolution could or could not do in the past." He believes that "A better scientific approach to assessing the quality of design is to study the actual biomechanics and functions of the foot." Burgess observes that "The requirements for agile bipedal movement are extremely demanding." After all, the foot must be "a compact multifunctioning precision device" which has to fulfill multiple requirements which are sometimes contradictory.

Bad-design proponents have asked why there are paired bones at the bottom of the leg above the ankle instead of a single bone. Burgess notes there are good reasons for this as fibula is "well known to provide stability to the ankle joint" via "a type of linkage system with multiple bars." He cites two specific advantages to having a fibula bone:

> One advantage of the fibula is that it increases the moment arm (mechanical advantage) of muscles acting on the ankle-foot complex. A second advantage is that the fibula increases the attachment area for muscles and therefore allows more muscle to act on the joint.

Burgess concludes:

> 1. There are four highly specialised design features in the ankle-foot complex
> 2. The ankle-foot complex is superior to human-engineered joints
> 3. Bad design arguments are contrary to scientific evidence
> 4. Engineering insight explains form and function

This last point is crucial because it shows that the very design and structure of the ankle-foot complex must exist to for it to perform its functions. According to Burgess, the system exhibits "very sophisticated engineering design."

- **Olen R. Brown and David A. Hullender, "Neo-Darwinism must Mutate to survive," *Progress in Biophysics and Molecular Biology*, 172: 24-38 (2022).**
  This peer-reviewed paper by ID-friendly authors published in the Elsevier journal *Progress in Biophysics and Molecular Biology* is highly critical of the modern synthesis:

  > There has been limited progress to the modern synthesis. The central focus of this perspective is to provide evidence to document that selection based on survival of the fittest is insufficient for other than microevolution.

The authors, Olen Brown and David Hullender, argue that calculations show the likelihood of microevolutionary processes adding up to macroevolutionary changes is highly improbable:

> Realistic probability calculations based on probabilities associated with microevolution are presented. However, macroevolution (required for all speciation events and the complexifications appearing in the Cambrian explosion) are shown to be probabilistically highly implausible (on the order of 10-50) when based on selection by survival of the fittest. We conclude that macroevolution via survival of the fittest is not salvageable by arguments for random genetic drift and other proposed mechanisms.

They go on to state, “We are critical, as previously explained, of the position that macroevolution is sufficiently explained by the processes useful for microevolution — in particular that mutations and survival of the fittest are adequate to the task,” and argue that “Microevolution does not explain speciation — only smaller changes.”

But clearly they share a critical perspective on neo-Darwinism that is very similar to that of the intelligent design community. Consider this striking passage:

> Survival of the fittest is adequate to select for such changes (gains) which occur within one genome primarily by single fixed mutations (and perhaps sometimes by horizontal gene transfer). Macroevolution, however, requires major changes necessitating multiple changes that logically most frequently occur in multiple genomes. Therefore, the concept survival of the fittest is inadequate to conserve individual changes in multiple genomes where the individual changes generate no increased fitness. … Thus, survival of the fittest is illogical when proposed as adequate for selecting the origination of all complex, major, new body-types and metabolic functions because the multiple changes in multiple genomes that are required have intermediate stages without advantage; selection would not reasonably occur, and disadvantage or death would logically prevail.

What they are saying is that when some feature requires multiple changes before providing an increase in fitness, the changes cannot be produced by mutation and selection alone. Their subsequent comments, read carefully, almost sound like an implicit endorsement of intelligent design:

> It is our perspective that the burden is too great for survival of the fittest to select evolutionary changes that accomplish all evolutionary novelty. Thus, evolution lacks a sufficient mechanism for multifactorial selections because a process that looks forward, is nonrandom, deterministic, or occurs by an unknown biological process, is required. The position of mainstream biologists regarding this aspect of evolution is that nature is always non-purposeful and, therefore, the proposed selection (process, force, tendency), could not possibly be natural (scientific). However, our perspective is that this is a supposition of necessity rather than an established principle. Logic demands that it be open to investigation. This first requires an openness to ideas and science must be open to new ideas.

They thus propose that evolution is only possible if it is “nonrandom, deterministic, or occurs by an unknown biological process” — something that some would reluctantly conclude “could not possibly be natural.” They continue:

> Darwin wrote in *On the Origin of Species*… : "If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down. But I can find out no such case." Today, Darwin's missing cases are abundant including each complex transition to a new body type, metabolic cycle, or metabolic chain. Multi-step processes are routinely required at every evolutionary step.

They then perform a probability calculation which shows that the likelihood of producing a necessary pathway would require such multi-step processes leading to probabilities below the plausibility bound they had previously set.

They use a case study of the origin of the Krebs cycle — a metabolic pathway involving 12 enzymes that is necessary for life. They believe that this is a useful test for evolution. They assume that the genome is "ripe" to produce each enzyme where a minimal number of mutations is needed for a gene to suddenly become functional. They therefore choose an incredibly generous value of 0.00001 as the probability that a given enzyme can be created by a single mutation.

They calculate the likelihood of producing all 12 enzymes needed to produce a selectable function as 10^{-51}. They note this is below 10^{-50}, a probability that was called "negligible" by French mathematician Émile Borel, who stated that "this process of evolution involves certain properties of living matter that prevent us from asserting that the process was accomplished in accordance with the laws of chance."

They also reject co-option and exaptation as possible explanations for the origin of the Krebs cycle:

> The idea that the complete, functioning Krebs cycle arose by purloining each intermediate step from other uses (Meléndez-Hevia, 1996) lacks empirical support. The discoveries that genes can be switched on and off, that codes read forward and backward, gene duplication, and the homeobox, are helpful but inadequate to save evolutionary theory without modification.

In the end, producing a complex feature like the Krebs cycle is just too improbable because "Selection based on survival of the fittest, for anything beyond single mutational changes in a genome, is insufficient scientifically and biologically." They conclude, "[T]here is something besides mutations and survival of the fittest needed to explain evolution."

- **David W. Snoke, "Spontaneous Appearance of Life and the Second Law of Thermodynamics," *BioCosmos*, 2 (1): 1-11 (2022).**
  This peer-reviewed article employs thermodynamic principles to critique claims that life originated from undirected physical processes. The author, David Snoke, is an ID-friendly professor of physics at the University of Pittsburgh. He defines entropy in terms of the number of microstates (i.e., specific arrangements of molecules in a system) that correspond to a macrostate (i.e., categorization of a set of microstates such as liquid water). Closed systems tend to transition from states of higher entropy to states of lower entropy. But this trend can be reversed if some "information processing system" selects a subset of states.

Snoke defines such a system as an engine. Life can maintain highly ordered states because it contains molecular machines that act as engines that harness the energy from concentration gradients and then direct it toward specified biological processes. Such engines do not violate the second law of thermodynamics because they represent low-entropy states. He then connects this insight to the origin of life by noting that the probability of engines spontaneously forming in a prebiotic setting is as improbable as a cell forming spontaneously without the engines due to both representing extremely low entropy states.

Snoke then addresses self-organizational processes that are purported to have generated living systems. He notes that the order such processes achieve, such as roll patterns (aka convection cells) in boiling water, corresponds to patterns with the natural length scales of the system. A self-organizational process acts like an information processing system, but it is only processing one bit of information. In the case of the roll patterns, the pattern only appears when the temperature crosses a threshold. The one bit corresponds to the yes/no answer to the question of when the temperature has exceeded the threshold. The challenge for life's origin is that cellular processes operate at multiple length scales and require vast amounts of information. Physical laws do not contain anywhere near the required amount to explain life's origin. Snoke summarizes this conclusion as follows:

> To make spontaneous information processing with additional bits, one must create a system with two, three, and more natural length scales analogous to the single natural length scale of convection cells discussed here. While such might be accomplished in the lab by carefully designed processes, for it to occur in nature would require that the laws of nature have multiple natural length scales written into them which can play the same role as gravity in a convection chamber, but which are different from gravity. While the convection chamber does show spontaneous information processing, it has exhausted all of the front-loaded resources it has, and cannot generate any more degrees of freedom for triggered macroscopic responses.

- **Gregory D. Sloop, "The Cardiovascular System of Antarctic Icefish Appears to Have Been Designed to Utilize Hemoglobinless Blood,"** ***BIO-Complexity*****, 2022: 2 (2022).**
  This peer-reviewed paper investigates the origin of fish species that live in extremely cold Antarctic waters. The paper argues that, "The circulatory system of Antarctic icefish may have been designed to prevent high blood viscosity at low temperatures by taking advantage of the increased solubility of oxygen at low temperatures, allowing use of hemoglobin-free blood." The author, medical researcher Gregory Sloop, argues that this complex system "could not have evolved via a series of gradual steps" because:

  > The hemoglobinless phenotype requires simultaneous customization of the heart, vasculature, and blood, including its viscosity. Simultaneous, coordinated acquisition of multiple unique features, as required by the absence of hemoglobin, is inconsistent with Darwinian evolution, which postulates that species develop by small, incremental changes over time.

  When liquids become cold they tend to become more viscous. Sloop observes, however, that "the viscosity of icefish blood at its native temperature, approximately 0°C, is very similar to that of human blood at 37°C." Fish that lives in very cold waters, such as Antarctic icefish, must therefore solve a problem: How are they able to pump blood through their bodies at such low temperatures?

One way that Antarctic icefish solve the problem is by having no erythrocytes (red blood cells) in their blood. So how do they deliver oxygen throughout their bodies? Some believe it's due to nitrous oxide (NO) dissolved in the bloodstream, which actually causes hypoxia in icefish tissues. But Sloop maintains that it is thanks to "a customized cardiovascular system [rather] than a conventional one that was pressed into service when a mutation caused the loss of hemoglobin expression." Some of these "cardiovascular customizations" include:

- Solubility of O_2 increases with lower temperature, allowing the blood to carry more O_2 at such a low temperature.
- Increased cardiac output.
- A special "high-output, low resistance circulation" where "trunk skeletal muscle capillaries are two to three times greater in diameter than those of typical teleosts, reducing vascular resistance" and "Icefish retinas are more densely vascularized than those of red-blooded notothenioids, increasing O_2 delivery to this metabolically active tissue."
- This larger cardiac output and special vasculature require "a blood volume two to four times greater than that of red-blooded fish" which "in turn requires a customized heart that is heavier and has a larger stroke volume than that of red-blooded notothenioids." As a result, "stroke volume of the icefish heart is 6 to 15 times greater than in other teleosts."
- To sustain this larger heart, special heart contractile cells called "cardiomyocytes" are in the icefish "relatively large and contain a relatively large number of mitochondria." Indeed, in one icefish species the percent of cardiomyocytes devoted to mitochondria are "the highest in any teleost and higher than in any vertebrate except for the Etruscan shrew."
- Special kidneys to accommodate the low-pressure blood circulation.
- Special "corpuscle" blood cells unique to icefish which convert carbon dioxide and water into carbonic acid.

The effect of all of these special features is to allow Antarctic icefish to have lower hematocrits (the percent volume used by red cells in the blood), which lowers blood viscosity, making it easier for the fish's heart to pump blood under such cold conditions. Sloop concludes:

> The customized icefish heart, vasculature, and blood form a system with mutually dependent parts. … The hemoglobinless phenotype requires simultaneous, coordinated acquisition of multiple unique features. This is difficult to explain with Darwinian evolution, which postulates that species develop by small, incremental changes over long periods. … Multiple customized components are necessary to utilize hemoglobinless blood. Actualizing the design for the icefish cardiovascular system requires each customized component to be in place simultaneously. This is more innovation than can be accomplished by random mutation as postulated in Darwinian evolution.

Sloop offers this potent observation: "Proponents of intelligent design see customizations to decrease blood viscosity as examples of teleology in biology."

- **David W. Swift, "The Diverse Early Embryonic Development of Vertebrates and Implications Regarding Their Ancestry,"** ***BIO-Complexity*****, 2022: 1 (2022).**
  Evolutionary biologists often argue that vertebrate embryos develop in highly similar manners, reflecting their common ancestry. This peer-reviewed paper shows that despite common claims and the predictions of evolution, vertebrates do not develop similarly:

  > It is well known that the embryonic development of vertebrates from different classes (e.g., fish, reptiles, mammals) pass through a "phylotypic stage" when they look similar, and this apparent homology is widely seen as evidence of their common ancestry. However, despite their morphological similarities, and contrary to evolutionary expectations, the phylotypic stages of different vertebrate classes arise in radically diverse ways. This diversity clearly counters the superficial appearance of homology of the phylotypic stage, and the plain inference is that vertebrates have not evolved from a common vertebrate ancestor. The diversity extends through all stages of early development — including cleavage and formation of the blastula, gastrulation, neurulation, and formation of the gut and extraembryonic membranes.

  Intelligent design does not require common ancestry to be false, but even a guided form of common ancestry might lead to different predictions from strictly unguided descent with modification. Thus, Darwin and subsequent evolutionists such as Ernst Haeckel found embryology to be a crucial line of evidence supporting Darwin's thesis. According to the author, common ancestry predicts that vertebrate development should exhibit striking homologies. But more than that, "If common ancestry is the explanation for homologies, not only should homologous organs be derived from equivalent embryonic tissues (the cardinal criterion for homology) but they should also develop by comparable processes."

  The paper argues that although vertebrate embryos do pass through a similar "phylotypic stage," the pathways of development are very different:

  > [D]espite their morphological similarities and contrary to evolutionary expectations, the striking fact is that the "phylotypic stages" of different groups of vertebrates arise in remarkably diverse ways, even with key tissues such as the germ layers (see below) deriving from completely different early embryonic sources. These observations clearly refute the presumed evolutionary homology of the vertebrate phylotypic stage, and hence undermine the inference of common ancestry based on that supposed homology.

  He reprints the "hourglass model" of vertebrate development and points out that this is merely an "observation" about development — not an explanation of how it arose. One of the key stages of development that leads to this similar "phylotypic stage" is gastrulation, which is crucial because it establishes the basic body plan and "leads to the establishment of the germ layers — ectoderm, mesoderm and endoderm — from which all of the body's tissues are derived."

  The author cites various specific differences in vertebrate development, especially in gastrulation: "from an evolutionary perspective we would surely expect gastrulation to be 'conserved'" but "for almost all of the major classes of vertebrates" there are key differences in gastrulation, including “the mechanism of gastrulation is significantly different from any of the others,” and “the source tissues of the germ layers are different.”

After reviewing mechanisms of gastrulation in various vertebrate classes, the author notes that “the wide variety of structures of the blastulas of different classes of vertebrate challenges the view that the resultant embryonic tissues can be considered equivalent or homologous.” Specifically, in different types of vertebrates, different parts of the blastula ultimately become the embryo itself. He describes these differences as follows:

- Chondrichthyans (lancelets): “It is a one-cell thick epithelial layer, forming the upper surface of the blastula.”
- Teleosts (bony fish, e.g., zebrafish): “It is a multiple-cell layer, beneath the overlying enveloping layer.”
- Amphibians: “It is the whole of the blastula, comprising the multilayered dome of the upper hemisphere and the mass of cells in the lower hemisphere.”
- Reptiles and birds: “It is the upper surface of the blastula, comprising a single-cell thick epithelial layer, overlying the hypoblast.”
- Placental mammals (e.g., primates): “It is part of the inner cell mass, within the outer trophoblast.”

The author cites further differences between which cells become the endoderm and which become the mesoderm, noting:

- in amniotes (reptiles, birds, mammals) cells that are internalized arise from a central area of the epiblast, i.e., the presumptive endoderm and mesoderm are surrounded by presumptive ectoderm; whereas
- in anamniotes (chondrichthyans, teleosts, amphibians) the cells that internalize are from the edge of the epiblast, i.e., the presumptive endoderm and mesoderm surround the presumptive ectoderm.

The author summarizes major differences in the mechanisms of gastrulation as follows:

- Chondrichthyans: by cells rolling over a posterior overhang of the epiblast.
- Teleosts: by involution around the edges of the epiblast as it spreads around the yolk.
- Amphibians: by involution through an annular blastopore.
- Reptiles: by involution through a canal-like blastopore.
- Birds: by cells ingressing through a primitive streak, formation of the primitive streak being accompanied by growth of an underlying endoblast.
- Placental mammals: by cells ingressing through a primitive streak.

These diverse modes of development cannot be considered homologous:

> In the light of these three substantial distinctions — the different overall structure of the blastulas, the different parts of the blastula that become the embryo, and the different relative positions of the presumptive ectoderm and mesoderm/endoderm in amniotes and anamniotes — there is no doubt that the tissues that become the embryo

> are not equivalent, and hence are far from being homologous across the various vertebrate classes.

According to Swift, these fundamental differences in early vertebrate mechanisms of development during gastrulation suggest that vertebrates do not share a common ancestry:

> The straightforward conclusion to draw from this radical diversity of their early embryonic development is that it shows the vertebrates have not evolved from a common vertebrate ancestor. This conclusion can be avoided only if there are credible explanations for how such diversity of early development might have arisen from the development prevailing in a common ancestor (whether or not similar to present-day cephalochordates) in an evolutionary way, via changes that (i) had a realistic probability of occurring, (ii) maintained viability, and (iii) offered, in most cases, significant advantage that could be favored by natural selection.

Meeting these evolutionary requirements poses a great challenge, however. The paper quotes developmental biologist Rudolf Raff: "One might reasonably expect mechanisms of early development to be especially resistant to modification because all subsequent development derives from early processes." The author calls this a "common-sense conclusion" because the complexity of vertebrate development demands that many coordinated modifications would be required to fundamentally change how development proceeds. The paper thus finds that "because of the interdependence of the mechanisms that are involved, constructive changes to embryonic development must entail coordinated production of and/or changes to several genes, e.g., for transcription factors and the DNA sequences on which they act, which is prohibitively improbable."

This evidence leads to a "waiting time" problem where multiple coordinated change would be required to transition from one developmental regime to another, posing "a formidable challenge to supposed evolutionary scenarios" as generating these changes would be "generally far in excess of the time available."

- **Samuel Haug, Robert J. Marks, and William A. Dembski, "Exponential Contingency Explosion: Implications for Artificial General Intelligence,"** ***IEEE Transactions on Systems, Man, and Cybernetics: Systems*****, 52 (5): 2800-2808 (2022).**
  Robert Marks and William Dembski are design theorists who have published numerous articles related to design detection and the limitations of evolutionary searches. This article illustrates how the number of operational uncertainties in a highly integrated complex system increases exceedingly rapidly with the number of internal and environmental variables. Consequently, the number of ways a complex system can fail, and thus the difficulty of designing it, also grows with increasing contingencies very rapidly. They applied their analysis to human designed systems, but it also directly applies to biological systems demonstrating the implausibility of their having originated through an undirected process. The authors summarize their work as follows:

  > The failure of complex artificial intelligence (AI) systems seems ubiquitous. To provide a model to describe these shortcomings, we define complexity in terms of a system's sensors and the number of environments or situations in which it performs. The complexity is not looked at in terms of the difficulty of design, but in the final performance of the system. As the complexity of AI, or any system, increases linearly

> the contingencies increase exponentially and the number of possible design performances increases as a compound exponential. In this worst case scenario, the exponential increase in contingencies makes the assessment of all contingencies difficult and eventually impossible.

The article models a complex system in terms of the number of its sensors, A, the number of sensor readings, s, and the number of performance or design rankings, C. The minimum number of possible designs, Y, is then,

$$Y = C^{s^A}$$

At least one design corresponds to one set of sensor readings and performance rankings. Only one design will operate at the highest performance for all possible sensor readings.

The authors illustrated their methodology with the example of a washing machine that has two sensors ($A = 2$) that each register two readings ($s = 2$):

Weight = (light, heavy) = (0, 1),
Turbidity = (mild, dirty) = (0, 1).

The washing machine can operate in four states or contingencies, x_i, corresponding to the sensor readings. A heavy load with mild turbidity would be $x_3 = (1, 0)$. Each contingency could correspond to two possible design rankings ($C = 2$): (failure, success) = (0, 1). Each of the 16 (2^{2^2}) designs corresponds to the performance for a set of readings (see Table 1). For instance, design y_7 corresponds to failure for light, mild loads, $x_1 = (0, 0)$, and success for all other contingencies: x_2, x_3, and x_4.

The challenge is that the number of design possibilities grows dramatically with increasing number of contingencies. Designing a system to operate properly in all situations quickly becomes an intractable problem. The challenge becomes even greater when a system must function in different environmental conditions.

In addition, designers often do not anticipate all the important contingencies. Such oversights are why AI systems often fail when initially launched. For instance, early self-driving cars mistook plastic bags for rocks, resulting in improper responses. The authors conclude by describing how these challenges can be mitigated by such strategies as designing components to operate more independently, adding redundancies, and differentiating tolerable failures from intolerable failures. The authors summarize their conclusions as follows:

> Increasing complexity increases operational contingencies. We can reasonably expect the increase in the number of contingencies will contain unexpected contingencies ranging from the annoying to the highly serious. The worst case of contingency growth is a highly connected, or conjunctive, system where the contingencies grow exponentially with respect to an increase in complexity. On the other end is the loosely connected disjunctive system where an increase in the number of sensors yields a linear increase in contingency count.

Such analyses help us to better understand the nature of designed systems and how designed systems must navigate constraints.

- **Ola Hössjer, Günter Bechly, and Ann Gauger, "On the waiting time until coordinated mutations get fixed in regulatory sequences,"** ***Journal of Theoretical Biology*****, Vol. 524: 110657 (2021).**
  This peer-reviewed paper in the *Journal of Theoretical Biology* is authored by three scientists who are part of the "Waiting Times" project. This project investigates a question of key interest to the theory of intelligent design: *How long does it take for traits to evolve when multiple mutations are required to give an advantage?* The paper opens by observing that "A classical problem of population genetics is to study the time until new genetic variants first appear through germline mutations and then get fixed, i.e. spread to all individuals of a species, as it adapts to a new environment and evolves over time." It notes that in previous studies, "analyzing evolution of whole DNA sequences of nucleotides of length L, written on the four letter alphabet A, C, G, T," the waiting time where each is neutral (i.e., gives no selective advantage) "increases either polynomially or exponentially with L."

  This paper develops a complex mathematical model for calculating the waiting time for the evolution of a trait that requires L nucleotides in order to function. Although this is strictly a methodological paper, one potential application could be the evolution of regulatory regions which control the expression of a gene. Changes to transcription are thought to be important to evolving new body plans or biological systems. Regulatory regions such as enhancers or promoters may have a length of 1000 nucleotides, and for expression to occur special proteins called transcription factors must bind to these regulatory regions at binding sites, which may be 6 to 10 nucleotides in length. They explain how this works:

  > The waiting time until the expression of the gene changes, is modeled as the time until the random walk hits the target, and it depends on the mutation rate, the selective advantage of the mutated regulatory sequence, the size of the population, the length of the regulatory sequence and the length of the binding site.

  However, evolving new traits is often far more complex than simply changing the expression of a single gene. Many traits are controlled by multiple genes, and the traits won't arise until expression of those genes is modified in a coordinated manner. The paper explains how their model might be applied to such an evolutionary question:

  > For more complex adaptations of a species, it is necessary that several genes are modified in a coordinated manner, either through mutations in the coding sequence, or through changed expression of these *m* genes. … In this paper we focus on the coordinated evolution of gene expression of existing genes, and ask the question how long time T_m it would take for a species to change the expression of *m* distinct genes. This corresponds to the time it would take for the required binding sites, in the regulatory sequences of *m* distinct genes, to evolve in a coordinated way. The microevolutionary process is then a random walk on a fitness landscape of regulatory arrays, that is, a random walk on *m* x *L* matrices, whose rows are the regulatory sequences of all *m* genes.

  The paper calculates how long it would take for m genes to evolve new regulatory sequences by chance, assuming that such changes in the expression of all of these genes would be required for some new complex adaptation to arise.

The introduction provides a rich review of examples of abrupt appearance from biological history, showing that their model is highly applicable to biological reality:

> For instance, the fossil record is often interpreted as having long periods of stasis, interrupted by more abrupt changes and "explosive" origins. These changes include, for instance, the evolution of life, photo-synthesis, multicellularity and the "Avalon Explosion", animal body plans and the "Cambrian Explosion", complex eyes, vertebrate jaws and teeth, terrestrialization (e.g., in vascular plants, arthropods, and tetrapods), insect metamorphosis, animal flight and feathers, reproductive systems, including angiosperm flowers, amniote eggs, and the mammalian placenta, echolocation in whales and bats, and even cognitive skills of modern man. Based on radiometric dating of the available windows of time in the fossil record, these genetic changes are believed to have happened very quickly on a macroevolutionary timescale. In order to evaluate the chances for a neo-Darwinian process to bring about such major phenotypic changes, it is important to give rough but reasonable estimates of the time it would take for a population to evolve so that the required multiple genetic changes occur.

Many complex features of living organisms appear abruptly in the fossil record, where it seems that multiple coordinated changes were necessary before any advantageous functional trait arose. The mathematical model developed in this paper is aptly suited to addressing whether neo-Darwinian mechanisms can explain the origin of complex biological features.

- **Steinar Thorvaldsen and Ola Hössjer, "Using statistical methods to model the fine-tuning of molecular machines and systems," *Journal of Theoretical Biology*, 501: 110352 (September 21, 2020).**

This paper represents an expressly pro-intelligent design approach, published in a major peer-reviewed journal, *The Journal of Theoretical Biology.* The authors are Steinar Thorvaldsen, a professor of information science at the University of Tromsø in Norway, and Ola Hössjer, a professor of mathematical statistics at Stockholm University. The paper begins by noting that while fine-tuning is widely discussed in physics, it needs to be considered more in the context of biology:

> Fine-tuning has received much attention in physics, and it states that the fundamental constants of physics are finely tuned to precise values for a rich chemistry and life permittance. It has not yet been applied in a broad manner to molecular biology.

The authors explain the paper's main thrust:

> [I]n this paper we argue that biological systems present fine-tuning at different levels, e.g. functional proteins, complex biochemical machines in living cells, and cellular networks. This paper describes molecular fine-tuning, how it can be used in biology, and how it challenges conventional Darwinian thinking. We also discuss the statistical methods underpinning finetuning and present a framework for such analysis.

They then explain how fine-tuning is defined. The definition is essentially equivalent to specified complexity:

> We define fine-tuning as an object with two properties: it must a) be unlikely to have occurred by chance, under the relevant probability distribution (i.e. complex), and b) conform to an independent or detached specification (i.e. specific).

Next, they explicitly introduce the concept of "design," and explain how humans are innately able to recognize it:

> A design is a specification or plan for the construction of an object or system, or the result of that specification or plan in the form of a product. The very term design is from the Medieval Latin word "designare" (denoting "mark out, point out, choose"); from "de" (out) and "signum" (identifying mark, sign). Hence, a public notice that advertises something or gives information. The design usually has to satisfy certain goals and constraints. It is also expected to interact with a certain environment, and thus be realized in the physical world. Humans have a powerful intuitive understanding of design that precedes modern science. Our common intuitions invariably begin with recognizing a pattern as a mark of design. The problem has been that our intuitions about design have been unrefined and pre-theoretical. For this reason, it is relevant to ask ourselves whether it is possible to turn the tables on this disparity and place those rough and pre-theoretical intuitions on a firm scientific foundation.

That last sentence is key: the purpose is to understand if there is a scientific method by which design can be inferred. They propose that design can be identified by uncovering fine-tuning. The paper explicates statistical methods for understanding fine-tuning, which they argue reflects "design":

> Fine-tuning and design are related entities. Fine-tuning is a bottom-up method, while design is more like a top-down approach. Hence, we focus on the topic of fine-tuning in the present paper and address the following questions: Is it possible to recognize fine-tuning in biological systems at the levels of functional proteins, protein groups and cellular networks? Can fine-tuning in molecular biology be formulated using state of the art statistical methods, or are the arguments just "in the eyes of the beholder"?

They cite the work of multiple leading theorists in the ID research community, and return to physics and the "anthropic principle," the idea that the laws of nature are precisely suited for life:

> Suppose the laws of physics had been a bit different from what they actually are, what would the consequences be? (Davies, 2006). … The chances that the universe should be life permitting are so infinitesimal as to be incomprehensible and incalculable. … The finely tuned universe is like a panel that controls the parameters of the universe with about 100 knobs that can be set to certain values. … If you turn any knob just a little to the right or to the left, the result is either a universe that is inhospitable to life or no universe at all. If the Big Bang had been just slightly stronger or weaker, matter would not have condensed, and life never would have existed. The odds against our universe developing were "enormous" – and yet here we are, a point that equates with religious implications…

However, rather than getting into religion, they apply statistics to consider the possibility of "design" as an explanation for the fine-tuning of the universe. The authors cite ID theorist William Dembski:

> William Dembski … regards the fine-tuning argument as suggestive, as pointers to underlying design. We may describe this inference as abductive reasoning or inference to the best explanation. This reasoning yields a plausible conclusion that is relatively likely to be true, compared to competing hypotheses, given our background knowledge. In the case of fine-tuning of our cosmos, design is considered to be a better explanation than a set of multi-universes that lacks any empirical or historical evidence.

The article offers additional reasons why the multiverse is an unsatisfying explanation for fine-tuning — namely that "multiverse hypotheses do not predict fine-tuning for this particular universe any better than a single universe hypothesis" and "we should prefer those theories which best predict (for this or any universe) the phenomena we observe in our universe."

The paper reviews the lines of evidence for fine-tuning in biology, including information, irreducible complexity, protein evolution, and the "waiting-time problem." Along the way it considers the arguments of many ID theorists, starting with a short review showing how the literature uses words such as "sequence code," "information," and "machine" to describe life's complexity:

> One of the surprising discoveries of modern biology has been that the cell operates in a manner similar to modern technology, while biological information is organized in a manner similar to plain text. Words and terms like "sequence code", and "information", and "machine" have proven very useful in describing and understanding molecular biology (Wills, 2016). The basic building blocks of life are proteins, long chain-like molecules consisting of varied combinations of 20 different amino acids. Complex biochemical machines are usually composed of many proteins, each folded together and configured in a unique 3D structure dependent upon the exact sequence of the amino acids within the chain. Proteins employ a wide variety of folds to perform their biological function, and each protein has a highly specified shape with some minor variations.

The paper cites and reviews the work of ID theorists Michael Behe, Douglas Axe, Stephen Meyer, and Günter Bechly. Some of these discussions are extensive. First, the article contains a lucid explanation of irreducible complexity and the work of Michael Behe:

> Michael Behe and others presented ideas of design in molecular biology, and published evidence of "irreducibly complex biochemical machines" in living cells. In his argument, some parts of the complex systems found in biology are exceedingly important and do affect the overall function of their mechanism. The fine-tuning can be outlined through the vital and interacting parts of living organisms. In "Darwin's Black Box" (Behe, 1996), Behe exemplified systems, like the flagellum bacteria use to swim and the blood-clotting cascade, that he called irreducibly complex, configured as a remarkable teamwork of several (often dozen or more) interacting proteins. Is it possible on an incremental model that such a system could evolve for something that does not yet exist? Many biological systems do not appear to have a functional viable predecessor from which

> they could have evolved stepwise, and the occurrence in one leap by chance is extremely small. To rephrase the first man on the moon: “That’s no small steps of proteins, no giant leap for biology.”
>
> […]
>
> A Behe-system of irreducible complexity was mentioned in Section 3. It is composed of several well-matched, interacting modules that contribute to the basic function, wherein the removal of any one of the modules causes the system to effectively cease functioning. Behe does not ignore the role of the laws of nature. Biology allows for changes and evolutionary modifications. Evolution is there, irreducible design is there, and they are both observed. The laws of nature can organize matter and force it to change. Behe’s point is that there are some irreducibly complex systems that cannot be produced by the laws of nature:
>
> “If a biological structure can be explained in terms of those natural laws [reproduction, mutation and natural selection] then we cannot conclude that it was designed. . . however, I have shown why many biochemical systems cannot be built up by natural selection working on mutations: no direct, gradual route exist to these irreducible complex systems, and the laws of chemistry work strongly against the undirected development of the biochemical systems that make molecules such as AMP1” (Behe, 1996, p. 203).
>
> Then, even if the natural laws work against the development of these ‘‘irreducible complexities”, they still exist. The strong synergy within the protein complex makes it irreducible to an incremental process. They are rather to be acknowledged as finetuned initial conditions of the constituting protein sequences. These structures are biological examples of nano-engineering that surpass anything human engineers have created. Such systems pose a serious challenge to a Darwinian account of evolution, since irreducibly complex systems have no direct series of selectable intermediates, and in addition, as we saw in Section 4.1, each module (protein) is of low probability by itself.

The article also reviews the peer-reviewed research of protein scientist Douglas Axe, as well as his 2016 book *Undeniable*, on the evolvability of protein folds:

> An important goal is to obtain an estimate of the overall prevalence of sequences adopting functional protein folds, i.e. the right folded structure, with the correct dynamics and a precise active site for its specific function. Douglas Axe worked on this question at the Medical Research Council Centre in Cambridge. The experiments he performed showed a prevalence between 1 in 1050 to 1 in 1074 of protein sequences forming a working domain-sized fold of 150 amino acids (Axe, 2004). Hence, functional proteins require highly organised sequences, as illustrated in Fig. 2. Though proteins tolerate a range of possible amino acids at some positions in the sequence, a random process producing amino-acid chains of this length would stumble onto a functional protein only about one in every 1050 to 1074 attempts due to genetic variation. This empirical result is quite analog to the inference from fine-tuned physics.
>
> […]

> The search space turns out to be too impossibly vast for blind selection to have even a slight chance of success. The contrasting view is innovations based on ingenuity, cleverness and intelligence. An element of this is what Axe calls ‘‘functional coherence”, which always involves hierarchical planning, hence is a product of finetuning. He concludes: ‘‘Functional coherence makes accidental invention fantastically improbable and therefore physically impossible” (Axe, 2016, p. 160).

They conclude that the literature shows “the probability of finding a functional protein in sequence space can vary broadly, but commonly remains far beyond the reach of Darwinian processes (Axe, 2010a).”

Citing the work of Günter Bechly and Stephen Meyer, the paper also reviews the question of whether sufficient time is allowed by the fossil record for complex systems to arise via Darwinian mechanisms. This is known as the “waiting-time problem”:

> **Achieving fine-tuning in a conventional Darwinian model: The waiting time problem**
> In this section we will elaborate further on the connection between the probability of an event and the time available for that event to happen. In the context of living systems, we need to ask the question whether conventional Darwinian mechanisms have the ability to achieve fine-tuning during a prescribed period of time. This is of interest in order to correctly interpret the fossil record, which is often interpreted as having long periods of stasis interrupted by very sudden abrupt changes (Bechly and Meyer, 2017). Examples of such sudden changes include the origin of photosynthesis, the Cambrian explosions, the evolution of complex eyes and the evolution of animal flight. The accompanying genetic changes are believed to have happen very rapidly, at least on a macroevolutionary timescale, during a time period of length t. In order to test whether this is possible, a mathematical model is needed in order to estimate the prevalence P(A) of the event A that the required genetic changes in a species take place within a time window of length t.

Lastly, the authors consider intelligent design as a possible explanation of biological fine-tuning, citing heavily the work of William Dembski, Winston Ewert, Robert J. Marks, and other ID theorists:

> Intelligent Design (ID) has gained a lot of interest and attention in recent years, mainly in USA, by creating public attention as well as triggering vivid discussions in the scientific and public world. ID aims to adhere to the same standards of rational investigation as other scientific and philosophical enterprises, and it is subject to the same methods of evaluation and critique. ID has been criticized, both for its underlying logic and for its various formulations (Olofsson, 2008; Sarkar, 2011).
>
> William Dembski originally proposed what he called an ‘‘explanatory filter” for distinguishing between events due to chance, lawful regularity or design (Dembski, 1998). Viewed on a sufficiently abstract level, its logics is based on well-established principles and techniques from the theory of statistical hypothesis testing. However, it is hard to apply to many interesting biological applications or contexts, because a huge

number of potential but unknown scenarios may exist, which makes it difficult to phrase a null hypothesis for a statistical test (Wilkins and Elsberry, 2001; Olofsson, 2008).

The re-formulated version of a complexity measure published by Dembski and his coworkers is named Algorithmic Specified Complexity (ASC) (Ewert et al., 2013; 2014). ACS incorporates both Shannon and Kolmogorov complexity measures, and it quantifies the degree to which an event is improbable and follows a pattern. Kolmogorov complexity is related to compression of data (and hence patterns), but suffers from the property of being unknowable as there is no general method to compute it. However, it is possible to give upper bounds for the Kolmogorov complexity, and consequently ASC can be bounded without being computed exactly. ASC is based on context and is measured in bits. The same authors have applied this method to natural language, random noise, folding of proteins, images etc (Marks et al., 2017).

[…]

The laws, constants, and primordial initial conditions of nature present the flow of nature. These purely natural objects discovered in recent years show the appearance of being deliberately fine-tuned. Functional proteins, molecular machines and cellular networks are both unlikely when viewed as outcomes of a stochastic model, with a relevant probability distribution (having a small P(A)), and at the same time they conform to an independent or detached specification (the set A being defined in terms of specificity). These results are important and deduced from central phenomena of basic science. In both physics and molecular biology, fine-tuning emerges as a uniting principle and synthesis – an interesting observation by itself.

In this paper we have argued that a statistical analysis of fine-tuning is a useful and consistent approach to model some of the categories of design: ‘‘irreducible complexity” (Michael Behe), and ‘‘specified complexity” (William Dembski). As mentioned in Section 1, this approach requires a) that a probability distribution for the set of possible outcomes is introduced, and b) that a set A of fine-tuned events or more generally a specificity function f is defined. Here b) requires some apriori understanding of what fine-tuning means, for each type of application, whereas a) requires a naturalistic model for how the observed structures would have been produced by chance. The mathematical properties of such a model depend on the type of data that is analyzed. Typically a stochastic process should be used that models a dynamic feature such as stellar, chemical or biological (Darwinian) evolution. In the simplest case the state space of such a stochastic process is a scalar (one nucleotide or amino acid), a vector (a DNA or amino acid string) or a graph (protein complexes or cellular networks).

A major conclusion of our work is that fine-tuning is a clear feature of biological systems. Indeed, fine-tuning is even more extreme in biological systems than in inorganic systems. It is detectable within the realm of scientific methodology. Biology is inherently more complicated than the large-scale universe and so fine-tuning is even more a feature. Still more work remains in order to analyze more complicated data structures, using more sophisticated empirical criteria. Typically, such criteria correspond to a specificity function f that not only is a helpful abstraction of an underlying pattern, such as biological fitness. One rather needs a specificity function

> that, although of non-physical origin, can be quantified and measured empirically in terms of physical properties such as functionality. In the long term, these criteria are necessary to make the explanations both scientifically and philosophically legitimate. However, we have enough evidence to demonstrate that fine-tuning and design deserve attention in the scientific community as a conceptual tool for investigating and understanding the natural world. The main agenda is to explore some fascinating possibilities for science and create room for new ideas and explorations. Biologists need richer conceptual resources than the physical sciences until now have been able to initiate, in terms of complex structures having non-physical information as input (Ratzsch, 2010). Yet researchers have more work to do in order to establish fine-tuning as a sustainable and fully testable scientific hypothesis, and ultimately a Design Science.

This article represents a major achievement: it gives the arguments of intelligent design theorists a hearing in a prominent mainstream scientific journal. And don't miss the purpose of the article, which is stated in its final sentence — to work towards "establish[ing] fine-tuning as a sustainable and fully testable scientific hypothesis, and ultimately a *Design Science*." The authors present compelling arguments that biological fine-tuning cannot arise via unguided Darwinian mechanisms. Some explanation is needed to account for why biological systems "show the appearance of being deliberately fine-tuned." Despite the noise that often surrounds this debate, for ID arguments to receive such a thoughtful and positive treatment in a prominent journal is itself convincing evidence that ID has intellectual merit. Claims of ID's critics notwithstanding, design science is being taken seriously by scientists.

- **Stuart Burgess, "A review of linkage mechanisms in animal joints and related bioinspired designs,"** ***Bioinspiration & Biomimetics*****, 16: 041001 (2021).**
  This peer-reviewed paper by engineering professor Stuart Burgess analyzes 10 linkage mechanisms in animal joints and asks whether they contain design principle which could be mimicked through biomimetics to improve human technology. He chose animal joints such as fish jaws, knee joints, and bird wings due to their extraordinary performance. Burgess praises the optimality of animal joint design and notes the potential for bioinspiration from studying animal joints:

> Ten different linkage mechanisms are presented. They are chosen because they cover a wide range of functionality and because they have potential for bioinspired design. Linkage mechanisms enable animal joints to perform highly sophisticated and optimised motions. A key function of animal linkage mechanisms is the optimisation of actuator location and mechanical advantage. This is crucially important for animals where space is highly constrained. Many of the design features used by engineers in linkage mechanisms are seen in nature, such as short coupler links, extended bars, elastic energy storage and latch mechanisms. However, animal joints contain some features rarely seen in engineering such as integrated cam and linkage mechanisms, nonplanar four-bar mechanisms, resonant hinges and highly redundant actuators. The extreme performance of animal joints together with the unusual design features makes them an important area of investigation for bioinspired designs.

The first four-bar linkage mechanism discussed is the mammalian knee — a joint that has been criticized as poorly designed. Burgess is familiar with constraints and design trade-offs, and discusses mammalian knee requirements: it must provide a 120° range of motion, be load bearing, and prevent overextension. An inverted four-bar linkage mechanism fulfills all these requirements. It enables a large extension range, but also has an *end stop* which locks the knee and decreases the amount of work required by the muscles to stand erect. The broad area of contact between the femur and tibia loads can be transferred through the joint and bore. The four-bar mechanism allows the center of rotation to move, which reduces muscular effort.

The second four-bar linkage mechanism discussed is the bird wing joint. Burgess notes the brilliant engineering in the avian elbow joint which enables wing tucking and extension. The elbow wing joint decreases 12.3% of a bird's need for force during flapping, according to research done with seagulls.

Various flying insects generate lift by flapping and rotating their wings at steep angles. Flapping occurs at a frequency of 20 to 1000 flapping cycles per second, which requires highly efficient hinges. Burgess observes that many insect wings have a small bar as part of their four-bar wing mechanism which ends up magnifying the wing rotation. This means that even minor movements on the insect's body can cause a considerable angle of movement in the wing. Of course, the insect's body must be correctly built to allow such mobility. Burgess also points out that flapping happens at a resonant frequency, which reduces the inertial energy required to flap significantly. This is only feasible because of the insect's body architecture.

The paper also examines fish jaws. The sling-jawed wrasse can hurl their jaws to capture prey using a quick suction approach. This design also minimizes the amount of swimming because pushing the jaw forward requires significantly less energy than swimming forward when food is nearby.

Burgess also describes the four-bar linkage mechanism of the mantis shrimp, which punches to eat. The force is produced by a four-bar linkage mechanism connected to a biological battery. When the shrimp is ready to punch, it relaxes a muscle, the latch is released, and the accumulated elastic energy delivers 1000 N of force, which is several orders of magnitude larger than the weight of the organism.

To conclude, the amazing design structures in organisms provide templates of inspiration for creating better products. Burgess provides three specific examples where direct study might improve human technology, including:

1. Improved 3D modeling of avian wing joints has important implications for aircraft wing design.
2. Jaw mechanisms may result in new and improved designs for robotic clamping.
3. The punching mechanism of the mantis shrimp could inspire new technology in the field of industrial design.

By studying the intricacies of natural mechanisms like four bar linkages, scientists can gain valuable knowledge that can potentially enhance human engineering practices.

- **Waldean A. Schulz, "An Engineering Perspective on the Bacterial Flagellum: Part 1 — Constructive View,"** ***BIO-Complexity*****, 2021: 1 (2021).**
  This peer-reviewed paper by PhD engineer Waldean Schulz "examines the bacterial flagellum from an engineering viewpoint," which aims to concentrate on the "the structure, proteins,

control, and assembly of a typical flagellum, which is the organelle imparting motility to common bacteria." This technique of examining biology through the eyes of engineering is not new — systems biologists have been doing it for years. However, since engineering is a field that tries to determine how to better design technology, the field of intelligent design promises to yield new engineering-based insights into biology. Schulz's paper is a prime example of such a contribution, and it yields a rigorous logical demonstration of the irreducible complexity of the flagellum.

Intelligent design is fundamentally a goal-directed approach to studying natural systems, where the various parts and components biological organisms are coordinated to work together in the top-down manner of engineering. Schulz's paper thus takes a "constructive approach" which requires a "top-down specification." Schulz explains how this approach works:

> It starts with specifying the purpose of a bacterial motility organelle, the environment of a bacterium, its existing resources, its existing constitution, and its physical limits, all within the relevant aspects of physics and molecular chemistry. From that, the constructive approach derives the logically necessary functional requirements, the constraints, the assembly needs, and the hierarchical relationships within the functionality. The functionality must include a control subsystem, which needs to properly direct the operation of a propulsion subsystem. Those functional requirements and constraints then suggest a few — and only a few — viable implementation schemata for a bacterial propulsion system. The entailed details of one configuration schema are then set forth.

Schulz introduces engineering methodologies to study the flagellum, which flow naturally from of an ID paradigm. He writes:

> A common engineering methodology, called the Waterfall Model, first produces a formal Functional Requirements Specification document. Then a design is proposed in a System Design Specification, which must comport with the Requirements Spec. Typically this methodology is often accompanied by a Testing Specification, which measures how well the subsequently constructed system satisfies the requirements. This methodology was and is successfully applied at Intel, Image Guided Technologies, and Stryker. A similar specification method can be used by a patent agent or attorney in helping inventors clarify in detail what they have invented for a patent application.

When applying this method, one examines "overall purpose for the proposed system, the usage environment, necessary functionality, available materials, tools needed for construction, and various parameters and constraints (dimensions, form, cost, materials, energy needs, timing, costs, and other conditions)." After doing this, "a design is proposed that logically comports with those requirements."

Schulz then applies this method to the flagellum, asking *What are the requirements for bacterial motility?* Schulz proposes a design for the bacterial flagellum to fulfill these requirements of flagellar motility. Some of the following requirements must be met:

- "the propulsion subsystem needs a source of power to operate"
- "there must be a power-to-motion transducer"

- "there must be sensors to detect whether the propulsion system should move the bacterium forward … there must be some external member physically interacting with the environmental medium containing the bacterium."

Schulz considers different designs to fulfill the requirements and determines that a rotary engine is the ideal schematic. Schulz develops a dependency network for these requirements showing their "interdependency relationships" which addresses all of the above constraints, including the "purpose, environment, required functions, constraints, and the logically implied static, structural requirements." Schulz further lists various components and properties of the flagellum and the rationale for their inclusion in the system. He notes that although there are a couple of different ways to build the system, "In either case, the specified bacterial motility system would be irreducibly complex" and that the "intricate coherence" of all of the parts, systems, and design requirements of the flagellum "is essentially irreducible." He concludes:

> Current evolutionary biology proposes that the flagellum could have been "engineered" naturalistically by cumulative mutations, by horizontal gene transfer, by gene duplication, by co-option of existing organelles, by self-organization, or by some combination thereof. See the summary and references by Finn Pond. Yet to date, no scenario in substantive detail exists for how such an intricate propulsion system could have evolved naturalistically piece by piece. Can any partial implementation of a motility system be even slightly advantageous to a bacterium? Examples of a partial system might lack sensors, lack decision logic, lack control messages, lack a rotor or stator, lack sealed bearings, lack a rod, lack a propeller, or lack redirection means. Would such partial systems be preserved long enough for additional cooperating components to evolve?

That is the key question — to be explored in future papers that Schulz aims to publish. Based upon the "intricate coherence" and "irreducible complexity" of the numerous parts and properties of the flagellum, the answers to these questions would seem to be no.

- **Waldean A. Schulz, "An Engineering Perspective on the Bacterial Flagellum: Part 2 — Analytic View,"** ***BIO-Complexity*****, 2021: 2 (2021).**

  This second paper on the design of the flagellum by ID-friendly engineer Waldean Shulz takes a "bottom up" approach, and reviews "the known 40+ protein components and the observed and inferred structure, control, and assembly of a typical bacterial flagellum." He provides a clear diagram of an "archetypical flagellum," labeling features such as the motor stator, filament, hook, and rod. Schulz notes that the assembly process requires a regular set of components and procedures in order to work properly. He quotes Cohen *et al.* (2017) from *Science* who state that "The bacterial flagellum exemplifies a system where even small deviations from the highly regulated flagellar assembly process can abolish motility and cause negative physiological outcomes."

  Schulz further explains that these protein components themselves are fine-tuned such that "all proteins in each rotary subassembly need to (non-covalently) bind tightly to themselves and to the proteins of the adjacent subassemblies. This is noteworthy: the combinatorial configurations of the ensemble of proteins must be very specifically orchestrated."

Schulz considers not just the design and construction of the flagellum, but also the biochemical basis of chemotaxis, explaining the complexity, elegance, and control of the system. He also explores the mechanisms by which the flagellum generates torque to spin the filament. While this process is not fully understood, he notes that the power output of the motor "is nearly 100% efficient," and proposes that it involves proteins that effectively function as "gears." Schulz then turns to the assembly of the flagellum and notes that they have remarkably similar control across different species: "All flagellar systems coordinate flagellar gene expression through a transcriptional hierarchy central to an integrated regulatory network of multiple regulatory components. These networks exhibit a number of conserved circuit architectures reflective of the strong conservation found within the structural components of the flagellum." In a series of illustrations, he diagrams the flagellar assembly process through various pathways and at major stages in the production of various subcomponents. He notes that the complexity of the flagellum poses a challenge to evolutionary biologists:

> The future work for an evolutionary biologist is twofold: (1) to provide a detailed explanation for how all the tightly constrained interlocking coherence described above could have evolved stepwise and naturalistically under real-world constraints; (2) to show evidence that such a scenario actually occurred in the past.

Schulz finds that a step-by-step evolutionary pathway is unlikely:

> [T]he evolutionary biological community has yet to hypothesize a likely, detailed, step-by-step scenario to explain how the flagellum and its control system could have been blindly engineered naturalistically. Yet even that would still fall short of real evidence that such a thing actually happened, given real-world constraints. The flagellum seemingly is irreducible. How would portions of an incomplete, nascent flagellum be protected from degradation for generations while the remainder was yet to be gradually added? If some of the subassemblies discussed above could be omitted, what function would result?

Although Schulz notes that these are "hard" questions, he says they should not be dismissed: "These are real questions, and the challenge is to answer them." In the meantime, despite our lack of total knowledge, he concludes that a design-option should remain on the table: "it seems disingenuous to dismiss teleology and intelligent causation, when so much is already known about the apparently ingenious, coordinated hierarchical assembly, control, and function of the flagellum."

- **Waldean A Schulz, "An Engineering Perspective on the Bacterial Flagellum: Part 3 — Observations,"** ***BIO-Complexity*****, 2021: 3 (2021).**
  This final paper on the engineering design of the flagellum by ID-friendly engineer Waldean Schulz concludes that a system as complex as the flagellum "seems profoundly unlikely to naturally evolve in the absence of foresight and mindful intent." Schulz begins by listing the various parts of the flagellum, detailing their functional-mechanical-biochemical relationships. Schulz shows that not only must the necessary mechanical parts be present for the flagellum to function, but they must be designed to interact in a chemically and mechanically coordinated manner that allows the molecular machine to function. He then examines six specifications of flagellar components: (1) molecular structure, (2) flexibility, (3) temporary binding relationships, (4) non-attractiveness to particular components, (5) size tolerances, and (6) temporal accuracy

of final bonding relationships (i.e., binding at the right time). Schulz insightfully observes that each constraint that was identified in the top-down analysis has a corresponding part that was observed in the bottom-up analysis: “Clearly there is high correlation between the top-down and bottom-up perspective. What is the implication of this correlation? It suggests the configuration of the flagellum is purposeful.”

Schulz then presents unique observations about the flagellum from widely different perspectives: that of an inventor, an engineer, a molecular biologist, an evolutionist, and a philosopher.

As an experienced inventor, Schulz observes that “many patents have been awarded simply for novel proteins. Yet the design of a single protein involves far less intellectual content and originality than would be required to design a coherent complex of proteins self-assembling into an organelle. This exposes a certain irony: the intellectual input of inventors is recognized in a human-designed protein but not in a natural protein — or in a coherent subsystem of proteins composing an organelle like the flagellum.” This calls to mind a paradox: our legal system is well situated to detect design and does so every time a person is convicted of a crime, yet science often resists making design inferences. He argues that an engineer’s perspective helps detect design in the flagellum:

> [A]n experienced engineer would fully appreciate the mental effort, insightful creativity, inventive genius, and foresight that even a rather simple device requires. It begins with observing a need or problem, implying purposeful insight. That is followed by identifying the available resources (materials, tools, existing parts), necessary functions, normal environment, physical constraints, and so on. Then such factual input is followed by one or more design schemata. While numerous design options may be conceived, a very few fully comply with the foregoing requirements and constraints. This whole process requires significant mental effort and is far from trivial or accidental. Nevertheless, all that abstract specification still does not instantiate a physical entity.

What is needed is foresight and planning to convert the abstract specification into physical reality — the very process of intelligent design. Schulz covers the engineering process which must be used to design a flagellum. A blind trial and error search won’t work. He observes that engineers at “Microsoft, Apple, or Google would never — could never — produce specified software by any blind search.” Inventors and engineers appreciate that intelligence is a far more efficient search process than blind trial and error.

The molecular biologist is less concerned with origins than with how systems work. Schulz envisions the molecular biologist observing that “each of the structural proteins of each of the flagellum’s subassemblies requires an extremely precise molecular configuration in order to simultaneously comply with several very specific required properties.” Schulz then gives new perspectives on some of the constraints that flagellar proteins must meet:

- Binding strength to overcome molecular forces.
- Proper folded geometry to produce overall shape.
- Matching of proper parts for protein-protein mechanical interactions.
- Binding to neighbors.

As for the observations of an evolutionist, Schulz quotes Aizawa (2009) admitting — from an evolutionary perspective — the beautiful design of the flagellum:

> Since the flagellum is so well designed and beautifully constructed by an ordered assembly pathway, even I, who am not a creationist, get an awe-inspiring feeling from its 'divine' beauty…. However, if the flagellum has evolved from a primitive form, where are the remnants of its ancestor? Why don't we see any intermediate or simpler forms of flagella than what they are today? How was it possible that the flagella have evolved without leaving traces in history?

Yet Aizawa says the flagellum "has been streamlined by evolution to minimize the time of the assembly process" and "has acquired its beauty by evolving…" Schulz explains this paradox: Aizawa has a "philosophical prior commitment to Naturalism."

Schulz notes that natural selection can *optimize* features but not *innovate* new ones. Without intelligent guidance, blind selection often gets stuck on local fitness peaks and cannot always traverse to highly adapted features sitting on other adaptive peaks: "without intelligently chosen, appropriate starting values — or a more sophisticated, robust algorithm — simpler algorithms often converge to local, suboptimal values."

He further quotes Merino (2009) making the crucial observation that "Comparison of the complete genome sequences of flagellated bacteria revealed that flagellar structural proteins are based on an ancient core set of 24 flagella genes that were present in the common ancestor to all Bacteria." In other words, there seems to be an irreducibly complex core of protein components common to all bacteria and these pose a severe challenge to evolutionary explanations of the origin of the flagellum. Schulz appreciates the implications of this irreducibility of the flagellar system: "Two dozen genes require quite a few innovative origins lacking detailed explanations — origins presumably occurring nearly simultaneously."

There is still much to learn about the flagellum, but Schulz argues we can consider design: "it seems disingenuous to pretend that questions about intelligent causation are irrelevant and inconsequential when so much is already known about the hierarchical assembly, control, and function of the flagellum." He concludes: "A motility organelle of this scope and scale seems profoundly unlikely to naturally evolve in the absence of foresight and mindful intent."

- **William Basener, Salvador Cordova, Ola Hössjer, and John Sanford, "Dynamical Systems and Fitness Maximization in Evolutionary Biology," *Handbook of the Mathematics of the Arts and Sciences*, 2021: 1-72 (2021).**
  In this chapter published in a peer-reviewed book, the authors survey the history of attempts in evolutionary theory to prove that fitness continuously increases in a population. They describe the development of Fisher's theorem of natural selection that purportedly proved that expectation. They demonstrate how the conclusion was inaccurate due to false assumptions about the distribution of mutation's fitness effects. A more accurate model developed by Basener and Sanford employs more realistic assumptions and demonstrates that fitness typically decreases. This portion of the chapter repeats much of the content from Basener and Sanford's journal article "The Fundamental Theorem of Natural Selection with Mutations" in the *Journal of Mathematical Biology*, which is included in this document. Their analysis undermines a key pillar in evolutionary theory.

The authors also describe several other simulations and experiments that demonstrate that fitness does not constantly move toward a maximum. Instead, it often oscillates or declines due to such factors as epistasis, high rates of deleterious mutations, and linkages between genes. In addition, they outline the different types of simulations and how they test for different factors in different situations. And they detail the results of Lenski's long-term evolutionary experiment that demonstrated that natural selection acts most effectively when it is favoring mutations that degrade function, and cite Michael Behe's critique of this research published in *Quarterly Review of Biology* in 2010. The authors summarize their conclusions as follows:

> Natural selection and presumed fitness maximization have often been cited for why biological systems can maximize their performance — even approaching the absolute limits of physics as discussed in section "Maximization of Net Biological Function." Mathematical models of natural selection provide no pathway to maximize fitness measured as net biological functionality, and selection operates on the level of the whole organism, and so cannot maximize biological systems just above the atomic level. This problem is profound, and is compounded by the fact that when natural selection is most effective, it is most often reductive in nature, involving loss of function (Behe 2010). Therefore, it seems incredible that natural selection could maximize functionality and performance to the level observed in biological systems.

If random mutation and natural selection tends to degrade function, some other cause is needed to explain how new functions are generated.

- **Daniel Andrés Díaz Pachón and Robert Marks, "Active Information Requirements for Fixation on the Wright-Fisher Model of Population Genetics,"** ***BIO-Complexity*****, 2020: 6 (2020).**
  This peer-reviewed article demonstrates the value of the concept of active information. It also allows for the reliability of mathematical evolutionary models to be assessed by comparing the active information they introduce into evolutionary process to experimental observations.

  The authors apply the formalism of active information to population genetics to demonstrate how models that employ natural selection and mutations add active information into evolutionary processes. They begin by examining the probability generated by the Wright-Fisher model for different gene alleles appearing in subsequent generations with specific frequencies given no selection, selection, and mutations. They derive the active information in the context of finding a given target. The active information equals the Shannon information associated with finding the target with selection and mutations (if present) minus the Shannon information associated with the probability of finding the target in the neutral model. The active information can be positive, zero, or negative depending on the nature of the selection and mutations.

  Basener and Sanford 2018 (reviewed in his document) demonstrated that a modified version of the Wright-Fisher model that includes realistic proportions of deleterious mutations predicts that the average fitness of a population tends to decrease. This result is consistent with the current analysis that predicts that negative active information will result from deleterious mutations greatly outnumbering beneficial mutations. The negative active information results in evolutionary searches performing worse than random searches in finding targets, namely evolutionary improvements.

The authors summarize the significance of their results as follows:

> In summary, we see at least two things: First, selection does not act in the model as an innocuous force. Selection adds information. Second, since selection is an information source (and mutations when they are present), it is not a free lunch, and the information it adds is compounded by the population size. Our research stands alongside the work of Basener and Sanford who through alternative analysis have demonstrated the ineffectiveness of the Wright-Fisher model to create information ex-nihilo.

- **Daniel Andrés Díaz-Pachón and Robert J. Marks II, "Generalized Active Information: Extensions to Unbounded Domains," *BIO-Complexity*, 2020: 3 (2020).**
  This peer-reviewed paper explores the utility of active information, a concept developed by theorists of intelligent design to measure the efficiency of unintelligent search algorithms to find their targets. The authors first respond to a criticism of active information made by Olle Häggström, a Swedish mathematician who claimed that "there is absolutely no a priori reason to expect that the 'blind forces of nature' should produce a fitness landscape distributed [uniformly]." They reply by observing, "It is not that out-of-equilibrium explanations are not allowed, it is that they must be accounted for."

  They then explain that active information can help us detect instances where probabilities depart from expected uniform distributions:

  > Active information can be viewed as a generalized instantiation of anomaly detection otherwise known as novelty filtering. The status quo of probabilistic uniformity is set and any significant deviation is flagged as novel. The degree of deviation from normalcy is measured by the active information. … [A]ctive information is the difference of the information for an event under equilibrium and nonequilibrium.

  As they observe, "Active information can also be seen as a statistical complexity measure." That is because it meets criteria previously laid out by mathematicians for building such metrics, including the fact that "Active information determines the information gap between the search of a target by pure chance and the input of an expert/dumb programmer." In light of these results, they predict that active information can be applied to build a useful model of population genetics.

- **Guillermo Gonzalez, "The Solar System: Favored for Space Travel," *BIO-Complexity*, 2020: 1 (2020).**
  As outlined in the book *The Privileged Planet*, by Guillermo Gonzalez and Jay Richards, the Earth is not only fine-tuned for life, but is also well designed to allow us to make scientific discoveries. This peer-reviewed *BIO-Complexity* paper by Guillermo Gonzalez, "The Solar System: Favored for Space Travel," extends privileged planet arguments to our ability to travel in space.

  Many known exoplanets are "super-Earths," planets with a mass up to 10X Earth's mass. These planets pose a problem for space travel: As the gravity of a planet increases, so does the amount of fuel needed for a rocket to escape its gravity and reach space. As Gonzalez puts it, "mass fraction [of fuel in a rocket] is an exponentially increasing function of delta-V relative to the exhaust velocity." Thus, as the surface gravity of a planet increases, the amount of fuel needed for a rocket to be blasted into space increases at an exponential rate until so much fuel would be needed that it would be impossible for the rocket to escape a planet's gravity.

Gonzalez finds "that the maximum payload mass is reduced by about 40 percent for a super-Earth only about 20 percent more massive than Earth. Beyond 1.65 Earth masses the Saturn V could not launch anything beyond the planet's atmosphere." In other words, a civilization on a planet larger than about 1.65 Earth masses would find it very difficult to engage in planetary exploration as we have done going to the moon.

A skeptic might ask, "Couldn't a more technologically advanced civilization develop new sources of fuel that require less mass?" Perhaps — one can always appeal to hypothetical or unknown scientific discoveries to explain away just about any problem. However, privileged planet arguments look at what we know, not what we don't know. Based upon what we know, the technological evolution of any civilization must presumably pass through "lower tech" phases (like we're in right now) before reaching "higher tech" phases. It thus seems "lucky" that less than 200 years from the start of the Industrial Revolution, we were able to explore space and land on the moon.

Gonzalez also asks how difficult it would be for a rocket to escape a solar system. He finds that "it is more difficult to launch interstellar missions from the circumstellar habitable zone of a low mass star." But our sun's size makes the production of such rockets feasible. This is another parameter which shows our solar system is fine-tuned not just for life but also for scientific discovery.

- **Jonathan Bartlett, "Measuring Active Information in Biological Systems," *BIO-Complexity*, 2020: 2 (2020).**
  This article by computer scientist Jonathan Bartlett addresses an important related question: How can we determine if a mutation is random and undirected, or if it was directed? In addressing this question, he finds new applications for the concept of active information.

  Active information tells us how much knowledge a search function has embedded in it about the location of the target. In the context of studying the effects of mutations on an organism, Bartlett explains: "What active information measures is the alignment of the genome itself to the problem of finding viable genetic solutions to selection pressures." In some cases, a mutation may be completely "random," meaning that it occurred due to mechanisms that were not preprogrammed to help the organism solve a problem. In other cases, a mutation may not be entirely "random," meaning that preprogrammed mechanisms internal to the organism directed the mutation to provide some potential benefit. Bartlett explains that non-random, directed mutations are essentially a reflection of the presence of active information in a genome to produce beneficial mutations:

  > This is wholly compatible with Behe's "First Rule of Adaptive Evolution," which states that evolution will "break or blunt any functional coded element whose loss would yield a net fitness gain." The question that is posed by active information is a separate one. Does the genome contain information about what changes are likely to yield benefit? It may be that the most likely way to yield benefit is to blunt or break some particular system. If active information is present, then the blunting and breaking will be

> measurably tilted towards blunting and breaking systems that are likely to yield selection benefit by doing so.
>
> The goal of active information is not to be a universal quantification of all aspects of information in biology, but rather to assess the narrow question of the information that cells contain that assist in their own evolution.

Bartlett notes that because living organisms tend to optimize across many variables over different timescales, measuring the amount of information could be difficult. However, he explains that the well-defined system of the adaptive immune system provides an environment where active information measurements can be readily calculated. He uses this observation to produce a general model for calculating active information in genomic mutations:

> The methodology described for the somatic hypermutation system can be generalized to any mutational system for which the following are reasonable parameters:
>
> - The cell reduces the mutation space to an area that still fully contains (or almost fully contains) the solution space.
> - The number of mutations that are required are small enough so that they can be reasonably thought of as the smallest mutation to accomplish the effect.

Lastly, Bartlett applies his method to an example offered by proponents of Darwinian evolution to supposedly demonstrate the power of random mutation and natural selection. The example is Long Term Evolution Experiment (LTEE) and the evolution of the Cit+ phenotype. As Bartlett explains, the first time Lenski and his team observed the evolution of the Cit+ phenotype, it required 31,500 generations to appear. However, in their paper, Hofwegen et al. (2016) witnessed the same trait arise in only about 12 generations and 30 days because of selection pressures. Bartlett predicts that the trait arose due to active information in the genome, responding to selection and thereby predisposing *E. coli* to evolve such a trait:

> *E. coli* contributes approximately 12.4 additional bits of information towards the search for the Cit+ mutation when under selection. This number is relative to the ordinary predisposition of E. coli to produce this mutation when not under selection, which has not been determined.

Bartlett shows that it is not random mutation alone that generates such complex traits in *E. coli.* What this indicates is that classical Darwinian evolution is not the mechanism at work here. Instead, preprogrammed mechanisms are designed to allow an organism to rapidly adapt to increase selection pressures. Were these preprogrammed mechanisms intelligently designed? That’s a separate question for another day, but what Bartlett has shown is that Darwinism didn’t produce this feature; something far smarter did. Intelligent design ideas are bearing fruit in our understanding of how evolution works.

- **Michael Egnor, “The Cerebral Windkessel as a Dynamic Pulsation Absorber,” *BIO-Complexity*, 2019: 3 (2019).**
  This peer-reviewed article by Michael Egnor, Professor of Neurosurgery at State University of New York Stony Brook Medical School, presents brain blood flow as an example of a designed system in the human body. When the heart pumps blood through the body, it creates a pulse of blood flow. Most of the capillaries in the human body can handle this pulse, however the

capillaries in our brain are so brittle that the typical blood flow pulse could destroy blood vessels in our brain. Egnor finds that our brains use a “suppression of the arterial pulse in the cranium which renders capillary blood flow smooth” which is called the “cerebral windkessel.” He finds that the best way to understand this blood flow pulse suppression is “by treating the cerebral windkessel as a designed system”:

> Arterial pressure and flow are normally synchronous, and (counterintuitively) the intracranial pressure (ICP) pulse slightly precedes the arterial blood pressure (ABP) pulse. Transfer function analysis of the ABP pulse to the ICP pulse shows a local minimum of amplitude response (a notch) at the heart rate, and abnormal intracranial dynamics attenuates the notch and shifts phase. I propose that these counterintuitive aspects of intracranial pulsatility may be understood by treating the cerebral windkessel as a designed system. On that basis, I here apply principles of reverse-engineering to model the ICP pulse first as a simple harmonic oscillator, then as a forced harmonic oscillator with one or two degrees of freedom. By including a model of the intra- and extra-capillary pathways, I show that ABP-ICP dynamics are characteristic of a dynamic pulsation absorber — a system of vibration suppression widely used in engineering.

This article this exemplifies how the design paradigm can be useful to scientists who seek to understand how biological systems function. By viewing biological system as designed, they ought to exhibit certain engineering principles that we observe in human-designed technology. This can help us solve questions that are vexing biologists. Egnor explains:

> Many aspects of the pulsatility of intracranial blood and CSF are difficult to understand, particularly because the pulsatile flow occurs in a rigid cranium which places obvious constraints on pulsatile dynamics. How is it that capillary blood flow is smooth, whereas the blood flow in the intracranial arteries and veins — sometimes only millimeters away from the capillaries — is quite pulsatile? Why does the pulsatility of the veins resemble the pulsatility of the CSF? Why do the CSF and venous pressure pulse waveforms have some characteristics of an arterial pulse? Why does the intracranial pressure (ICP) pulse normally precede the arterial blood pressure (ABP) pulse, but lag with intracranial hypertension?
>
> I propose that a useful approach to understanding these counterintuitive aspects of intracranial pulsatility is to consider the dynamics of the cerebral windkessel as that of a designed system. Such a system manifests design principles that accomplish specified goals, which for the cerebral windkessel is the buffering of arterial pulsatility — an unwanted ‘vibration’ — in cerebral blood flow, while at the same time maintaining optimal cerebral blood flow and minimizing energy dissipation. This approach to exploring intracranial pulsatility entails reverse engineering of the cerebral windkessel, in accordance with established engineering principles of vibration control.

Egnor’s conclusion that “[t]he cerebral windkessel is a dynamic pulsation absorber” is based upon analysis of the signal of blood flow in the body and the brain. This model is inspired by the view that many aspects of the human body were designed based upon rational engineering principles and has analogues in many human-designed systems:

> Despite its anatomical and mathematical complexity, the windkessel is in principle simple and elegant. The cerebral windkessel has analogues in mechanical engineering (a dynamic vibration absorber), electrical engineering (a wavetrap circuit), acoustic engineering (a cavity resonator) and systems analysis (a band stop filter).

Such design-inspired models not only reaffirm the conclusion of design — they can also lead to improved therapies and medical treatments:

> Windkessel dysfunction causes impairment of cerebral blood flow, loss of capillary integrity, and cerebral edema, which may in turn result in markedly increased intracranial elastance and a cascade of windkessel impairment.
>
> Adjustment of heart rate or other parameters on which the windkessel depends may restore normal windkessel function. Restoration of windkessel function is possible, at least in theory, with any derangement of intracranial dynamics.
>
> Aided by the principles of reverse engineering, we should explore the theoretical, physical, and physiological implications of this elegant system of pulsation absorption in the cranium. The difficult process of understanding the cerebral windkessel may provide new and counterintuitive insight into disorders of intracranial dynamics.

In other words, intelligent design is not only leading to a better understanding of how biology works, but the assumption that biology was engineered is also helping us to develop improved medical treatments.

- **Chongjing Cao, Stuart Burgess, and Andrew T. Conn, "Toward a Dielectric Elastomer Resonator Driven Flapping Wing Micro Air Vehicle,"** ***Frontiers in Robotics and AI*****, 5: 137 (January 2019).** This peer-reviewed article co-authored by pro-ID engineer Stuart Burgess demonstrates how the design of dragonflies inspired the development of new materials and models for micro air vehicles (MAVs). The use of biomimetics to build MAVs further illustrates how biological systems are optimally designed, and it challenges the evolutionary assumption that biology should often display suboptimal design. The authors describe how dragonflies inspired the development of new materials that resonate at the same frequency as MAVs' wing beat frequency:

> In the last two decades, insect-inspired flapping wing micro air vehicles (MAVs) have attracted great attention for their potential for highly agile flight. Insects flap their wings at the resonant frequencies of their flapping mechanisms. Resonant actuation is highly advantageous as it amplifies the flapping amplitude and reduces the inertial power demand. Emerging soft actuators, such as dielectric elastomer actuators (DEAs) have large actuation strains and thanks to their inherent elasticity, DEAs have been shown a promising candidate for resonant actuation.

They also explain why insect flight is so energy efficient:

> One challenge all flapping wing MAV researchers have been facing is the extremely high power demands required for autonomous flight at micro scales. In nature, insects solve this problem by taking advantage of their elastic thorax and muscle system as a damped oscillator and flap their wings at its resonant frequency.

The authors describe how MAVs have employed springs in the past to mimic insect wings' resonance with their beat frequency. Yet new materials better model the elastic properties of insect muscles, so they should allow for even greater energy efficiency. The authors also present biologically inspired models for MAVs.

- **Ola Hössjer and Ann Gauger, "A single-couple origin is possible," *BIO-Complexity*, 2019: 1 (2019).**
  This peer-reviewed paper is the culmination of a project conducted by biologist Ann Gauger and mathematician Ola Hössjer to address how deep into the past an initial couple had to live in order to account for modern human genetic diversity. They published two previous papers in *BIO-Complexity* developing a mathematical population genetics model which can test these questions. This paper applies their model and allows for an initial pair of humans to be given "designed variants" of genes representing "primordial diversity" built into the initial genomes of Adam and Eve. Under their model, natural biological processes then govern the subsequent genetic history of the human race. They find that "a single-couple origin of humanity as recent as 500kya is consistent with data. With only minor modifications of our parsimonious model assumptions, we suggest that a single-couple origin 100kya, or more recently, is possible."

- **David Nemati and Eric Holloway, "Expected Algorithmic Specified Complexity," *BIO-Complexity*, 2019: 2 (2019).**
  This peer-reviewed paper expands upon research into Algorithmic Specified Complexity (ASC) as a means of design detection by demonstrating conservation rules. The authors demonstrate that ASC under a chance hypothesis is always negative. They use this result to prove that the expected ASC is conserved under stochastic processing, and the complexity for individual events is conserved under deterministic and stochastic processing.

  The authors define ASC as the measure of meaningful information in a pattern in a particular context, and they describe the advantage of using the ASC measure:

  > The fundamental advantage is that the use of an independent external context allows ASC to measure whether an event refers to something beyond itself, i.e. is meaningful. … ASC's use of an independent context enables novel contextual specifications to be derived from problem domain knowledge, and then applied to identify meaningful patterns, such as identifying non-trivial functional patterns in the game of life.

  The ASC measure provides a much clearer picture of meaningful information than measures that do not consider a particular context.

  It is the difference between the Shannon surprisal or complexity measure of *x* and the conditional algorithmic information or specification measure of *x*. The authors illustrate calculating ASC in poker. The Shannon surprisal would be the probability for any hand of poker appearing. The conditional algorithmic information would relate to the number of hands corresponding to a particular category such as a royal flush. The Shannon surprisal of every hand is the same, but the conditional algorithmic complexity is smaller for rarer hands. Therefore, the ASC for rarer hands is larger.

The authors prove that the expected ASC for the chance hypothesis always being negative must entail conservation rules:

> Standard information theory cannot account for meaningful information. Algorithmic specified complexity can, but it is a probabilistic quantity. One question we have addressed is: can the expected ASC be positive? We proved the expected ASC is negative … We then use the negativity of expected ASC to prove a conservation of expected ASC under stochastic processing, and deterministic and stochastic conservation of complexity for individual events.

- **Günter Bechly, "Chrismooreia michaelbehei gen. et sp. nov. (Insecta: Odonata: Asiopteridae), a new fossil damsel-dragonfly from the Early Jurassic of England,"** ***BIO-Complexity*****, 2018:1 (2018).**
  This paper, authored by pro-ID paleontologist Dr. Günter Bechly, describes a new species of dragonfly, dating to the early Jurassic period, about 191 million years ago, with an estimated wingspan of 4.5 inches. The fossil was supplied to Bechly by the British fossil collector Chris Moore. The genus is therefore named in his honor (*"Chrismooreia"*) and the species is named after leading intelligent design advocate and biochemist Michael Behe (*"michaelbehei"*). The specimen is incredibly well preserved, and its characters indicate a classification of this species within the now extinct family Asiopteridae, belonging to the insect order Odonata. It is to-date the most complete specimen among the Asiopteridae family, which was hitherto only documented from isolated wings. This meant that, for the first time, scientists could elucidate the body characters of Asiopteridae – including "compound eyes that meet dorsally, robust thorax, legs with short spines, and very long leaf-like cerci."

  What is the significance of this paper for intelligent design? The paper notes an incongruent pattern of similarities between this fossil and other documented species belonging to the order Odonata. Bechly comments,

  > In any case the high degree of homoplasy shows that the overall pattern of similarity is very incongruent and does not readily align with a hierarchical system required by evolutionary classification. While surprising from the perspective of common ancestry, such incongruences would not be surprising from the perspective of common design. To avoid a dilemma here, I recommend basing classification on maximum similarity rather than assumed common descent. Also on this basis I here tentatively retain Sphenophlebiidae as a distinct family and attribute the new taxon to Asiopteridae, with which it shares most features of the wing venation (the only known character complex in the other genera of Asiopteridae).

  The paper thus challenges the nested hierarchical distribution of traits predicted by evolution, and suggests that common design is a more satisfying account of the evidence.

- **James C. LeMaster, "Evolution's Waiting-Time Problem and Suggested Ways to Overcome It — A Critical Survey,"** ***BIO-Complexity*****, 2018: 2 (2018).**
  This paper reviews literature on the waiting times problem in population genetics and provides a survey and critique of four mechanisms that are proposed to reduce these waiting times to within a reasonable timeframe for evolution to operate. The author begins by reviewing the work of Douglas Axe, Ann Gauger, and Mariclaire Reeves on the rarity of stable and functional

protein folds and the consequent difficulty of attaining new protein structures. He also discusses the work of Richard Sternberg on the waiting time of attaining two co-dependent mutations in the evolution of aquatic whales from terrestrial mammals, based on equations from a 2008 paper by Rick Durrett and Deena Schmidt. Sternberg estimates that the waiting time would be in excess of 43 million years, significantly longer than the amount of time documented by the fossil record for the evolution of the whale from terrestrial mammals such as *Pakicetus* (which has been estimated to be no more than around 9 million years. LeMaster also discusses estimates of the waiting time for two co-dependent mutations in humans which, again, exceeds the amount of time afforded by the fossil record.

The paper evaluates four proposed mechanisms that are thought to reduce the necessary waiting times. Symbiogenesis involves the merging of two distinct organisms to form a single more complex organism (thought to account for the origins of mitochondria and chloroplasts). However:

> [S]ince numerous modifications would have been needed to transform a newly acquired symbiont to an organelle, it is unclear whether the required timescale is actually reduced by this hypothesis. One can imagine the central absorption event happening quite rapidly, but, while Cavalier-Smith postulates how various stages of symbiogenesis might have occurred, he does not provide details about how long pre- and post-absorption stages must have taken in order for the changes to be fixed throughout the eukaryotes. In addition, he offers no calculation to show that required times are less than available times.

DNA. Can relocations of transposable elements, by enlarging genome diversity, reduce the necessary waiting times for biological change? The author writes:

> [T]he time savings in one step of the process point to significant time costs in other steps. Besides moving DNA segments, transposition and retrotransposition require enzymes (transferase and reverse transcriptase, respectively). They also require numerous complex regulatory mechanisms, many of which critically defend organisms from highly damaging effects TEs can cause when they are expressed. Some of these protective mechanisms include “repressive protein complexes, histone methylation, RNA interference (RNAi), and RNA-directed DNA methylation, as well as recombinational regulatory complexes”. Moreover, even if TEs speed diversity, Fedoroff admits, “The epigenetic mechanisms that control homology-dependent recombination . . . slow the pace of genome restructuring to an evolutionary time scale”.

The third mechanism discussed in the paper is the horizontal gene transfer (HGT) between organisms. Though some argue HGT accelerates evolutionary change, the paper notes:

> HGT would require complex transposition and regulation enzymes (both in the source organism and in the host organism). Moreover, the likelihood of harmful effects is even greater with HGT, since the genetic material comes from a foreign body. In order to mitigate damage to the host, the HGT process would require specialized mechanisms to inhibit or silence the transposons’ expression. Fedoroff reports that prokaryotes (and presumably eukaryotes as well) possess “systems that discriminate endogenous DNA from that Over thirty years ago, Erwin and Valentine wrote about HGT through viral

> infection as an accelerator of evolution, albeit clarifying that it would only happen with "the aid of other evolutionary processes." Mathematically speaking, this concern could be partly compensated for if the gross number of organisms experiencing HGT's were massive. Whether this compensating situation exists or has existed will require more research and calculation, in order to clarify how many HGT's would be necessary to overcome the deleterious effects. acquired through horizontal gene transfer and bacteriophage infection". As with transposition, the overall waiting times for evolving these specialized enzymes and mechanisms could offset any short-term time savings brought by the rapid influx of genetic material.

Finally, the author considers whether alternative genetic pathways to a novel function could serve to reduce the needed waiting time. He notes that Douglas Axe took into account alternative routes in his calculations, nonetheless concluding that "Protein sequences that perform particular functions are far too rare to be found by random sampling." Moreover, the waiting times are so prohibitive, that the problem cannot be resolved even on the hypothetical that multiple mutational solutions to the same problem exist. The paper concludes:

> Conceptually, teleological agency could drastically shorten waiting times for complex biological features. Teleology is neither blindly deterministic nor purely random, nor merely a combination of the two. Rather, it intentionally innovates by foreseeing goals and learning and inventing paths to overcome obstacles. Consequently, it can rapidly rule out large swaths of unlikely search space, focusing only on potentially successful solutions.

In other words, intelligent causes are capable of visualizing complex end goals in a way that cannot be replicated by a mindless search. Thus, teleological explanations are a more satisfying explanation of the many transformations seen in the history of life.

- **Chongjing Cao, Stuart Burgess, and Andrew T. Conn, "Flapping at Resonance: Realization of an Electroactive Elastic Thorax," *2018 IEEE International Conference on Soft Robotics*, July 5, 2018, 327-332.**

This peer-reviewed paper in an engineering journal is lead authored by Stuart Burgess, a professor of engineering design at Bristol University, who has written extensively on the evidence for design in life. It focuses on biomimetics, the idea that life's design can help improve human technology. The authors presented a flapping wing micro air vehicle (MAV) that was modeled after the design of insect wings. They described why insect wings operate with such high efficiency:

> Insects take advantage of their elastic thorax and muscle system as a damped oscillator and flap their wings at its resonant frequency … This highly elastic natural oscillator enables resonant excitation to take advantage of the amplified the flapping stroke and greatly reduced inertial power demands.

Their design for a MAV included dielectric elastomer actuators (DEAs) that mimic the properties of insect muscles. They achieved large strains that are like those in muscles, and their inherent elasticity allowed them to store and release inertial energy like the highly efficient resilin protein found in the thorax of insects.

The team detailed the design of the MAV, and they described how different parameters affected flapping frequency and power requirements. They also calculated and then measured the resonant frequencies based on the materials used for the DEA. And they measured the power requirements of the MAVs for the different number of membrane layers in the DEA.

The team demonstrated that their design performed far better than other designs not mimicking insects. The summarized their results as follows:

> We show that the insect-inspired wings can have a peak flapping stroke of 63° at 18 Hz. While this flapping performance requires further optimization towards generating enough lift for flight, this prototype far outperforms previous DEA-based flapping mechanisms in terms of stroke amplitude and wingbeat frequency …

They conclude by listing ways they wish to improve future MAVs such as using improved materials, optimizing the actuator and flapping mechanism, and employing better manufacturing techniques. Future versions will also further optimize the coupling between the DEA and flapping mechanism and the relatively low resonance frequencies that can be achieved for long wings. Such research shows that the design of life exhibits efficient features that best human technology, with major implications for how living systems arose.

- **Winston Ewert, "The Dependency Graph of Life,"** ***BIO-Complexity*****, 2018: 3 (2018).**
  One of the most popular arguments for common ancestry is the ability to classify biological data into a nested hierarchical tree-like pattern. While intelligent design is not necessarily incompatible with common ancestry, this paper shows that it is possible for design to contribute to our understanding of phylogenetic data. In this paper, Winston Ewert offers an alternative hypothesis to account for this tree-like resemblance – based on the idea that a designer may re-use code modules for different projects, often called "common design." The abstract reads:

> The hierarchical classification of life has been claimed as compelling evidence for universal common ancestry. However, research has uncovered much data which is not congruent with the hierarchical pattern. Nevertheless, biological data resembles a nested hierarchy sufficiently well to require an explanation. While many defenders of intelligent design dispute common descent, no alternative account of the approximate nested hierarchy pattern has been widely adopted. We present the dependency graph hypothesis as an alternative explanation, based on the technique used by software developers to reuse code among different software projects. This hypothesis postulates that different biological species share modules related by a dependency graph. We evaluate several predictions made by this model about both biological and synthetic data, finding them to be fulfilled.

Ewert notes that the common descent and dependency graph models have important similarities:

> Taxonomic categories appear in both: in common descent they are represented by their most recent common ancestral species. In the dependency graph, they are modules. Both can explain the nested relationship of taxonomic categories. In common descent, this is because one species descended from another. In the dependency graph, this is because one module depends on another.

Ewert explains, however, that the models “differ on one crucial point” — under a design-based dependency graph view, traits need not always be distributed within a nested hierarchy:

> [A] species conventionally has one ancestral species, but a module typically has multiple dependencies. … All marine species depend on a marine module, and the echolocating species depend on the echolocation module. The dependency graph is essentially a tree with extra flexibility; the modules can explain genes shared between species thought to be only distantly related by common descent. A module is not restricted to reusing code from a single source, but can freely reuse from multiple sources. Compare this to common descent where each species must almost exclusively draw from a single source: its ancestral species.

Thus, a prediction of the dependency graph is that there will be re-usage of elements in a manner that is dissimilar to a tree-like structure. Ewert reviews specific examples with a view towards evaluating the respective merits of a tree and a dependency graph. For instance,

> *Gallus gallus* (chickens) and *Meleagris gallopavo* (turkeys) are closely related birds, and thus are expected to share many genes by common descent. On the other hand, despite the similarity in names, *Taeniopygia guttata* (zebra finch) and *Danio rerio* (zebra fish) are only distantly related because one is a bird and the other a fish. As such, it should be relatively improbable to find genes shared *only* between these two species. But according to the Hegenom dataset, there are nineteen gene families found only in this pair of species. The dependency graph model can assign high probabilities to both of these combinations by postulating a module shared between the pairs of species.

Ewert finds that his model is viable when compared to the data:

> The predictions of the dependency graph hypothesis set out in this paper have been shown to be correct. The biological data was a better fit to a dependency graph than to a tree. The data produced by a simulated process of common descent was a better fit to a tree than to a dependency graph. The data produced by a compiler was both a better fit to a dependency graph than a tree, and a better fit to a tree than to the null model. The inferred biological dependency graphs contained were not simply the tree of life with a few additions, but instead contained many additional modules.

After analyzing the distribution of gene families in nine diverse types of animals, Ewert’s preliminary analysis found that a common design-based dependency graph model fit the data 10^{3000} times better than a traditional Darwinian phylogenetic tree. His ID-based dependency graph model predicted reuse of parts much better than neo-Darwinism. This paper shows that intelligent design can make contributions to diverse scientific fields, such as phylogenetics and the relationships between different organisms.

- **Eric Holloway and Robert Marks, “Observation of Unbounded Novelty in Evolutionary Algorithms Is Unknowable,” *Lecture Notes in Computer Science (Including Subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 10841 LNAI: 395-404 (2018).**

Eric Holloway and Robert Marks are computer scientists and design theorists, with Marks being a professor at Baylor University. This peer-reviewed article refutes claims that evolutionary algorithms have demonstrated limitless novelty. The authors prove that unbounded novelty is unknowable:

> Open ended evolution seeks computational structures whereby creation of unbounded diversity and novelty are possible. However, research has run into a problem known as the "novelty plateau" where further creation of novelty is not observed. Using standard algorithmic information theory and Chaitin's Incompleteness Theorem, we prove no algorithm can detect unlimited novelty. Therefore observation of unbounded novelty in computer evolutionary programs is nonalgorithmic and, in this sense, unknowable.

They list several definitions of novelty and then describes novelty in the case of computer algorithms:

> In all these domains, novelty has common characteristics. Novelty is
> – defined relative to a typical population,
> – measured using a distance, and
> – unanticipated.

Within a computational domain, everything can be represented by a bitstring. We can measure a bitstring's distance from a population in many ways. A large distance signifies something outside of the typical population. We can characterize the typical population by the smallest program that can produce the population, the size of which is the Kolmogorov complexity of the population. When a member is added to the population that requires the program size to increase, then the member is atypical albeit not necessarily novel. Note if a member is novel, then it is atypical, thus it will increase the population's Kolmogorov complexity.

The authors then present an analysis of the limits of measuring novelty generated by computer algorithms based on the noncomputability of Kolmogorov complexity and Chaitin's Incompleteness Theorem. They show that one cannot measure the Kolmogorov complexity of a bitstring above a certain limit. A bitstring in an evolutionary algorithm represents an individual organism in a population, and identifying novelty requires measuring the increase in a bitstring's complexity. Consequently, the limit set by the theorem corresponds to the limit in the increase of novelty that can be observed. The authors summarize their work as follows:

> A reliable method of identifying an endless amount of novelty would also imply the ability to calculate a lower bound of arbitrary size on Kolmogorov complexity. Since every axiomatic system has a limit to the lower bound it can calculate, due to Chaitin's incompleteness theorem, the reliable method of novelty detecting introduces a contradiction. This same contradiction results if we have a program we know only generates novel bitstrings.
>
> As such, we must conclude there is no reliable method of identifying an endless degree of novelty, nor of producing only novel bitstrings. We can only reliably detect novelty to a finite amount, and not significantly more than the Kolmogorov complexity of the axioms used for detection.

- **Ola Hössjer, Günter Bechly, and Ann Gauger, "Phase-type distribution approximations of the waiting time until coordinated mutations get fixed in a population." Chapter 12 in: Silvestrov, S., Malyarenko, A. & Rancic, M. (eds):** ***Stochastic Processes and Algebraic Structures - From Theory Towards Applications. Volume 1: Stochastic Processes and Applications. Springer Proceedings in Mathematics and Statistics*****, 271: 245-313 (2018).**
  This peer-reviewed paper provides a method of calculating "the waiting time until a number of coordinated mutations occur in a population." The authors note that waiting times studies have many applications:

  > The waiting time problem for coordinated mutations has several applications. It is widely believed, for instance, that many types of cancer occur when several somatic mutations spread in a population of cells within a tissue (Knudson). This has been analyzed mathematically by Komarova et al., Iwasa et al., Nowak, and Schinazi. A second related application is immune system response, where coordinated somatic mutations are triggered in reaction to certain antigens (Radmacher et al.). A third application is to analyze the waiting time until multiple germline mutations arrive in duplicate genes in order to make them functional (Behe and Snoke, Lynch). A fourth application is coordinated germline mutations in regulatory regions, where changes at two different binding sites have to occur in a given order (Carter and Wagner, Durrett and Schmidt). A fifth application is coordinated mutations in bacterial populations, where each surviving mutant gives rise to a daughter population that grows at an exponential rate (Axe).

  This research has important implications for the viability of standard evolutionary mechanisms because some systems may require waiting times far longer than that allowed by the fossil record, suggesting some different type of cause was at work in their origin.

- **William F. Basener and John C. Sanford, "The Fundamental Theorem of Natural Selection with Mutations,"** ***Journal of Mathematical Biology*****, 76 (7): 1589-1622 (2018).**
  Two ID-friendly scientists critique Fisher's fundamental theorem of natural selection. The fundamental theorem states that the average fitness of a population increases at a rate equal to the genetic variance of a species. But it does not consider mutations, so selection only removes deleterious mutations resulting in a decrease in variance. After the variance approaches zero, the population fitness approaches a constant value. Fisher added Fisher's Corollary that mutations would add a continuous supply of variance resulting in a perpetual increase in mean fitness.

  Basener and Sandford demonstrate that Fisher's conclusions are false by presenting an alternative version of his model that includes mutations with more realistic distributions of selection coefficients. They run several simulations with their model to demonstrate that populations do not generally increasing in average fitness. Instead, the average fitness often continuously decreases. Consequently, they undermine one of the foundational pillars of evolutionary theory.

  Basener and Sanford describe their approach as follows:

  > The goal of this paper is to develop a version of Fisher's theorem analogous to that presented by Crow and Kimura (1970), but with the additional capability of tracking the effects of mutations to new genetic varieties over time. This new formulation is proven

> as Theorem 2, where we derive a formula that gives the rate of change of mean fitness as a function of both the variance in fitness and the mutation effects on population fitness. In this manner, we provide the ability to mathematically analyze Fisher's Corollary (Point (B)).

The authors also review numerous experimental and observational studies that demonstrate that most mutations are deleterious or nearly neutral. The largest impact on fitness comes from those mutations that are not so deleterious that selection efficiently removes them and not so neutral that they have no impact on fitness. These "very slightly deleterious mutations" generally drive populations to lower fitness.

The authors summarize their conclusions as follows:

> After we re-formulated Fisher's model, allowing for dynamical analysis and permitting the incorporation of newly arising mutations, we subsequently did a series of dynamical simulations involving large but finite populations. We tested the following variables over time: (a) populations without new mutations; (b) populations with mutations that have a symmetrical distribution of fitness effects; and (c) populations with mutations that have a more realistic distribution of mutational effects (with most mutations being deleterious). Our simulations show that; (a) apart from new mutations, the population rapidly moves toward stasis; (b) with symmetrical mutations, the population undergoes rapid and continuous fitness increase; and (c) with a more realistic distribution of mutations the population often undergoes perpetual fitness decline.

Such research suggests that blind evolutionary mechanisms are unable to preserve the fitness of a species. Some other causes are needed.

- **Jonathan Bartlett, "Evolutionary Teleonomy as a Unifying Principle for the Extended Evolutionary Synthesis," *BIO-Complexity*, 2017: 2 (2017).**
  This peer-reviewed paper identifies the unifying principle undergirding the Modern Synthesis as the primacy of three processes driving evolution: mutation, fluctuation in genetic frequencies, and differential reproduction. They result in biological systems appearing to act with purpose to generate biological novelties, but the novelties' origin is through a historical process without purpose. Biologists Colin Pittendrigh and Ernst Mayr promoted the term teleonomy to signify biological entities acting with a purpose due to a program. Bartlett demonstrates that the different mechanisms promoted by the Extended Synthesis do not appear entirely random, but they display teleonomy (aka purpose), which is a hallmark of design:

  > For more than a century, biology has struggled with the concept of teleology. Teleology is the orientation of objects (often organisms) towards ends. That is, organisms have purposes which are reflected in their behaviors. What makes biology unique as a subject is that while the study of rocks or atoms rarely makes reference to purpose, the study of biology is almost exclusively concerned with purpose.

  Bartlett describes how the Extended Synthesis adds the following features to evolutionary theory:

  - Extended inheritance: organisms inherit more than just genes.

- Reciprocal causation: organisms shape their environments, which then act on them.
- Nonrandom phenotypic variation: organisms biased change in specific directions.
- Variable rates of change: the effects of mutations are nonlinear.
- Organism-centered perspective: entire organisms have causal role in their evolution.
- Macro-evolutionary processes: the additional modes of inheritance lead to additional macro-evolutionary processes.

He argues that each of these processes demonstrates teleonomy, so teleonomy is the unifying principle that undergirds the Extended Synthesis. This use of teleonomy differs from the Modern Synthesis since it is not simply the result of the evolutionary process, but it drives evolution. In niche inheritance, a program directs organisms to shape their environment for the benefit of the organism. In sexual selection, organisms are directed by a program to choose mates that generate healthy offspring. In epigenetic inheritance, a program modulates genes in response to environmental circumstances to affect the evolutionary outputs in the next generation. And mechanisms cause mutations affecting development to manifest themselves in ways that do not significantly alter the organism.

Recognizing the centrality of teleonomy can help redirect investigators interpretation of biological data. Traditionally, biologists have interpreted observations of genetic changes assuming mutations were random, and different alleles' frequencies were simply the result of differential survival due to the advantage or disadvantage they brought to the organism. Within a framework undergirded by teleonomy, researchers can attempt to identify how teleonomy might direct evolution toward specific outcomes.

Bartlett summarizes his analysis as follows:

> Throughout the twentieth century, the Modern Synthesis dominated as the unifying principle for biological evolution, focused on the idea that evolution happens to an organism, and that the organism itself does not have a significant causative effect in its own evolution. The Extended Evolutionary Synthesis claims to provide a new way of looking at evolution, but has failed to generate a set of unifying principles for biologists. We have proposed Evolutionary Teleonomy — the idea that organisms can actively affect their evolution on every level — as the new foundational principle of evolutionary biology. Evolutionary Teleonomy unifies many of the independent topics of the Extended Evolutionary Synthesis under a single, understandable label.

This return to purpose / teleonomy is evidence biology is moving closer to a design-based framework.

- **Winston Ewert and Robert J. Marks II, "Conservation of Information in Coevolutionary Searches,"** ***BIO-Complexity*****, 2017: 1 (2017).**
  Winston Ewert and Robert Marks are design theorists who have published extensively on design detection and the limitations of evolutionary algorithms. This article overturns the claim that incorporating coevolutionary interactions could overcome the limitations of traditional evolutionary algorithms by demonstrate that coevolutionary algorithms perform even less efficiently than traditional ones. Ewert and Marks demonstrate that coevolutionary processes

will not overcome limitations on evolutionary searches imposed by the No Free Lunch (NFL) theorem:

> A number of papers show that the *No Free Lunch* theorem does not apply to coevolutionary search. This has been interpreted as meaning that, unlike classical full query searches, coevolutionary searches do not require extensive a priori knowledge about the domain. Alternately, coevolutionary searches can be viewed as providing incomplete information about fitness and differ from standard evolutionary searches where queries provide full fitness information. Knowing the full value of a fitness is better than knowing partial subjacent fitness information. Consequently, coevolution can be viewed as a degradation of search performance in this sense…. Coevolution does not allow an escape from the necessity of exploiting prior information in search processes and remains bounded by conservation of information in general and the *No Free Lunch theorem* in particular.

The NFL theorem states that no search algorithm will on average find a target any faster than a random search. Consequently, evolutionary processes are incapable of generating complex novelties without outside infusions of information about targets. Critics responded by asserting that coevolutionary processes could overcome this constraint since changing environmental conditions and the presence of coevolving species change the fitness landscape, which represents the fitness of an organism with given traits.

The authors overturn this claim by demonstrating that algorithms that incorporate coevolutionary interactions are even less efficient than traditional algorithms. They illustrate how a coevolutionary algorithm must generate a query matrix where a row is assigned to each candidate state and each column corresponds to a different factor affecting fitness such as interactions with a particular species. Many cells in this matrix are often not known, whether due to computational or other practical limitations. Various methods are employed to assign each trial solution (row) an aggregate fitness value based on the limited knowledge. The algorithm then proceeds as with traditional models. Since the information available to the algorithm is less than with traditional searches, the authors postulate that the performance should be inferior to traditional searches, not more efficient.

The authors then demonstrate the accuracy of their prediction through several examples. They first describe searching through a series of books for a treasure map. A coevolutionary process corresponds to the need to check through a book multiple times before determining if it contains the map, decreasing the efficiency of the search. They also provide examples of searching for an effective insecticide and searching for the oldest students in several classrooms, which also show decreased efficiency. The authors then prove theorems related to the inferiority of coevolutionary algorithms. And they apply their theorems to several standard search algorithms including *Needle in the Haystack*, *Horizontal*, *Vertical*, *Depth Search*, and *So-far so-good*. In no situation can a coevolutionary component enable a search algorithm to overcome the NFL theorem:

> We conclude that there is nothing special in a coevolutionary algorithm that absolves it from the necessity of making use of prior information to solve non-trivial searches. If the full query algorithm requires prior knowledge, so do the coevolutionary algorithms because they perform worse than the full query algorithm. None of the free lunch

> proofs provide evidence that less prior knowledge is required for coevolutionary algorithms. If these apparent free lunches do not provide a mathematical justification for success, what does? The success of coevolutionary algorithms like any other algorithms depends on the use of prior knowledge. The algorithms are designed to exploit the characteristics of the problem being solved.

- **Wolf-Ekkehard Lönnig, "Mendel's Paper on the Laws of Heredity (1866): Solving the Enigma of the Most Famous 'Sleeping Beauty' in Science,"** ***eLS*** **(Jon Wiley & Sons, 2017).**
  In this peer-reviewed paper, geneticist Wolf-Ekkehard Lönnig asks why Gregor Mendel's accurate theories of heredity developed in the 19th century were initially rejected or ignored by many other scientists. He concludes that it is because at that time, the scientific community was completely enamored with Darwinian evolution and unwilling to consider ideas that did not fit with Darwin's models of evolution and inheritance. As Lönnig puts it:

  > His [Mendel's] analysis, discernment and exposition of the laws of heredity as well as his views on evolution diametrically defied and contradicted the ideas and convictions of Darwin and his followers. … [T]he basic reason for the neglect of the laws of heredity was essentially this: To imply something like a static definition of the species by constant hereditary elements right into a momentous process vigorously favouring the Darwinian revolution (continuous evolution by natural selection without any teleology intimately combined with the inheritance of acquired characteristics, to underscore the latter, often forgotten point once more) was met – although usually silently – with skepticism, deliberate ignorance and strong opposition. And there is no doubt concerning Darwin's overwhelming victory in the battle for the scientific minds in the nineteenth century, so much so that Mendel's performance before the Natural History Society of Brünn was even met with 'scornful laughter'….

  Lönnig quotes Italian biologist Guiseppe Sermonti who concurs with this explanation: "What really happened was that Mendel ruled out almost all the forces that Darwin had invoked to explain evolution."

  Because Mendel's theory of inheritance produces "all-or-nothing traits," Lönnig explains that this conflicted with Darwin's ideas about gradual evolution:

  > [P]erhaps even more important, Mendel's discoveries cast doubt on another definitely decisive and essential part of Darwin's theory: continuous evolution, for which Darwin had postulated 'infinitesimally small inherited variations', 'steps not greater than those separating fine varieties' and 'insensibly fine steps', 'for natural selection can act only by taking advantage of slight successive variations; she can never take a leap, but must advance by the shortest and slowest steps'.

  According to Lönnig, "[I]n Mendel's view, endless evolution was neither probable for cultivated plants nor for species in the wild."

- **Roman Yampolskiy, "On the origin of synthetic life: attribution of output to a particular algorithm,"** ***Physica Scripta*****, 92 (1): 013002 (2017).**
  This peer-reviewed paper by computer scientist Roman Yampolskiy proposes a research program to distinguish between life-like entities observed in nature resulting from evolutionary

processes from those engineered by intelligent agents. His article further demonstrates the legitimacy and benefit of applying design-detection methodologies to life. The author lists methods for design detection which strongly overlap with those present by such design theorists as William Dembski and Stephen Meyer:

> It seems it is possible to estimate the scientific knowledge and minimum intelligence necessary to produce, or at least duplicate, a particular artifact by analyzing its complexity, prerequisite components and evidence of tools used in the production, be it an artifact/data or an abstract algorithm. … Such telltale signs include: complexity in the absence of probabilistic resources, watermarking, multilevel encoding, support for future features, physical computation, evidence of degradation from the original design, and the engineer's signature, etc. It may even be possible for intelligent agents to perform this analysis on themselves to discover their origins.

He also proposes that even within a materialistic scientific paradigm, observed forms of life are often expected to result from intelligent agents:

> Unless evidence to the contrary exists, a given life form is statistically more likely to have its origins as a product of engineering and so our priors should be adjusted accordingly. This type of reasoning also applies to Earth: we are also likely to have our origins as synthetic life, as suggested by the theory of directed panspermia, seeding or some other similar variants. In fact the approximate probability of being produced by unaided laws of physics rather than engineering is equal to one divided by the total number of self-reproducing biological robot species all the generations of intelligent beings around the universe have ever produced. In our estimate (based on Drake's equation) this tends to zero as the age of the universe increases.

He also challenges the synthetic biology community to design a biological component that could not have evolved to demonstrate that the theory of evolution is falsifiable:

> Consequently, we propose a challenge to the synthetic biology community to purposefully design and produce an organism with an unevolvable component, which meets Darwin's criteria for falsifying his theory. Can such a feat be accomplished? Can it be mathematically proven that a particular design is not evolvable, or at least statistically very unlikely? We believe those are important questions to be answered by genetic engineers and which would reconfirm the falsifiability of the Theory of Evolution [86].

If such a challenge were ever accepted, synthetic biologists would likely either demonstrate that evolutionary theory is unfalsifiable, or they would further demonstrate that living systems were designed.

- **Elizabeth A. Siewert and Thomas A. Siewert, "The Need for a Quantifiable Model of Evolution,"** ***Journal of Bio Innovation*****, 6:5: 685-694 (2017).**
  In this paper, Elizabeth Siewert and Thomas Siewert describe and offer a critique of, two quantitative models of the innovative potential of evolution proposed by Fred Hoyle and Richard Dawkins. In his book, *Evolution from Space,* Hoyle contended that "the chance of obtaining" the enzymes needed for primitive life by chance is "only one part in $10^{40,000}$". Siewert

and Siewert note that Hoyle does not correctly model evolutionary theory, which "states that complexity is build up slowly step by incremental step – not all at once and suddenly."

A much simpler model is offered by Richard Dawkins. In his book, *The Blind Watchmaker*, Dawkins puts forward a model of 'evolving' the phrase "METHINKS IT IS LIKE A WEASEL" in small incremental steps. At each iteration, Dawkins randomly changed characters for each of the twenty-eight positions, retained the characters that corresponded to the target sequence and continued to change those that did not. Dawkins noted that, if we had attempted to produce the target in one step, the probability would be astronomically small -- 1 in 10^{40}. But by changing only one character at a time, the target sequence was arrived at in only a handful of iterations. However, as Siewert and Siewert point out, this exercise "had a predefined goal. He knew, as the programmer, what phrase he wanted to reach and defined each incremental 'success' with respect to that predefined goal." The authors of this paper conclude that neither of these two models offers an accurate representation of Darwinian evolution. Instead, "we need an example that is simple enough to depict the small *incremental* steps of evolution, and undefined enough to model an *undirected* process of evolution."

The authors instead propose their own model, which more accurately reflects the process of evolution as envisioned by Charles Darwin and his modern exponents. As a case study, the authors choose the human eye to illustrate their model, noting that,

> Critics of Darwin cite the human eye as an example of a complex structure to illustrate the falsehood of Darwin's theory. However, these critics make the same mistake that Hoyle made in that the fully developed human eye is too complex. In contrast, proponents of Darwin respond by stating that the human eye didn't happen all at once…They hypothesize that the earliest eye might have been just a patch of light - sensitive cells on the skin. Then, through random mutations, a depression in the light-sensitive spot developed and slowly evolved into a retina, and over more time, perhaps a lens developed. (Nilsson and Pelger, 1994)

The authors focus on the hypothesized patch of light-sensitive cells, which is often proposed as an evolutionary precursor to vision. They ask:

> How difficult would it be for a *Chlamydomonas* [i.e. a motile, single-celled green alga] without a functional eyespot to develop a primitive eyespot that is functional enough to confer an evolutionary benefit? The organism would need to solve several problems to gain this minimum functionality. It would need to be able to detect the presence of light (the eyespot), the ability to swim toward that light (the flagella), and a signaling system from the primitive eyespot to the flagella. Otherwise, given that it could swim, and could detect where it wanted to swim, if there are no means of communication between the eyespot and the flagella, there is not a functional advantage.

To be conservative, they make several simplifying assumptions that are favorable to evolutionary mechanisms. They assume that "the *Chlamydomonas* already has the ability to swim toward the light (if it could detect that light) and the signaling system from the (yet non-functioning) eyespot to the flagella." Moreover, they assume that, of the more than 200 proteins involved in the eyespot of *Chlamydomonas*, only ten additional ones are required for a functional eyespot. Furthermore, they assume that "the chloroplast is already functioning –

presumably being used when the 'blind' *Chlamydomonas* happens to be in sunlight." They also assume that each of the ten proteins is a hundred residues in length. This is particularly generous since, as they note, the photoreceptor proteins found in the *Chlamydomonas* eyespot are approximately 700 residues in length. They further assume, generously, that, instead of needing to build the proteins out of the twenty amino acids found in modern proteins, we only need to select from four generic amino acids that represent the four broad types – basic; acidic; neutral and hydrophobic; and neutral and hydrophilic.

Recall that the authors assume that only ten proteins are required of the more than 200 proteins that are involved in the *Chlamydomonas* eyespot. Given that the number of possible combinations of 100-residue long proteins using the four broad types of amino acids is 4^{100}, the number of ways of making ten of these proteins is $(4^{100})^{10}$, or 10^{602}. Thus, the probability of making these ten proteins is 1 in 10^{602}.

The authors next offer a generous estimate of the probabilistic resources available. They note that "Since the *Chlamydomonas* lives in water, it is logical to calculate the probability of this eyespot developing by chance somewhere in the oceans of the world." A calculation of the upper bound on the available probabilistic resources (based on absurdly generous assumptions) estimates the number of possible attempts as 10^{77}. The authors then "calculate the probability of these ten proteins forming somewhere in the oceans in earth's history by the equation $P = 1 - (1 - 10^{-602})^{10\text{^}77}$, which comes out to 10^{-525}. This is a vanishingly low probability."

Based on their analysis, the authors suggest, we should re-evaluate our assumptions about the causal efficacy of undirected processes in explaining systems such as the origins of a light-sensitive spot.

- **Granville Sewell, "On 'compensating' entropy decreases,"** ***Physics Essays*****, 30:1 (2017).**
  In 2011, mathematician Granville Sewell was disallowed from publishing an article in the journal *Applied Mathematics Letters* (*AML*) simply because it was critical of Darwinian evolution. Then, that non-published paper was later critiqued in the journal *Mathematical Intelligencer*, even though it was never published in the first place. Even worse, his critics doubled-down on censorship by disallowed him from publishing a rebuttal within that journal. Obviously his arguments must hold merit if technical journals are willing devote space to rebutting them. This paper in the journal *Physics Essays* grants Sewell the space to respond to his critics.

  Defenders of Darwinian evolution sometimes argue that decreases in entropy in living organisms due to evolutionary processes do not violate the second law of thermodynamics if those decreases are "compensated for" by increases of entropy elsewhere in the universe. Sewell rejoins that "there is no such total entropy, and that the compensation argument is not a valid way to dismiss the claim that evolution violates the second law." To appreciate the absurdity of the compensation argument, Sewell proposes an imaginary scenario where "a tornado turns a town into rubble, then a second tornado turns this rubble back into houses and cars." Of course, this is wildly improbable, but if the town is an open system, and total entropy of the universe still increases, then according to the compensation argument "the second tornado does not pose any conflict with the second law." Sewell documents that, unfortunately, various physics textbooks make precisely this sort of mistake. He continues:

> [T]o argue that evolution does not violate the second law, you cannot simply dismiss the problem by saying, the Earth is an open system so any decreases in entropy here are easily compensated by increases elsewhere, you have to argue that thanks to the influx of solar energy, it is not really impossibly improbable that the four fundamental, unintelligent forces of physics alone could rearrange the fundamental particles of physics into computers, science libraries, airplanes, and iPhones. Common sense tells us that the fact that order can increase in an open system does not mean that tornados can turn rubble into houses and cars, or that computers can appear on a barren planet as long as the planet receives solar energy. Something must be entering the open system which makes the appearance of computers not extremely improbable, for example, computers.

Sewell then turns to the improper handling of his 2011 *AML* paper, noting that "the reason my accepted *AML* paper was withdrawn was because it seemed to support intelligent design (ID) theory," even though article "did not explicitly promote intelligent design." He then recounts the conclusion of that paper:

> Of course, one can still argue that the spectacular increase in order seen on Earth does not violate the second law because what has happened here is not really extremely improbable. And perhaps it only seems extremely improbable, but really is not, that, under the right conditions, the influx of stellar energy into a planet could cause atoms to rearrange themselves into nuclear power plants and spaceships and digital computers. But one would think that at least this would be considered an open question, and those who argue that it really is extremely improbable, and thus contrary to the basic principle underlying the second law of thermodynamics, would be given a measure of respect, and taken seriously by their colleagues, but we are not.

In this paper, he offers a similar conclusion:

> If Darwin was right, then evolution does not violate the second law because, thanks to natural selection of random mutations, and to the influx of stellar energy, it is not really impossibly improbable that advanced civilizations could spontaneously develop on barren, Earth-like planets. Getting rid of the compensation argument would not change that; what it might change is, maybe science journals and physics texts will no longer say, sure, evolution is astronomically improbable, but there is no conflict with the second law because the Earth is an open system, and things are happening elsewhere which, if reversed, would be even more improbable.

The publication of this peer-reviewed paper by Sewell might be evidence that physics texts will one day move in the right direction.

- **Paul A. Nelson and Richard J.A. Buggs, "Next Generation Apomorphy: The Ubiquity of Taxonomically Restricted Genes," in *Next Generation Systematics*, ed. Peter D. Olson, Joseph Hughes, and James A. Cotton (Cambridge: Cambridge University Press, 2016), pp. 237-263.** In this book chapter from a Cambridge University Press volume, Paul Nelson and Richard Buggs discuss the challenge to evolution from the existence of taxonomically-restricted genes (TRGs) — that is, genes that are limited to a small set of taxa, without apparent homologues among other taxonomic groups. Nelson and Buggs note that when TRGs were first identified, it was generally assumed that the phenomenon was an artifact of incomplete sampling, and that further sampling would identify orthologs of these genes and thereby reduce the number of genes that were taxonomically-restricted. However, as more taxa have been sampled, there has been an increase in the number of documented genes that are taxonomically-restricted. They comment,

> Perhaps surprisingly, this expectation was not borne out. The majority of early genome sequences were of bacteria and a 2005 study of 122 bacterial genomes showed that the number of TRGs found was rising in a linear fashion with number of genomes sequenced, showing no signs of a plateau (Wilson et al. 2005). More recently, Beiko (2011) surveyed over a thousand complete bacterial and archaeal genomes, noting that no plateau for new TRGs can yet be envisaged. 'Given the amount of novel genetic information in new genomes,' he writes, 'and the increasing rate at which genomes are being sequenced, there is consequently no reason to suspect that the rate of accumulation of novel genes will decrease in the near future'.

Nelson and Buggs survey literature pertaining to bacteria, viruses, and eukaryotes, showing that there exists a positive correlation between the number of sampled taxa and the number of TRGs.

The authors note that many TRGs have an elucidated function, and list four lines of general evidence for TRG function. First, the fact that they have been annotated is typically a consequence of expressed sequence tag (EST) data aligning to them. The fact that they are expressed, therefore, provides some evidence that they are functional. Second, a methodology developed by Wilson *et al*. (2007) for determining the probability of a protein being functional suggests that many TRGs are functional. Third, when TRGs with varying levels of taxonomic restriction are compared, it is found that there are features that correlate with the extent of taxonomic restriction (e.g. GC content and gradual decline in length). Nelson and Buggs note that "The continuum of characteristics between widespread, functionally characterized genes and restricted, little-studied genes has been taken as evidence that the latter are functional, and not artefacts." Finally, "If TRGs are functional, their frequency should correlate with the degree to which their species is ecologically or taxonomically removed from other species whose genomes have been sequenced – this seems to be the case." The authors proceed to give five specific examples of documented TRG function, drawn from viruses, archaea, bacteria, and two eukaryotic phyla (Cnidaria, and Mollusca).

They then discuss the origins of evolution of TRGs. Standard approaches to explaining the origins of novel genes are inadequate to explain TRGs, since these depend on the "duplication, reshuffling, retrotransposition and/or horizontal transfer of pre-existing coding regions." But these processes are expected to "leave behind traceable putative-progenitor sequences, detectable by similarity searches." The fact that TRGs do not resemble possible progenitor sequences does not comport well with the hypothesis of gradual evolution.

Another scenario that is often invoked to account for the evolution of TRGs is *de novo* gene birth from noncoding sequences. Nelson and Buggs note:

> Some researchers cite this mechanism for TRG s without identifying an orthologous non-coding region in a close relative (Levine et al. 2006; Begun et al. 2007; Zhou et al. 2008;

> Toll-Riera et al. 2009); as such ‘ de novo gene evolution ’ is more an observation of orphan gene existence than an understood mechanism of gene origination.

Nonetheless, other researchers have identified cases where a purported *de novo* gene can in fact be associated with orthologous non-coding sequences in other taxa. However, as Nelson and Buggs note, one could also postulate that the coding sequences gave rise to the noncoding sequences, rather than the reverse — that is to say, the non-coding orthologs could be pseudogenes. This would seem to be a more probable explanation given the implausibility of functional genes arising *de novo* by chance from noncoding sequences. For this reason, Nelson and Buggs conclude that “pseudogenization may be a more parsimonious explanation for the patterns seen.” Moreover, “Mutational hotspots could lead to non-negligible probabilities of parallel (homoplastic) disabling mutations.”

The authors note that it is unfortunate that some researchers have ignored TRGs, presuming them to be an artifact of incomplete genome drafts:

> For example, two pioneering studies of gene evolution in humans (Knowles and McLysaght 2009; Wu et al. 2011) excluded over 200 genes that had no detectable orthologs in other primates, on the assumption that their TRG status was simply due to incompleteness of other primate genome drafts. Similarly, in an analysis of gene family evolution across 12 *Drosophila* genomes, Hahn et al. (2007) ‘found 23 070 families that consisted of a single gene and that appear ed to have evolved on a terminal lineage (i.e. they are found in only a single species). These single-gene families were regarded as artefacts of the annotation process, and were removed from further analysis.

By contrast, what does a data-driven approach look like? The authors explain,

> A data-driven approach would treat TRGs that align to EST sequences as unique functional genes until proven otherwise. As Nichols et al. (2011, p. 147) argue, ‘ evolutionary conservation is not a reliable indicator of the importance of an orphan to the organism ... orphans may have evolved to fulfill an important but specialized function required by the niche of the organism ’ . It is notable that in cancer research, human genomics has led to a data- first approach that has yielded insights unanticipated by hypothesis- first approaches (Golub 2010). Similarly, genome sequencing of multiple genomes across the diversity of life is yielding insights for evolution, which were unanticipated by current paradigms (e.g. Koonin and Wolf 2008;Koonin 2009; Boto 2010).

The paper concludes by noting that, though most genes (with the exception of core genes involved in informational processing) are, to some extent, taxonomically-restricted, it has been a surprise to discover that there are many genes that are restricted to a single species or genus. This presents an enigma for the standard evolutionary account, according to which all genes are descended with modification from previously-existing ones.

- **Ola Hössjer, Ann Gauger, and Colin Reeves, “Genetic Modeling of Human History Part 2: A Unique Origin Algorithm,” *BIO-Complexity*, 2016: 4 (2016).**
  In their prior paper, these authors laid out a framework for testing models of human origins where humans share a common ancestor with chimpanzees, and also models where humans

experienced a “unique origin” and were “created with considerable diversity.” This second paper presents mathematical algorithms “for testing different historical scenarios of the human population,” including common ancestry models, and models where humans “all descend from one single couple.” Their mathematical approach can simulate human history by varying different parameters, including population expansion, bottlenecks, colonization and migration patterns, mating and reproduction schemes, and various types of mutations in automosomal chromosomes, sex chromosomes, and mitochondrial DNA. Additionally, “[a]n important parameter of the model is the created diversity of the founder generation, since it facilitates a higher degree of genetic diversity for a relatively young population within autosomal and X chromosomal regions, and possibly also for mitochondrial DNA.”

Their algorithms incorporate what they identify as the six major mechanisms of genetic change, (i) genetic drift, (ii) genetic recombination, (iii) colonization and migration, (iv) mutations, (v) natural selection, and (vi) initial created founder diversity. They note that “common descent models only include the first five mechanisms, but (vi) is important in order to generate enough diversity for a population with only one founding couple.” Indeed, they observe that a “particularly important parameter is the created diversity, which makes it possible to obtain a substantial amount of genetic diversity for nuclear autosomal and X-chromosome DNA, during a relatively short period of time.”

After going through a detailed mathematical analysis of the model they conclude, “[i]n subsequent papers, we plan to simulate human DNA data from our proposed model in order to assess how well it fits real data,” with the ultimate goal of finding “the best fitting population history within a unique origin framework, and then to compare it with a best fitting common ancestry model.”

- **Ola Hössjer, Ann Gauger, and Colin Reeves, “Genetic Modeling of Human History Part 1: Comparison of Common Descent and Unique Origin Approaches,” *BIO-Complexity*, 2016: 3 (2016).**
  Did humans evolve from apelike creatures or were they intelligently designed? According to the standard evolutionary view, humans share a common ancestor with chimpanzees, and our lineage diverged about 6 million years ago in Africa and then evolved by unguided evolutionary mechanisms into its present form. This paper evaluates the assumptions underlying the standard evolutionary model of human origins and finds “it is full of gaps and weaknesses.” Instead, the authors maintain that “a unique origin model where humanity arose from one single couple with created diversity seems to explain data at least as well, if not better.”

  After reviewing five main mechanisms invoked by standard evolutionary models of population genetics to explain human genetic diversity (mutation, genetic drift, natural selection, recombination, and colonization and migration), the paper observes that:

  > Neo-Darwinism accounts for the above-mentioned mechanisms I–V, and among them germline mutations are essentially the only way by which novel DNA can arise. The theory does not allow for large amounts of new and suddenly appearing diversity. The reason is that neo-Darwinism is framed within methodological naturalism. This prevailing approach to science only allows for natural hypotheses. But if an intelligent designer is invoked as a possible explanation, and if humanity originates from one single

> couple, it is possible that their chromosomes were created with considerable diversity from the beginning.

Thus, the authors report discovery of “a sixth mechanism of genetic change,” one which is almost universally ignored by evolutionary models: “Created founder diversity is biologically plausible for DNA of non-sex chromosomes.”

With these mechanisms in mind, the article compares standard evolutionary “common ancestry” models of human origins with “unique origin” models, where an initial pair of humans was created with significant founder diversity. There are two main common ancestry models of human origins: the Out-of-Africa model, where humans evolved in Africa and then migrated out one single time, and the Multiregional Evolution model, where humans evolved in Africa but migrated out multiple times, with different human populations around the world evolving in parallel. There are also two “unique origin” models: An African Ancestry model, where the initial created pair was located in Africa, and a Middle East ancestry model, where an initial couple was created in the Middle East and then humans migrated around the world.

The authors note that the “main argument against a unique origin is that the nucleotide diversity of human DNA data seems too high in order make a single founding couple possible.” But they argue it is possible that humans are descended from an initial couple if “they were created with genetic diversity in their autosomal and X-chromosome DNA.” What about the location of the initial couple? Non-African populations of humans seem more genetically similar compared to African humans, and they note that “the Middle East ancestry model faces some challenges, in particular to explain why African DNA looks older than non-African DNA.” However, a Middle East origin model could explain the data if “the age of humanity is much more recent” than common ancestry models predict, and if African populations experienced higher rates of genetic change and lived in isolated communities where unique diversity was easily fixed into small populations. They cite previous literature to support these ideas, making the Middle East unique origin model a realistic possibility.

The authors conclude that “Any common descent model faces a challenge to explain the genetic differences rather than the similarities with other species, the consequences of inbreeding depression and increased genetic entropy, human DNA mixture with archaic populations, and that our DNA resembles a mosaic of about four founder genomes.” Thus, they find that “The provisional conclusion is that a unique origin model seems more plausible.” But which unique origin model best explains the data? They urge future research is needed to test the two unique origins models, which is what the authors plan to do in subsequent papers. It may be that multiple models can explain the data, in which case they conclude that “the common descent model of our origin from ape-like ancestors can no longer be claimed as conclusive proof that there could not have been a single first pair.”

- **Steinar Thorvaldsen, “A Mutation Model from First Principles of the Genetic Code,” *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13 (5): 878-886 (2016).**
  This paper by Steinar Thorvaldsen, a design-friendly professor of information science at the Arctic University of Norway, presents a mathematical model to assess the impact of genetic decay on genomes. He demonstrates that proteins in bacteria appear to continuously decay, which challenges standard assumption that evolutionary processes tend to improve or at least maintain genetic information.

Thorvaldsen developed a model for neutral evolution where amino acids transition into other amino acids with a probability based on the genetic code, and he compared it to the Point Accepted Mutation (PAM) model. He demonstrates that any gene sequence free to randomly accumulate mutations would eventually approach sequences with the same equilibrium distribution of amino acids that he calls the stationary distribution. The extent to which a protein sequence genetically decayed corresponds to the extent to which the distribution of amino acids and the stationary distribution match:

> The paper presents a neutral Codons Probability Mutations (CPM) model of molecular evolution and genetic decay of an organism. … Genetic decay is quantified as a similarity between the amino acid distribution of proteins from a (group of) species on one hand, and the equilibrium distribution of the Markov chain on the other. Amino acid data for the eukaryote, bacterium, and archaea families are used to illustrate how both the CPM and PAM models predict their genetic decay towards the equilibrium value of 1.

In future studies, he hopes to expand his model to include observed functional constraints on which mutations can be tolerated.

He determined from empirical data that bacteria with shorter generation times tend to display greater levels of genetic decay:

> The results are displayed in Fig. 8, and show an overall tendency of closer distance to the steady state in warm environment bacterial proteins than in their cold environment equivalents. In total, 45 of the 66 proteins have higher steady state similarity in their warm version than in the cold version.

This observation suggests that natural selection is often not able to preserve proteins from genetically decaying since it acts on the entire organism, not individual proteins:

> Selection operates on the organism level, not on the protein level, and there may also be selection breakdown for the great majority of mutations that have small impact on fitness, and this will effect equally to both beneficial and deleterious mutations. In a recent simulation study Nelson and Sanford concluded that only a very small fraction of all non-neutral mutations are selectable within large genomes.

- **Scott T. Matuscak and Change Laura Tan, "Who are the parents of *Mycoplasma mycoides* JCVI-syn1.0?," *BIO-Complexity*, 2016: 2 (2016).**
  In 2010, the noted biotechnologist J. Craig Venter seemingly bolstered the idea that blind mechanistic processes could create life when his team announced the creation of "the first self-replicating species we've had on the planet whose parent is a computer." This peer-reviewed paper scrutinizes that research and finds that in actuality, the true parents of the bacterium *M. mycoides* were previous bacteria of the same species, with small amounts of input from yeast and *E. coli*, as well as the ingenuity of humans. After analyzing the methods used in the research, they find that "the computer was only used, passively, to store genome sequence information. It did not generate a single molecule necessary for the survival or arrival of" the bacterial cells. According to their analysis, the vast majority of the bacteria's genome was based upon DNA from the genomes of living bacteria. To be precise:

> [T]he final complete genome, 98.55% of the genome sequence was based on the natural *M. mycoides* genome sequence, 0.94% was the yeast cloning vector sequence, and 0.08% came from bacterial insertions. The last 0.43% was designed by humans in the form of watermarks, using a computer as a tool to convert the letters, numbers, and punctuation into DNA sequences.

They further observe that “the human-engineered watermark sequences do not produce any functional products within the cell, so even the small percentage of sequences that were actually designed by humans using computers do not affect the cell with respect to function (except perhaps as a burden to maintain those sequences.”) Thus, they argue that “If one were to classify the parents of an organism on the basis of the providers of the genetic sequence, then we should consider the parent of *M. mycoides* JCVI-syn1.0 to be *M. mycoides* because it provides almost 99% of the genome sequence.” They conclude that “regardless of which criteria one chooses to use in order to define what constitutes the actual parent for the *M. mycoides* JCVI-syn1.0 cells, the computer would be the least plausible candidate. It was just a place that was used by humans to store the sequences in transit. The sequence on a computer will not give birth to even a single DNA, RNA, or protein molecule of any cell.” In Venter’s research, no blind mechanisms created any new species.

- **Dustin J. Van Hofwegen, Carolyn J. Hovde, and Scott A. Minnich, “Rapid Evolution of Citrate Utilization by *Escherichia coli* by Direct Selection Requires citT and dctA,” *Journal of Bacteriology*, 198 (7): 1022-1034 (2016).**
  For years, Richard Lenski’s Long Term Evolution Experiment (LTEE) has been touted as showing that *E. coli* bacteria evolved a “new” complex trait — the ability to uptake and metabolize the molecule citrate. The LTEE required 30,000 generations and many years to acquire the supposedly “new” trait. But this peer-reviewed research study, co-authored by biologist Scott Minnich, witnessed the same trait arise in only about 12 generations and 30 days. This suggests that this trait is not very genetically complicated, and that there is more to the story than has been told. Indeed, this paper shows that no new genetic information arose during the evolution of this trait.

  LTEE proponents often fail to acknowledge that *E. coli* normally have the ability to feed on citrate — the bacteria just cannot uptake and metabolize citrate under oxic conditions. In the LTEE, bacteria evolved the ability to uptake citrate under oxic conditions (the “Cit+ phenotype”). But did anything new evolve? At the genetic level, Minnich and his coauthors’ research says the answer is “no.” To understand why, review the three primary mutations required to produce the Cit+ phenotype:

  - A mutation allowed the *E. coli* to express an antiporter protein, CitT, under oxic conditions. CitT permits one molecule of citrate to be imported into the cell in exchange for one of three less ‘valuable’ molecules with less carbon: succinate, fumarate, or malate. However, gene for this antiporter protein already existed previously, so no new gene evolved.

    CitT is usually switched off in *E. coli* when oxygen is present, but this mutation allowed it to be turned on. What caused it to become turned on? Biochemically speaking, a switch that normally represses expression of the gene that produces CitT under oxic conditions was broken via the mutation, so the citrate-uptake pathway got turned on under oxic conditions.

This isn't the evolution of a new molecular feature; it's the breaking of a molecular feature — a repressor switch.

- There was a duplication mutation of the gene for the CitT antiporter protein, allowing the bacteria to produce more of that protein. This allowed more citrate to be uptaken under oxic conditions. This too does not involved the evolution of anything new — it only involves making more of something already present.

- Another gene duplication mutation occurred for the gene that produces the protein DctA, a succinate importer. This allowed some of the succinate that had been lost in exchange for citrate to be recovered and transported back into the cell. Again, this is just making more of something already present; nothing new arose.

Thus, the mutational pathway observed in the LTEE which generated the Cit+ phenotype involves: (i) Breaking something at the molecular level (a repressor), (ii) Making more of something already present (citrate importer), and (iii) Making more of something already present (succinate importer). Such changes — breaking features at the molecular level, or making more of some pre-existing components — have been long known to be possible under Darwinian evolution. As Minnich and his coauthors explain in their paper: "No new genetic information (novel gene function) evolved." They also write, "the LTEE has not substantiated evolution in the broader sense by generation of new genetic information, i.e. a gene with a new function." They conclude:

> Finally, because this adaptation did not generate any new genetic information and only required expanded expressions of two existing transporters (citT and dctA), generation of *E. coli* Cit+ phenotypes in our estimation do not warrant consideration as a speciation event.

For microbiologists, however, a key question is why did this paper's research observe the Cit+ phenotype arise so rapidly, whereas Lenski's LTEE required a long time for the same? A commentary in the Journal of Bacteriology that accompanied this paper research paper explains:

> [T]he primary message of the paper by Van Hofwegen et al. is that the series of events used to explain adaptation in the short-transfer LTEE (and in speciation) might need to be revised. … It would appear that the delay in the LTEE experiments may not reflect need for a neutral potentiation step, but the difficulty of intermittent selection to act on frequent copy number variants. The bottleneck is in serial dilutions is hard to cross when initial improvements are due to an unstable copy number variant that is counter-selected during the intervening rapid growth period. (John Roth and Sophie Maisnier-Patin, "Re-interpreting long-term evolution experiments -- Is delayed adaptation an example of historical contingency or a consequence of intermittent selection," *Journal of Bacteriology*, Vol. 198:1009-1012 (April, 2016).)

The phrase "may not reflect need for a neutral potentiation step" means that no complex sequence of neutral mutations was needed to produce the Cit+ phenotype. Essentially this research shows that when one imposes strong selection for growth on citrate, the story isn't one of neutral evolution evolving a complex feature, but one where each step gave a successive advantage (and no step creates anything genetically new). Under the right selection pressures, this relatively simple phenotype can arise very quickly. This research shows that Lenski's work not the impressive story of a complex evolutionary pathway many claimed it was.

Most importantly, this paper shows that Lenski's work did not demonstrate the evolution of any new biochemical features. Rather, it takes pre-existing transporter proteins and over-expresses them in an unusual environment — but only by breaking a molecular switch. Biochemically, these molecules are only doing what they were already designed to do. Nothing "new" evolved here — and in that sense no new genetic information was produced.

- **Douglas D. Axe and Winston Ewert, "*Stylus* Experiments Made Easy — A Free App for Personal Computers," *BIO-Complexity*, 2016: 1 (2016).**
  Stylus is a computer program that models Darwinian evolution *in silico* by trying to evolve Chinese characters. Because Chinese characters have a structure that is related to their function, testing the evolution of Chinese characters provides a meaningful analogue for testing the evolvability of new proteins. *Stylus* thus models the Darwinian process in a more biologically realistic manner than many other would-be evolutionary simulations. This peer-reviewed paper describes and announces a free *Stylus* app for use on personal computers (Mac, PC, Linux). As the paper explains, the *Stylus* app allows users to test the evolvability of various genes (Chinese characters) provided in a library included with the program.

  Within the *Stylus* app, genes can be subjected to various types of mutations chosen in experiments run by the user. The program also shows mutation statistics, showing "the effects of point mutations on the selected gene." The degree to which mutations have optimized gene function can be displayed and exported graphically. The goal is that "the major improvement in ease of use [of *Stylus*] brought about by this new app will attract new users among professional researchers, teachers and students," creating a growing base of users, and allowing more research on protein evolution to take place.

- **Douglas D. Axe and Ann K. Gauger, "Model and Laboratory Demonstrations That Evolutionary Optimization Works Well Only If Preceded by Invention — Selection Itself Is Not Inventive," *BIO-Complexity*, 2015: 2 (2015).**
  This paper reports original experimental and theoretical research which challenges the evolvability of new protein functions. In a previous paper ("Enzyme Families--Shared Evolutionary History or Shared Design? A Study of the GABA-Aminotransferase Family"), the authors tried to experimentally convert proteins to perform the functions of other closely related proteins, and showed that such an enzyme conversion would require more mutations than would be feasible over the history of life. Darwinian evolutionists often invoke the "promiscuity hypothesis," wherein a protein has a primary function but might also have some side activity with a weakly selectable function. In time, that side-activity might be refined and optimized to perform some new function very well, and the original primary function may even be lost. In the previous paper, the authors used starting proteins with functions very different from the functions of the target proteins, which precluded promiscuity from successfully aiding the evolution of the new target protein function. This paper, however, tested the promiscuity hypothesis through both experimental lab-work and theoretical simulations.

  Experimentally, this study began with a "junk" protein with weak activity against the antibiotic ampicillin, but without a properly folded enzymatic structure for that function. It could not be improved by three rounds of random mutation and selection. In contrast, a weakly functional protein with a destabilized but properly folded structure could rapidly be optimized to wild-type levels of activity. This suggests the that promiscuity hypothesis only works if a protein already has the right kind of functional protein fold. Without that, protein promiscuity cannot lead to the evolution of a new feature.

The authors tested this same question through a theoretical study using *Stylus*, a computer model co-developed by Douglas Axe that simulates Darwinian evolution in a biologically realistic manner by evolving Chinese characters. They started with a random sequence whose product had very weak similarity to the target character, and then sought to evolve the target through random mutation and selection. This was unsuccessful. Next, they tested whether an already-existing character with some weak similarity to the target could be evolved by mutation and selection to a proficient version of the target character. Once again, this could not be done. However, they found that if the starting character was only six mutations away from optimization, it improved rapidly upon mutation and selection.

This paper thus presents both experimental and theoretical research that converge on a common conclusion: selection and mutation can refine things that already have a well-honed function, in particular where the starting protein already exists as a functional fold of the right design. But if the starting point isn't already near the final target, then unguided evolutionary mechanisms cannot generate new protein folds or novel functions.

- **Winston Ewert, "Overabundant mutations help potentiate evolution: The effect of biologically realistic mutation rates on computer models of evolution,"** ***BIO-Complexity*****, 2015: 1 (2015).** Computer simulations of evolution are often cited as demonstrating the efficacy of the Darwinian mechanism to create new complex features. But do these computer models accurately represent biological reality? In this peer-reviewed paper, computer scientist Winston Ewert analyzes computer models of evolution and finds that they use unrealistically high mutation rates which allow the artificial simulations to evolve new features much more easily than would be feasible in real biological systems. For example, Ewert finds that the programs Avida and *Ev* use "a substitution mutation rate of 0.0025 per instruction" and "a substitution rate of approximately 0.0038 per nucleotide," respectively. Yet in the real world, "viruses have mutation rates ranging from 10^{-4} to 10^{-8} per base pair per generation" and "higher organisms sho[w] mutation rates ranging from 10^{-7} to 10^{-11}." According to Ewert, "the most rapidly mutating viruses undergo mutations at a rate an order of magnitude less than these computer models." He thus finds:

  > The computer models developed thus far do not solve simple problems when using a biologically realistic mutation rate. … [W]hen using realistic mutation rates, these models no longer function effectively. This undermines the argument that they support Darwinian evolution and raises a serious challenge to claims of the effectiveness of Darwinian evolution in solving real-world biological challenges.

  In particular, Ewert finds that the overestimation of real-world mutation rates within evolutionary simulations creates severe problems for Darwinism when the evolution of a feature requires potentiating mutations — mutations that have no effect when they initially occur, but are required later in the pathway to allow some function to emerge. Ewert explains:

> The models fail due to the necessity and difficulty of obtaining potentiating mutations. That is, in each of the models, it is impossible to evolve the solution one beneficial mutation at a time. Some of the mutations necessary to solve the problem will be neutral or deleterious when they first arise. These are called potentiating mutations because they are not helpful by themselves, but introduce the potential for other mutations to be beneficial.

Using computer simulations with biologically realistic parameters, Ewert finds that biologically realistic mutation rates are simply too low to generate needed potentiating mutations. He concludes: "We have argued based on computer models and biological data that [1] potentiating mutations are necessary for adaptation, [2] individual potentiating mutations are very improbable, and [3] there are only a handful available at any point in time. If these three facts are true, there is no way that Darwinism can account for human evolution. For Darwinism to be true, one or more will have to be overturned."

- **Bhakti Niskama Shanta, "Life and consciousness - The Vedantic view,"** ***Communicative & Integrative Biology*****, 8(5): e1085138 (2015).**
This peer-reviewed paper in a mainstream biology journal promotes goal-directed, teleological, nonmechanistic, and nonreductionist Vedantic views of biology that are friendly to intelligent design. The article notes that while mainstream science "presumes life as just a chance occurrence," the Vedantic view holds that "the origin of everything material and nonmaterial is sentient and absolute (unconditioned)." It finds evidence for this viewpoint in the basic biological principle *omne vivum ex vivo* — "life comes from life," which parallels a Vedantic proverb implying that "An 'organic whole' cannot arise from parts that have to be assembled. That process can only produce inorganic, mechanical or chemical processes, not living organisms." The article then explains that Darwinian evolution cannot explain the "goal-oriented or teleological activities" found in living organisms:

> Life's ability to preserve its own species offers a significant challenge to Darwinian gradualism. Living organisms exhibit many such overtly noticeable goal-oriented or teleological activities (self-determination, self-formation, self-preservation, self-reproduction, self-restitution and so on), which make them distinct from insentient mechanical and chemical systems. Darwin's Origin of Species invokes natural selection to explain the goal-driven activities of the living organisms, but insists that random mutations are exclusively responsible for the gradual but steady appearance of more complicated organisms. This irrational inability to scientifically explain how novel body types arise in study of life and its evolution is the major deficiency of Darwinism.

These problems apply not only to the physical properties of organisms, but also to their behaviors, since "Both abiogenesis and evolution theory are outcomes of mechanistic or reductionistic thinking and that is why they cannot explain how organisms have cognitive features like thinking, feeling and willing." According to the article, consciousness is not explainable in mechanistic terms, for "Life and its evolution cannot be understood by imposing simplistic Darwinian mechanistic reductionism on sentient biological systems. Evidence is forcing biologists to go beyond physics and chemistry to properly comprehend the science of consciousness." While some may argue that these Vedantic views are different from intelligent design, such teleology in biological origins is in fact totally consonant with an intelligent paradigm of biology.

- **Winston Ewert, William A. Dembski, Robert J. Marks II, "Measuring meaningful information in images: algorithmic specified complexity," *IET Computer Vision*, 9 (6): 884-894 (2015).**
  This peer-reviewed paper applies algorithmic specified complexity (ASC) as a measure of meaning vs. randomness in a dataset, providing a rigorous mathematical analytical tool for detecting design. The authors test this methodology by comparing computer "images which contain content from those which are simply redundancies, meaningless or random noise." According their design detection model:

  > For an image to be meaningfully distinguishable, it must relate to some external independent pattern or specification. The image of the sunset is meaningful because the viewer experientially relates it to other sunsets in their experience. Any image containing content rather than random noise fits some contextual pattern. Naturally, any image looks like itself, but the requirement is that the pattern must be independent of the observation and therefore the image cannot be self-referential in establishing meaning. External context is required. If an object is both improbable and specified, we say that it exhibits 'specified complexity'."

  How can we detect whether an image contains specified complexity? They explain that it must be both uncompressible (complex) and match a pattern:

  > The more the image can be described in terms of a pattern, the more compressible it is, and the more specified. For example, a black square is entirely described by a simple pattern, and a very short computer programme suffices to recreate it. As a result, we conclude that it is highly specified. In contrast, an image of randomly selected pixels cannot be compressed much if at all, and thus we conclude that the image is not specified at all. Images with content such as sunsets take more space to describe than the black square, but are more specified than random noise. Redundancy in some images is evidenced by the ability to approximately restore groups of missing pixels from those remaining.

  A simple black square might be compressible and specified, but it is not complex. As they note, "The random image is significantly more complex, whereas the solid square is much less complex." But these are relatively easy cases. They then try to tackle more difficult images, such as a photograph of the famous scientist Louis Pasteur with increasing amounts of random noise added. As ASC predicts, the more noise that's added to the image, the lower the ASC. Similarly, resizing an image of Einstein causes it to lose clarity, and its ASC decreases. This is what their model predicts.

  What about a picture of "stick men on a sea of noise"? They found that ASC was still able to detect the presence of a complex and specified feature even when surrounded by noise. They conclude that ASC is an effective methodology for distinguishing random image data from meaningful images:

  > We have estimated the probability of various images by using the number of bits required for the PNG encoding. This allows us to approximate the ASC of the various images. We have shown hundreds of thousands of bits of ASC in various circumstances. Given the bound established on producing high levels of ASC, we conclude that the

> images containing meaningful information are not simply noise. Additionally, the simplicity of an image such as the solid square also does not exhibit ASC. Thus, we have demonstrated the theoretical applicability of ASC to the problem of distinguishing information from noise and have outlined a methodology where sizes of compressed files can be used to estimate the meaningful information content of images.

The applicability to intelligent design is clear: if ASC is a useful tool for distinguishing designed images from random ones or ones produced by some unguided algorithm, then perhaps it can be applied to biological systems or other natural structures to detect design there as well.

- **David W. Snoke, Jeffrey Cox, and Donald Petcher, "Suboptimality and Complexity in Evolution,"** ***Complexity*****, 21(1): 322-327 (September/October, 2015).**
  This article, by physicists David Snoke, Jeffery Cox, and Donald Petcher, begins by observing that in order to produce a new system, evolution must first try many new variations upon which natural selection can act in order to "find" something useful to retain. But that comes with a potentially fatal cost, since most new variations won't function, leading to the accumulation of "junk." As the authors put it: "[T]here is an additional energy cost to increased complexity. ... In real systems, building new systems is costly, and the cost of carrying along useless or redundant systems is one of the arguments for the efficiency of existing living systems, as excess baggage is dropped as too costly. The problem can be circumvented by providing an incentive system or reward for trying out new variations. This poses a catch-22 for Darwinian evolution: If the "reward" isn't high enough, nothing new ever evolves. On the other hand, if the reward is too high, too many new things are tried, many of which don't do anything useful, and the system accumulates much deleterious junk. As they explain:

  > There are two competing processes. On one hand, the energy cost of carrying vestigial systems makes them weakly deleterious, not neutral, which tends to reduce their number. Conversely, without stabs in the dark, that is, new systems which might eventually obtain new function but as yet have none, no novelty can ever occur, and no increase of complexity. Thus, if the energy cost of vestigial systems is too high, no evolution will occur.

  Evolutionary biologists often attempt to resolve this dilemma by claiming it's easy to evolve new structures, but lots of junk accumulates. These authors observe that such reasoning "has historically led evolutionary theorists to expect, that living systems carry a significant fraction of vestigial, or nonfunctional, elements, as well as quasivestigial elements which function with much less than optimal efficiency." To test this evolutionary expectation, they constructed a model that rewards evolving a new function, but that exacts a price for evolving systems that require lots of parts before providing an advantage. They found that when the model was optimized to reward the evolution of new features, it did evolve new features. Some of those features were useful. But the vast majority were not. But there was a cost for the ability to evolve something new. Before the simulation finished, the population experienced a crash because the organisms accumulated so much genetic garbage — new features that were in fact no more than useless freeloaders — that fitness dropped precipitously. Thus, the authors observe another problem: "nature does not reward complexity per se, it rewards functions that enhance survival and reproduction" and "there may be many paths to the same function, some simpler and some more complex, and all will be rewarded roughly the same whether or not the function is done elegantly or not; only the overall energy cost will deter some versions of obtaining the function." Their model tries to accommodate these facts by incorporating "(1) an energy cost for increasing number of elements produced and (2) multiple paths to beneficial functions." There is thus a ratio of reward to the cost of trying out something new:

- If the ratio is too low, then it's costly to try new things, and they will be eliminated right away. New features don't evolve.
- If the ratio is high, then new features will evolve quite easily. Initially, new complexity is generated, and strongly harmful or costly vestigial traits are eliminated. But trying lots of new variation means slightly deleterious traits cannot be weeded out. Over time unhelpful traits accumulate. Eventually such mutations pile up to an extent that the population reaches a crisis point, and crashes. The junk has become an unbearable burden. The organisms go extinct.

According to their simulation, Darwinian evolution thus either produces (1) nothing new, or (2) large amounts of junk that is ultimately deadly. In case (2), the reward for trying new things is high compared to the cost of building new structures. But in order for the ratio to be high enough for complexity to increase, the cost of building new things must be negligible. Novelties proliferate, but the fraction of the beast that's vestigial grows, and the organism is eventually swamped and overwhelmed by harmful vestigial features. However, when trying to avoid the problem of (2) by making the reward-to-cost ratio lower, as in (1), then nothing new ever evolves. Real biological organisms are closer to position (1), because there are efficient ways to get rid of nonfunctional features that exact a cost and because we don't observe systems that are full of dead weight. But if organisms are in position (1), that suggests new complex features cannot be built because it's very difficult to try new things. They conclude:

> In existing living systems, the fitness collapse seen in this model appears to be prevented by mechanisms which quickly eliminate nonfunctional elements, while leaving functional elements untouched. This type of mechanism would seem to prevent 'stabs in the dark' of any great magnitude, and thus prevent ongoing increase of complexity.

When it comes to generating viable living systems, Darwinian evolution faces a 'damned if you do, damned if you don't' dilemma. Whatever cause generated the complex functional biological features we observe, it was not unguided Darwinian evolution.

- **Wolf-Ekkehard Lönnig, "Transposons in Eukaryotes (Part B): Genomic Consequences of Transposition,"** ***eLS [Encyclopedia of Life Sciences]*****. John Wiley & Sons, Ltd: Chichester, DOI:10.1002/9780470015902.a0026265 (August, 2015).**
This peer-reviewed article reviews the role of transposable elements (TEs) and, citing to the work of Michael Behe, argues that "irreducibly complex" structures may defy explanation by TEs or standard Darwinian mechanisms:

> [M]utation and selection may not be the full explanation for the origin of species; that is, the factors of the neo-Darwinian scenario may find their limits, for example, in the generation of 'irreducibly complex structures' (Behe, 2006, 2007). This is a term used to describe structures that, according to Behe, cannot be explained by a piecemeal production via intermediate steps. Among the examples discussed by Behe are the origins of (1) the cilium, (2) the bacterial flagellum with filament, hook and motor

> embedded in the membranes and cell wall and (3) the biochemistry of blood clotting in humans. Moreover, the traps of *Utricularia* (Lönnig, 2012) and some other carnivorous plant genera as well as several further apparatus in the animal and plant world appear to pose similar problems for the modern synthesis (joints, echo location, deceptive flowers, the reproductive system of the Australian gastric brooding frog *Rheobatrachus silus*, the mechanical gears of the nymph stage of the leaf hopper *Issus coleoptratus* etc.). Up to now, none of these systems has been satisfactorily explained by neo-Darwinism. Whether accelerated TE activities with all the above named mutagenic consequences can solve the questions posed remains doubtful in the eyes of the critical observer. Moreover, natural selection itself may not have the stringency usually ascribed to it (for details, see ReMine, 1993; Lönnig, 2001, 2012, 2014).

While unguided mutational processes involving TEs seem incapable of producing irreducibly complex structures, the article notes that there may be "teleologic benefits" from TE activities: "Concerning the totally unexpected and extraordinarily high level of current DNA transposition activities in bats in clear contrast to near extinction or absence of such elements in all other mammals, Huang *et al.* (2012) give sympathetic consideration to 'teleologic benefits' (among others) promoting active DNA transposons in the order Chiroptera (perhaps via HT; Tang *et al.*, 2015). A 'pacemaker proponent' *sensu lato* may perhaps ask whether teleologic benefits could also be involved in an independent origin of the *Transip* TEs and the immune system of jawed vertebrates (not to mention teleology in the sense of Behe, 2006, 2007)."

The article also cites ID authors such as Jonathan Wells and Richard Sternberg while noting that they and other authors think that non-coding DNA is largely functional:

> In the wake of the ENCODE (encyclopedia of DNA elements) project, several authors are even favouring positions that almost approach the assumption of 100% functional DNA in all genomes, that is, there is no junk DNA in the genomes of plants and animals at all (Shapiro and von Sternberg, 2005;Wells, 2011).

It concludes by noting that "several lines of evidence" including "irreducibly complex systems" challenge current evolutionary models and should spur us to follow the evidence "wherever it may lead."

- **Mohit Mishra, Utkarsh Chaturvedi, K. K. Shukla, "Heuristic algorithm based on molecules optimizing their geometry in a crystal to solve the problem of integer factorization," *Soft Computing*, DOI 10.1007/s00500-015-1772-8 (July 23, 2015).**
  This peer-reviewed paper does not argue for intelligent design, but it uses core ID concepts as a heuristic for solving certain kinds of mathematical problems. In that regard, the paper favorably cites and employs the work of ID researchers William Dembski and Robert Marks of the Evolutionary Informatics Laboratory. The paper discusses integer factorization, or how we determine what prime numbers can be multiplied to yield another particular integer. This is essentially a search problem with applications in cryptography and other computer science questions. This is a very difficult problem but some algorithms have been developed to solve it. But which search algorithms are more efficient than others at solving the search? Such a fitness question is precisely what Dembski and Marks address in their research. The paper states:

> To quantify the quality of an objective function, we analyze our objective functions based on conservation of information in search theory (Dembski and Marks 2009).

Dembski and Marks have developed a principle of “conservation of information” which holds that if an algorithm does better than blind search, that is because it was given prior information, where the amount of prior information equals at least the measure of how far the algorithm outperforms blind search. Searches can thus perform better than a random search when they are fed information (called “active information”) to help find the target. According to their methodology, Exogenous information ($I_{‡}$) represents the difficulty of a search in finding its target with no prior information about the target's location. Active information (I_+) is the amount of information smuggled in by intelligence to aid the search algorithm in finding its target. Endogenous Information (I_S) then measures the difficulty the search will have in finding its target after the addition of Active Information. Thus, $I_+ = I_{‡} - I_S$.

After discussing various methods of solving the problem of integer factorization, this paper asks how the methods work, writing: “In this section, we analyze our objective function based on conservation of information in search (Dembski and Marks 2009).” The authors then cite to Dembski and Marks’s concepts like “endogenous information,” “exogenous information,” and “active information.” After discussing how this methodology relates to solving a search question, they conclude, “The conservation of information in search provides a way to quantify the quality of an objective function.”

What does all this have to do with Darwinian evolution? The research by Dembksi and Marks is applicable to essentially any search function. While this paper focuses on solving the problem of searching for prime numbers that can be multiplied to yield a given integer, Darwinian evolution is, at its heart, also a search algorithm. It uses a trial-and-error process of random mutation and unguided natural selection to find genotypes (i.e., DNA sequences) that lead to phenotypes (i.e., biomolecules and body plans) characterized by high fitness (i.e., fostering survival and reproduction). According to Dembski and Marks, unless you start off with some information indicating where peaks in a fitness landscape may lie, any search — including a Darwinian one — is on average no better than a random search. In some cases, even a random search can work when you have lots of probabilistic resources (i.e., time and opportunities for computation) or when there are lots of targets out there waiting to be found. Thus, Darwinian evolution can work when only one mutation is needed to give some advantage and when evolution takes place within a large, rapidly reproducing population (like we often see in bacteria).

But when targets are rare and there aren't many opportunities for the search (e.g., trying to evolve a complex multimutation feature in long-lived organisms like humans with small effective breeding populations), then such a random search won't work. The paper under discussion here doesn't address such questions. It does, however, affirm the utility of Dembski and Marks's ideas in testing the efficiency of a search function — an extremely important question in the context of evaluating Darwinian evolution.

- **Winston Ewert, W. A. Dembski and Robert J. Marks II, “Algorithmic Specified Complexity in the Game of Life,” *Systems, Man, and Cybernetics: Systems, IEEE Transactions*, 45(4): 584-594 (April 2015).**
  This paper develops algorithmic specified complexity (ASC) as an improved method of measuring the functional meaning of biological (and other forms of) information and detecting

design. The authors begin by observing that “Neither fundamental Shannon nor Kolmogorov information models are equipped” to measure “meaningful” information. Complex and specified information (CSI) has long been cited as a method of measuring the functional meaning of information. ASC is a new flavor of CSI which can measure the degree to which information is meaningful:

> The arranging of a large collection of parts into a working machine is highly improbable. However, *any* arrangement would be improbable regardless of whether the configuration had any functionality whatsoever. For this reason, neither Shannon nor KCS [Kolmogorov-Chaitin-Solomonoff] information models are capable of directly measuring meaning. Functional machines are specified — they follow some independent pattern. When something is both improbable and specified, we say that it exhibits *specified complexity*. An elaborate functional machine exemplifies high specified complexity. We propose a model, algorithmic specified complexity (ASC), whereby specified complexity can be measured in bits.

ASC is similar to KCS in that it assumes a computer environment which can describe some scenario in terms of commands in a programming language. This can allow, as they put it, a “quantitative measurement of specified complexity.”

To illustrate, they study patterns in the “Game of Life” computer simulation, such as “gliders” which move across the screen, or “Gemini,” a complex pattern which can copy itself. Ewert, Dembski, and Marks use these features of “Game of Life” to test the utility of ASC for detecting design. They find that some patterns are “simple enough that they arise from random configurations of cell space,” but “[o]thers required careful construction.” Their model predicts that high ASC patterns would arise by design, and that patterns which are known to appear randomly would have low ASC. They found that ASC is generally a good predictor of whether patterns appear at random or require design:

> We have merely calculated the probability of generating the pattern through some simply random process not through the actual Game of Life process. We hypothesized that it was close enough to differentiate randomly achievable patterns from one that were deliberately created. This appears to work, with the exception of the unix pattern. However, even that pattern was less than an order of magnitude more probable than the bound suggested. This suggests the approximation was reasonable, but there is room for improvement.
>
> We conclude that many of the machines built in the Game of Life do exhibit significant ASC. ASC was able to largely distinguish constructed patterns from those which were produced by random configurations. They do not appear to have been generated by a stochastic process approximated by the probability model we presented.

In other words, many high ASC patterns in Game of Life don’t arise randomly. But is that surprising? After all, the “Game of Life” is a computer program created by intelligent agents that’s designed to mimic living systems — systems which also have high ASC, and don’t arise randomly. As they conclude, “Our work here demonstrates the applicability of ASC to the measure of functional meaning.”

- **Stuart Burgess, Robert Lock, Jun Wang, Gene Sattler, and J. Douglas Oliver, "The Energy Benefits of the Pantograph Wing Mechanism in Flapping Flight: Case Study of a Gull," *International Journal of Micro Air Vehicles*, 7 (3): 275-284 (2015).**
  This paper, lead authored by professor of engineering design Stuart Burgess, further illustrates how life demonstrates optimal engineering principles that can inspire human engineering. Bird wings employ a 4-bar pantograph mechanism in the forearm, which reduces the required number of muscles in the wing by coupling the elbow and wrist joint together. The authors analyzed the amount that this design saves on power usage. They developed a theoretical model of inertial power for flapping flight based on the ring-billed gull. The investigators calculated the wing inertia and the flapping frequency. They then calculated the power required for the downward acceleration phase using the equation provided by another study (Berg and Rayner 1995). The also compensated for the power expended in breaking. And they calculated the power required for the upward acceleration phase by accounting for the 50% reduced inertia due to wing attraction. Finally, they calculated the minimum total power from the equation provided by another study (Norberg 1990). They determined that the 4-bar mechanism reduces the inertial power by 6.1% and the total power by .6%, which is a significant savings.

  The authors also described the efficiency of the overall wing design:

  > The inertia of bird wings is low due to a skeletal structure made from bone with high strength-to-weight and stiffness-to-weight ratios, along with multi-link lightweight feathers (Dumont 2010). In addition, the wing inertia is minimised with a mechanism in the forearm section of the wing which enables the bicep and triceps muscles to actuate the wrist joint through actuation of the elbow joint. This reduces the number of muscles in the forearm section of the wing and hence reduces the wing inertia.

  In addition, they described how the wing design could help guide the design of FMAVs (flapping micro air vehicles):

  > This paper has shown that the energy-saving advantages of the 4-bar pantograph mechanism are desirable to replicate in a human-design FMAV. Not only does energy-saving result in a better power-to-weight ratio but it also increases the range of the vehicle. An additional advantage of the pantograph mechanism is that the wing is more compact and this allows the wings to be more slender and aerodynamically efficient. … it constrains the wrist and elbow joint to move together resulting in a more co-ordinated deployment and retraction of wings.

  The implications are profound: If life appears engineered and can even be mimicked to improve human technology, can we say life itself was not designed?

- **John Sanford, Wesley Brewer, Franzine Smith, and John Baumgardner, "The waiting time problem in a model hominin population," *Theoretical Biology and Medical Modelling*, 12: 18 (2015).**
  This paper cites the research of ID theorists Michael Behe, Douglas Axe, and Ann Gauger and uses a computer simulation of Darwinian evolution to address the question, "How long does it take for the simplest biological text strings to arise and be fixed, within a hominin population?" The authors begin by noting that "Given the unique capabilities of humans, an evolving hominin

population would need to establish a great deal of new information, leading to new functionalities." They observe that Haldane's Dilemma suggests that very long time periods are required to fix multiple mutations that are required for some trait. Thus, "waiting for just the right mutation to arise in just the right location can be a rate-limiting factor in terms of the long-term evolution of any relatively small population" and "the generation and fixation of multiple specific mutations needed to combine to create a new function can require inordinately long waiting times." After favorably reviewing the work of Behe, Axe, Gauger, and others, the paper seeks to take a "fresh approach" and "use biologically realistic numerical simulations to analyze waiting times for the generation and fixation of specific strings of nucleotides of various lengths, given different mutation rates, given different selection pressures, and given different population sizes." The numerical simulation, Mendel's Accountant, allows a user to model an evolving population while modulating relevant different parameters of that population. After running the simulation, they find that "the waiting time problem is a significant constraint on the macroevolution of the classic hominin population" since "[r]outine establishment of specific beneficial strings of two or more nucleotides becomes very problematic." Indeed, they found that "For nucleotide strings of moderate length (eight or above), waiting times will typically exceed the estimated age of the universe – even when using highly favorable settings." They conclude: "To the extent that waiting time is a serious problem for classic neo-Darwinian theory, it is only reasonable that we begin to examine alternative models regarding how biological information arises."

- **Laurence A Cole, "The Evolution of the Primate, Hominid and Human Brain,"** ***Journal of Primatology*****, 4 (1), DOI:10.4172/2167-6801.1000124 (2015).**
  In this peer-reviewed paper, biochemist Laurence Cole argues that guided evolutionary processes were involved in the origin of the human brain. Cole who earned his PhD in biochemistry from the Medical College of Wisconsin and is a former faculty at Yale and the University of New Mexico, argues that larger brain sizes in humans and other primates were permitted by the development of a molecule called hyperglycosylated chorionic gonadotropin (HCG). In his view, the evolution of this molecule allowed increased nutrients to pass through the placenta during human development, allowing primate brains to grow larger.

  Cole offers a hypothesis of guided evolution of human brain enlargement where an intelligent agent — whom he identifies as "God" — was behind the process. His model requires that four specific evolutionary steps caused new biomolecules to arise which allowed increased nutrients passing through the placenta, which in turn allowed larger brain growth, which in turn allowed higher intelligence. Many other genes would have been involved in this process as well, and Cole appreciates that the whole evolutionary pathway — including these four specific events — are highly unlikely to occur by chance. He thus writes:

  > It is the evolution of CG and hyperglycosylated CG alone that led to the four clear steps in the development of the human brain and presented in the "CG/hyperglycosylated CG human evolution model". Yes it is important that these primates' brains were continuously promoted by seven brain growth genes and their coded proteins. But brain growth, however, was only permitted by the evolution of forever improving promoters of hemochorial placentation and implantation, CG and hyperglycosylated CG.
  >
  > Considering Darwin's evolution model, the human evolution model described here is somewhat strange. Normally, positive mutations, such as those which occurred with CG

> and hyperglycosylated CG might take on 100 or more functions. Positive mutation may cause a hardening of a beak or mouth leading to better eating, a strengthening of any one of 50 muscles leading to increased strength, and improvement in liver enzyme functions, an improvement in vocal functions, better wiggling of toes, and so on. Furthermore, most mutation do not lead to positive outcomes. Mutation may not happen at all. As such the odds of a mutation in the CG gene leading to increased CG biological activity may be very small, perhaps 1 in 1000 or 1 in 10,000 offspring. In the "CG/hyperglycosylated CG human evolution model", it appears like four mutation in the CG gene leading to major improvement in brain size occurred in a row, prosimian primate -(1)- lower simian primate -(2)- advanced simian primate -(3)- early hominids -(4)- humanoids. Four 1 in 1000 or 1 in 10,000 events occurring in a row appears like planned evolution rather than Darwinian evolution with remote odds of anywhere between 1 in a trillion and 1 in 10 quadrillion. This indicates that human brain development may have been planned rather than randomly evolved through Darwinian evolution. In this respect "the CG/hyperglycosylated CG human evolution model" could be suggestive of God's involvement in planning human creation as indicated in the Bible.

This model of intelligently guided evolution reflects an understanding that the likelihood of many specific mutations occurring is too low to be feasible under Darwinian evolution. The appearance of such models in the literature indicates that scientists are increasingly taking seriously the concept of intelligent design.

- **Mariclair A. Reeves, Ann K. Gauger, and Douglas D. Axe, "Enzyme Families–Shared Evolutionary History or Shared Design? A Study of the GABA-Aminotransferase Family,"** ***BIO-Complexity*****, 2014: 4 (2014).**
  When Michael Behe published *Darwin's Black Box* in 1996, he outlined irreducible complexity as a biochemical challenge to Darwinian evolution. Evolutionists responded by claiming that irreducibly complex features can be built through co-option, where a gene may be duplicated, and then the extra copy borrowed and retooled, or "co-opted," to perform some new function. This peer-reviewed research paper from protein scientists at Biologic Institute experimentally tests the co-option model, showing it's very difficult for proteins to evolve new functions.

  The project began in 2011, when Biologic researchers Ann Gauger and Douglas Axe published results of laboratory experiments trying to convert one enzyme (Kbl_2) to perform the function of another enzyme ($BioF_2$). Because these two proteins have a similar structure and are members of the same family, they are thought to be very closely related. Converting one protein to perform the function of a closely related protein is the sort of change which ought to be easily accomplished under the co-option model. However, after trying multiple combinations of different mutations, Gauger and Axe found, "successful functional conversion would in this case require seven or more" mutations. This posed a severe problem for Darwinian evolution, since a 2010 paper by Axe found that features which would require more than two harmful mutations, or more than six neutral mutations, before providing an advantage could not arise in the entire history of the earth. Axe and Gauger's 2011 study only investigated the evolvability of two proteins. Now in this 2014 paper, Axe, Gauger, and biochemist Mariclair Reeves, present new research on additional proteins from the same family, showing that they too are not amenable to an evolutionary conversion.

Their experiments examined nine other closely related enzymes to see if it is possible to convert them to perform the function of $BioF_2$. They induced all possible single mutations in the nine enzymes, and many other combinations of mutations, to determine if the enzymes could "evolve" the $BioF_2$ function. They found that this co-option scenario would require at least four mutations to convert an enzyme to function like $BioF_2$, including mutations to duplicate the gene and over-express it. Given that some of these mutations (such as duplication) would initially pose a disadvantage, it would take some 10^{15} years for the necessary mutations to arise to co-opt a protein to function like $BioF_2$ – over 100,000 times longer than the age of the earth. Clearly this is not a feasible evolutionary scenario, as they conclude: "when all laboratory experience with enzyme conversion is considered collectively in this light, it seems quite clear both that the classical recruitment explanation of enzyme diversity is severely undermined and that there is no credible evolutionary alternative."

- **David Snoke, "Systems Biology as a Research Program for Intelligent Design,"** ***BIO-Complexity*****, 2014: 3 (2014).**
  This article reviews the field of systems biology and argues that it is far more compatible with intelligent design than with unguided evolution: "Opponents of the intelligent design (ID) approach to biology have sometimes argued that the ID perspective discourages scientific investigation. To the contrary, it can be argued that the most productive new paradigm in systems biology is actually much more compatible with a belief in the intelligent design of life than with a belief in neo-Darwinian evolution. This new paradigm in system biology, which has arisen in the past ten years or so, analyzes living systems in terms of systems engineering concepts such as design, information processing, optimization, and other explicitly teleological concepts. This new paradigm offers a successful, quantitative, predictive theory for biology. Although the main practitioners of the field attribute the presence of such things to the outworking of natural selection, they cannot avoid using design language and design concepts in their research, and a straightforward look at the field indicates it is really a design approach altogether." After observing, "It has become an extremely productive paradigm in biology to look for biological systems that exhibit the properties of sophisticated engineered systems, i.e., ones that resemble methods developed by human engineers over the past few hundred years to accomplish complicated tasks," Snoke lists various features in biology that have been found to function like goal-directed, top-down engineered systems. After recounting such seemingly engineered aspects of biology, of the kind that systems biology studies, Snoke asks why systems biology has done such a good job of identifying these features of biology. He finds that the success of systems biology can be attributed to the assumptions it makes. And what are those? Snoke provides a list of assumptions that overlaps neatly with many of the assumptions of intelligent design. For example, he argues that systems biology assumes "teleology," which is to say "top-down" rather than "bottom up" design. As he puts it, systems biology assumes that biological systems were built "starting with a goal, and then working backwards to see what is needed and used to accomplish that goal." Snoke even quotes from proponents of systems biology urging biologists to recognize "the much-neglected teleological side of molecular biology." Snoke's closing words neatly deflect the objections of critics: "Many have demanded that the intelligent design paradigm must come up with a successful, predictive, quantitative program for biology, but it seems that such a program already exists right under our noses."

- **Stuart Burgess, Robert Lock, Jun Wang, Gene Sattler, and J. Douglas Oliver, "The Effect of Aerodynamic Braking on the Inertial Power Requirement of Flapping Flight: Case Study of a Gull,"** ***International Journal of Micro Air Vehicles*****, 6 (2): 117-127 (2014).**

This paper further illustrates how life demonstrates optimal engineering principles that can inspire human engineering. The lead author, Stuart Burgess, is a professor of engineering design at Bristol University, and has written extensively on the evidence for design in life. This observation directly conflicts with a central evolutionary assumption that life should often illustrate a suboptimal design logic.

The authors modeled the aerodynamic braking forces on the wing of ring-billed gull during wing deceleration. Their study was motivated by a desire to gain insights on how to better design FMAVs (flapping micro air vehicles). The investigators used a terminal velocity experiment to measure a gull's lift coefficient. They also calculated such parameters as the wing inertia, the excursion angle during flapping, and flapping frequency. And they drew from other research to determine the flapping frequency (Pennycuick 1996) and total wing flap angle (Scholey 1983). They then calculated the inertial power exerted for accelerating and decelerating the wings for the downstroke and upstroke in flight.

Their analysis identified how the dynamics of flight were optimized for energy efficiency:

> The wings are more extended during the down-stroke in order to maximise lift for flight (see Fig. 3(a) and Fig. 3(b)). The wing is partly folded during the upstroke to reduce inertia and reduce drag (see Fig. 3(c) and Fig. 3(d)). The feathers also have a structure that tends to give a one-way flow of air that further reduces resistance on the upstroke (King and McLellan, 1984).

The authors estimated the inertial power requirement to be 8.5% of the total power requirement for minimum power speed. And 50% of the kinetic energy is converted into useful aerodynamic work.

In the discussion, the investigators identified how their analysis provided insights on how to improve FMAV design:

> The analysis of aerodynamic braking on the gull has given insight into how to reduce the inertial drag of flapping micro air vehicles. The aerodynamic braking of flapping micro air vehicles can be maximised by maximising flap angle, maximising wing length (for a given inertia), minimising inertia and maximising lift coefficient. If aerodynamic braking is desired then it is important to select an actuator system that allows intermittent actuation of the wing.

If biological systems perform better than human-designed systems and can help us improve human technology, what does this say about their origin?

- **Jonathan Wells, "Membrane Patterns Carry Ontogenetic Information That Is Specified Independently of DNA,"** ***BIO-Complexity*****, 2014: 2 (2014).**
  With over 400 citations to the technical literature, this peer-reviewed article by Jonathan Wells demonstrates compellingly that embryogenesis depends on crucial sources of information that exist outside of the DNA. This ontogenetic information guides the development of an organism, but because it is derived from sources outside of the DNA, it cannot be produced by mutations in DNA. Jonathan Wells concludes that because the neo-Darwinian model of evolution requires

that variation is produced by DNA mutations, neo-Darwinism cannot account for the origin of such epigenetic and ontogenetic information that exists outside of DNA.

Wells begins by observing that for decades, biologists accepted the “central dogma” of molecular biology — without qualification — which claims genes encoded by DNA entirely determine an organism. This view essentially says “DNA makes RNA makes protein makes us.” Wells writes:

> The emphasis on genetic programs owes much to evolutionary theory — specifically, to the modern synthesis of Darwinian evolution and Mendelian genetics. According to the modern synthesis, new heritable variations originate in genetic mutations. In a 1970 interview, Monod said that with the establishment of the central dogma, “and the understanding of the random physical basis of mutation that molecular biology has also provided, the mechanism of Darwinism is at last securely founded”.

No one doubts that DNA encodes RNA, and RNA is translated to make proteins, but many other sources of information can enter the process along the way that do not stem directly from information encoded in DNA. For example, Wells observes that some of the basic axes of organismal development are in place *before* the initiation of developmental gene regulatory networks (dGRNs): “Spatial anisotropies precede — and are causally upstream of — the embryo’s dGRNs.”

Another non-DNA form of information Wells identifies is the “sugar code,” determined by complex patterns of sugar molecules, called glycans, on membrane surfaces. These molecules can carry high amounts of information since “carbohydrates can form branching chains that are far more elaborate than linear chains of nucleotides and amino acids.”

Wells also explains that “ion currents, transmembrane voltage potentials and [Endogenous Electric Fields] play significant roles in ontogeny comes from artificially disrupting them in vivo and then observing the effects of their disruption on morphogenesis,” but the information determining these electric fields is not in the DNA.

Population genetics — the mathematical basis for modern neo-Darwinian theory — is predicated upon the view that traits are encoded in DNA, and mutations in DNA produce new traits for natural selection to act upon. But since many traits aren’t determined by DNA, mutations in DNA cannot produce those traits. The very basis of the theory falls apart. Wells explains:

> As we have seen, however, the idea that embryo development is controlled by a genetic program is inconsistent with the biological evidence. Embryo development requires far more ontogenetic information than is carried by DNA sequences. Thus Neo-Darwinism is false.

This is cutting-edge biology — and Wells grounds it in hundreds of citations to the peer-reviewed literature. Papers like this show that when freed from the “central dogmas” of neo-Darwinian evolution, a theory of intelligent design can open up promising and fruitful avenues of research and thinking in biology.

- **Winston Ewert, “Complexity in Computer Simulations,” *BIO-Complexity*, 2014: 1 (2014).** Computer scientist Winston Ewert reviews the literature claiming to evolve irreducible complexity through evolutionary computer simulations and finds that “Behe’s concept of irreducible complexity has not been falsified by computer models.” After reviewing the models, including Avida, Ev, Steiner trees, geometric model, digital ears, and Tierra, Ewert finds that in many cases, the “parts” that compose the irreducibly complex systems are “too simple,” in that the programs are designed such that systems which the programs deem “functional” are very likely to evolve. “Almost all of the cases of proposed irreducible complexity consist of parts simple enough that a system of several components could be produced by chance, acting without selection. As such, they fail to demonstrate that their models can evolve irreducibly complex systems, especially on the scale of biological complexity,” he writes. This leads to a conundrum for evolutionary theorists. Since “Darwinian evolution is an ateleological process,” this means that “If a model is designed to assist the evolution of an irreducibly complex system, it is not a model of Darwinian evolution” and “Any decision in the construction of a model made with an eye towards enabling the evolution of irreducible complexity invalidates the model.” Ewert finds that this is precisely where many of these models fail. In the one case that a truly irreducibly complex system was found in a program, he found it was “designed as part of the ancestor used to seed the … simulation,” and thus did not actually evolve. According to Ewert’s analysis, computational attempts to explain the evolution of irreducible complexity have “failed on a number of fronts”:

  > Two of the models fail to satisfy the knockout test, in that they maintain functionality after parts have been removed. Almost all of the models use parts that are trivially complex, on the order of an amino acid rather than a protein in complexity. None of the models attempt to show why the mechanism used necessarily requires its parts. Finally, some of the models have been carefully designed to evolve. Thus, none of the models presented have demonstrated the ability to evolve an irreducibly complex system.

  He concludes, “The prediction of irreducible complexity in computer simulations is that such systems will not generally evolve apart from intelligent aid” and finds that this prediction “has thus far stood the test in computer models.”

- **Guillermo Gonzalez, “Setting the Stage for Habitable Planets,” *Life*, 4: 35-65 (2014).** How do habitable planets form? Are ID theorists contributing to the body of scientific literature that bears on these important questions? This peer-reviewed scientific paper by astronomer Guillermo Gonzalez (co-author of *The Privileged Planet*) reviews zones of habitability in the solar system, galaxy, and universe where life can potentially exist.

  Many have proposed that habitability zones might be expanded if life unlike that which we find on Earth is considered. Gonzalez points out that no viable examples of other forms of life have been provided: “alternative kinds of chemistry upon which life might be based are sometimes considered, but such explorations are highly speculative and have not produced viable instances.”

  ID-critics sometimes confuse those conditions which are sufficient with those that are necessary for life. Many habitability parameters are necessary for life to exist — such as a planet existing within the circumstellar habitable zone (CHZ) where liquid water can exist. But such conditions are not sufficient to bring life into existence. In fact, most ID proponents would maintain that the laws and conditions we find in nature are necessary for life to exist, but are not sufficient to bring it into existence. Gonzalez helps explain this helpful distinction:

> The conditions required for the continued existence of life on a planet are probably different and less specific than the conditions required for its origin. For example, some origin-of-life scenarios require dry land to be present and go through dry-wet cycles, something not possible on a "water world". A planet that fails to be in the required "window" for the origin of life early in its history could later be within the CHZ, but lack life. Contrariwise, a planet that was once habitable can go through a sterilization phase; it could return to a habitable state, but lack life.

A common assumption in astrobiology is that liquid water present anywhere on a planet is sufficient to make it habitable. Gonzalez argues that although we know that many planets in our solar system have or had liquid water, it is planets like earth — which is unique in our solar system for presently having liquid water on the surface — that are most likely to be habitable:

> Class I habitats maintain liquid water on the surface and are exposed to light form the host star. Earth is an example of a Class I habitat. A Class II habitat begins with surface water, but loses it within a few billion years. Mars and Venus are in Class II. Class III habitats have a subsurface water ocean that interacts with the silicate interior. Europa is an example of this class. Class IV habitats have liquid water above an ice layer, separating the liquid water from the silicate core. Ganymede and Callisto are probably examples of a Class IV habitat. In the present review, we will only consider Class I habitats, as this is the most likely class to be potentially habitable.

Gonzalez notes that at least three concepts are necessary to render a planet habitable:

1. The Circumstellar Continuously Habitable Zone (CCHZ) pertains to planets that can "maintain liquid water on its surface … over at least a few billions of years." It requires the proper "energy balance between a terrestrial planet and its host star" — an energy balance which requires multiple parameters, including distance from the host star, the nature of the planet's orbit (e.g., not tidally locked), the nature of the planet's atmosphere (e.g., not to high a greenhouse effect), the nature of the radiation coming from the host star (e.g., not too much radiation), and the stability of the host star (e.g., constant luminosity and not too many superflares).
2. The Galactic Habitable Zone (GHZ) is a concept co-developed by Gonzalez which "describes the regions of the Milky Way most likely to contain habitable planetary systems." It pertains to regions of the galaxy that contain sufficient heavy metallic elements to produce rocky habitable planets, and regions of the galaxy sufficiently removed from threats to life such as "gamma ray bursts, supernovae, comet showers and encounters with interstellar clouds."
3. The Cosmic Habitable Age (CSA) is "not a spatial zone, but rather, a temporal zone of habitability over the course of the evolution of the Universe." Gonzalez explains that "chemically-based life is not possible in the very early Universe before atoms formed or in the distant future, after all the stars burn out" and "Other considerations indicate that the boundaries of the CHA are much narrower than these extreme limits."

Gonzalex notes that exoplanets — planets outside our solar system — further show the rarity of habitable planets. According to Gonzalez, as more and more exoplanets have been discovered "it quickly became apparent that exoplanetary systems do not resemble the Solar System; this is also true when detection biases are taken into account." One common type of exoplanet is "hot Jupiters" which are large planets "in very short period orbits," or planets with "longer period eccentric orbits." Additional planets have been discovered "between the mass of Earth and Neptune ('super Earths'), as well as an abundance of Neptune mass planets." According to Figure 3 of his paper, no exoplanets have been discovered that hat an earth-like mass and earth-like planetary radius. He finds that "exoplanetary systems are generally not like the Solar System."

The Moon is vital to Earth's habitability, but Gonzalez also asks, "How likely is it for a system like the Earth and Moon to form in the protoplanetary disk?" He notes that the Earth-Moon system appears finely-tuned to remain stable where "a small decrease in the Earth-Moon angular momentum or a small increase in the Moon's mass would have caused the obliquity to be chaotic. In other words, the Moon is near its maximum mass while still avoiding chaotic obliquity variations."

Another important parameter of habitability is the presence of water — something difficult to explain since, "Earth formed in a region of the early Solar System that was very dry." One possible explanation that water was delivered to Earth on comets is problematic because it "can only account for about 10% of its crustal water inventory." For our Solar System to sustain habitable planets, some degree of fine-tuning is needed: "With a modestly different set of initial conditions and historical trajectory, as exemplified in exoplanetary systems, the Solar System would have had markedly different Jovian and terrestrial planet architectures."

Questions about the requirements for habitable planets are highly relevant to determining whether Earth, our solar system, and the Milky Way galaxy appear finely-tuned for life. This paper shows that pro-ID scientists are publishing research that is directly relevant to advancing our knowledge regarding these questions.

- **Stuart Burgess, Andrew King, and Rick Hyde, "An analysis of optimal structural features in the peacock tail feather,"** ***Optics and Laser Technology*****, 38: 329-334 (2014).**
  This peer-reviewed paper demonstrates that the peacock feather ornamentation demonstrates a highly sophisticated design strategy that is optimized for both function and beauty. The degree of optimization both provides evidence of design, and it conflicts with the evolutionary prediction that life should often demonstrate suboptimal design.

  The authors explain how peacock feathers are comprised of a stem, barbs, and smaller barbules that are arranged in a hierarchical pattern and employ a thin-film design. This strategy optimizes feathers for strength and lightness:

  > Thin-film structures give inherently high levels of stiffness and strength. The stem, barb and barbule all have a thin-film structure. In each case, the thin-film consists of a low-density foam core surrounded by one or more layers of a keratin film. … The existence of layers of a keratin skin around a low-density core leads to high structural efficiency because when a beam is subjected to bending loads, the highest stresses occur at the outer fibres.

In addition, the feathers employ several design strategies to produce a high-resolution, brightly colored display:

> The fan layout of the peacock display is very precise with each feather pointing to a common centre, as shown in Fig. 1. In addition, the eye feathers are spaced apart with a remarkable degree of uniformity. … The peacock tail feathers have an optical function of producing attractive and bright colours. The colours in the peacock tail are not pigment colours but structural colours which are produced by thin-film interference. The barbules are dark purple in the 'pupil' of the eye, blue in the 'iris' of the eye, bronze around the iris and green on the fringes.

The authors note that engineers rarely attempt to optimize a product for both utility and beauty at the same time:

> In man-made design it is generally recommended to separate functions because it is considered impossible to optimize the carrier of several combined functions. However, the peacock feather is a structure which is an exception to this design rule. The peacock is extremely optimized for several different functions simultaneously.

- **Stuart Burgess and Appolinaire C. Etoundi, "Performance Maps for a Bio-Inspired Robotic Condylar Hinge Joint,"** ***Journal of Mechanical Design*****, 136 (11): 115002 (2014).**
  This paper, lead authored by ID-friendly engineering professor Stuart Burgess, refutes the claim that the human knee appears poorly designed by demonstrating that a robotic knee modeled after the human knee most effectively meets multiple goals. The paper also demonstrates the difficulty of properly setting the parameters of the knee architecture for it to functional optimally, which demonstrates that the human knee was designed. The authors describe how their design of a robotic knee was modeled after the human knee:

  > The joint mimics the human knee joint by copying the curved surfaces of the femur and tibia and by copying the four-bar motion of the cruciate ligaments [1]. The joint is called a condylar joint because of the curved (convex–concave) interface between the femur and tibia. The motion of the cruciate ligaments can be modeled as an inverted parallelogram four-bar mechanism [2,3].

  They map several aspects of performance as parameters in their artificial knee design are changed:

  > This paper presents performance charts that map the design space of a bio-inspired robotic condylar hinge joint. The purpose of the charts is to enable designers to visualize the limits of performance of the joint and to gain insights into tradeoffs between individual aspects of performance such as mechanical advantage, sliding ratio, and range of movement.

  They identify the difficulty of engineering an efficient knee since the different components must properly interact with other components. A notable example is the part that parallels the human tibia:

> For each four-bar mechanism, the tibia profile had to be generated based on the unique motion of that four-bar mechanism and taking into account the profile of the femur condyle. This is a nontrivial task because each four-bar mechanism has a unique kinematic motion and because the cam motion of the femur–tibia must be exactly compatible with the motion of the four-bar mechanism.

The authors also described multiple complex tradeoffs in performance related to such aspects as maximum angle of defection, strength, and stability. Their analysis both demonstrates the genius of the design of the human knee and the difficulty of setting parameters properly.

- **Steinar Thorvaldsen and Peter Øhrstrøm, "Darwin's Perplexing Paradox intelligent design in nature," *Perspectives in Biology and Medicine*, 56 (1): 78-98 (Winter, 2013).**
  This paper in a prominent medical journal asserts that Darwin himself did not completely reject intelligent design and encourages modern Darwinians to consider following the same path. According to the authors, though Darwin rejected Paley's arguments for design, "he was never able to ignore the powerful experience of the beauty and complexity of an intelligently designed universe, as a whole." Contrary to ID-critics who claim ID is a recent mutation of creationism, these authors observe:

  > The term "intelligent design" is not new. It was used and discussed by Charles Darwin (1809–1882) in the years immediately after the publication of his *On the Origin of Species by Means of Natural Selection* (1859). He applied the term in an 1861 letter to Sir John F.W. Herschel (1792–1871).

  But they were not the first to use the term as "Darwin and Herschel are likely to have got the term 'intelligent design' from Professor William Whewell of Trinity College, Cambridge (1794–1866), who seems to have been the first to use it." They quote Whewell writing in 1833 nature shows "clear evidence of intelligent design, of arrangement with a benevolent end." Indeed they observe that "the conversations regarding 'design in nature' are much older, dating back to the Greeks."

  The authors seek to propose ways to blend Darwin's idea with intelligent design, noting that "neither Darwin nor any of his contemporaries found it unscientific when [Asa] Gray stated that 'variation has been led along certain beneficial lines,'" where Gray "accepted natural selection as the cause of new species, but he did not believe it to be the only cause of variation, which he considered to be initiated by some inherent power, imparted in the beginning by divine design." In their view, Darwin himself did not reject all forms of teleology in nature, arguing:

  > Darwin made a distinction between two kinds of intelligent design, one general (or cosmological), and one specific (related to the individual species). He accepted the former as a basis for a reasonable understanding of the origin of the universe, whereas he rejected the latter as relevant for a proper understanding of the living world. … For Darwin himself, the idea of a divine designer was not the problem. In fact, he had nothing against the view that universe as a whole was intelligently designed, a notion that was part of the common worldview. However, the idea of a detailed, intelligent design was in conflict with his theory of natural selection.

They argue “both sides of the modern debate can benefit significantly by investigating the arguments and views formulated in the intelligent design debate of the 1860s and 1870s.” Specifically, they propose:

> [B]oth sides may find it clarifying to refer to Darwin’s distinction between the two kinds of intelligent design. The critics of intelligent design should take into consideration that the other side actually has an interesting argument when they appeal to teleology, conceived as “teleology with teleology” (Brenner 2012), and modern advocates of intelligent design should understand why their view is considered provocative.

While ultimately the authors do not directly take a position on design in nature, they argue that the debate over design is a legitimate one which, in their view, “has yet to be generally settled.”

- **Winston Ewert, William A. Dembski, Robert J. Marks II, “Active Information in Metabiology,” *BIO-Complexity*, 2013: 4 (2013).**
  The authors analyze “metabiology,” a field developed by the Argentine-American computer scientist and mathematician Gregory Chaitin, to use mathematics and computer simulations to formally prove that Darwinian mechanisms can create new information. Metabiology uses a gene-centered model of evolution, where a simulated “genetic code” (a hypothetical computer program) can be “mutated,” and when the program “halts” or stops running, it outputs a number that correlates with the program's fitness. If the number goes up as the evolutionary simulation proceeds, this is said to show Darwinian processes can create new information. Chaitin calls metabiology an “answer” to David Berlinski’s “stinging critique of Darwinism,” but the paper’s authors find the program deviates from biological reality, requiring informational inputs donated by an intelligent source — called “active information” — and does not truly demonstrate that unguided processes can produce new information.

  Significantly, the paper finds that metabiology “pays no attention to resource limitations” and grants itself “unbounded resources and unbounded time,” thereby failing to adequately model real-world biological processes where probabilistic resources (e.g., time and population sizes) are limited. As they put it, “Metabiology’s math obscures the huge amounts of time required for the evolutionary process.” A related, unrealistic aspect of metabiology that it can systematically simulate all possible programs, which in effect allows it to completely rewrite its evolving program instantly. Such a process would never happen to genomes in biological organisms, meaning metabiology unrealistically grants access to the equivalent of unlimited computing resources.

  The authors also explain that metabiology uses a halting oracle as a source of “active information.” A halting oracle is a hypothetical meta-program that can indicate whether a given program will ever stop running. They note Chaitin admits that the halting oracle in metabiology, “is where all the creativity is really coming from in our program,” but also he admits that such an oracle is “mathematical fantasy.” The authors thus aptly observe: “A computer tool proven not to exist is admittedly at the outset an obvious major strike against a theory purporting to demonstrate reality.” They conclude:

  > In order for evolution to occur in these models, external knowledge must be imposed on the process to guide it. Metabiology thus appears to be another example where its designer makes an evolutionary model work. ... Consistent with the laws of conservation

of information, natural selection can only work using the guidance of active information, which can be provided only by a designer.

Properly understood, these programs show that evolution requires intelligent design.

- **Michael J. Denton, "The Types: A Persistent Structuralist Challenge to Darwinian Pan-Selectionism," *BIO-Complexity*, 2013: 3 (2013).**
In this paper, Michael Denton challenges the view that biological organisms are accidents of random mutation and natural selection but instead adopts a structuralist viewpoint, where body plans are like Platonic "types," programmed into the fabric of nature. According to Denton, this view, popular before Darwin wrote *Origin of Species* in 1859, "was supported by two fundamental observations: that the homologies appeared to be *non-adaptive abstract patterns*, and that in some cases they appear to have remained *invariant for hundreds of millions* of years in diverse lineages." As examples of persistent, non-adaptive patterns, he cites the pentadactyl limb structure in vertebrates, the insect body plan, or the pentamerous symmetry of echinoderms. Denton contends that structuralism can account for these non-adaptive features that pervade life.

  The Darwinian view, in contrast, is "functionalist," wherein "organisms are in essence like machines, complexes of functional parts arranged to serve particular adaptive ends." A structuralist view does not deny that adaptations exist, as structuralism "implies that organic order is a mix of two completely different types of order, generated by two different causal mechanisms: a primal order generated by natural law, and a secondary adaptive order imposed by environmental constraints (by natural selection according to Darwinists, by Lamarckian mechanisms and by intelligent design according to current design theorists)." But Denton argues that the functionalism required by Darwinian evolution cannot account for seemingly non-adaptive features. This is a major problem for Darwinism, as Denton cites "a vast universe of non-adaptive forms and patterns in nature which no biologist, not even the most convinced functionalist or Darwinist, has ever claimed to serve specific adaptive functions." Thus, "neither Darwin nor any subsequent Darwinist has ever provided cogent reasons for accepting the grand claim that all complexity in biology (including all currently non-adaptive forms) has resulted from past adaptive and purposeful shaping of structures to serve functional ends."

  So what can explain the origin of these features? Denton proposes that a structuralist view can be rehabilitated since "during the 20th century several advances in different fields have provided new support for the pre-Darwinian idea of life and its deep structures as immanent in the world order." These discoveries include the fine-tuning of the universe for life, covered by Denton in a previous paper (*BIO-Complexity*, Vol. 2013 (1).) Here, Denton adds some new parameters from biochemistry:

  - *DNA:* The chemical stability of the double-helical shape of DNA which allows it to "perform one of the most important of biological functions," including the fact that "its base sequence may contain 'complex specified information'."
  - *Protein folding:* "the rules that generate the thousand-plus known protein folds have now been largely elucidated and remarkably they amount to a set of 'laws of form' of precisely the kind sought after by early 19th-century biologists."

  - *Lipids:* Lipid membranes "arise mainly from the self-organization of the membranes themselves, by energy minimization without any direction from anything like a genetic blueprint."
  - *Microtubules:* According to Denton, "The microtubular aster is another example of a molecular form that clearly arises directly out of the intrinsic self-organizing properties of its basic constituents."

Denton explains that the specification of these structures in the genetic code is not enough to explain their functionality, and "Rather, in every case the primary natural self-organizing propensity of a particular category of matter is exploited and secondarily modified to serve some adaptive end." He likewise suggests that cell form, and even organismal form, might heavily depend on natural laws to take their shapes. In his view, "organic form at all levels of the biological hierarchy, not just at the cellular level, is essentially emergent and epigenetic, arising from complex dynamic self-organizing mechanisms during development."

Denton concludes that: "After 150 years of focused functionalist effort, the grand taxonomic system and the ascending hierarchy of homologous patterns has still not been adequately accounted for in functionalist/adaptive/Darwinian terms." The structuralist view of biology he proposes is not exactly the same as intelligent design, but it's quite compatible with a designed universe, where the laws of nature are finely-tuned to allow for complex life to exist. Just as Darwinism cannot explain these laws, these laws cannot explain all the adaptive complexity of life. Structuralist views leave plenty of room for intelligent design.

- **Stephen C. Meyer, *Darwin's Doubt: The Explosive Origin of Animal Life and the Case for Intelligent Design* (HarperOne, 2013).**
  Charles Darwin knew that there was a significant event in the history of life that his theory did not explain. In what today is known as the "Cambrian explosion," 530 million years ago, many animals suddenly appeared in the fossil record without apparent ancestors in earlier layers of rock. In *Darwin's Doubt*, Stephen C. Meyer tells the story of the mystery surrounding this explosion of animal life — a mystery that has intensified, not only because the expected ancestors of these animals have been not found, but also because scientists have learned what it takes to construct an animal. Meyer argues that the theory of intelligent design — which holds that certain features of the universe are best explained by an intelligent cause, not an undirected cause such as natural selection — is ultimately the best explanation for the origin of the Cambrian explosion. The publisher, HarperOne, conducted an external peer-review with two distinguished paleontologists and two evolutionary biologists.

- **Granville Sewell, "Entropy and Evolution," *BIO-Complexity*, 2013: 2 (2013).**
  In this paper, mathematician Granville Sewell explores whether the second law of thermodynamics poses difficulties for Darwinian evolution. Some early critics of Darwinism argued that the second law "must" pose a problem because evolutionary models require a decrease in entropy. Sewell avoids such unsophisticated arguments, but nonetheless reframes the issue to show that the second law *could potentially* be an obstacle.

  Sewell observes that evolutionists responded to older second-law criticisms via a "compensation argument," claiming that "because the Earth is an open system" that therefore "entropy can decrease in an open system, provided the decrease is compensated by entropy increases outside the system." Sewell is skeptical of that rejoinder and points out that:

> the fact that order can increase in an open system does not mean that tornados can turn rubble into houses and cars without violating the second law. And it does not mean that computers can appear on a barren planet as long as the planet receives solar energy. Something must be entering from outside which makes the appearance of computers not extremely improbable, for example, computers.

Can unguided natural causes provide the "something" to produce the kind of order required for life. Sewell again explains why the "compensation argument" fails:

> In an open system you just have to take into account what is entering (and leaving) the system when deciding what is extremely improbable and what is not. When thermal entropy decreases in an open system, there is not anything macroscopically describable happening that is extremely improbable from the microscopic point of view; rather, something is crossing the boundary that makes the decrease not extremely improbable.

He would thus formulate the following rule: "Natural (unintelligent) forces do not do macroscopically describable things that are extremely improbable from the microscopic point of view." What this means is that given the second law of thermodynamics, the compensation argument does not necessarily solve the problem for Darwinian evolution, and the second law *could* potentially be a problem for Darwinism. If Darwinian advocates were willing to candidly examine the improbabilities faced by their theory, they would see that serious questions about the second law -- among many others, of course -- remain to be answered.

- **Michael J. Denton, "The Place of Life and Man in Nature: Defending the Anthropocentric Thesis," *BIO-Complexity*, 2013: 1 (2013).**
  In this paper, Michael Denton argues that the "the order of nature is uniquely suitable for life as it exists on earth (Terran life), and specifically for living beings similar to modern humans." He opens by observing that after "the Copernican revolution and particularly after the publication of Darwin's *On the Origin of Species* … mankind, so it seemed, had no special place in nature." But this article reviews "discoveries in chemistry and biochemistry" of the past 100 years which "have reopened the 'grand debate' by providing intriguing new support for the old and seemingly obsolete anthropocentric paradigm." However, "To make the radical claim that the universe is designed for our existence," Denton observes, we must demonstrate "a cosmos where the laws of nature are uniquely fit for Terran life" rather than "exotic biochemistries" like "Star Treklike aliens." Toward this end, Denton observes that many of the basic chemical constituents on Earth -- water, carbon dioxide, oxygen and organic compounds – are specially fit for life as we know it:

  - *Carbon:* According to Denton, "carbon is unique in its ability to combine with other atoms, forming a vast and unparalleled number of compounds in combination with hydrogen, oxygen and nitrogen." Moreover "the general 'metastability' of carbon bonds and the consequent relative ease with which they can be assembled and rearranged by living systems contributes greatly to the fitness of carbon chemistry for biochemical life," and means "that no other atom is nearly as fit as carbon for the formation of complex biochemistry."
  - *Water:* Denton observes that water is "is able to hold in solution an enormous, unequalled range of diverse chemical compounds" and thus has a power as a "far greater than that of

almost any other common fluid." It has also been discovered that "the temperature range in which water is a fluid, 0–100°C, overlaps with the temperature range in which chemical bonds can be readily manipulated by biochemical system." These properties form an essential role in protein folding and the formation of the cell membrane.

- *Carbon dioxide:* CO_2 is special because it "not only distributes carbon to all corners of the hydrosphere, it also maintains the acid-base balance of the hydrosphere, generating a controlled aqueous environment in which the carbon it distributes can be assembled into living systems." In Denton's view, "No less than water, then, CO_2 is uniquely fit for carbon-based life."
- *Oxygen:* Denton points out that "The fact that oxidations, particularly of carbon and hydrogen, provide more energy than nearly all other types of chemical reactions is of particular importance."

Denton also cites "'cosmic coincidences,' the notion that the fundamental physical constants that determine the overall structure of the universe and the laws of nature must be very close to the values observed to generate a universe capable of harboring life." For example, "the 'lucky' fact that the nuclear resonances of the isotopes ^{12}C and ^{16}O are exactly what they need to be if carbon is to be synthesized and accumulate in any quantity in the interior of stars." He further finds that these finely-tuned parameters are more important for complex human physiology than simpler life, such as bacteria.

Denton closes by asking, "Can we infer that anthropocentric fine-tuning is the result of intelligent design?" He argues that "it is very hard not to be struck by the fact that the properties of the members of the vital ensemble are peculiarly fit for life as it is on earth, in a profoundly synergistic and parsimonious way," and thus "new discoveries in organic chemistry and biochemistry, unrecognized at the time, were providing the first hint that life on earth might after all be the result of design."

- **Berkley E. Gryder, Chase W. Nelson, and Samuel S. Shepard, "Biosemiotic Entropy of the Genome: Mutations and Epigenetic Imbalances Resulting in Cancer," *Entropy*, 15: 234-261 (2013).**
  ID encourages scientists to understand biological systems like designed objects. This paper thus shows how ID proponents can apply ID thinking to help approach scientific problems, like the causes of cancer. Using this approach, this paper compares living organisms to semiotic – i.e., symbol or language-based – systems in order to understand cancer. It observes:

> Recognizing living organisms as semiotic systems allows for useful analogies to be drawn from other semiotic systems. Such analogies are powerful because: (1) they give insight and understanding by relating the unfamiliar in terms of the familiar and, (2) lessons learned from other semiotic spheres (such as principles of efficient information storage and retrieval in computer science) can generate predictions and hypotheses for new frontiers in biology (such as a tree-like database structure for information storage and retrieval in the human genome). This is evidenced by the fact that biologists frequently use analogies from the familiar semiotic systems of human language and computers.

They further observe: "The DNA message is read, copied, edited, transcribed, and translated. It is striking that the most fitting terms used to describe the biochemical mechanics of life are rooted not in biology, chemistry or mechanics, but rather, in language." If the best analogies for biological systems are to designed objects, what does that say about the nature and origin of biological systems? How can this analogy help us deal with cancer? Since "cancer is a disease of genome alterations," then it is a disease caused by "deterioration of biological sign systems," which they call "biosemiotic entropy." It is the breakdown in transmission of DNA's language-based information – or biosemiotic entropy – which causes cancer. They conclude, "Understanding the existing biosemiotic systems within individuals, the parameters affecting their entropy, and their eventual deterioration leading to cancer may aid hypothesis generation for more effective treatments."

- **Richard Lock, Ravi Vaidyanathan, and Stuart Burgess, "Impact of Marine Locomotion Constraints on a Bio-Inspired Aerial-Aquatic Wing: Experimental Performance Verification," *Journal of Mechanisms and Robotics*, 6: 1 (September 11, 2013).**
  This peer-reviewed paper co-authored by ID-friendly engineer Stuart Burgess reports a model of an avian wing capable of aerial and aquatic locomotion that was inspired through the process of biomimetics. They describe the aim of their research as follows:

  > The main aim of this research is to determine optimal kinematic parameters for marine locomotion that maximize nondimensionalized performance measures (e.g., propulsive efficiency), derived from analysis of avian wing morphing mechanisms that balance competing demands of both aerial and aquatic movement. Optimization of the kinematic parameters enables the direct comparison between outstretched (aerial) and retracted (aquatic) wing morphologies and permits trade-off studies in the design space for future robotic vehicles.

  The authors tested a retracted wing as a means of propulsion in water, and they compared their experimental results to previous numerical simulations. They concluded the following:

  - Given the demonstrated thrust generation, the use of a retracted foil is a feasible flapping foil propulsion mechanism
  - Utilizing a driving mechanism that can achieve operations atSt0.8 will maximize performance of the retracted foil profile
  - Aquatic mission lengths of 1.4–10.7 h shown to be achievable utilizing retracted foil
  - The swept back foil profile reduces the required power to drive the motion to approximately a 1=4 of the equivalent extended foil profile for the same kinematic conditions, but this comes with a reduction in thrust production
  - At equivalent Strouhal numbers, the retracted foil achieves the same level of propulsive efficiency and thrust coefficient values as the extended orientation
  - Increasing flapping frequency demonstrated an improvement in foil performance, useful when considering the task-space performance measures
  - Flapping foil propulsion, either with an extended or retracted wing, is inefficient at slow speeds (<0.2 m/s)
  - Numerical model validated as potential design tool, due to tendency to over-estimate values hence introducing a factor of safety prior to actual design.

  Such research shows the utility of turning to nature to improve human technology.

- **Richard Lock, Stuart Burgess, and Ravi Vaidyanathan, "Multi-Modal Locomotion: From Animal to Application," *Bioinspiration & Biomimetics*, 9: 1: 011001 (December 16, 2013).**

This peer-reviewed paper on biomimetics analyzes the locomotive strategies of animals that move in different mediums, such as aerial and terrestrial, to gain insights on how to design automated vehicles with similar capacities. They state:

> By analysing morphologies of multi-modal locomotion in animals and understanding why specific combinations perform particularly well together, fundamental lessons and paradigms can be elucidated. These can provide a foundation for design analysis in future engineering projects. These characteristics can then be used as inspiration when considering future mobile robotic platforms.

The authors list for several animals the locomotive strategies and their performance measure in different modes of locomotion including aerial, terrestrial, aquatic, and underground. They also rank their overall performance and the extent they compromise in one area for the sake of another. They distinguish animals that use the same structures in different modes from those that use separate structures for moving in different environments.

In some birds, extended wings are used for flight and retracted wings are used for swimming. In others, wings are used for flight and legs are used for swimming. The authors observed that those animals that use different locomotion mechanisms for different modes do not completely separate their use:

> The wings actually help reduce the cost of transport of the Svalbard rock ptarmigan (*Lagopus muta hyperborea*), transitioning from walking gait, then grounded running followed by aerial running.

They summarize their conclusions as follows:

> It would appear from this initial qualitative analysis that the two multi-modal operations that would benefit from utilizing the same mechanism in both mediums is the flapping mechanism exhibited by birds in aerial/aquatic operations, and snaking and anguilliform swimming in terrestrial/aquatic operations, a lesser number than the authors had expected. In future mobile robotic platforms, engineers should attempt to identify ways in which discrete locomotion mechanisms can be used to assist additional modes through a secondary function, such as aiding stability, assisting mode transitions and increasing performance.

- **Appolinaire Etoundi, Robert Lock, Ravi Vaidyanathan, and Stuart Burgess, "A Bio-Inspired Condylar Knee Joint for Knee Prosthetics,"** ***International Journal of Design & Nature and Ecodynamics*****, 8 (3): 213-225 (2013).**
  This peer-reviewed paper on biomimetics is co-authored by Stuart Burgess, a professor of engineering design at Bristol University, who uses biomimetics to illustrate evidence for design in life. The authors present a novel prosthetic knee joint inspired by the design of the human knee. They begin by outlining the mechanics of the human knee joint and its dynamics during walking, running, and squatting. They identify key features that they wished to mimic in their prosthetic design:

    - Separation of structural (compression joint) and kinematic (four-bar mechanism) functions.

- Curved (condylar) joint giving high conformity and, therefore, high stiffness and strength.
- Moving centre of rotation giving potential for optimal mechanical advantage.
- Simplicity of design giving potential for compactness and robustness.
- Locking in upright position.

The authors then describe how their prosthetic knee models the human knee in its curved profiles to achieve the benefits of high stiffness and strength. The design also copies the four-bar motion of the ligaments with some modifications. The modified four-bar design provides stability and alleviates the need for additional ligaments to surround the joint. It also incorporates femur and tibia components that taper down to a 35-mm circular section close in size to the human bone counterparts. The curvature of the components was designed to match the moving center of rotation of the human knee's four-bar mechanism.

The authors then detail their testing of the prosthetic knee's performance. They summarize the results as follows:

> The joint mimics the condylar surfaces of the femur and tibia bones in the human knee joint and also mimics the four-bar motion of the cruciate ligaments. The bio-inspired design has the same desirable features of a human knee joint including a moving centre of rotation, high strength, high stiffness, compactness and locking in the upright position. The bio-inspired design could be used for artificial legs or for knee implants. Experimental tests have verified the kinematic, stiffness and life performance of the joint.

- **Vladimir I. shCherbak and Maxim A. Makukov, "The 'Wow! Signal' of the terrestrial genetic code,"** ***Icarus*****, 224 (1): 228-242 (May, 2013).**
  This peer-reviewed paper in the respected scientific journal *Icarus* proposes that "patterns of symbolic language" in our DNA might contain an "intelligent signature." Since "the actual scenario for the origin of terrestrial life is far from being settled," the paper argues, "the proposal that it might have been seeded intentionally cannot be ruled out." Their proposed methods for detecting design are not entirely dissimilar from those commonly proposed by ID proponents:

  > To be considered unambiguously as an intelligent signal, any patterns in the code must satisfy the following two criteria: (1) they must be highly significant statistically and (2) not only must they possess intelligent-like features, but they should be inconsistent in principle with any natural process, be it Darwinian or Lamarckian evolution, driven by amino acid biosynthesis, genomic changes, affinities between (anti)codons and amino acids, selection for the increased diversity of proteins energetics of codon-anticodon interactions, or various pre-translational mechanisms.

  The authors seem to argue for a natural, extraterrestrial intelligence, as they posture their argument as similar to a biological version of SETI. Nonetheless, the fact remains that this paper is attempting to argue for design detection within biology, placing it within ID thinking proper.

- **Winston Ewert, William A. Dembski and Robert J. Marks II, “Conservation of Information in Relative Search Performance,” *Proceedings of the 2013 IEEE 45th Southeastern Symposium on Systems Theory (SSST)*, Baylor University, March 11, 2013, pp. 41-50.**
According to this paper, the “No Free Lunch” theorems studied by William Dembski predict that “all search algorithms have the same performance on the average.” Some might argue that when search performance is compared in a relative manner, “Some algorithms look to perform better than others.” The authors find, however, that this claim does not hold, once you examine the average performance across related searches:

  > [T]his advantage is lost when averaging is over a group of related algorithms. Every advantage against one algorithm is balanced by a disadvantage against a related algorithm.

  The investigators consider the example of three treasure-hunters on an island, each searching in different places. One treasure-hunter might be able to look at the empty holes dug by another to learn that the treasure wasn’t found in that location, thereby improving his search performance. Some “searches” might have more information about the target than others, but when you take the average of the treasure-hunters performance across the entire island, they collectively perform no better than a random search. The authors conclude:

  > In order to best an algorithm, active information is required from extra knowledge of the problem. This parallels the case of the NFL requiring information about the fitness function in order to improve performance. Finally, random search exhibits the same average performance regardless of which algorithm it faces. Thus no way exists to gain an advantage on average over random search. The principle of conservation of information still applies in the case of relative performance metrics. The appearance of free lunches in relative performance metrics does not give us any way to exploit them to create generally superior optimizers.

  The implication is that Darwinian evolution, on average, can’t ever perform better than a random search.

- **Winston Ewert, William A. Dembski and Robert J. Marks II, "On the Improbability of Algorithmically Specified Complexity,'' *Proceedings of the 2013 IEEE 45th Southeastern Symposium on Systems Theory (SSST)*, Baylor University, March 11, 2013, pp. 68-70.**
The classical formulation of detecting design seeks to find complexity and specification. In other work, the Evolutionary Informatics Lab has developed algorithmic specified complexity (ACS) as a method of quantifying specification. But can ACS be a measure of the probability, or complexity of an event as well? In this paper, the authors “show a bound on the probability of obtaining a particular value of algorithmic specified complexity.” They conclude that “high ASC objects are improbable,” and useful for detecting design – objects which they call “special” compared to normal natural events.

  ACS incorporates the concept of Kolmogorov complexity, defined as the “shortest computer program length required to reproduce a specified bitstring description of an object.” This metric allows the authors to identify objects which are unlikely, but also follow predictable patterns:

  > The usefulness of this definition depends on the wide variety of constructs that are compressible. This includes for example simple pattern, such as “01” repeated 32 times. It

> also includes valid English text, which given a knowledge of the English language can be compressed. It also include complex functioning systems because they can be described by their functionality rather then the system that produces that functionality. Thus Kolmogorov complexity captures a wide variety of objects that we deem "special." Thus we can usefully apply this metric to a wide variety of objects.

They conclude, "that an object exhibiting high ASC is unlikely to arise," thus fulfilling part of the criteria for detecting design.

- **Winston Ewert, William A. Dembski, Ann K. Gauger, Robert J. Marks II, "Time and Information in Evolution,"** ***BIO-Complexity*****, 2012: 4 (2012).**
  This paper responds to a 2010 paper in *Proceedings of the U.S. National Academy of Sciences* (*PNAS*) titled "There's plenty of time for evolution," by Herbert S. Wilf and Warren J. Ewens, a biologist and a mathematician at the University of Pennsylvania. There's little doubt that Wilf and Ewens intended to respond to ID arguments. Though strategically lacking any citations to ID literature, their *PNAS* paper's abstract starts by stating, "Objections to Darwinian evolution are often based on the time required to carry out the necessary mutations," and arguing that "there has been ample time for the evolution that we observe to have taken place." Dembski, Gauger, and Marks then offer a long list of reasons why the Wilf and Ewens model of evolution isn't biologically realistic because "within their model are implicit information sources, including the equivalent of a highly informed oracle that prophesies when a mutation is 'correct,' thus accelerating the search by the evolutionary process." They also find that Wilf and Ewens "simplify the search" and incorrectly assume "no epistasis between beneficial mutations, no linkage between loci, and an unrealistic population size and base mutation rate, thus increasing the pool of beneficial mutations to be searched." In effect, Wilf and Ewens ignore the problem of non-functional intermediates, wrongly assuming that all intermediate stages will be functional, or lead to some functional advantage. Because of these, and other problems, the authors argue, Wilf and Ewens' "conclusion that there's plenty of time for evolution is unwarranted."

- **Matti Leisola, Ossi Pastinen, and Douglas D. Axe, "Lignin -- Designed Randomness,"** ***BIO-Complexity*****, 2012: 3 (2012).**
  We are used to thinking of design as a positive presence. What if the things we don't see are missing for a reason also? Lignin, a complex organic polymer found in wood, is the second most abundant biopolymer on the planet, and higher gram for gram in stored energy than the most abundant biopolymer, cellulose. Yet nothing living can directly use lignin as an energy source. Why? In this peer-reviewed paper, the authors argue that the answer is because the indigestibility of lignin may be an essential requirement for the balance of life. Lignin is an essential component of wood, but its indigestibility slows the degradation of wood, thus allowing the buildup of humus in the soil, which in turn permits plant growth and all resulting life that depends on plants. This paper thus extends design arguments into the realm of ecology.

  The authors begin by recognizing that lignin poses a conundrum for Darwinism. Neo-Darwinian theory claims that new molecular functions readily evolve but this means:

  > The Darwinian account must somehow reconcile 400 million years of failure to evolve a relatively modest innovation — growth on lignin — with a long list of spectacular innovations thought to have evolved in a fraction of that time.

They thus ask: “How can microorganisms have failed to exploit lignin as an energy source while much less evolvable species have, on innumerable occasions, acquired solutions to problems that appear to be considerably harder?” In their view:

> That tension vanishes completely when the design perspective is adopted. Terrestrial animal life is crucially dependent on terrestrial plant life, which is crucially dependent on soil, which is crucially dependent on the gradual photo- and biodegradation of lignin. Fungi accomplish the biodegradation, and the surprising fact that it costs them energy to do so keeps the process gradual. The peculiar properties of lignin therefore make perfect sense when seen as part of a coherent design for the entire ecosystem of our planet.

They conclude that lignin makes an argument for not just design in microbiology, but also in ecology: “Perhaps the oddest aspect of this is that Darwin’s theory is unable to make sense of a situation that otherwise makes perfect sense. If life is the product of intelligent design, it stands to reason that the whole design must be considered — not just the functions of molecules and cells and tissues and organs and organisms, but also the functions of entire ecosystems, all the way up to the global ecosystem.”

- **Fernando Castro-Chavez, “A Tetrahedral Representation of the Genetic Code Emphasizing Aspects of Symmetry,” *BIO-Complexity*, 2012: 2 (2012).**
  The beauty of the organization of the periodic table has long been recognized as an artifact of the aesthetic design embedded in nature. This article by Fernando Castro-Chavez, of the Department of Medicine at Baylor College of Medicine, develops new methods of visualizing the organization of the genetic code. Much like the periodic table finds there are geometric patterns to the properties of elements, Castro-Chavez proposes that “a geometric representation of the code will only be as compelling as the harmony between the chosen geometry and the biological reality.” He uses a tetrahedral shape to organize the code, where 16 of the 64 codons appear one each side. The four endpoints of the tetrahedron represent the start and stop codons, with the inner four triangles representing codons that encode hydrophobic amino acids, and wherever possible, “amino acids are grouped by salient properties.” He proposes this beautiful arrangement can lead to “new insights” into the code.

- **Winston Ewert, William A. Dembski, and Robert J. Marks II, “Climbing the Steiner Tree — Sources of Active Information in a Genetic Algorithm for Solving the Euclidean Steiner Tree Problem,” *BIO-Complexity*, 2012: 1 (2012).**
  ID-critics like mathematician David Thomas have argued that genetic algorithms mimicking natural selection can solve the Steiner tree problem, a classic problem in evolutionary computation which seeks to find the shortest pathway interconnecting a set of points. In this paper, researchers at the Evolutionary Informatics Lab argue that intelligence is necessary to solve problems like the Steiner tree. The authors explain that, “A genetic algorithm is a search algorithm that uses procedures that mimic natural selection and random mutation to determine which candidate solutions to try next,” but their research has developed a method of determining how much “active information” has been “through incorporating sources of information derived from the programmer’s prior knowledge.”

  They respond to Thomas arguing that “Thomas is under the misapprehension that intelligent design advocates claim that the actual answer is encoded into the algorithm,” whereas “This is not in fact what intelligent design advocates claim." Rather, the claim is that programmers can import active information into programs in more subtle ways, using prior knowledge to fine-tune the algorithm to find the solution. While this might be a good programming strategy, it is nothing like the blind and unguided process of Darwinian evolution since "success is due to prior knowledge being exploited to produce active information in the search algorithm." They conclude, "Only a teleological process guided by some form of intelligence can function in this way. Insofar as simulations of evolution make use of prior knowledge, they are not simulations of Darwinian evolution in any meaningful sense."

- **John C. Sanford and Chase W. Nelson, "The Next Step in Understanding Population Dynamics: Comprehensive Numerical Simulation," In: M. Carmen Fusté (ed.), *Studies in Population Genetics* (Intech Open, 2012), pp. 117-136.**
  This paper discusses a numerical simulator, Mendel's Accountant, "that can simultaneously model all the major known factors that affect genetic change, as well as their relevant interactions, to better approximate what occurs in the real world." The user can specify the species and its reproductive structure (i.e. haploid vs. diploid, genome size, mode of reproduction, etc.). Second, the user can determine the population characteristics (i.e. population size, number of generations, etc.). Third, the user can select reproductive details. Sanford and Nelson note that "The reproductive rate must always be high enough to create a population surplus each generation, such that this surplus can then be selectively removed each generation." The user can also determine the number of chromosomes and linkage blocks. Fourth, "the experimenter needs to specify the mutations that will be added to the population." The authors note that,

  > Mendel assigns mutations to individuals randomly, following a Poisson distribution. The experimenter specifies a mutation rate appropriate for the species under study (or one that is of theoretical interest). Likewise, the experimenter must specify a distribution of mutational fitness effects. Typically this distribution will include deleterious, neutral, and beneficial mutation s. The mutations that are added to the population are drawn randomly from a user-specified pool of potential mutations (usually having a Weibull distribution of fitness effects). Drawing from such a distribution, some mutations will have large effects, but most will have small (nearly-neutral) effects (Kimura, 1983), as occurs in nature (Eyre-Walker & Keightley, 2007). Each new mutation has an identifier for tracking purposes, a fitness effect, a specified degree of dominance, and a chromosomal location (i.e., a designated linkage block).

  Hundreds of millions of new mutations can be simulated during the course of an experiment. Each of these mutations "is tracked through all generations, until it is either lost or goes to fixation, or until the experiment is complete." Throughout the course of the experiment, the program monitors and plots "the average number of mutations per individual, individual and average fitness, population size history, the fitness distributions of accumulating mutations, selection threshold histories, linkage block net fitness values, and mutant allele frequencies."

  A surprising result, from an evolutionary perspective, to come out of the simulation experiments, is that the number of deleterious mutations, and of beneficial mutations, per individual have a tendency to increase over time at a constant rate. The authors observe that, though "the rapid amplification of high-impact beneficial mutations is as would be as [*sic*] expected," a striking observation was "that the large majority of beneficial mutations are too subtle to respond to selection." For the overwhelming majority of mutations (with the exception of rare strongly beneficial mutations), selection did not significantly alter the ratio of beneficial to deleterious mutations. The authors note that "Since it is well known that deleterious mutations arise much more frequently than do beneficial mutations, this means that many more functional nucleotide sites are being disrupted than are being established, even with intense selection."

The consequence of this finding is that "there should be a strong natural tendency toward net loss of genetic information over time, even while a limited number of beneficial mutations are being strongly amplified." This is surprising from an evolutionary point-of-view, since it renders it implausible that mutation and selection could be causally adequate to account for the many complex innovations that have occurred throughout the history of life.

- **Robert W. Carter and John C. Sanford, "A new look at an old virus: patterns of mutation accumulation in the human H1N1 influenza virus since 1918," *Theoretical Biology and Medical Modelling*, 9: 42 (2012).**
  This paper by two ID-friendly biologists demonstrates how mutational accumulation degrades genetic code over time. The authors present a comprehensive historical analysis of mutational changes within the influenza virus H1N1, examining over 4100 fully sequenced H1N1 genomes. Their results document multiple extinction events, including the previously known extinction of the human H1N1 lineage in 1957 and an apparent second extinction of the human H1N1 lineage in 2009. They state that the extinctions seem to be due to continuous genetic erosion from the accumulation of mutations in the lineages.

  > It is therefore reasonable to ask if the striking reduction in H1N1 mortality might be due, in part, to natural attenuation resulting from deleterious mutation accumulation. Herd immunity is undoubtedly an important factor in reduced H1N1 mortality since 1918, but this may not be sufficient to explain the continuous decline in H1N1-related mortality over multiple human generations or the eventual extinction of the viral strain. Likewise, improved medical treatments, such as antibiotic treatment for flu-related pneumonia, were certainly a significant factor reducing H1N1 mortality, but these do not appear to fully explain the nature of the pattern of mortality decline seen for H1N1. For example, the exponential decline in mortality began before the invention of antibiotic treatment.

  This paper shows the degenerative effects of mutations even in the H1N1 virus, which has access to large population sizes and causal efficacy of natural selection. Thus, this paper shows that mutations break code apart rather than build novel code using the example of the H1N1 virus. They show that the H1N1 genome has been systematically degrading since 1918.

  > This [referring to systemic degradation] is evidenced by continuous, systematic, and rapid changes in the H1N1 genome throughout its history. For example, there was an especially rapid and monotonic accumulation of mutations during a single pandemic. Similarly, there was a continuous and rapid accumulation of mutations over the entire history of the virus, including a similar steady increase in nonsynonymous amino acid substitutions. While mutations accumulated in the human H1N1s, there was a parallel accumulation of mutations in the porcine H1N1 lineage.

The authors conclude that while some beneficial mutations occur, many more deleterious mutations are also occurring at the same time. They also observed an erosion of codon bias over time without a net movement towards any single host preference). They conclude:

> It appears that the H1N1 strains currently in circulation are significantly attenuated and cannot reasonably be expected to back-mutate into a non-attenuated strain. The greatest influenza threat, therefore, is the introduction of a non-attenuated strain from some natural reservoir. This suggests that a better understanding of the origin of such non-attenuated strains should be a priority. Our findings suggest that new strategies that accelerate natural genetic attenuation of RNA viruses may prove useful for managing future pandemics and, perhaps in the long run, precluding the genesis of new influenza strains.

Design-based thinking sheds light on even the most important of topics, such as how viruses spread through populations.

- **Joseph A. Kuhn, "Dissecting Darwinism,"** ***Baylor University Medical Center Proceedings*****, 25 (1): 41-47 (2012).**
  This article by Dr. Joseph Kuhn of the Department of Surgery at Baylor University Medical Center appeared in the peer-reviewed journal *Baylor University Medical Center Proceedings*. It poses a number of challenges to both chemical and biological evolution, including:

  > 1. Limitations of the chemical origin of life data to explain the origin of DNA
  > 2. Limitations of mutation and natural selection theories to address the irreducible complexity of the cell
  > 3. Limitations of transitional species data to account for the multitude of changes involved in the transition.

  Regarding the chemical origin of life, Kuhn points to the Miller-Urey experiments and correctly observes that "the experimental conditions of a low-oxygen, nitrogen-rich reducing environment have been refuted." Citing Stephen Meyer's *Signature in the Cell*, he contends that "the fundamental and insurmountable problem with Darwinian evolution lies in the remarkable complexity and inherent information contained within DNA." Kuhn also explains that "Darwinian evolution and natural selection could not have been causes of the origin of life, because they require replication to operate, and there was no replication prior to the origin of life," but no other known cause can organize the information in life.

  Dr. Kuhn then turns to explaining the concept of irreducible complexity, citing Michael Behe's book *Darwin's Black Box* and noting that "irreducible complexity suggests that all elements of a system must be present simultaneously rather than evolve through a stepwise, sequential improvement, as theorized by Darwinian evolution." Further, "The fact that these irreducibly complex systems are specifically coded through DNA adds another layer of complexity called 'specified complexity.'" As a medical doctor, Kuhn proposes that irreducibly complex systems within the human body include "vision, balance, the respiratory system, the circulatory system, the immune system, the gastrointestinal system, the skin, the endocrine system, and taste." He concludes that "the human body represents an irreducibly complex system on a cellular and an organ/system basis."

Kuhn also explores the question of human/ape common ancestry, citing Jonathan Wells's book *The Myth of Junk DNA* and arguing:

> DNA homology between ape and man has been reported to be 96% when considering only the current protein-mapping sequences, which represent only 2% of the total genome. However, the actual similarity of the DNA is approximately 70% to 75% when considering the full genome, including the previously presumed "junk DNA," which has now been demonstrated to code for supporting elements in transcription or expression. The 25% difference represents almost 35 million single nucleotide changes and 5 million insertions or deletions.

In Dr. Kuhn's view, this poses a problem for Darwinian evolution because the "[t]he ape to human species change would require an incredibly rapid rate of mutation leading to formation of new DNA, thousands of new proteins, and untold cellular, neural, digestive, and immune-related changes in DNA, which would code for the thousands of new functioning proteins."

Kuhn also observes that a challenge to neo-Darwinism comes from the Cambrian explosion:

> Thousands of specimens were available at the time of Darwin. Millions of specimens have been classified and studied in the past 50 years. It is remarkable to note that each of these shows a virtual explosion of nearly all phyla (35/40) of the animal kingdom over a relatively short period during the Cambrian era 525 to 530 million years ago. Since that time, there has been occasional species extinction, but only rare new phyla have been convincingly identified. The seminal paper from paleoanthropologists J. Valentine and D. H. Erwin notes that the absence of transitional species for any of the Cambrian phyla limits the neo-Darwinian explanation for evolution.

Despite Texas's call for discussing the scientific strengths and weaknesses of Darwinian evolution, Kuhn closes by noting, "In 2011, when new textbooks were presented to the State Board of Education, 9 out of 10 failed to provide the mandated supplementary curricula, which would include both positive and negative aspects of evolution (44)." Citing Discovery Institute's Report on the Texas Textbooks, he laments:

> [S]everal of the textbooks continued to incorrectly promote the debunked Miller-Urey origin of life experiment, the long-discredited claims about nonfunctional appendix and tonsils, and the fraudulent embryo drawings from Ernst Haeckel. In essence, current biology students, aspiring medical students, and future scientists are not being taught the whole story. Rather, evidence suggests that they continue to receive incorrect and incomplete material that exaggerates the effect of random mutation and natural selection to account for DNA, the cell, or the transition from species to species.

Kuhn concludes, "It is therefore time to sharpen the minds of students, biologists, and physicians for the possibility of a new paradigm."

- **Kirk K. Durston, David K.Y. Chiu, Andrew K.C. Wong, and Gary C.L. Li, "Statistical discovery of site inter-dependencies in sub-molecular hierarchical protein structuring,"** ***EURASIP Journal on Bioinformatics and Systems Biology*****, 2012: 8 (2012).**

Lead author Kirk Durston is a design theorist who has published extensively on design detection methods and their application. He and his team developed a methodology that identifies how different amino acids in a protein coordinate to perform different functions. Their tool assists in identifying the design principles underlying protein structure and activities. It has already been used by another design-friendly researcher to study a region of a complex protein that was assumed by many biologists to be nonfunctional since different versions of it varied considerably in different species. The tool helped demonstrate that the region was functional. Each version is likely fine-tuned for the needs of the species that possesses it.

The authors explain how their methodology compares sequences of different versions of a protein using sophisticated statistical methods to identify how different amino acids cooperate. Clusters of cooperating amino acids are then associated with specific functions. They report on the application of their methodology to two proteins, which demonstrated its reliability:

> An important goal of our proposed work is to extend our understanding of sub-molecular, internal relationships within the 3D structure of proteins by analyzing their multiple sequence alignments. In this article, we introduce a powerful new form of analysis based on the concept of granular computing and the k-modes attribute clustering algorithm (k-modes algorithm for abbreviation) to reveal statistical associations among multiple amino acids, using the aligned sequence data of both the ubiquitin and transthyretin protein families as the test bed. … The ETM, mentioned earlier, forms clusters of highly conserved sites that, when mapped to a 3D model, are correlated with a function such as binding.

The tool proved effective in identifying coordinated amino acids and their related functions for the test proteins:

> All of the major clusters were found to be either functionally or structurally significant (Table 2). Some clusters in particular were found to have an important internal structural relationship… This result suggests that the method presented here is able to pick up local structural associations remarkably well. Furthermore, there are some cases where the associated sites of the clusters are located at a distance (e.g., sites 30, 43, 68, and 69) with binding site relationships, or other structural or functional relationships.

- **David L. Abel, "Is Life Unique?,"** ***Life*****, 2: 106-134 (2012).**
  What is it that distinguishes life from non-living entities? This peer-reviewed paper attempts to answer that question, noting that "Life pursues thousands of biofunctional goals," whereas "Neither physicodynamics, nor evolution, pursue goals." Is it possible that unguided evolution and strictly material causes produced life's purposeful processes? According to this paper, the answer is no. Life's goals include the use of "symbol systems" to maintain "homeostasis far from equilibrium in the harshest of environments, positive and negative feedback mechanisms, prevention and correction of its own errors, and organization of its components into Sustained Functional Systems." But the article notes that "the integration and regulation of biochemical pathways and cycles into homeostatic metabolism is programmatically controlled, not just physicodynamically constrained." This programming is termed "cybernetic" — yet according to the paper cybernetic control "flows only from the nonphysical world of formalism into the physical world through the instantiation of purposeful choices." Indeed, "Only purposeful choice contingency at bona fide decision nodes can rescue from eventual deterioration the

organization and function previously programmed into physicality." Life thus cannot be the result of unguided material processes — some cause capable of programming "purposeful choices" is necessary.

- **Stuart Burgess, J Wang, and Ravi Vaidyanathan, "A comparison of the efficiency of the bicycle with analogous systems in nature," *International Journal of Design & Nature and Ecodynamics*, 6 (2): 97-108 (2011).**
  This peer-reviewed paper, lead-authored by engineer Stuart Burgess, catalogues similarities in design features between birds and bicycles and argues for the optimality of biological design. Both points reinforce the argument that birds are the products of design, and they challenge the evolutionary framework, which predicts that life should often display suboptimal design.

  The authors compare the power usage of bicycles and birds at different velocities. They note that the power usage always increases for bicycles with increasing velocity, but it drops to a minimum at an intermediate velocity for birds. They compare the optimal features of bicycles and birds as follows:

  > There are several analogies between the optimal features of bicycles and the optimal features in nature. The coasting ability of a bicycle is analogous with the coasting ability of birds; the chain transmission has an analogy with the four-bar linkage in the skeletal structure of bird wings; the spoke-rim wheel layout has analogies with natural web structures; and the tyre is analogous with some of the shock absorbing structures in animals. The numerous analogies should not be surprising because the bicycle is designed primarily for speed and efficiency and has been optimised for over 100 years. Many creatures are likewise optimised for speed and efficiency.

  The authors also note that birds can use thermal inclines to increase their efficiencies beyond that of bicycles:

  > Nature shows that the bicycle is well optimised and there are no obvious areas for making dramatic improvements of efficiency in the bicycle design itself. However, one key difference with nature is that coasting animals like birds avoid steep gradients by flying on a level course or by using thermals to gain altitude. Where a cycle route has hills, they significantly increase journey time and the energy demand.

- **Douglas D. Axe, Philip Lu, and Stephanie Flatau, "A *Stylus*-Generated Artificial Genome with Analogy to Minimal Bacterial Genomes," *BIO-Complexity*, 2011: 3 (2011).**
  This peer-reviewed paper is a follow-up up to the 2008 *PLoS One* paper co-authored by Axe and Lu on *Stylus*, a computer simulation of evolution which is more faithful to biological reality than many others. This 2011 paper explains that the "functions" of the digital organisms in other simulations are often divorced from real-world meaning. They designed *Stylus* to present a more accurate picture:

  > The motivation for *Stylus* was the recognition that prior models used to study evolutionary innovation did not adequately represent the complex causal connection between genotypes and phenotypes.

  Stylus aims to correct these deficiencies by simulating Darwinian evolution in a manner that more accurately reflects the biological relationship between genotype and phenotype. It is also more realistic because it solves real-world problems. As the paper explains, "Functional specificity therefore has a structural basis in the *Stylus* world, just as it does in the real world." *Stylus* manipulates digital objects that have real-world meaning: the targets of evolution in *Stylus* are Chinese characters. As the paper explains:

> These translation products, called vector proteins, are functionless unless they form legible Chinese characters, in which case they serve the real function of writing. This coupling of artificial genetic causation to the real world of language makes evolutionary experimentation possible in a context where innovation can have a richness of variety and a depth of causal complexity that at least hints at what is needed to explain the complexity of bacterial proteomes.

These characters not only have real-world meaning, but their function-related shapes bear interesting analogies to proteins. An additional similarity between Chinese characters and proteins is that just as protein domains are re-used throughout many proteins, so particular shapes, called "strokes," are found commonly throughout Chinese characters.

Basic to life is an information conversion, where the information carried in genes (the genotype) is converted into an organism's observable traits (the phenotype). Those biological structures then perform various functions. Another way of framing this information conversion is therefore: sequence → structure → function. Axe, Lu and Flatau explain that many previous computer programs attempting to simulate evolution achieve part of this conversion, but not the whole thing.

For example, Conway's famous Game of Life starts with a structure, and in some instances that structure can perform a function. But there is no sequence involved in the conversion. Avida starts with a sequence of programming commands, and when successful performs certain logic functions. But in Avida there is no structure to mediate between sequence and function. *Stylus*, on the other hand, is more advanced in that it simulates the full sequence → structure → function information transfer. It does this by starting with a programmed genome. As the paper explains:

> [The] *Stylus* genome encodes a special kind of text, namely, one that describes how to decode the genome. That is, the desired genome will encode a sequence of Chinese characters (in the form of vector proteins) that tells a reader of Chinese how *Stylus* genes are translated into vector sequences, and how those sequences are processed to make readable vector proteins.

The paper explains: "What *Stylus* offers that no other model offers, to our knowledge, is an artificial version of gene-to-protein genetic causation that parallels the real thing."

In the world of *Stylus*, a Chinese character is like a protein. So how can we determine if a functional "protein" has evolved? According to the paper, "At the core of *Stylus* software is an algorithm that quantifies the likeness of a given vector protein to a specified Chinese character." This complicated algorithm is described as follows:

> *Stylus* endows these graphical constructs with interesting similarities to their molecular counterparts by uncovering and exploiting a pre-existing analogy -- the analogy between the set of characters used in Chinese writing and the set of protein structures used in life.

> Specifically, vector proteins are drawn objects that may function as legible Chinese characters if they are suitably formed. ... *Stylus* is unique in its use of real function that maps well to molecular biology. It therefore represents a significant advance in the field of evolutionary modeling. (internal citations omitted)

The paper presents a set of Chinese characters that can be used for simulating the evolutionary process in the *Stylus* world. But can these Chinese character groups, which have many qualities that parallel real-world protein families, evolve by random mutation and natural selection? That's the sort of question the creators of *Stylus* hope to answer. The results of such simulations will probably be fleshed out in future papers. But the current paper leaves us with a strong sense of where this is all heading:

> Evolutionary causation is intrinsically tied to the relationship between genotype and phenotype, which depends on low-level genetic causation. It follows that evolutionary explanations of the origin of functional protein systems must subordinate themselves to our understanding of how those systems operate. In other words, the study of evolutionary causation cannot enjoy the disciplinary autonomy that studies of genetic causation can.
>
> In view of this, the contribution of *Stylus* is to make evolutionary experimentation possible in a model world where low-level genetic causation has the essential role that it has in the real world. Combined with the free *Stylus* software, the complete *Stylus* genome made freely available with this paper paves the way for analogy-based studies on a wide variety of important subjects, many of which are difficult to study by direct experimentation. Among these are the evolution of new protein folds by combining existing parts, the optimality and evolutionary optimization of the genetic code, the significance of selective thresholds for the origin and optimization of protein functions, and the reliability of methods used for homology detection and phylogenetic-tree construction.

There probably will never be a perfect computer simulation of biological evolution, but *Stylus* brings new and improved methods to the field of evolutionary modeling. This tool will help those interested in testing the viability of Darwinian claims to assess whether complex features can be created by random mutations at the molecular level.

- **S.C. Burgess, J. Wang, A.C. Etoundi, R. Vaidyanathan, and J.D. Oliver, "A functional analysis of the jaw mechanism in the sling-jaw wrasse," *International Journal of Design & Nature and Ecodynamics*, 6 (4): 258-271 (2011)**
  This paper lead-authored by ID-friendly engineer Stuart Burgess uses the assumption of efficient design to guide his research. The authors uncover the design principles in the mechanism of the sling jaw wrasse. The sling-jaw wrasse is a common reef fish with a deployable mouth that it slings forward to capture prey. Burgess et al. start the reverse engineering process by visualizing a hierarchy of goals for the jaw. This is akin to a requirements analysis, which is an essential phase in any engineering process. Burgess then used a computed tomography methodology to collect data on the sling-jaw mechanism. Through analysis, they determine that the sling-jaw is a 4-bar mechanism, similar to the 4-bar Ackerman steering devices in cars or the scissors lifts at hardware stores. They then generate a numerical model of a swimming fish, including jaw deployment. When these equations are solved, it is possible to show quantitatively that the sling-jaw reduces the amount of time it takes to reach food by seven times when compared to swimming. The authors further demonstrate that catching food with the sling-jaw required 50

times less energy than using the entire body. Important takeaways include that the sling jaw wrasse contains a design motif that is also used in human engineering. Statements like "the linkage mechanism in the sling-jaw wrasse is a sophisticated mechanism that enables fast linear actuation" show Burgess et al. have uncovered key design principles for why the wrasse is designed with a sling-jaw.

- **Andrew Conn, Chung Seng Ling, and Stuart Burgess, "Biomimetic Analysis of Insect Wing Kinematics for Flapping MAVs," *International Journal of Micro Air Vehicles*, 3 (1): 1-11 (March 1, 2011).**
  In this peer reviewed paper co-authored by ID-friendly engineer Stuart Burgess, the authors apply biomimetics — the idea that living organisms can help us improve human technology. The authors analyze the design and operations of insect wings to identify how to best engineer micro air vehicles (MAVs). They began by identifying the relevant wing and flight variables and the values observed in different insects. The chosen model insect was the Hawkmoth. The also identified how insects adjusted the variables for flight stability and maneuvering. One key observation was that insects have redundant control mechanisms to increase precision over each maneuver.

  The authors then describe how the wings exploit unsteady aerodynamic mechanisms. For instance, wings moving at the right angle will create a leading-edge vortex that produces lift. They also observed that the careful timing between stroke reversal and wing rotation allows for effective fight control. The precise interaction of the wings also affects unsteady aerodynamic mechanisms to increase lift. The authors identified other examples.

  The authors then listed how their analysis of insect flight mechanics and dynamics provides direction in designing MAVs. They identified the details of insect flight that are most important to implement. They summarized their conclusions as follows:

  > Insects are believed to utilise a form of control redundancy to aid their high manoeuvrability, by having more control inputs (kinematic parameters) than controllable DOF. It may not be necessary to replicate control redundancy in a flapping MAV, but it is critical that at least one of the most influential kinematic parameters is made adjustable, namely the angle of attack, stroke amplitude and mean flapping angle of each wing. Insects rely on several unsteady aerodynamic mechanisms to augment lift production above steady-state values. Rotational lift, dynamic stall of leading edge vortices and wing-wake interactions are all influenced by the angle of attack throughout the wing stroke. Additionally, rotational lift forces have been shown to be controllable via the phase of pronation or supination relative to stroke timing, which has potential significance towards flight control.

  The implication of this sort of research is that life's design suggests it too was engineered, but in a superior manner to human technology.

- **Stephen C. Meyer and Paul A. Nelson, "Can the Origin of the Genetic Code Be Explained by Direct RNA Templating?," *BIO-Complexity*, 2011: 2 (2011).**
  This peer-reviewed paper had its origins in a debate at Biola University in 2009 where Stephen Meyer debated two critical biologists. One of those scientists was Arthur Hunt from the University of Kentucky, who had previously cited the research of Michael Yarus which proposed

that certain chemical affinities between RNA triplets and amino acids could have formed a chemical basis for the origin of the genetic code. According to Hunt, Yarus's research showed that "chemistry and physics … can account for the origin of the genetic code" and thus "the very heart of Meyer's thesis (and his book [Signature in the Cell]) is wrong." Meyer and Nelson's *BIO-Complexity* paper responds to Yarus's claims, showing that when challenged, ID proponents can produce compelling technical rebuttals. According to their detailed response, Yarus's (and Hunts') claims fail due to "selective use of data, incorrect null models, a weak signal even from positive results, … and unsupported assumptions about the pre-biotic availability of amino acids." Rather than refuting design, the research shows the need for "an intelligently-directed" origin of the code.

- **Ann K. Gauger and Douglas D. Axe, "The Evolutionary Accessibility of New Enzyme Functions: A Case Study from the Biotin Pathway," *BIO-Complexity*, 2011: 1 (2011).**
  This paper reports research conducted by Biologic Institute scientists Ann Gauger and Douglas Axe on the number of minimum changes that would be required to evolve one protein into another protein with a different function. The investigators studied two proteins, Kbl and BioF, with different functions but highly similar structures -- thought by evolutionists to be very closely related. Through mutational analysis, Gauger and Axe found that a minimum of *seven* independent mutations -- and probably many more -- would be necessary to convert Kbl to perform the function of its allegedly close genetic relative, BioF. Per Axe's 2010 *BIO-Complexity* paper, "The Limits of Complex Adaptation: An Analysis Based on a Simple Model of Structured Bacterial Populations," they report that this is beyond the limits of Darwinian evolution:

  > The extent to which Darwinian evolution can explain enzymatic innovation seems, on careful inspection, to be very limited. Large-scale innovations that result in new protein folds appear to be well outside its range. This paper argues that at least some small-scale innovations may also be beyond its reach. If studies of this kind continue to imply that this is typical rather than exceptional, then answers to the most interesting origins questions will probably remain elusive until the full range of explanatory alternatives is considered.

- **Ann K. Gauger, Stephanie Ebnet, Pamela F. Fahey, and Ralph Seelke, "Reductive Evolution Can Prevent Populations from Taking Simple Adaptive Paths to High Fitness," *BIO-Complexity*, 2010: 2 (2010).**
  This research, published by molecular biologist Ann Gauger of the Biologic Institute, Ralph Seelke at the University of Wisconsin Superior started by breaking a gene in the bacterium *Escherichia coli* required for synthesizing the amino acid tryptophan. When the gene was broken in just one place, random mutations in the bacteria's genome were capable of "fixing" the gene. But when two mutations were required to restore function, Darwinian evolution could not do the job. Such results show that it is extremely unlikely for blind and unguided Darwinian processes to find rare amino-acid sequences that yield functional proteins. In essence, functional proteins are multi-mutation features in the extreme.

- **Michael J. Behe, "Experimental Evolution, Loss-of-Function Mutations, and 'The First Rule of Adaptive Evolution,'" *The Quarterly Review of Biology*, 85 (4): 1-27 (December 2010).**
  This peer-reviewed paper by Michael Behe in the journal *Quarterly Review of Biology* helps explain why we don't observe the evolution of new protein functions. After reviewing many studies on bacterial and viral evolution, he concluded that most adaptations at the molecular level "are due to the loss or modification of a pre-existing molecular function." In other words,

since Darwinian evolution proceeds along the path of least resistance, Behe found that organisms are far more likely to evolve by a losing a biochemical function than by gaining one. He thus concluded that “the rate of appearance of an adaptive mutation that would arise from the diminishment or elimination of the activity of a protein is expected to be 100-1000 times the rate of appearance of an adaptive mutation that requires specific changes to a gene.” If Behe is correct, then molecular evolution faces a severe problem. If a loss (or decrease) of function is much more likely than a gain-of-function, logic dictates that eventually an evolving population will run out of molecular functions to lose or diminish. Behe’s paper suggests that if Darwinian evolution is at work, something else must be generating the information for new molecular functions.

- **Douglas D. Axe, “The Limits of Complex Adaptation: An Analysis Based on a Simple Model of Structured Bacterial Populations,” *BIO-Complexity*, 2010: 4 (2010).**
  The ability of Darwinian evolution to produce features that require multiple mutations before providing a benefit has been an issue long debated between proponents of intelligent design and proponents of neo-Darwinism. This paper responds to arguments from Michael Lynch and Adam Abegg, finding that they made a mistake -- actually two mistakes -- in their calculation of the length of time required for multiple mutations to occur when there is no adaptive benefit until all mutations are in place.

  The purpose of Axe’s paper is then to mathematically determine how much time is needed to evolve traits that require multiple mutations before any adaptive benefit is conferred on the organism. He notes that there are essentially three models that might be invoked to explain the origin of these complex features: molecular saltation, sequential fixation, and stochastic tunneling. Axe’s paper tackles stochastic tunneling, a model that is in a sense midway between the molecular saltation and sequential fixation models. According to Axe, stochastic tunneling “differs from sequential fixation only in that it depends on each successive point mutation appearing without the prior one having become fixed.” However, because the prior mutations are not yet fixed in the larger population, this means that the number of organisms that have the prior mutations may be small. Thus, this mechanism “must instead rely on the necessary mutations appearing within much smaller subpopulations,” or as Axe models it, bacterial lines. This model resembles molecular saltation in that it depends on all required mutations eventually appearing by chance -- but anticipates this will happen after mutations are fixed in smaller subpopulations. Axe explains why all of these models face unavoidable statistical improbabilities: “in view of the fact that the underlying limitation is an unavoidable aspect of statistics -- that independent rare events only very rarely occur in combination -- it seems certain that all chance-based mechanisms must encounter it.”

  Axe thus aims to accurately model the evolution of a multi-mutation feature. He investigates two cases: (1) when intermediate mutations are slightly disadvantageous, and (2) when intermediate mutations are selectively neutral. Axe seeks to give neo-Darwinian evolution a generous helping of probabilistic resources by modeling the evolution of bacteria -- asexual organisms that reproduce quickly and have very large effective population sizes. Unsurprisingly, Axe found that Darwinian evolution has great difficulty fixing multiple mutations when those mutations have negative selection coefficients (i.e., they are disadvantageous, or maladaptive). Neutral mutations have a better shot at becoming fixed, but even here Axe finds that the ability of neo-Darwinian evolution to produce multi-mutation features is severely limited. The implications of this analysis for Darwinian evolution are large and negative. Axe’s model made assumptions which were very generous towards Darwinian evolution. He assumed the existence of a huge population of asexually reproducing bacteria that could replicate quickly -- perhaps nearly three times per day -- over the course of billions of years. In these circumstances, complex adaptations requiring up to six mutations with neutral intermediates can become fixed. Beyond that, things become implausible. If only slightly maladaptive intermediate mutations are required for a complex adaptation, only a couple of mutations (at most two) could be fixed. If highly maladaptive mutations are required, the trait will never appear. Axe discusses the implications of his work:

> In the end, the conclusion that complex adaptations cannot be very complex without running into feasibility problems appears to be robust. ... Although studies of this kind tend to be interpreted as supporting the Darwinian paradigm, the present study indicates otherwise, underscoring the importance of combining careful measurements with the appropriate population models.

Axe's paper, because it focuses on bacteria, does not model the evolution of sexually reproducing organisms. In sexually reproducing eukaryotic organisms, the longer generation times and lower effective population sizes would dramatically lower the number of mutations that could be fixed before acquiring some adaptive benefit. In vertebrate evolution, the probabilistic resources available to Darwinian evolution would be much smaller than those available to bacteria, and the result proportionately difficult to explain along Darwinian lines. Some other mechanism must be generating complex multi-mutation features.

- **Wolf-Ekkehard Lönnig, "Mutagenesis in *Physalis pubescens* L. ssp. *floridana*: Some further research on Dollo's Law and the Law of Recurrent Variation," *Floriculture and Ornamental Biotechnology*, 1-21 (2010).**
  This original research paper on mutagenesis in plants favorably cites "intelligent design proponents," including Michael Behe, William Dembski, Jonathan Wells, and Stephen Meyer, as advocating one of various legitimate "scientific theories on the origin of species." Citing skeptics of neo-Darwinism such as Behe and "the almost 900 scientists of the Scientific Dissent from Darwinism," the paper notes that:

  > Many of these researchers also raise the question (among others), why -- even after inducing literally billions of induced mutations and (further) chromosome rearrangements -- all the important mutation breeding programs have come to an end in the Western world instead of eliciting a revolution in plant breeding, either by successive rounds of selective "micromutations" (cumulative selection in the sense of the modern synthesis), or by "larger mutations" ... and why the law of recurrent variation is endlessly corroborated by the almost infinite repetition of the spectra of mutant phenotypes in each and any new extensive mutagenesis experiment (as predicted) instead of regularly producing a range of new systematic species...

  Lönnig focuses on the origin of a particular trait found in some angiosperms, where longer sepals form a shelter for developing fruit called inflated calyx syndrome, or "ICS." According to Lönnig, phylogenetic data indicate that under a neo-Darwinian interpretation, this trait was either lost in multiple lineages or evolved independently multiple times. If the trait evolved multiple times independently, then why do so many plants still lack such a "lantern" protective shelter? After noting that some proponents of neo-Darwinism make unfalsifiable appeals to unknown selective advantages, he concludes that neo-Darwinism is not making falsifiable predictions and finds that this "infinity of mostly non-testable explanations (often just-so-stories) itself may put the theory outside science."

However, there is another possibility, namely the scientific hypothesis of intelligent design. In contrast to neo-Darwinism, the author notes the ID view can "be falsified by proving (among other points) that the probability to form an ICS by purely natural processes is high, that specified complexity is low, and finally, by generating an ICS by random mutations in a species displaying none." Lönnig recounts the many phrases Darwin used to explain that his theory of evolution requires "innumerable slight variations," and argues that the ICS could not evolve in such a stepwise fashion. After reviewing the multiple complex steps involved in forming an ICS, he states that his research "appears to be in agreement with Behe's studies (2007): it seems to be very improbable that the current evolutionary theories like the modern synthesis (continuous evolution) or the hopeful monster approach (in one or very few steps) can satisfactorily explain the origin of the ICS." In closing, Lönnig cites further Behe's concept of irreducible complexity and Dembski's arguments regarding the universal probability bound, contending that the ICS may be beyond the edge of evolution. Nevertheless, he leaves the present question open for further research, which he enthusiastically invites. Yet, citing the work of Stephen Meyer, William Dembski, and Robert Marks, he concludes that "it appears to be more than unlikely to generate the whole world of living organisms by the neo-Darwinian method."

- **George Montañez, Winston Ewert, William A. Dembski, and Robert J. Marks II, "A Vivisection of the ev Computer Organism: Identifying Sources of Active Information,"** ***BIO-Complexity*****, 2010: 3 (2010).**
  This paper continues the work of the Evolutionary Informatics Lab showing that some cause other than Darwinian mechanisms is required to produce new information. Thomas Schneider's "ev" program has been widely cited as showing that Darwinian processes can increase information. In this peer-reviewed paper, William Dembski and his coauthors demonstrate that, contrary to such claims, the "ev" program is in fact rigged to produce a particular outcome. According to the paper ev "exploit[s] one or more sources of knowledge to make the [evolutionary] search successful" and this knowledge "predisposes the search towards its target." They explain how the program smuggles in active information:

  > The success of ev is largely due to active information introduced by the Hamming oracle and from the perceptron structure. It is not due to the evolutionary algorithm used to perform the search. Indeed, other algorithms are shown to mine active information more efficiently from the knowledge sources provided by ev.
  >
  > Schneider claims that ev demonstrates that naturally occurring genetic systems gain information by evolutionary processes and that "information gain can occur by punctuated equilibrium." Our results show that, contrary to these claims, ev does not demonstrate "that biological information...can rapidly appear in genetic control systems subjected to replication, mutation, and selection." We show this by demonstrating that there are at least five sources of active information in ev.
  >
  > 1. The perceptron structure. The perceptron structure is predisposed to generating strings of ones sprinkled by zeros or strings of zeros sprinkled by ones. Since the binding site target

is mostly zeros with a few ones, there is a greater predisposition to generate the target than if it were, for example, a set of ones and zeros produced by the flipping of a fair coin.

2. The Hamming Oracle. When some offspring are correctly announced as more fit than others, external knowledge is being applied to the search and active information is introduced. As with the child's game, we are being told with respect to the solution whether we are getting "colder" or "warmer."

3. Repeated Queries. Two queries contain more information than one. Repeated queries can contribute active information.

4. Optimization by Mutation. This process discards mutations with low fitness and propagates those with high fitness. When the mutation rate is small, this process resembles a simple Markov birth process that converges to the target.

5. Degree of Mutation. As seen in Figure 3, the degree of mutation for ev must be tuned to a band of workable values.

A critic might claim that some of these items represent a proper modeling of Darwinian evolution. However, the way that ev uses these processes is unlike Darwinian evolution. For example, in (1), we see that the program's use of a "perceptron" causes the output to be highly biased towards matching the target. It's a way of cheating to ensure the program reaches its target sequence. Likewise, in (2) and (4), the program can effectively look ahead and march in the right direction towards the target, whereas unguided Darwinian evolution would have no "look ahead" capability. The active information in the Hamming Oracle makes a sharp contrast with the evolution of real binding sites where there may be no binding capability until multiple mutations are fixed.

Mutation and selection are not the causes of success in these genetic algorithms. Yes, random mutation occurs and yes, there is selection. But selection is performed by a fitness function that is encoded by the programmer. And in programs like ev, the programmer intentionally shapes the fitness function to be amenable to stepwise Darwinian evolution. This effectively assumes the truth of Darwinian evolution. But in the real world of biology, fitness functions might look very different: there might be lonely islands of function in a vast sea of nonfunctional sequences. Indeed, if one uses a randomized fitness function, the search performs poorly and might not even outperform a blind search.

Thus choosing the right fitness function (from the set of possible fitness functions) requires as much or more information than choosing the right string from the set of possible strings in your search space. The fitness function itself is an information-rich structure. The program starts with this information-rich fitness function, and then produces something much less information rich -- the target sequence. And as the paper shows, ev does this in a relatively inefficient way: using the same information-rich fitness function, you can find the target 700 times more efficiently than by using simple single-agent stochastic hill climbing. Active information is smuggled into the fitness function. Rather than showing that information can arise by Darwinian evolution, ev shows that intelligence is required.

- **William A. Dembski and Robert J. Marks II, "The Search for a Search: Measuring the Information Cost of Higher Level Search,"** ***Journal of Advanced Computational Intelligence and Intelligent Informatics*****, 14 (5): 475-486 (2010).**
  This paper by leading ID theorists William Dembski and Robert Marks argues that without information about a target, anything greater than a trivial search is bound to fail: "Needle-in-the-haystack problems look for small targets in large spaces. In such cases, blind search stands no hope of success." They cite "No Free Lunch theorems," according to which "any search technique will work, on average, as well as a blind search." However, in such a case, "Success requires an assisted search. But whence the assistance required for a search to be successful?" Dembski and Marks thus argue that "successful searches do not emerge spontaneously but need themselves to be discovered via a search." However, without information about the target, the search for a search itself is still no better than a blind search: "We prove two results: (1) The Horizontal No Free Lunch Theorem, which shows that average relative performance of searches never exceeds unassisted or blind searches, and (2) The Vertical No Free Lunch Theorem, which shows that the difficulty of searching for a successful search increases exponentially with respect to the minimum allowable active information being sought." The implication, of course, is that without the ultimate input from an intelligent agent -- active information -- such searches will fail.

- **Richard Lock, Ravi Vaidyanathan, Stuart Burgess, and John Loveless, "Development of a Biologically Inspired Multi-Modal Wing Model for Aerial-Aquatic Robotic Vehicles through Empirical and Numerical Modelling of the Common Guillemot, Uria Aalge,"** ***Bioinspiration & Biomimetics*****, 5: 4 (2010).**
  The authors, who include ID-friendly engineering professor Stuart Burgess, investigated the aerial and aquatic flight modes of the guillemot for inspiration on how to design robotic vehicles that can operate in aerial and aquatic environments. The bird's anatomy appears to have optimized the competing design tradeoffs between flight and swimming. The authors identified the locomotive adjustments the bird performs when driving:

  > Once at the hunting ground the birds dive underwater, morphing their wings, and utilize the same flapping mechanism in water as they do in air. Other kinematic changes also take place, such as the flapping frequency reducing from approximately 9 to 2.5 Hz when moving from air to water, and the forward velocities reduce from 19.1 to 1.52 m/s, respectively.

  They calculated the guillemot's locomotive power requirements in air and sea, and they ran an experiment to test their calculations. They manufactured a wing model to measure the drag in air and water. They also created a numerical model to estimate the drag forces. The authors summarize their results as follows:

  > Empirically determined values associated with the profile drag of the common guillemot confirm a potential 50% reduction in profile drag due to the retraction of the wing. Using these determined values along with previously determined values associated with parasitic drag [10], the overall drag associated with the guillemot is found to be lower in water than values calculated by theory for aerial locomotion. … Through the use of the numerical model, the retracted wing formation is found to consistently reduce the power requirement of the flapping motion compared to the extended wing, highlighting

the benefit of the folding arrangement. Inertial dynamic contributions are also found to be consistently lower for the retracted wing.

- **Douglas D. Axe, "The Case Against a Darwinian Origin of Protein Folds," *BIO-Complexity*, 2010: 1 (2010).**
This paper by Biologic Institute director Douglas Axe argues that amino-acid sequences that produce functional protein folds are too rare to be discovered by the trial-and-error processes of Darwinian evolution. It begins by observing that when the genetic code was first discovered, "The code had made it clear that the vast set of possible proteins that could conceivably be constructed by genetic mutations is far too large to have actually been sampled to any significant extent in the history of life. Yet how could the highly incomplete sampling that has occurred have been so successful? How could it have located the impressive array of protein functions required for life in all its forms, or the comparably impressive array of protein structures that perform those functions? This concern was raised repeatedly in the early days of the genetic code, but it received little attention from the biological community." After reviewing the problem, Axe concludes that "With no discernable shortcut to new protein folds, we conclude that the sampling problem really is a problem for evolutionary accounts of their origins." He argues that "a search mechanism unable to locate a small patch on a grain of level-14 sand is not apt to provide the explanation of fold origins that we seek. Clearly, if this conclusion is correct it calls for a serious rethink of how we explain protein origins, and that means a rethink of biological origins as a whole."

- **Winston Ewert, George Montañez, William Dembski and Robert J. Marks II, "Efficient Per Query Information Extraction from a Hamming Oracle," *42nd South Eastern Symposium on System Theory*, pp. 290-297 (March, 2010).**
This paper continues the peer-reviewed work co-published by William Dembski, Robert Marks, and others affiliated with the Evolutionary Informatics Lab. Here, the authors argue that Richard Dawkins's "METHINKSITISLIKEAWEASEL" evolutionary algorithm starts off with large amounts of active information -- that is, information intelligently inserted by the programmer to aid the search. This paper covers all of the known claims of operation of the WEASEL algorithm and shows that in all cases, active information is used. Dawkins's algorithm can best be understood as using a "Hamming oracle" as follows: "When a sequence of letters is presented to a Hamming oracle, the oracle responds with the Hamming distance equal to the number of letter mismatches in the sequence." The authors find that this form of a search is very efficient at finding its target -- but that is only because it is preprogrammed with large amounts of active information needed to quickly find the target. This preprogrammed active information makes it far removed from a true Darwinian evolutionary search algorithm. An online toolkit of programs called "Weasel Ware" accompanies the paper and can be found at http://evoinfo.org/weasel.

- **David L. Abel, "Constraints vs Controls," *The Open Cybernetics and Systemics Journal*, 4: 14-27 (January 20, 2010).**
This article explains that the organization of matter in life requires non-material causes such as "mental choice of tokens (physical symbol vehicles) in a material symbol system" which then "instantiates non-physical formal Prescriptive Information (PI) into physicality." It also acknowledges that life is fundamentally based upon information: "Life, on the other hand, is highly informational. Metabolic organization and control is highly programmed. Life is marked by the integration of large numbers of computational solutions into one holistic metasystem. No as-of-yet undiscovered law will ever be able to explain the highly informational organization of

living organisms." The article explains that "choice contingency" is a concept where the outcome is determined by the choice of an intelligent agent:

> Whereas chance contingency cannot cause any physical effects, choice contingency can. But choice contingency, like chance contingency, is formal, not physical. So how could non-physical choice contingency possibly become a cause of physical effects? The answer lies in our ability to instantiate formal choices into physical media. As we shall see below, formal choices can be represented and recorded into physicality using purposefully chosen physical symbol vehicles in an arbitrarily assigned material symbol system. Choices can also be recorded through the setting of configurable switches. Configurable switches are physicodynamically indeterminate (inert; decoupled from and incoherent with physicodynamic causation). This means that physicodynamics plays no role in how the switch is set. Physicodynamic factors are equal in the flipping of a binary switch regardless of which option is formally chosen. Configurable switches represent decision nodes and logic gates. They are set according to arbitrary rules, not laws. Here arbitrary does not mean random. Arbitrary means "not physicodynamically determined." Rules are not constrained by physical nature. Arbitrary means "freely selectable" -- choice contingent.

Only an intelligent cause -- an "agent" -- could implement such choice contingency. The article further explains that physical constraints are not what govern life, but rather choice controls, which cannot be explained by metaphysical naturalism:

> Volition (choice contingency) is every bit as repeatedly observable, predictable (given any form of true organization), and as potentially falsifiable as any naturalistic hypothesis. Volition and control are no more metaphysical than acceleration, wave/particle duality, weight, height, quarks, and light. We cannot label volition and control "metaphysical," and quantum mechanics and statistical mechanics "physical." Mathematics and the scientific method themselves are non-physical. Volitional controls (as opposed to mere constraints) are a fact of objective reality. If this fact does not fit within the perimeter of our prized lifelong worldview, perhaps it is time to open our minds and reconsider the purely metaphysical presuppositions that shaped that inadequate worldview. Philosophic naturalism cannot empirically or logically generate organizational bona fide controls. It can only generate self-ordering, low-informational, unimaginative constraints with no formal cybernetic capabilities. Metaphysical naturalism is too small a perimeter to contain all of the pieces. Naturalism is too inadequate a metanarrative to be able to incorporate all of the observable scientific data.

The article concludes that the formalisms we see in life "arise only in the minds of agents."

- **David L. Abel, "The GS (genetic selection) Principle,"** ***Frontiers in Bioscience*****, 14: 2959-2969 (January 1, 2010).**
  This paper studies the genetic code, observing that "Nucleotides function as physical symbol vehicles in a material symbol system." But it argues that teleology is necessary to explain the choice controls in such systems: "The challenge of finding a natural mechanism for linear digital programming extends from primordial genetics into the much larger realm of semantics and semiotics in general. Says Barham: 'The main challenge for information science is to naturalize the semantic content of information. This can only be achieved in the context of a naturalized teleology (by 'teleology' is meant the coherence and the coordination of the physical forces

which constitute the living state)'. The alternative term 'teleonomy' has been used to attribute to natural process 'the appearance of teleology'. Either way, the bottom line of such phenomena is selection for higher function at the logic gate programming level." The article explains why natural selection is inadequate to explain many features we observe in biology, and why instead we require a cause that can anticipate function: "Programming selections at successive decision nodes requires anticipation of what selections and what sequences would be functional. Selection must be for potential function. Nature cannot anticipate, let alone plan or pursue formal function. Natural selection can only preserve the fittest already-existing holistic life."

- **D. Halsmer, J. Asper, N. Roman, and T. Todd, "The Coherence of an Engineered World," *International Journal of Design & Nature and Ecodynamics*, 4 (1): 47-65 (2009).**
  This peer-reviewed scientific paper argues that we live in an "engineered world." It observes that "Human-engineered systems are characterized by stability, predictability, reliability, transparency, controllability, efficiency, and (ideally) optimality. These features are also prevalent throughout the natural systems that make up the cosmos. However, the level of engineering appears to be far above and beyond, or transcendent of, current human capabilities." The paper cites the fine-tuning of the universe for life, such as the special properties of water, the prevalence of elements needed for life (e.g. hydrogen, oxygen, and carbon), the expansion rate of the universe, as well as the Galactic Habitable Zone, a concept developed by Discovery Institute senior fellow Guillermo Gonzalez:

  > On the universal scale, however, one can see that our planet is in a comparatively narrow region of space known as the "Galactic Habitable Zone." This zone allows for the right surface temperature, stable climate metallicity, ability to hold liquid water, and many other conditions necessary for life. There is no practical reason why the universe has to contain life, but the fact that it does gives great importance to this zone for the benefit of our existence.

  The authors then explain Gonzalez and Jay Richards's "Privileged Planet" argument:

  > Not only does this zone satisfy the requirements of life but also it endowed humans with a prime position to view the wonders of the universe. There are many qualities that make the earth an excellent place from which to study the universe. First of all is the transparency of the atmosphere. Our atmosphere admits the radiation necessary for life while blocking most of its lethal energy. This transparency also allows humans to see into space without the distortions caused by a thick atmosphere as would be the case on Venus. Secondly, the regularity of our solar system's orbits makes time calculation of planetary events more predictable, even allowing for estimations of planetary orbits millions of years ago. Finally, the gas and dust in our region of the Milky Way are diffuse compared to other regions in the local mid-plane. This allows humans to view 80% of the universe without blockage. If our solar system was moved farther away, perpendicularly to the mid-plane, we would be able to see the other 20%. However, this would cause a large percentage of our current view to be blocked by dust as well as the luminosity of stars in close proximity. Humanity's place in the universe is amazingly unique when it comes to discovery. Planet earth is in prime position for the gleaning of knowledge from the stars.

The paper also focuses on fine-tuning in biology as evidence of biological design, citing the work of a variety of noteworthy proponents of intelligent design, including Walter Bradley, Michael Behe, Jonathan Wells, and William Dembski. The paper examines the engineering of life, noting that "[b]iological systems are constantly undergoing processes that exhibit modularity, specificity, adaptability, durability, and many other aspects of engineered systems." It quotes from William Dembski and Jonathan Wells's book *The Design of Life*, stating: "Many of the systems inside the cell represent nanotechnology at a scale and sophistication that dwarfs human engineering. Moreover, our ability to understand the structure and function of these systems depends directly on our facility with engineering principles." The authors further cite the work of Michael Behe's, such as *Darwin's Black Box* and *The Edge of Evolution*, explaining that biological systems display "irreducible complexity" which requires a goal-directed process or "'bottom up-top down' design." After examining the engineering of our universe from the macro- to microscope scales, they conclude: "An interdisciplinary study of the cosmos suggests that a transcendently engineered world may be the most coherent explanation for the reality we experience as human beings."

- **Ossi Turunen, Ralph Seelke, and Jed Macosko, "*In silico* evidence for functional specialization after genome duplication in yeast," *Federation of European Microbiological Societies (FEMS) Yeast Research*, 9: 16-31 (2009).**
  This paper by ID-friendly biologists discusses the evidence for gene duplication in yeast, and the implications for Darwinian evolution. They argue that when gene duplicates acquire "new" functions, it's not because a "new" function evolved, but rather because the original gene had multiple functions, some of which are then lost, as the gene becomes more "specialized." Called the promiscuous model of protein evolution, it proposes that examples of evolution by gene duplication results more from loss, rather than gain, of function:

  > [T]here appears to be a trend that the complexity of the genes (amount of functions in one gene) is slowly decreasing due to gene duplication and subsequent divergence. Functional reduction of the fast-evolving genes in the duplicated gene pairs is also seen in the finding that they have less protein-protein interactions.

  This could have important implications for Darwinian evolution, since a mechanism that tends to reduce complexity and protein-protein interactions obviously cannot account for the ultimate origin of genes.

- **Andy C. McIntosh, "Biomimetic inspiration from fire and combustion in nature, including the bombardier beetle," *Biomimetics and Bioinspiration*, 7401 (2009).**
  In this peer-reviewed conference paper, Andy McIntosh discusses two of the three examples discussed in his earlier paper, "Combustion, fire, and explosion in nature – some biomimetic possibilities," (*Journal of Mechanical Engineering Science* Vol. 221, 2007, 1157-1163), summarized previously. The two examples considered are the knobcone pine and the Bombardier beetle. Regarding the knobcone pine, McIntosh notes that the resin of the tree suggests "biomimetic applications" because "This tough resin (liquefying at 203°C) has possible applications to fireproofing of materials and needs more careful study to investigate its properties." Regarding the bombardier beetle, McIntosh notes multiple biomimetic possibilities:

  > There are industrial applications in three main areas. The first is pharmaceutical sprays where nebulisers are used for efficient drug delivery and small droplet sizes are

> important. The second application is to fuel injectors for the auto industry. This of course would involve using gasoline, but the principle of vapour explosion technology carries over to any fluid. Current injection technology using atomisers involves extremely high pressures (above 1000 bar). The µMist™ spray system enables the same to be done using pressures of the order of 10-20 bar. The third application is to fire extinguishers which would require the larger droplet size.
>
> What perhaps is of greatest interest to all applications is the reduction in the environmental impact of current high performance mist technologies. This is particularly true of pharmaceutical sprays where current carriers used for drug delivery are gases like propane which are potential pollutants for the atmosphere. The µMist™ spray system for this application would be entirely water based, and thus offers an environmentally friendly solution. Fire extinguishers also use gas ejection systems which involve pollution, and again the µMist™ spray being water based, overcomes this problem. For fuel injection systems in road vehicles, current atomisation techniques lead to some hydrocarbon particulate formation in the exhaust (soot). The new µMist™ spray system would lower such emissions and thus reduce the environmental pollution. As well as this, the greater efficiency of combustion of small droplet sprays (coupled with improved engine performance) leads to less hydrocarbon wastage in combustion, and so indirectly has a further positive environmental impact.

McIntosh concludes:

> The use of such extremes in natural devices shows the intricacy of design features which biomimetic engineers have come to expect in the rich and diverse mechanisms in biological systems in nature. Both studies are exploratory but show that there are potential advantages in studying the material properties of the knobcone pine and resin, and the explosion characteristics of the bombardier beetle. The development of a fast spray mass ejection device has a number of application to pharmaceutical drug delivery devices, fire extinguishers and fuel injectors.

That biological systems so often surpass human designed technology in their engineering ingenuity, and that they can serve to inspire design innovations, is best explained if these biological systems are themselves the products of design.

- **Richard A. Carnhart and Adam Cenian, "Implication of Proven Limits on Scientific Knowledge: Gödel's Proof, Quantum Uncertainty, Chaos Theory and Specified Complexity of Information Theory," *Bulletin de la Société Des Sciences Et Des Lettres de Łódź*, Vol. LIX (Série: Recherches Sur Les Déformations LVIII): 7-18 (2009).**
  This article in a French scientific journal argues that "four discoveries of modern science: Gödel's incompleteness theorems, quantum uncertainty, chaos theory, and, tentatively, complex specified information theory, show us specific ways in which our ability to know and control nature is limited in principle, not only in practice." After observing that the scientism of atheists like Peter Atkins "rules out the idea that the universe was created for a purpose or was designed," they argue that other factors lead to the opposite conclusion. In particular, one factor they cite is "specified complexity":

> Even organisms made of a single cell have a large genetic code in the form of a base 4 coding system (using the letters A., C., G. T). This genetic code is like a computer program. An arbitrary single sequence of a million of these letters is extremely improbable. Further, the vast majority of such sequences would not allow an organism to form, much less function. Only very specific sequences can code for the processes in the organism's living cell. These processes are many, highly complex, and highly coordinated with one another. The term "specified complexity" has been suggested to describe such living systems.

But where does specified complexity come from? According to the paper, "In the entire experience of the human race apart from living systems, no such specified complex systems, very rich in information, ever raise except as the result of design and action of an intelligent source." They argue that "it may be necessary to postulate action of an intelligence inside or outside of the natural order to explain the origin of complex specified information (CSI) in living systems." The authors recognize, however, that the scientific community is closed to this conclusion, and urges them to keep an open mind:

> It seems that the scientific community may be so comfortable with Neo-Darwinism that it has not invested in the scientific development of life-related information theory. This is a genuine issue of freedom of inquiry in intellectual life, whether in the university or the academy. This author recommends: give free inquiry a chance!

The authors conclude that the evidence suggests "a more encompassing world view than mere ontological naturalism."

- **A.S. Boxerbaum, R.J. Bachmann, R.D. Quinn, R.M. Harkins, T. Dunbar, S.C. Burgess, and Vaidy Anathan, "Design and Testing of a Highly Mobile Insect-Inspired Autonomous Robot in a Beach Environment,"** ***International Journal of Design & Nature and Ecodynamics*****, 4 (4): 319-336 (2009).**

  This paper shows how complex designs in nature can help inspire and improve human technology through the field of biomimetics. The paper includes observations about how cockroaches run, turn, and navigate obstacles. The authors recognize that this lowly insect has a wealth of design information to share about how to navigate different surfaces and climb over obstacles. Accordingly, this team studied the cockroach and specifically mimicked its tripod gait, gait modulation, and flexion joints to design a robot to navigate a beach.

  Navigating beach terrain has many unique challenges. For example, the robot must be able to handle soft sand, go over objects, and deal with hard-packed sand. To construct a robot to meet these requirements includes, but is not limited to, a specific design of the robot's structure, cable steering, foot design, component layout, enclosure, heat dissipation, weight distribution, gait control mechanism, communication, control, performance simulation, and the electronic hardware and controller design.

  Using knowledge gleaned from building the prototype robot, the team then subsequently designed an amphibious, surf-zone robot that can move on the sea floor as well as the beach. During their component layout, many requirements were considered before a plan for organizing the components was put into place. For example, the overall size of the robot compared to the size of the components needing to be housed within the structure (sensors and related electronics) was considered. Then the positioning of the components relative to their position of action in the system was considered. To do this type of analysis requires understanding of the system, goals, and knowledge about how to optimally arrange components:

> The front body segment will leave as much room as possible for sensors and related electronics. It will only contain the drive motor, steering servos, and a speed controller.

They then describe a design decision that resulted from the change between the prototype robot and the amphibious robot:

> In previous Whegs™ robots, the compliant mechanisms were contained inside the frame. However, there is no need to waterproof these mechanisms, so they have been moved outside the sealed frame to save space. All drive chains run along the sides to prevent dividing up the usable space.

Evidence of the success of mimicking the cockroach is present in this summary of what the team was able to accomplish:

> Our Beach Whegs™ robot is designed with active and passive mechanisms for maximum mobility and terrain adaptability. The robot is propelled by a single motor to move in a cockroach-like tripod gait normally, but passively adapts its gait for mobility on different terrains. Through extensive field testing, we have isolated, tested, and integrated a range of subsystems designs to create a robot suited for autonomous operation. These innovations have resulted in a robust robot well suited to autonomous operation in the beach and other sandy/rocky environments.

This paper shows how design processes can enhance our appreciation of biological design and the obstacles inherent in system design. This demonstrates how intricate designs in nature can be used to inspire and develop human technology via the discipline of biomimetics. Furthermore, biomimetics as a discipline leads to a better understanding of what it takes to create a cockroach. If the design of such an amphibious robot necessitates this component layout design process, then shouldn't the design of the imitated system necessitate a similarly intelligent, mind-based process for component layout?

- **Winston Ewert, William A. Dembski, and Robert J. Marks II, "Evolutionary Synthesis of Nand Logic: Dissecting a Digital Organism,"** ***Proceedings of the 2009 IEEE International Conference on Systems, Man, and Cybernetics*****, pp. 3047-3053 (October, 2009).**
  In 2003, researchers at the University of Michigan published in *Nature* the results of a computer simulation of evolution called Avida. The *Nature* paper's authors expressly framed "Avida" as a refutation of ID arguments, claiming the program shows "that complex adaptive traits do emerge via standard Darwinian mechanisms." But does Avida truly model "standard Darwinian mechanisms"? In 2009, four researchers at the pro-ID Evolutionary Informatics Lab furthered this scientific debate in a peer-reviewed paper titled, "Evolutionary Synthesis of Nand Logic: Dissecting a Digital Organism." Building upon concepts previously established by William Dembski and Robert J. Marks, the paper argues that Avida's programmers smuggle in "active information" to allow their simulation to find its evolutionary targets. According to the paper, sources of intelligently programmed "active information" in Avida include the following:

  - “Active information from Avida’s initialization” where “[t]he initialization in Avida recognizes the essential role of the nop-C instruction in finding the EQU.”
  - “Mutation, fitness, and choosing the fittest of a number of mutated offspring.”
  - Most importantly, there is “Stair step active information” where the digital “mutations” in Avida are essentially pre-programmed to perform a useful function, and are rewarded for doing so.

Ewert, Dembski, and Marks focus on this third point, noting that, “The importance of stair step active information is evident from the inability to generate a single EQU [the target function] in Avida without using it.” They ask, “What happens when no stair step active information is applied?” and note what the original authors of the Avida paper in *Nature* reveal:

> At the other extreme, 50 populations evolved in an environment where only EQU was rewarded, and no simpler function yielded energy. We expected that EQU would evolve much less often because selection would not preserve the simpler functions that provide foundations to build more complex features. Indeed, none of these populations evolved EQU, a highly significant difference from the fraction that did so in the reward-all environment.

But does real biology “reward” mutations to the extent that Avida does? The passage quoted above shows that when Avida is calibrated to model actual biology -- where many changes may be necessary before there is any beneficial function to select for (irreducible complexity) -- “none of these populations evolved” the target function. Avida’s creators trumpet its success, but Ewert, Dembski, and Marks show that Avida uses “stair step active information” by rewarding forms of digital “mutations” that are pre-programmed to yield the desired outcome. It does not model true Darwinian evolution, which is blind to future outcomes and cannot use active information. The implications may be unsettling for proponents of neo-Darwinian theory: Not only is Darwinian evolution “on average… no better than blind search,” but Avida is rigged by its programmers to succeed, showing that intelligence is in fact necessary to generate complex biological features. An online toolkit of programs called “Mini Vida” accompanies the paper and can be found at http://evoinfo.org/minivida.

- **William A. Dembski and Robert J. Marks II, “Bernoulli’s Principle of Insufficient Reason and Conservation of Information in Computer Search,” *Proceedings of the 2009 IEEE International Conference on Systems, Man, and Cybernetics*, pp. 2647-2652 (October, 2009).**
In his 2001 book *No Free Lunch*, William Dembski argued that Darwinian evolutionary searches cannot produce new complex and specified information, and information that is “found” by Darwinian searches actually reflects information that was smuggled in by an intelligence external to the search. This peer-reviewed paper co-written with Robert J. Marks furthers Dembski’s arguments, contending that in all searches -- including Darwinian ones -- information is conserved such that “on average no search outperforms any other.” The implication of their principle of “Conservation of Information” (COI) is that Darwinian evolution, at base, is actually no better than a random search. To make their argument, the paper develops a methodology for measuring the information smuggled into a search algorithm by intelligence. Exogenous Information (I_Ω) represents the difficulty a search in finding its target with no prior information about its location. Active Information (I_+) is the amount of information smuggled in by intelligence to aid the search algorithm in finding its target. Endogenous Information (I_s) then measures the difficulty the search will have in finding its target after the addition of Active

Information. Thus, $I_+ = I_\Omega - I_S$. Having laid this theoretical groundwork, Dembski and Marks begin to apply their ideas to evolutionary algorithms which claim to produce new information. They argue that computer simulations often do not properly model truly unguided Darwinian evolution: “COI has led to the formulation of active information as a measure that needs to be introduced to render an evolutionary search successful. Like an athlete on steroids, many such programs are doctored, intentionally or not, to succeed,” and thus “COI puts to rest the inflated claims for the information generating power of evolutionary simulations such as Avida and ev.” They conclude that when trying to generate new complex and specified information, “in biology, as in computing, there is no free lunch,” and therefore some assistance from intelligence is required to aid Darwinian evolution find unlikely targets in search space.

- **William A. Dembski and Robert J. Marks II, “Conservation of Information in Search: Measuring the Cost of Success,” *IEEE Transactions on Systems, Man, and Cybernetics-Part A: Systems and Humans*, 39 (5): 1051-1061 (September, 2009).**
  This peer-reviewed article by William A. Dembski and Robert J. Marks II challenges the ability of Darwinian processes to create new functional genetic information. Darwinian evolution is, at its heart, a search algorithm that uses a trial and error process of random mutation and unguided natural selection to find genotypes (i.e., DNA sequences) that lead to phenotypes (i.e., biomolecules and body plans) that have high fitness (i.e., foster survival and reproduction). Dembski and Marks’s article explains that unless you start with some information about where peaks in a fitness landscape may lie, any search -- including Darwinian searches -- are on average no better than a random search. After assessing various examples of evolutionary searches, Dembski and Marks show that attempts to model Darwinian evolution via computer simulations, such Richard Dawkins famous “METHINKSITISLIKEAWEASEL” exercise, start off with, as Dembski and Marks put it, “problem-specific information about the search target or the search-space structure.” According to the paper, such simulations only reach their evolutionary targets because there is pre-specified “accurate information to guide them,” or what they call “active information.” The implication, of course, is that some intelligent programmer is required to front-load a search with active information if the search is to successfully find rare functional genetic sequences. They conclude that “Active information is clearly required in even modestly sized searches.” This paper is in many ways a validation of some of Dembski’s core ideas in his 2001 book *No Free Lunch: Why Specified Complexity Cannot Be Purchased without Intelligence*, which argued that some intelligent input is required to produce novel complex and specified information. Dembski has written about this article at Uncommon Descent, explaining how it supports ID: “Our critics will immediately say that this really isn’t a pro-ID article but that it’s about something else (I’ve seen this line now for over a decade once work on ID started encroaching into peer-review territory). Before you believe this, have a look at the article. In it we critique, for instance, Richard Dawkins METHINKS*IT*IS*LIKE*A*WEASEL (p. 1055). Question: When Dawkins introduced this example, was he arguing pro-Darwinism? Yes he was. In critiquing his example and arguing that information is not created by unguided evolutionary processes, we are indeed making an argument that supports ID.”

- **David L. Abel, “The Universal Plausibility Metric (UPM) & Principle (UPP),” *Theoretical Biology and Medical Modelling*, 6: 27 (2009).**
  Materialists often vaguely appeal to vast periods of time and boundless probabilistic resources in the universe to make their scenarios sound plausible. But is “mere possibility” sufficient justification to assert “scientific plausibility”? This peer-reviewed article in *Theoretical Biology and Medical Modelling* answers that question, arguing that “[m]ere possibility is not an

adequate basis for asserting scientific plausibility” because “[a] precisely defined universal bound is needed beyond which the assertion of plausibility, particularly in life-origin models, can be considered operationally falsified.” The paper observes that “Combinatorial imaginings and hypothetical scenarios can be endlessly argued simply on the grounds that they are theoretically possible,” but then argues that the unwillingness of materialists to consider certain origin of life models to be false is actually stopping the progress of science, since “at some point our reluctance to exclude any possibility becomes stultifying to operational science.” The paper observes that “Just because a hypothesis is possible should not grant that hypothesis scientific respectability,” an important rejoinder to materialists who propose speculative stories about self-organization or co-option to explain the origin of biological complexity. The author then rigorously calculates the Universal Plausibility Metric (UPM), incorporating the maximum probabilistic resources available for the universe, galaxy, solar system, and the earth:

${}^{c}\Omega_{u}$ = Universe = 10^{13} reactions/sec X 10^{17} secs X 10^{78} atoms = 10^{108}
${}^{c}\Omega_{g}$ = Galaxy = $10^{13} \text{ X } 10^{17} \text{ X } 10^{66} = 10^{96}$
${}^{c}\Omega_{s}$ = Solar System = $10^{13} \text{ X } 10^{17} \text{ X } 10^{55} = 10^{85}$
${}^{c}\Omega_{e}$ = Earth = $10^{13} \text{ X } 10^{17} \text{ X } 10^{40} = 10^{70}$

The author concludes that consideration of Universal Plausibility Metrics allow for falsification of speculative origin of life scenarios: “The application of The Universal Plausibility Principle (UPP) precludes the inclusion in scientific literature of wild metaphysical conjectures that conveniently ignore or illegitimately inflate probabilistic resources to beyond the limits of observational science.” When hypotheses require probabilistic resources that exceed these metrics, the author argues that they “should be considered not only operationally falsified hypotheses, but bad metaphysics on a plane equivalent to blind faith and superstition.” It concludes that the complexity we see in life requires an agent-based cause that can make choices: “Symbol systems and configurable switch-settings can only be programmed with choice contingency, not chance contingency or fixed law, if non-trivial coordination and formal organization are expected.”

- **David L. Abel, “The Capabilities of Chaos and Complexity,” *International Journal of Molecular Sciences*, 10: 247-291 (2009).**
  This paper seeks to address the question, “If all known life depends upon genetic instructions, how was the first linear digital prescriptive genetic information generated by natural process?” The author warns materialists that there is an easy solution to the challenges posed by intelligent design: “To stem the growing swell of Intelligent Design intrusions, it is imperative that we provide *stand-alone natural process* evidence of non-trivial self-organization at the edge of chaos. We must demonstrate on sound scientific grounds the formal capabilities of naturally occurring physicodynamic complexity.” However, while the author notes that much effort has been spent “arguing to the lay community that we *have proved* the current biological paradigm,” he concludes that the actual evidence for self-organization is “sorely lacking” and has been “inflated.” The author emphasizes a distinction between “order” and “organization,” arguing that self-ordered structures like whirlpools are readily constructed by natural processes, but “have never been observed to achieve 1) programming, 2) computational halting, 3) creative engineering, 4) symbol systems, 5) language, or 6) bona fide organization” -- all hallmarks of living organisms. In contrast, living organisms are built upon programming and are highly organized, but “physicodynamics alone cannot organize itself into formally functional systems requiring algorithmic optimization, computational halting, and circuit integration.” His solution offers a positive argument for design: “No known natural process exists that spontaneously

writes meaningful or functional syntax. Only agents have been known to write meaningful and pragmatic syntax." He notes that the kind of "sophisticated formal function" found in life "consistently requires regulation and control," but "Control always emanates from choice contingency and intentionality, not from spontaneous molecular chaos."

- **David L. Abel, "The biosemiosis of prescriptive information,"** ***Semiotica*****, 174 (1/4): 1-19 (2009).** This article explains that classical measures of information, such as Shannon Information, are inadequate to explain biological function, suggesting that functional biological information be measured as prescriptive information ("PI"). It argues that the choice of an intelligent agent is necessary to produce PI: "PI arises from expedient choice commitments at bona fide decision nodes. Such decisions steer events toward pragmatic results that are valued by agents. Empirical evidence of PI arising spontaneously from inanimate nature is sorely lacking. Neither chance nor necessity has been shown to generate prescriptive information. Choice contingency, not chance contingency, prescribes non-trivial function." According to the article, agent choice is required to generate the formalisms found in living organism: "Formalisms of all kinds involve abstract ideas and agent-mediated purposeful choices. Inanimate physics and chemistry have never been shown to generate life or formal choice-based systems."

- **A. C. McIntosh, "Information and Entropy — Top-Down or Bottom-Up Development in Living Systems,"** ***International Journal of Design & Nature and Ecodynamics*****, 4 (4): 351-385 (2009).** This paper expressly endorses intelligent design after exploring a key question in ID thinking. "The ultimate question in origins must be: Can information increase in a purely materialistic or naturalistic way? It is not satisfactory to simply assume that information has to have arisen in this way. The alternative of original design must be allowed and all options examined carefully." A professor of thermodynamics and combustion theory, McIntosh is well acquainted with the workings of machinery. His argument is essentially twofold: (1) First, he defines the term "machine" (a device which locally raises the free energy) and observes that the cell is full of machines. Such machines pose a challenge to neo-Darwinian evolution due to their irreducibly complex nature. (2) Second, he argues that the information in living systems (similar to computer software) uses such machines and in fact requires machines to operate (what good is a program without a computer to run it?). An example is the information in DNA. From a thermodynamics perspective, the only way to make sense of this is to understand that the information is non-material and constrains the thermodynamics so that the local matter and energy are in a non-equilibrium state. McIntosh addresses the objection that, thermodynamically speaking, highly organized low entropy structures can be formed at the expense of an increase in entropy elsewhere in the universe. However, he notes that this argument fails when applied to the origin of biological information:

  > whilst this argument works for structures such as snowflakes that are formed by natural forces, it does not work for genetic information because the information system is composed of machinery which requires precise and non-spontaneous raised free energy levels -- and crystals like snowflakes have zero free energy as the phase transition occurs.

  McIntosh then tackles the predominant reductionist view of biological information which "regards the coding and language of DNA as essentially a phenomenon of the physics and chemistry of the nucleotides themselves." He argues that this classical view is wrong, for "biological structures contain coded instructions which ... are not defined by the matter and energy of the molecules carrying this information." According to McIntosh, Shannon information is not a good measure of biological information since it is “largely not relevant to functional information at the phenotype level.” In his view, “[t]o consider biological information as simply a 'by product' of natural selective forces operating on random mutations is not only counter-intuitive, but scientifically wrong.” According to McIntosh, one major reason for this is “the irreducibly complex nature of the machinery involved in creating the DNA/mRNA/ribosome/amino acid/protein/DNA-polymerase connections.” He continues:

> All of these functioning parts are needed to make the basic forms of living cells to work. ... This, it may be argued, is a repeat of the irreducible complexity argument of Behe, and many think that that debate has been settled by the work of Pallen and Matzke where an attempt to explain the origin of the bacterial flagellum rotary motor as a development of the Type 3 secretory system has been made. However, this argument is not robust simply because it is evident that there are features of both mechanisms which are clearly not within the genetic framework of the other. That is, the evidence, far from pointing to one being the ancestor of the other, actually points to them both being irreducibly complex. In the view of the author this argument is still a very powerful one.

Further citing *Signature in the Cell*, McIntosh states: “What is evident is that the initial information content in DNA and living proteins rather than being small must in fact be large, and is in fact vital for any process to work to begin with. The issue of functional complexity and information is considered exhaustively by Meyer who argues that the neo-Darwinist model cannot explain all the appearances of design in biology.” So how do biological systems achieve their highly ordered, low-entropy states? McIntosh’s argument is complementary to that of Stephen Meyer’s, but it takes a more thermodynamic approach. According to McIntosh, information is what allows biological systems to attain their high degrees of order: “the presence of information is the cause of lowered logical entropy in a given system, rather than the consequence. In living systems the principle is always that the information is transcendent to, but *using raised free energy* chemical bonding sites.” McIntosh solves the problem of the origin of information by arguing that it must arise in a “top-down” fashion requiring the input of intelligence:

> [T]here is a perfectly consistent view which is a top-down approach where biological information already present in the phenotypic creature (and not emergent as claimed in the traditional bottom-up approach) constrains the system of matter and energy constituting the living entity to follow intricate non-equilibrium chemical pathways. These pathways whilst obeying all the laws of thermodynamics are constantly supporting the coded software which is present within ... Without the addition of outside intelligence, raw matter and energy will not produce auto-organization and machinery. This latter assertion is actually repeatedly borne out by experimental observation -- new machinery requires intelligence. And intelligence in biological systems is from the non-material instructions of DNA.

This thinking can be applied to DNA: since “the basic coding is the cause (and thus reflects an initial purpose) rather than the consequence, [the top-down approach] gives a much better paradigm for understanding the molecular machinery which is now consistent with known thermodynamic principles.” McIntosh explains that the low-entropy state of biological systems is the result of the workings of machines, which must be built by intelligence: “It has often been asserted that the logical entropy of a non-isolated system could reduce, and thereby new information could occur at the expense of increasing entropy elsewhere, and without the involvement of intelligence. In this paper, we have sought to refute this claim on the basis that this is not a sufficient condition to achieve a rise in local order. One always needs a machine in place to make use of an influx of new energy and a new machine inevitably involves the systematic raising of free energies for such machines to work. Intelligence is a pre-requisite." He concludes his paper with an express endorsement of intelligent design: "the implication of this paper is that it supports the so-called intelligent design thesis -- that an intelligent designer is needed to put the information into the biological system."

- **A.C. McIntosh, "Evidence of design in bird feathers and avian respiration," *International Journal of Design & Nature and Ecodynamics*, 4 (2): 154-169 (2009).**
  In this peer-reviewed paper, Leeds University professor Andy McIntosh argues that two systems vital to bird flight -- feathers and the avian respiratory system -- exhibit "irreducible complexity." The paper describes these systems using the exact sort of definitions that Michael Behe uses to describe irreducible complexity:

  > [F]unctional systems, in order to operate as working machines, must have all the required parts in place in order to be effective. If one part is missing, then the whole system is useless. The inference of design is the most natural step when presented with evidence such as in this paper, that is evidence concerning avian feathers and respiration.

  Regarding the structure of feathers, he argues that they require many features to be present in order to properly function and allow flight:

  > [I]t is not sufficient to simply have barbules to appear from the barbs but that opposing barbules must have opposite characteristics -- that is, hooks on one side of the barb and ridges on the other so that adjacent barbs become attached by hooked barbules from one barb attaching themselves to ridged barbules from the next barb (Fig. 4). It may well be that as Yu *et al.* suggested, a critical protein is indeed present in such living systems (birds) which have feathers in order to form feather branching, but that does not solve the arrangement issue concerning left-handed and right-handed barbules. It is that vital network of barbules which is necessarily a function of the encoded information (software) in the genes. Functional information is vital to such systems.

  He further notes that many evolutionary authors "look for evidence that true feathers developed first in small non-flying dinosaurs before the advent of flight, possibly as a means of increasing insulation for the warm-blooded species that were emerging." However, he finds that when it comes to fossil evidence for the evolution of feathers, "None of the fossil evidence shows any evidence of such transitions."

  Regarding the avian respiratory system, McIntosh contends that a functional transition from a purported reptilian respiratory system to the avian design would lead to non-functional intermediate stages. He quotes John Ruben stating, "The earliest stages in the derivation of the avian abdominal air sac system from a diaphragm-ventilating ancestor would have necessitated selection for a diaphragmatic hernia in taxa transitional between theropods and birds. Such a debilitating condition would have immediately compromised the entire pulmonary ventilatory apparatus and seems unlikely to have been of any selective advantage." With such unique constraints in mind, McIntosh argues that "even if one does take the fossil evidence as the record of development, the evidence is in fact much more consistent with an *ab initio* design position -- that the breathing mechanism of birds is in fact the product of intelligent design."

McIntosh's paper argues that science must remain at least open to the possibility of detecting design in nature, since "to deny the possibility of the involvement of external intelligence is effectively an assumption in the religious category." Since feathers and the avian respiratory system exhibit irreducible complexity, he expressly argues that science must consider the design hypothesis:

> As examples of irreducible complexity, they show that natural systems have intricate machinery which does not arise in a "bottom up" approach, whereby some natural selective method of gaining small-scale changes could give the intermediary creature some advantage. This will not work since, first, there is no advantage unless all the parts of the new machine are available together and, second, in the case of the avian lung the intermediary creature would not be able to breathe, and there is little selective advantage if the creature is no longer alive. As stated in the introduction, the possibility of an intelligent cause is both a valid scientific assumption, and borne out by the evidence itself.

- **David L. Abel, "The 'Cybernetic Cut': Progressing from Description to Prescription in Systems Theory," *The Open Cybernetics and Systemics Journal*, 2: 252-262 (2008).**
  This article tries to explain how scientists can produce artificial intelligence and bridge the "cybernetic cut" -- from programmed reactions to real choices. It thus states: "How did inanimate nature give rise to an algorithmically organized, semiotic and cybernetic life? Both the practice of physics and life itself require traversing not only an epistemic cut, but a Cybernetic Cut. A fundamental dichotomy of reality is delineated. The dynamics of physicality ('chance and necessity') lie on one side. On the other side lies the ability to choose with intent what aspects of ontological being will be preferred, pursued, selected, rearranged, integrated, organized, preserved, and used (cybernetic formalism)." The article contends that choice contingency is necessary to produce functional biological life forms, for: "Choice contingency, on the other hand, involves purposeful selection from among real options. Unlike chance contingency, with choice contingency an internalized goal motivates each selection." The paper further notes that "The capabilities of chance contingency are often greatly inflated," suggesting that "agent steerage" is necessary to explain biological features. According to the paper "Purposeful choices are needed to achieve sophisticated formal utility. The chance and/or necessity of physicodynamics alone have never been observed to generate a nontrivial formal control system."

- **Andrew Conn, Stuart Burgess, and Chung Seng Ling, Ravi Vaidyanathan, "The Design Optimization of an Insect-Inspired Micro Air Vehicle," *International Journal of Design & Nature and Ecodynamics*, 3 (1): 12-27 (March 7, 2008).**
  This peer-reviewed paper, co-authored by ID-friendly engineer Stuart Burgess is based upon the principle that life exhibits optimal engineering principles that can inspire human engineering. The authors identify principles in insect wing design that can be employed in micro air vehicles (MAVs) to improve their power efficiency and maneuverability. Their article begins by describing the value of this comparison:

> Agile indoor flight is, therefore, a daunting engineering challenge, yet insects, aided by non-orthogonal flight forces and unsteady aerodynamic phenomena, regularly display remarkable flight performance that eclipses these criteria.
>
> The discovery and continuously improving understanding of the low Reynolds number unsteady aerodynamic mechanisms employed by insects is central to applying biomimetic or bio-inspired design to extract flapping wing MAV solutions. Reproducing these designs, hence enabling characteristics of their advanced performance, is a promising approach to allow flapping MAVs to generate greater lift and manoeuvrability than conventional mechanisms for indoor flight, such as rotary wings.

The authors also describe how engineers previously implemented insects' "optic flow method" to avoid obstacles and their mechanoreceptors as novel strain sensors. The describe our ability to fully implement biological designs is constrained by the limits of our existing technologies.

The authors calculate the power requirements of MAVs and design constraints for MAVs to better mimic the flight abilities of insects:

> For agile and manoeuvrable flight comparable to that of insects, it is crucial that the MAV flapping mechanism produces a dynamically adjustable output so that the wing kinematics (i.e. angle of attack, stroke amplitude and timing) are controllable.

Two solutions are presented to help meet these criteria. The first is an "artificial muscle" made from silicone dielectric elastomer films. It can maximize power output and incorporate embedded elastic storage. The second is implementing a parallel crank-rocker mechanism that generates a flapping and pitching output motion. The performance of the two solutions was tested and recommended improvements were suggested. The work done per stroke could be improved by minimizing the elastomer film thickness, and using a higher power brushless DC motor could increase the wingbeat frequency. The fact that life is so well-engineered that it can be used to improve human technology directly conflicts with a central evolutionary assumption that life should often illustrate a suboptimal design logic.

- **Richard v. Sternberg, "DNA Codes and Information: Formal Structures and Relational Causes,"** ***Acta Biotheoretica*****, 56 (3): 205-232 (September, 2008).**
  This article by pro-ID evolutionary biologist Richard Sternberg compares the information processing ability of the cell to computer programming. Sternberg observes that non-physical symbols and codes underlie biology, stating that "There are no chemical constraints or laws that explain the 64-to-20 mapping of codons to amino acids and stop sites -- the relations are 'arbitrary' with respect to the molecular components in the sense that mappings can be reassigned." According to Sternberg, the genetic code is like computer codes in that it contains the following properties: "Redundancy, Error dampening capability, Symbolic and semantic flexibility, Output versatility, Multiple realizability, and Text editing." There is also a computer-like form of recursivity in molecular biology, "as a protein product can in turn be part of the transcriptional, RNA processing, or translational apparatus -- even binding to its own mRNA." He explains the interdependent nature of DNA and other biomolecules, stating "Any DNA code is but the domain of a larger system; the larger system in turn depends on DNA codes (at least in part)." The author's conclusion is that the workings of biology, fundamentally, are not reducible to material molecules but rather resides in information, symbols, and sets of mathematically

logical rules: “The mathematical structures that proteins (and RNAs!) are the result of are not ‘in’ a gene. Instead, the DNA sequence is the material platform for the symbol strings that allow information to be accessed. In this sense, then, DNA is less than its Central Dogma interpretation because it is not ontically informational. Yet DNA enables many more code systems tha[n] commonly acknowledged and in this way is more than just a collection of codons.”

- **Douglas D. Axe, Brendan W. Dixon, Philip Lu, “*Stylus*: A System for Evolutionary Experimentation Based on a Protein/Proteome Model with Non-Arbitrary Functional Constraints,” *PLoS One*, 3 (6): e2246 (June, 2008).**
  Computer simulations of evolution such as Avida have been widely touted as having refuted intelligent design. But close scrutiny of these simulations reveal that they do not model true Darwinian processes because they are essentially pre-programmed to evolve complex systems. This peer-reviewed paper by ID-proponents attempts to present a computer simulation that fixes these defects by modeling Darwinian evolution in a biologically accurate manner, superior to that used by other evolutionary simulations such as Avida.

- **Wolf-Ekkehard Lönnig and Heinz-Albert Becker, “Carnivorous Plants,” In: Keith Roberts (ed.), *Handbook of Plant Science* (Wiley, 2007), pp. 1493-1499.**
  This peer-reviewed book chapter, coauthored by ID-friendly plant geneticist Wolf-Ekkehard Lönnig, cites irreducible complexity while presenting a review of carnivorous plants, which, by employing “enormously different and ingenious trap mechanisms,” trap and digest insects.

  The authors discuss the evolutionary origins of carnivorous plants, observing an impressive level of convergence – that is, complex features that have apparently arisen independently multiple times in the history of life:

  > Although the carnivorous nature of *Roridula* sp., *Paepalanthus bromelioides* and *Brocchinia reducta* is still doubted by some authors, most writers agree that the nine fully substantiated families belong to six different plant orders already clearly show that carnivory in plants must have arisen several times independently of each other. In a scenario of strong convergence based on morphological data the pitchers might have arisen seven times separately, adhesive traps at least four times, snap traps two times and suction traps possibly also two times.

  The authors further note that convergence of complex traits has been thought by many to be so intrinsically unlikely that the conclusion that they arose multiple times independently has been strongly resisted. However, “molecular comparisons have corroborated the independent origin of at least five of the carnivorous plant groups.” They quote earlier work that has questioned the ability of unguided evolutionary processes to account for the origins of carnivory in plants:

  > Nachtwey raised the question of how the origin from a leaf tip should be envisioned and went on to task: ‘Which nondirectional mutation should have occurred first in a normal leaf tip and subsequently displayed any selective advantage? Without an advantage it would have been lost as trivial. The modern synthesis strongly emphasizes that mutation and section have to cooperate to generate new structures. So, by which blind mutations should the suction trap have originated?’ And regarding the problem of further evolutionary stages the writer continues: ‘Even a perfect suction trap displaying

> the astonishing ability to rapidly catch animals would have no advantage in the struggle for life because the prey would not be digested. Conversely, the production of highly effective digestive juices would be of no avail for the tip of a leaf as long as it could not capture the prey, which is absolutely necessary. But even if suction trap and digestive juices cooperated, nothing would be gained in the struggle for life. The dissolved proteins must also be absorbed and metabolized to species-specific proteins. The formation of the suction trap requires the perfect cooperation of many different genes and developmental factors. At the end a benefit is reached in the struggle for life, but not by any evolutionary stage.' Nachtwey concluded that none of the contemporary evolutionary theories was able to answer these questions, proposing that the answer might lie outside the present scientific paradigms.

The authors also observe:

> Juniper *et al.,* who favor the functional proposition of Schnell quoted above, also agree with Nachtwey on the intricacy of the evolutionary problem, stating that 'no adequate evolutionary sequence can yet be constructed even to present a speculative path for the origin of what appears to be a relatively homogenous group (1989, p. 43). As for this problem, they continue that *Ultricularia* 'is a complex bit of mechanism and offers, as yet, an intractable problem in evolution' (1989, p. 117).

This challenges gradual evolution:

> Yet, even authors preferring 'gradual evolutionary change through unimaginable aeons of time (Slack, 2001, p. 19) admits the depth of the origins problem for carnivorous plants: 'Unfortunately this is a question which we cannot hope to answer without suitable fossil evidence and one can offer a mere hypothesis.' (Slack pp. 18/19). Moreover, it appears to be hard even to imagine clearcut selective advantages for all the thousands of posulated intermediate steps in a gradual scenario, not to mention the formulation and examination of scientific (i.e. testable) hypotheses for the origin of the complex carnivorous plant structures examined above.

Finally, the authors positively refer to the work of Michael Behe who, in his 1996 publication *Darwin's Black Box*, sought to take up Charles Darwin's challenge in the *Origin of Species* that "If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down." The authors note:

> Michael J. Behe (1996, p. 39) has refined Darwin's statement by introducing and defining his concept of 'irreducibly complex systems', specifying: 'By *irreducibly complex* I mean a single system composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning.
>
> Some biologists believe that the trap mechanism(s) of *Utricularia*and several other carnivorous plant genera (*Dionaea, Aldovanda, Genlisea*) come at least very near to 'such a case' of irreducible complexity. It is to be hoped that future research will fully clarify these questions.

Thus, the paper highlights features of carnivorous plants that exhibit irreducible complexity (a feature characteristic of designed systems), citing the work of leading intelligent design proponent, Michael Behe, and discussing how the irreducibly complex nature of carnivorous plants presents a formidable challenge to evolutionary accounts of their origins. This challenge is also further compounded, as the paper notes, by the apparent independence with which carnivory in plants has arisen in multiple lineages – an observation that is, again, less surprising on a design thesis.

- **Michael Sherman, "Universal Genome in the Origin of Metazoa: Thoughts About Evolution,"** ***Cell Cycle*****, 6 (15): 1873-1877 (August 1, 2007).**
  This striking paper supports intelligent design advocates who view life as being "front-loaded" to allow for biological evolution. For example, the paper states, "This model has two major predictions, first that a significant fraction of genetic information in lower taxons must be functionally useless but becomes useful in higher taxons, and second that one should be able to turn on in lower taxons some of the complex latent developmental programs, e.g., a program of eye development or antibody synthesis in sea urchin." In other words, lower taxa somehow have the genetic tools to produce systems that they do not have, but that do exist in higher taxa. As the article states: "Genes that are seemingly useless in sea urchin but are very useful in higher taxons exemplify excessive genetic information in lower taxons. It is unclear how such genetic complexity could have evolved." When discussing the convergent use of pax-6 in widely diverse organisms, it states: "So, how does it happen that convergently evolved systems have the same developmental switches? These findings are very difficult to explain within the context of Darwinian ideas." The author proposes a hypothesis where some pre-Cambrian ancestor that had "a Universal Genome that encodes all major developmental programs essential for every phylum of Metazoa emerged in a unicellular or a primitive multicellular organism." This common ancestor then lost much genetic information in many lineages: "The proposed model of a Universal Genome implies that a lot of information encoded in genomes is not utilized in each individual taxon, and therefore is effectively useless." The article suggests that microevolution is at work, but that Darwinian macroevolution cannot be credited with major innovations: "Furthermore, genetic evolution in combination with natural selection could define microevolution, however, within this model it is not responsible for the emergence of the major developmental programs." This is an evolutionary model, but it challenges the sort of unguided and random evolution inherent to neo-Darwinism, and supports a front-loading intelligent design model.

- **Kirk K. Durston, David K. Y. Chiu, David L. Abel, Jack T. Trevors, "Measuring the functional sequence complexity of proteins,"** ***Theoretical Biology and Medical Modelling*****, 4:47 (2007).**
  This article devises a method of measuring the functional sequence complexity of proteins, which in turn permits "distinguishing between order, randomness, and biological function." The authors suggest that "If genes can be thought of as information processing subroutines, then proteins can be analyzed in terms of the products of information interacting with laws of physics." The metric of functional sequence complexity advanced by these authors is highly similar to the notion of complex and specified information.

- **Andrew Conn, Stuart Burgess, and Chung Seng Ling, "Design of a Parallel Crank-Rocker Flapping Mechanism for Insect-Inspired Micro Air Vehicles,"** ***Proceedings of the Institution of***

***Mechanical Engineers, Part C: Journal of Mechanical Engineering Science*, 221 (10): 1211–1222 (2007).**
Can the design of living organisms help us improve human technology? This peer-reviewed engineering paper co-authored by ID-friendly engineer Stuart Burgess, suggests the answer is yes. Burgess and his co-authors engineered a novel micro air vehicle (MAV) that they modeled after the design of insect wings. They presupposed that insects embody the optimal design for MAVs and then attempted to mimic their mechanical logic. The authors described the reasons for insects' power efficiency:

> Insect wings possess several features that maximize their lift-to-drag ratio while maintaining excellent mass efficiency. The arrangement and orientation of veins, which provide stiffness, ensure that insect wings have regions of favourable flexion lines within the compliant wing membrane [13]. The wings also have an inherently twisted and cambered shape that again increases the lift-to-drag ratio. Spanwise veins are often also arranged in peaks and troughs resulting in wing corrugation which improves stiffness. Also, the veins have a high mass efficiency, becoming elliptical in cross-section in areas where the loading is predominantly unidirectional.

The authors then described their guidelines for mimicking insect wings. They identified the optimal wing angles and beat frequencies based on insect wing dynamics to generate a leading-edge vortex to enhance lift. They focused on larger insects, which most resemble the dimensions of human-designed MAVs. They copied the adjustments insect wings perform during maneuvering. And they implemented similar elastic energy storage, flapping frequency resonance, mechanical advantage with levers, and vein shapes and locations.

They tested a prototype for its performance, and they compared their design with other designs for performance and complexity. Their design was comparable in complexity to other designs, but it demonstrated improved performance. The main challenge they encountered was that the wing-beat frequency was 5.5 Hz, much lower than expected. They attempted to increase the frequency with springs that mimics insects' ability to store elastic energy at stroke reversal. The adjustment slightly increased the frequency. They hoped to further increase the frequency with better springs in future models. The application of biomimetics — using biology to improve human engineering — has implications friendly to the idea that that life itself may have been designed.

- **David L. Abel, "Complexity, self-organization, and emergence at the edge of chaos in life-origin models," *Journal of the Washington Academy of Sciences*, 93: 1-20 (2007).**
  This article suggests that intelligent mind is responsible for the complexity of life, stating: "In computer science, only the programmer's mind determines which way the switch knob is pushed. In evolution science we say that environmental selection 'favors' the fittest small groups. But selection is still the key factor, not chance and necessity. If physicodynamics set the switches, the switches would either be set randomly by heat agitation, or they would be set by force relationships and constants. Neither chance nor necessity, nor any combination of the two, can program. Chance produces only noise and junk code. Law would set all of the switches the same way. Configurable switches must be set using 'choice with intent' if 'computational halting' is expected."

- **Novid Beheshti and Andy C. Mcintosh, "The bombardier beetle and its use of a pressure relief valve system to deliver a periodic pulsed spray,"** ***Bioinspiration & Biomimetics*****, Vol. 2 (2007), 57-64.**
  In this paper, Novid Beheshti and Andy Mcintosh argue that certain features of the anatomy of the bombardier beetle's combustion chamber function as inlet and outlet valves, and that "the intake and exhaust valve mechanism involves a repeated (pulsating) steam explosion." The bombardier beetle is a remarkable insect that possesses a defensive mechanism against predators, whereby it is able to squirt a hot spray consisting of water and steam at boiling temperature (including noxious chemicals that are dissolved in the water) on birds, ants and frogs. The defensive mechanism of the Bombardier beetle involves the combination of two key chemical components: hydroquinones and hydrogen peroxide. These are stored separately in specialized glandular chambers within the beetle's abdomen. When the beetle feels threatened, muscular contractions force these two chemicals into a reaction chamber, where enzymes catalyze their explosive chemical reaction. This reaction produces a volatile and extremely hot mixture that can reach temperatures of up to 100 degrees Celsius within milliseconds. Simultaneously, the reaction generates a rapid release of gases, causing a pressure buildup within the beetle's reaction chamber. To discharge the defensive spray, the Bombardier beetle employs a unique valve mechanism, consisting of a sphincter-like muscle and a pair of specialized tubes called glandular ducts, which connect the reaction chamber to two small openings called the pygidial glands located on the beetle's abdomen. The beetle can control the direction and intensity of the spray by adjusting the angles at which the ducts and pygidial glands are oriented. When the valve is opened, the highly pressurized and scalding hot spray forcefully shoots out of the pygidial glands with a characteristic popping sound. This models the same design logic seen in human engineering.

- **Felipe Houat de Brito, Artur Noura Teixeira, Otávio Noura Teixeira, Roberto C. L. Oliveira, "A Fuzzy Intelligent Controller for Genetic Algorithm Parameters," in** ***Advances in Natural Computation*** **(Licheng Jiao, Lipo Wang, Xinbo Gao, Jing Liu, Feng Wu, eds, Springer-Verlag, 2006); Felipe Houat de Brito, Artur Noura Teixeira, Otávio Noura Teixeira, Roberto C. L. Oliveira, "A Fuzzy Approach to Control Genetic Algorithm Parameters,"** ***SADIO Electronic Journal of Informatics and Operations Research*****, 7 (1): 12-23 (2007).**
  This paper (published in two different venues) uses genetic algorithms that are controlled by an "intelligent agent based on fuzzy logic" and finds that such a method is more efficient than a random search typical of Darwinism. Citing the Intelligent Design and Evolution Awareness (IDEA) Center, it states: "The success achieved in the implementation of an intelligent agent controlling the evolutionary process is somewhat similar to the controversial approach of the Intelligent Design Theory, which is defended by many scientists as an answer to several aspects that are not well explained by the neo-Darwinist Theory."

- **Stuart C. Burgess, "Multi-Functioning and Multi-Optimisation in Feathers,"** ***International Journal of Design & Nature*****, 1 (1): 1-10 (2007).**
  One way to recognize design is by finding forms of complexity and elegance in biological systems which resemble that found in human technology. But what happens when the complexity and elegance of biological systems exceeds what we find in human-designed technology? Can the superior designs we find in biology help us improve our own technology? In this peer-reviewed paper, ID-friendly engineer Stuart Burgess argues that this superior design is in fact exactly what we find when we examine bird feathers — and that this can help us to improve the efficiency of human technology:

> Natural organisms often have multiple functions and multi-optimisation in a single component or mechanism. In addition, natural organisms are highly integrated assemblies. … One of the interesting characteristics of natural organisms from a design point of view is the existence of multiple functions and multi-optimisation in a single component or mechanism. In addition, natural organisms are highly integrated assemblies with several sub-systems being closely integrated together. In contrast, human design has traditionally avoided multi-functioning in single components because of the difficulties this presents in the design process. Multi-functioning and multi-optimisation are very challenging because there are more constraints in the design process and therefore fewer possible solutions. In practice, multi-functioning leads to a need for very sophisticated design solutions.

Of course, there are many design benefits from using multi-functional components, as Burgess explains:

> Multi-functioning and integration have obvious benefits. The number of components in a device can be dramatically reduced and this can lead to compactness and low mass. Compactness and low mass can lead to many improved aspects of mechanical performance such as energy and space efficiency and speed of operation. Low part count can also lead to high levels of reliability and easier maintenance.

Yet integrated, multi-functional components are exactly what we find in biology: "Integration and multi-functioning are very common in nature." How do we see these sorts of properties in bird feathers? According to Burgess, "The flight feathers of birds can be considered to have three major functions: an aerodynamic function, a fail-safe function and a lightweight structural function. … Despite having three complex functions, the feather is a single integrated structure."

Burgess explains that the aerodynamic function is facilitated by its asymmetric which allows one-way airflow that prevents the wing from being pushed downwards. Its fail-safe mechanism is self-healing, facilitated by its hierarchical design where barbs hook into barbules which allows the structure of the feather to be unzipped and "re-zipped", allowing the original structure to be reformed. Burgess further explains that its hierarchical layout is also "optimal from a structural point of view because the feather transfers loads from a surface to a point. Its overall design using keritan provides "optimal material and shape properties" — both lightweight and strong. Keratin also allows bird feathers to exhibit multiple colors, serving a display function.

The multi-functionality we find in biological systems is difficult to engineer, which is why it is so rare in human-designed systems:

> When designing an engineering device, it has traditionally been recommended to design each component for one main function in order to make the behaviour of the device easier to understand and predict. For example, in material selection methodology it has traditionally been assumed that components generally have one main function. Another reason for avoiding multi-functioning in the past is the lack of multidisciplinary design teams and a lack of suitable technology. Observations of past engineering devices show that they do indeed generally possess limited multi-functioning and integration of parts. … Multi-functioning and multi-optimisation are very challenging because there are more

> constraints in the design process and hence fewer possible solutions. In addition, the design team must have wide cross-discipline knowledge to know what is feasible and optimal.

But by studying biological systems, this can change because "Nature can be a rich source of ideas and inspiration that can help to achieve multi-functioning in engineering." From a design-perspective, the argument flows naturally: the superior elegance, efficiency, and functionality we find in life is because these systems were designed, and thus they can help us improve the design of our own human technology.

- **Andy C. McIntosh, "Combustion, fire, and explosion in nature – some biomimetic possibilities," *Journal of Mechanical Engineering Science*, 221: 1157-1163 (2007).**
In this paper, engineer Andy C. McIntosh discusses possible biomimetic applications for biological systems involving fire and/or explosions. He explains:

> There are a number of examples in the natural world of engineering sophistication which highlight the immensely sophisticated design features in the world around us and the great resource there is for inventiveness.

McIntosh focuses on three of these involving fire and/or explosions – namely, the knobcone pine, the scotch broom seed, and the combustion chamber of the bombardier beetle (the latter the author describes as "perhaps the most ingenious" of the systems discussed).

First, cones of the knobcone pine (*Pinus attenuata*) can remain closed for years or even decades until opened by the heat of a forest fire. The pinecone is sealed with a hard resin, which is melted at a high temperature of 203 degrees. Upon release, the seedlings are sufficient to plant a new forest. How is the seed itself not damaged by the fire? First, the cones have thick, sturdy scales that insulate the seeds. The seeds themselves have a relatively high moisture content, acting as a natural barrier. Moreover, as the tree is burned by the fire, the seeds are insulated from burning by the emission of the vaporized resin. McIntosh comments that "categorizing the critical temperature and humidity for each type of cone" has biomimetic applications. Furthermore, "the touch resin which liquefies at 203°C has potential "for biomimetic applications to fireproofing."

The second example is the Scottish broom seed (*Cytisus scoparius*). The seeds of the are dispersed by exploding from the mature pods when they dry out and split open, which propels the seeds one to four meters away. McIntosh summarizes the potential biomimetic applications:

> To have a propulsive device which simply depended on two warped pieces of material under tension with a small barrel or funnel, and triggered open by either mechanically or by drying (as with the broom) may serve as a more precise means of delivery than conventional heterogeneous sprays.

The final example is the bombardier beetle — a remarkable insect that possesses a defensive mechanism against predators, whereby it squirts a hot spray consisting of water and steam at boiling temperature (including noxious chemicals that are dissolved in the water) on birds, ants and frogs. The defensive mechanism of the Bombardier beetle involves the combination of two key chemical components: hydroquinones and hydrogen peroxide. These are stored separately in specialized glandular chambers within the beetle's abdomen. When the beetle feels threatened, muscular contractions force these two chemicals into a reaction chamber, where enzymes catalyze their explosive chemical reaction. This reaction produces a volatile and extremely hot mixture that can reach up to 100°C within milliseconds. Simultaneously, the reaction generates a rapid release of gases, causing a pressure buildup within the beetle's reaction chamber. The beetle possesses an outlet nozzle that can be targeted in any direction.

McIntosh notes that the bombardier beetle's combustion chamber works in a manner akin to the pulse combustor that powered the V1 flying bomb used by Germany during WWII. He explains:

> This engine worked on the basis of a cycle of low and high pressure where first the fuel (petrol) is injected into the combustion chamber and then the air brought in via a one way valve. These react forming a high pressure because of the expanding gases which closes the inlet valve and propels the exhaust gases out through a tail pipe. As the pressure drops, the inlet valve reopens so that more air comes in for the next combustion cycle and so on. The beetle does the same but instead of an air intake it has hydrogen peroxide as an oxidant.

In regard to biomimetic applications, McIntosh notes:

> The research has also investigated a scaled up version of the beetle chamber where the chamber is 2 cm long and thus about 20 times the size of the beetle. CFD simulations showed that such a device was feasible using the same vapour explosion technique and good mass ejection efficiency has been demonstrated. The advantage this could give gas turbine igniters is a promising biomimetic application, where injecting vaporized fuel into the part of the combustion chamber where the combustion has ceased can be a pyrotechnic method of reignition.

McIntosh highlights that the three examples discussed in the paper reveal "the intricacy of design features which biomimetic engineers have come to expect in the rich and diverse mechanisms in biological systems in nature." That biological systems so often surpass human designed technology in their engineering ingenuity, and that they can serve to inspire design innovations, is best explained if these biological systems are themselves the products of design.

- **Wolf-Ekkehard Lönnig, Kurt Stüber, Heinz Saedler, Jeong Hee Kim, "Biodiversity and Dollo's Law: To What Extent can the Phenotypic Differences between *Misopates orontium* and *Antirrhinum majus* be Bridged by Mutagenesis," *Bioremediation, Biodiversity and Bioavailability*, 1 (1): 1-30 (2007).**
  This study attempts to trace the evolutionary history of two taxa of flowering plants that evolutionary biologists believe to be closely related. The authors tried to use mutagenesis experiments to cause the plants' traits to revert to a more "primitive" form, but found that such basic mutagenesis experiments were unable to cause the reversion of the taxa to the "'primitive' state." The authors have an explanation for their observations that explains a long-standing law of evolution, and supports the basic tenets of intelligent design: "since most new characters arise, not by simple additions but by integration of complex networks of gene functions rendering many systems to be irreducibly complex (Behe 1996, 2004; for a review, see Lönnig 2004), such systems cannot -- in agreement with Dollo's law -- simply revert to the

original state without destroying the entire integration pattern guaranteeing the survival of a species." They conclude that, "for the rise of these taxa as well as for the inception of irreducible complex systems, the debate continues whether mutations and selection alone will be sufficient to produce all the new genetic functions and innovations necessary for the cytoplasm, membranes, and cell walls." The article favorably cites works from ID-friendly scientists such as Doug Axe's articles in *Journal of Molecular Biology*; Michael Behe's *Darwin's Black Box*; Behe and Snoke's 2004 article in *Protein Science*; David Berlinski's writings in *Commentary*; William Dembski's books *The Design Inference*, *No Free Lunch*, and *The Design Revolution*; Stephen C. Meyer's article in *Proceedings of the Biological Society of Washington*, and his work in *Darwinism, Design, and Public Education*; and also cites pro-ID entries from *Debating Design*.

- **Novid Beheshti and Andy C McIntosh, "A Biomimetic Study of the Explosive Discharge of the Bombardier Beetle," *International Journal of Design & Nature*, 1 (1): 61-69 (2007).**
  This paper focuses on the Bombardier beetle. The researchers model the scaled-up chamber and suggest an application for the high-velocity ejection of vaporized fuel in biomimetics, specifically in gas turbine igniters. According to the paper's abstract:

  > A biomimetic study of the bombardier beetle's explosive discharge apparatus was undertaken using numerical (CFD) modelling, first, of the beetle's combustion chamber, and then of a scaled-up combustion chamber with a view to its application to devices such as gas turbine relighters. The new findings about the existence of a pressure release valve at the beetle's combustion chamber exit yield a clearer understanding of the physics of the beetle's mass ejection mechanism. The scaled-up chamber (about 1 cm in length) is modelled by considering the chamber to be filled with liquid hexane which then undergoes vapour explosion through a pressure release valve at the exit. The ejection of vaporised fuel at high exit velocities has a number of applications, including gas turbine igniters.

  Biomimetics is a field that seeks to draw inspiration from nature's designs, processes, and systems to solve engineering problems. In this case, Beheshti and McIntosh note,

  > A numerical model of the very small bombardier beetle combustion chamber (approximately 1 mm long) has demonstrated that the significant physical behaviour behind the mass ejection efficiency is a cavitation explosion from hot water under pressure. Sudden decompression kicks the boiling liquid out of its moveable turret rear nozzle.
  >
  > A scaled-up version of the same type of combustion chamber (20 mm long) has been numerically modelled using the same vapour explosion technique and a good mass ejection efficiency has been demonstrated. The advantage this could give gas turbine igniters is a promising biomimetic application.

  The fact that nature's designs can inspire creative innovations in engineering underscores how much more sophisticated biological systems are than human designed ones. It also reveals the heuristic value, and practical applicability, of a design-based framework.

- **Wolf-Ekkehard Lönnig, "Mutations: The Law of Recurrent Variation," *Floriculture, Ornamental and Plant Biotechnology*, 1: 601-607 (2006).**

Citing *Darwin's Black Box* and other articles by Michael Behe about irreducible complexity, as well as the work of William Dembski and Stephen Meyer, this article states: "all the models and data recently advanced to solve the problem of completely new functional sequences and the origin of new organs and organ systems by random mutations have proved to be grossly insufficient in the eyes of many researchers upon close inspection and careful scientific examination." Citing the work of Meyer, it further notes the "limits of the origin of species by mutations."

- **David L. Abel and Jack T. Trevors, "Self-organization vs. self-ordering events in life-origin models,"** ***Physics of Life Reviews*****, 3: 211-228 (2006).**
  This article, co-authored by a theoretical biologist and an environmental biologist, explicitly challenges the ability of Darwinian mechanisms or self-organizational models to account for the origin of the language-based chemical code underlying life. They explain that "evolutionary algorithms, neural nets, and cellular automata have not been shown to self-organize spontaneously into nontrivial functions." The authors observe that life, "typically contains large quantities of prescriptive information." They further argue that "[p]rescription requires choice contingency rather than chance contingency or necessity," entailing a necessary appeal to an intelligent cause. Throughout the paper, the authors use positive arguments referencing the creative power of "agents" as they cite the work of Discovery Institute fellows and ID-theorists William Dembski, Charles Thaxton, and Walter Bradley. Critiquing models of self-organization, they conclude that "[t]he only self that can organize its own activities is a living cognitive agent."

- **David L. Abel and Jack T. Trevors, "More than Metaphor: Genomes Are Objective Sign Systems,"** ***Journal of BioSemiotics*****, 1 (2): 253-267 (2006).**
  This article argues for intelligent design, observing that only intelligence capable of making choices can create the complexity we see in human beings. The authors state: "Neither chance contingency (quantified by Shannon theory) nor any yet-to-be-discovered law of nature can generate selection contingency. Yet selection contingency is abundantly evident throughout nature." The sort of cause that is needed looks like this: "If the brain's decision nodes were constrained by natural law, our decisions would not be real. If our choices were constrained by chance or necessity, we should stop holding engineers responsible for building collapses, and stop holding criminals responsible for their behavior. Real selection/choice contingency not only predates the existence of human metaphor and heuristic use of analogy, it produced human mentation." According to the authors, "Sign systems in human experience arise only from choice contingency at successive decision nodes, not chance contingency or necessity."

- **Øyvind Albert Voie, "Biological function and the genetic code are interdependent,"** ***Chaos, Solitons and Fractals*****, 28: 1000-1004 (2006).**
  In this article, Norwegian scientist Øyvind Albert Voie examines an implication of Gödel's incompleteness theorem for theories about the origin of life. Gödel's first incompleteness theorem states that certain true statements within a formal system are unprovable from the axioms of the formal system. Voie then argues that the information processing system in the cell constitutes a kind of formal system because it "expresses both function and sign systems." As such, by Gödel's theorem it possesses many properties that are not deducible from the axioms which underlie the formal system, in this case, the laws of nature. He cites Michael Polanyi's seminal essay "Life's Irreducible Structure" in support of this claim. As Polanyi put it, "the structure of life is a set of boundary conditions that harness the laws of physics and chemistry their (the boundary conditions') structure cannot be defined in terms of the laws that they

harness." As he further explained, "As the arrangement of a printed page is extraneous to the chemistry of the printed page, so is the base sequence in a DNA molecule extraneous to the chemical forces at work in the DNA molecule." Like Polanyi, Voie argues that the information and function of DNA and the cellular replication machinery must originate from a source that transcends physics and chemistry. In particular, since as Voie argues, "chance and necessity cannot explain sign systems, meaning, purpose, and goals," and since "mind possesses other properties that do not have these limitations," it is "therefore very natural that many scientists believe that life is rather a subsystem of some Mind greater than humans."

- **Kirk Durston and David K. Y. Chiu, "A Functional Entropy Model for Biological Sequences," *Dynamics of Continuous, Discrete & Impulsive Systems: Series B Supplement* (2005).**
  This peer-reviewed article by ID-proponents seeks to offer definitions of information that measure information in terms of functionality. The authors' approach mirrors the concept of specified complexity. They explain that "The purpose of this paper is to show that Shannon entropy can also be redefined as a function of the joint patterns between data and functionality, thus incorporating a functional interpretation into the measure." They explain that their methods can also be used to measure the degree of mutational changes necessary to convert one functional protein into another: "The difference in functional entropy between the two different sequences not only provides an estimate for the amount of information required to change the starting sequence into the final sequence, but it also calculates the estimated number of trials to achieve the final sequence in evolution" and thus "The functional entropy change calculated … can be interpreted as a quantifier of evolutionary change." Their paper experimentally tests their methods, calculating difference in functional entropy between a *Hox* enzyme found in insects and crustaceans, thought to be homologous. They write: "Since the novel function as expressed did not come into effect until all 6 mutations were in place, the evolutionary path was modeled as a random walk" and yielded a change of ~26 bits. According to Axe (2010), this of course pushes the limit of what can be produced by Darwinian evolution.

- **David L. Abel and Jack T. Trevors, "Three subsets of sequence complexity and their relevance to biopolymeric information," *Theoretical Biology and Medical Modeling*, 2 (29): 1-15 (August 11, 2005).**
  This article recognizes the important point that biological information must be defined in terms of the specific type of information it represents. Shannon information and Komologorov information are said to be inadequate measures of information. Instead, the authors recommend using functional sequence complexity, a concept essentially identical to specified complexity, to measure biological information. The article also refers to "choice contingency" entailing an "arbitrary intelligent choice" as a known cause: "Compression of language is possible because of repetitive use of letter and word combinations. Words correspond to reusable programming modules. The letter frequencies and syntax patterns of any language constrain a writer's available choices from among sequence space. But these constraints are the sole product of arbitrary intelligent choice within the context of that language. Source and destination reach a consensus of communicative methodology before any message is sent or received. This methodology is called a language or an operating system. Abstract concept ('choice contingency') determines the language system, not 'chance contingency,' and not necessity (the ordered patterning of physical 'laws.')" It then argues that true organization, such as that studied in biology, requires this "choice contingency," implying intelligent design: "Self-ordering phenomena are observed daily in accord with chaos theory. But under no known circumstances can self-ordering phenomena like hurricanes, sand piles, crystallization, or

fractals produce algorithmic organization. Algorithmic 'self-organization' has never been observed despite numerous publications that have misused the term. Bone fide organization always arises from choice contingency, not chance contingency or necessity."

- **Wolf-Ekkehard Lönnig, "Mutation Breeding, evolution, and the law of recurrent variation," *Recent Research and Developments in Genetics and Breeding*, 2: 45-70 (2005).**
  This paper by plant geneticist Wolf-Ekkehard Lönnig criticizes random mutation as a mechanism for generating biological diversity. The article states: "An essential experimental discovery supporting the improbability of the origin of all life forms due to mutation, recombination and selection alone is the fact (well-known for decades) that − after repetitive mutagenic treatment of all the lines and species tested so far − the spectrum of mutants will only slightly be increased." The result is that "the number of mutants with new phenotypes asymptotically approaches a saturation line in persistently large mutation experiments." Moreover, observed mutations "are mostly losses-of-function-mutations (often including many alleles with a series of gradually reduced functions) and they are either neutral or slightly disadvantageous for the organisms thus affected." He argues that new functions are not produced by mutations:

  > However, what has never been achieved by accidental mutations, is the creation of entirely new functional DNA-sequences constituting new genes and new gene reaction chains for novel synorganized anatomical structures and/or physiological functions.

  He further notes that many scientists are beginning to doubt neo-Darwinism on this basis:

  > In contrast to the neo-Darwinians quoted in the introduction, the unanimous conclusion of these authors - among them now again several Nobel laureates in their relevant disciplines (Sir John Eccles (23), Karl von Frisch (26), Ragnar Granit (29), Charles Townes (89), Eugene P. Wigner (94), and others, see (50)) - is that mutations (in cooperation with natural selection) constitute only a partial solution to cope with the complex task of the origin of species and higher systematic taxa and thus alternatives must be looked for and carefully considered. In contrast to the neo-Darwinians quoted in the introduction, the unanimous conclusion of these authors - among them now again several Nobel laureates in their relevant disciplines (Sir John Eccles (23), Karl von Frisch (26), Ragnar Granit (29), Charles Townes (89), Eugene P. Wigner (94), and others, see (50)) - is that mutations (in cooperation with natural selection) constitute only a partial solution to cope with the complex task of the origin of species and higher systematic taxa and thus alternatives must be looked for and carefully considered.

  Multiple ID-friendly scientist are cited along the way in this paper, including Michael Behe, David Snoke, William Dembski, David Berlinski, Stephen Meyer, and others. He concludes that "the origin of the world of living organisms must be explained on a basis different from that given by the synthetic theory of evolution."

- **Heinz-Albert Becker and Wolf-Ekkehard Lönnig, "Transposons: Eukaryotic," *Encyclopedia of Life Sciences* (John Wiley & Sons, 2005).**
  This encyclopedia entry recounts that some biological systems may be irreducibly complex, stating: "A general difficulty to be mentioned in this context (but not inherent in the selfish DNA hypothesis) is that mutation and selection may not be the full explanation for the origin of species; i.e. the factors of the neo-Darwinian scenario may find their limits, for example, in the

generation of ‘irreducibly complex structures’ (Behe, 1996). This is a term used to describe structures that, according to Behe and co-workers, cannot be explained by a piecemeal production via intermediate steps.” The article elaborates on Behe’s argument stating, “Among the examples discussed by Behe are the origins of (1) the cilium, (2) the bacterial flagellum with filament, hook and motor embedded in the membranes and cell wall and (3) the biochemistry of blood clotting in humans.” The article then proposes that additional systems may challenge Darwinian explanations, stating: “Moreover, the traps of Utricularia (and some other carnivorous plant genera) as well as several further apparatuses in the animal and plant world appear to pose similar problems for the modern synthesis (joints, echo location, deceptive flowers, etc.). Up to now, none of these systems has been satisfactorily explained by neo-Darwinism. Whether accelerated TE activities with all the above named mutagenic consequences can solve the questions posed remains doubtful.”

- **John A. Davison, “A Prescribed Evolutionary Hypothesis,” *Rivista di Biologia/Biology Forum*, 98: 155-166 (2005).**
  Otto Schindewolf once wrote that evolution postulates “a unique, historical course of events that took place in the past, is not repeatable experimentally and cannot be investigated in that way.” In this peer-reviewed article from an Italian biology journal, John A. Davison agrees with Schindewolf. Since “[o]ne can hardly expect to demonstrate a mechanism that simply does not and did not exist,” Davison attempts to find new explanations for the origin of convergence among biological forms. Davison contends that “[t]he so-called phenomenon of convergent evolution may not be that at all, but simply the expression of the same preformed ‘blueprints’ by unrelated organisms.” While discussing many remarkable examples of “convergent evolution,” particularly the marsupial and placental saber-toothed cats, Davison is unmistakable in his meaning. The evidence, he writes, “bears, not only on the questions raised here, but also, on the whole issue of Intelligent Design.” Davison clearly implies that this evidence is expected under an intelligent design model, but not under a Neo-Darwinian one.

- **Guillermo Gonzalez, “Habitable Zones in the Universe,” *Origins of Life and Evolution of Biospheres*, 35: 555-606 (2005).**
  This peer-reviewed scientific paper by astronomer Guillermo Gonzalez (co-author of *The Privileged Planet*) reviews zones of habitability in the universe where life can exist. The Circumstellar Habitable Zone (CHZ) has been long-recognized as the “range of distances from the Sun that an Earth-like planet can maintain liquid water on its surface.” But Gonzalez explores additional habitable zones, including a concept which Gonzalez co-developed called the “Galactic Habitable Zone” (GHZ) which is defined as regions of the galaxy that can support advanced life. Parameters that define the GHZ include “the radial gradients of the supernova rate and the gas metallicity in the disk.” Another relevant habitable zone pertains to time rather than space — the “Cosmic Habitable Age” (CHA), which describes time periods of the universe which would allow life to exist, such as the point at which stars could appear with earthlike planets.

  Gonzalez reviews studies of the CHZ, GHZ, and CHA and proposes improvements and refinements to their definitions, even proposing that it might be possible to develop a unified theory of habitability:

> Today, the CHZ, GHZ, and CHA are treated as separate concepts. Eventually, it should be possible to unify them into a single broad understanding of habitability for every galaxy and spanning the entire history of the universe.

Questions about the prevalence of habitability are highly relevant to determining the extent to which our planet, solar system, galaxy, and universe appear finely-tuned for life. Papers like this thus show pro-intelligent design scientists conducting and publishing research precisely in areas of mainstream scientific interest that are directly relevant to the evidence for intelligent design.

- **Douglas D. Axe, "Estimating the Prevalence of Protein Sequences Adopting Functional Enzyme Folds," *Journal of Molecular Biology*, 341: 1295-1315 (2004).**
  This experimental study shows that functional protein folds are extremely rare, finding that "roughly one in 10^{64} signature-consistent sequences forms a working domain" and that the "overall prevalence of sequences performing a specific function by any domain-sized fold may be as low as 1 in 10^{77}." Axe concludes that "functional folds require highly extraordinary sequences." Since Darwinian evolution only preserves biological structures that confer a functional advantage, it would be very difficult for such a blind mechanism to produce functional protein folds. This research also shows that there are high levels of specified complexity in enzymes, a hallmark indicator of intelligent design. Axe himself has confirmed that this study adds to the evidence for intelligent design: "In the 2004 paper I reported experimental data used to put a number on the rarity of sequences expected to form working enzymes. The reported figure is less than one in a trillion trillion trillion trillion trillion trillion. Again, yes, this finding does seem to call into question the adequacy of chance, and that certainly adds to the case for intelligent design." See Scientist Says His Peer-Reviewed Research in the Journal of Molecular Biology "Adds to the Case for Intelligent Design".

- **Michael Behe and David W. Snoke, "Simulating evolution by gene duplication of protein features that require multiple amino acid residues," *Protein Science*, 13 (10): 2651-2664 (2004).**
  In this article, Lehigh University biochemist Michael Behe and University of Pittsburgh physicist Snoke show how difficult it is for unguided evolutionary processes to take existing protein structures and add novel proteins whose interface compatibility is such that they could combine functionally with the original proteins. According to their analysis, mechanisms in addition to standard Darwinian processes are required to generate many protein-protein interactions:

  > The fact that very large population sizes — 10^9 or greater — are required to build even a minimal MR feature requiring two nucleotide alterations within 10^8 generations by the processes described in our model, and that enormous population sizes are required for more complex features or shorter times, seems to indicate that the mechanism of gene duplication and point mutation alone would be ineffective, at least for multicellular diploid species, because few multicellular species reach the required population sizes. Thus, mechanisms in addition to gene duplication and point mutation may be necessary to explain the development of MR features in multicellular organisms.

  By demonstrating inherent limitations to unguided evolutionary processes, this work gives indirect scientific support to intelligent design and bolsters Behe's case for intelligent design in answer to some of his critics.

- **Wolf-Ekkehard Lönnig, “Dynamic genomes, morphological stasis, and the origin of irreducible complexity,” in Valerio Parisi, Valeria De Fonzo, and Filippo Aluffi-Pentini eds., *Dynamical Genetics* (2004).**
  Biology exhibits numerous invariants -- aspects of the biological world that do not change over time. These include basic genetic processes that have persisted unchanged for more than three-and-a-half billion years and molecular mechanisms of animal ontogenesis that have been constant for more than one billion years. Such invariants, however, are difficult to square with dynamic genomes in light of conventional evolutionary theory. Indeed, Ernst Mayr regarded this as one of the great unsolved problems of biology. In this paper Dr. Wolf-Ekkehard Lönnig, Senior Scientist in the Department of Molecular Plant Genetics at the Max-Planck-Institute for Plant Breeding Research (now retired), employs the design-theoretic concepts of irreducible complexity (as developed by Michael Behe) and specified complexity (as developed by William Dembski) to elucidate these invariants, accounting for them in terms of an explicit intelligent design hypothesis.

- **Stuart C. Burgess and Andrew M. King, “The Application of Animal Forms in Automotive Styling,” *The Design Journal*, 7 (3): 41-52 (2004).**
  This paper investigates how animal forms are mimicked in automotive styling and describes how design in nature may be used to inspire and produce aesthetically pleasing automotive designs.

  The authors discuss recognizable animal-like features in cars, such as a waist that mimics the human hourglass shape, facial features such as elliptical eyes, aggressive expressions, kind expressions, fish gills, and an expanded rear tail. They also expound on direct similarities between animals and automobiles, such as the fact that they both typically have four points of contact with the ground, consume fuel, and expel waste. The paper examines six aspects of automotive design — curves, symmetry, wholeness, distinctive facial features, and body profiles — and describes how each aspect is seen in the animal kingdom and has been copied by automotive engineers. For example:

  > There are strong parallels between the faces of animals and the front end of cars. In the same way that an animal has vision through the eyes, so a car driver has vision with the help of headlights. In the same way that animals have eyelids to cover their eyes, so some cars have deployable covers over the headlights. In the same way that an animal has ears to detect what is around, so a car has wing mirrors to enable the driver to see what is around.

  Burgess and King also emphasize the impressive designs within the animal kingdom, discussing how some animal forms optimized for speed have curves that give them highly efficient aerodynamic profiles:

  > [T]he animal can minimize aerodynamic drag by having a low frontal area. This is achieved by having a low body profile and slender body. From this equation it can also be seen that the animal can minimize aerodynamic drag by having a low drag coefficient. A low drag coefficient is produced by body shapes that enable air to pass smoothly around the body with the minimum of change of direction in the flow lines. Therefore, shapes with low drag coefficients tend be smoothly rounded … a cheetah has both a low body profile and highly rounded shape that is aerodynamically efficient.

They also discuss the functional role of symmetry in animal designs and how exceptions to a rule of symmetry often have specific engineering optimization function:

> Animals contain a great deal of symmetry in their body and limbs because it helps them maintain balance in locomotion. This symmetry produces an elegant layout. It is important to note that there are some exceptions to the symmetry rule in nature, although these exceptions actually help to prove the rule. For example many owls have asymmetrically placed ears for the purpose of increasing the sensitivity of hearing. The fact that asymmetry can be produced where necessary shows that symmetry is not an inevitable by-product of animal growth but a deliberately specified feature. The high level of symmetry in creatures shows that symmetry is important for balance and sensing.

They emphasize the incredible design and engineering rationale for animal features:

> Animals are acknowledged to be supremely efficient. For example, in the case of the airfoil shape on aircraft wings, there is virtually no difference between the shape of a trout and the shape of a classical airfoil shape.

They close by discussing advantages of using animal design forms in automotive design. They note that one of the first scientists to be intrigued by this was Leonardo di Vinci. They state that many of the reasons for similarity between animal and automotive designs come down to the convergence of design variables due to their similar functions, stating:

> [T]he use of animal forms is inherently compatible with functional requirements because of the high level of optimization of natural forms.

The preeminence of design in nature and the utility of mimicking natural designs is a concept championed by the intelligent design community, which proposes that nature's designs are optimized not merely by natural selection but by an engineering-like process where multiple variables are considered and the best possible outcome given relevant constraints was achieved. Thus, biomimetics is a successful design practice.

- **Stuart Burgess and D. Pasini, "Analysis of the structural efficiency of trees,"** ***Journal of Engineering Design*****, 15 (2): 177-193 (2004).**
  This study investigates the mass-efficiency of the structural shapes and forms found in trees. The authors, which include ID-friendly engineer Stuart Burgess, explain that the purpose is "to understand how high levels of mass-efficiency are achieved [in trees] and to identify lessons for engineering designers." To classify the function of structural features of a tree, they use a methodology called a function-means tree. This is a graphical means of providing a hierarchy of functions, beginning with the highest and then depicting how these are fulfilled by lower-level functions. Building this hierarchy of objectives is a very important step in reverse engineering because it helps one to understand the functional reasons for structures observed in nature.

  Through their expertise and with the help of a design lens, the authors reverse engineer the structural design of trees. The authors investigate the engineering importance of a tree's tapered trunk and the structural hierarchy of little branches being supported by bigger branches. They discuss the weight of the tree trunk and note that the compressive stress is not significant even for large trees because of their structure. Also, since trees grow straight up and then have branches emerging from all sides, much of the bending stress is alleviated through this excellent design of counterbalance. Another important aspect of tree design is its hierarchical structure. First there is the trunk, then the main branches, then secondary branches, and finally tertiary branches and leaves. This provides several advantages. The hierarchy allows the surface area of the tree's canopy to be linked to its source efficiently, and allows a relatively direct load path from the canopy to the trunk. It also mediates the ability for gradual growth. Key structural features in the trunk include tapering and residual stresses, which allows maximum bending to vary the least at the bottom and the most at the top, and reduces the amount of necessary biomass. The design of the trunk to bend also enables pre-stressing. This helps to improve the strength of the tree by reliving stress a little at a time instead of all at once in a devastating snap.

Burgess and Pasini observe that trees seem to be structurally designed more for strength. This is especially clear when looking at the smaller branches of a tree and its leaves, which readily deform in the wind, thereby minimizing aerodynamic loading. Despite their extreme flexibility, the design of the leaves still keep them stable enough to provide a flat surface for light collection. In engineering, this is called high bending stiffness but low torsional stiffness.

Hold-down bolts in concrete (what connects a building to its foundation) are comparable to sinker roots, a type of root that grows deep into the soil. Unlike hold-down bolts, roots are multifunctional, providing not only structural support but also water uptake. The authors explain that the lateral roots extend perpendicular to the sinker roots and provide an anchoring system through the creation of a plate of soil to which the tree structure is bound. For some trees with high growth rates, buttresses provide additional support as the underground root systems develop more slowly than canopy growth. They also observe the efficient design of wood's microstructure, which is that of hollow cells with a hexagonal shape. They note that being hollow reduces the overall density of wood, which reduces the load needed to be borne by the trunk and branches.

The authors describe how trees are incredibly well-designed structures to withstand the forces of their own weight and the wind. To do this they have smart structural design features like a multilayered hierarchy, counterbalance of loads, tapering to preserve resources, flexibility for minimal aerodynamic loading, and an appropriate microstructure. They conclude that trees still offer additional inspiration for engineers, especially when it comes to "multi-functioning structures with smart, adaptable behavior." By understanding the good design of trees, humans can practice biomimetics and improve our own technology.

- **Wolf-Ekkehard Lönnig and Heinz-Albert Becker, "Carnivorous Plants," in *Nature Encyclopedia of Life Sciences*, 2: 1493-1498 (2004).**
  This 2004 entry carnivorous plants in the peer-reviewed *Nature Encyclopedia of Life Sciences* notes that "it appears to be hard even to imagine the clearcut selective advantages for all the thousands of postulated intermediate steps in a gradual scenario, not to mention the formulation and examination of scientific (i.e. testable) hypotheses for the origin of the complex carnivorous plant structures examined above." They go on to favorably cite the work of Michael Behe, stating:

The reader is further invited to consider the following problem. Charles Darwin provided a sufficiency test for his theory (1859, p. 219): "If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down." Darwin, however, stated that he could "not find such a case." Biochemist Michael J. Behe (1996, p. 39) has refined Darwin's statement by introducing and defining his concept of "irreducible complexity", specifying: "By *irreducibly complex* I mean a single system composed of several well-matched interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning."

Some biologists believe the trap mechanism(s) of *Utricularia* and several other carnivorous plant genera (*Dionaea*, *Aldrovanda*, *Genlisea*) come at least very near to "such a case" of irreducible complexity.

- **Stephen C. Meyer, "The origin of biological information and the higher taxonomic categories," *Proceedings of the Biological Society of Washington*, 117 (2): 213-239 (2004).**
  This article argues for intelligent design as an explanation for the origin of the Cambrian fauna. Not surprisingly, it created an international firestorm within the scientific community when it was published. (See David Klinghoffer, "The Branding of a Heretic," *Wall Street Journal*, Jan. 28, 2005, as well as the following website by the editor who oversaw the article's peer-review process: http://www.richardsternberg.net/.) The treatment of the editor who sent Meyer's article out for peer-review is a striking illustration of the sociological obstacles that proponents of intelligent design encounter in publishing articles that explicitly defend the theory of intelligent design.

  John Angus Campbell and Stephen C. Meyer, *Darwinism, Design, and Public Education* (East Lansing, Michigan: Michigan State University Press, 2003; published as part of the peer-reviewed Rhetoric and Public Affairs Series).
  This is a collection of interdisciplinary essays that addresses the scientific, philosophical, and educational controversies concerning the theory of intelligent design. According to Michigan State University Press's original description of the book: "Darwinism, Design, and Public Education examines ID as a science, a philosophy, and a movement for educational reform. In this book, leading design theorists present their scientific case for intelligent design, their criticisms of contemporary Darwinism and their arguments for a pluralistic controversy-based model of science education." The book was peer-reviewed by a philosopher of science, a rhetorician of science, and a professor in the biological sciences from an Ivy League university. The book includes five scientific articles advancing the case for the theory of intelligent design, the contents of which are summarized below.

- **Stephen C. Meyer, "DNA and the Origin of Life: Information, Specification and Explanation," pp. 223-285, in John Angus Campbell and Stephen C. Meyer, *Darwinism, Design, and Public Education* (East Lansing, Michigan: Michigan State University Press, 2003.**
  Meyer contends that intelligent design provides a better explanation than competing chemical evolutionary models for the origin of the information present in large bio-macromolecules such as DNA, RNA, and proteins. Meyer shows that the term information as applied to DNA connotes not only improbability or complexity but also specificity of function. He then argues that neither chance nor necessity, nor the combination of the two, can explain the origin of information starting from purely physical-chemical antecedents. Instead, he argues that our knowledge of

the causal powers of both natural entities and intelligent agency suggests intelligent design as the best explanation for the origin of the information necessary to build a cell in the first place.

- **Michael J. Behe, "Design in the Details: The Origin of Biomolecular Machines," pp. 287-302, in John Angus Campbell and Stephen C. Meyer, *Darwinism, Design, and Public Education* (East Lansing, Michigan: Michigan State University Press, 2003.**
  Behe sets forth a central concept of the contemporary design argument, the notion of "irreducible complexity." Behe bases his argument on a consideration of phenomena studied in his field, biochemistry, including systems and mechanisms that display complex, interdependent, and coordinated functions. Such intricacy, Behe argues, defies the causal power of natural selection acting on random variation, the "no end in view" mechanism of neo-Darwinism. On the other hand, he notes that irreducible complexity is a feature of systems that are known to be designed by intelligent agents. He thus concludes that, compared to Darwinian theory, intelligent design provides a better explanation for the presence of irreducible complexity in the molecular machines of the cell.

- **Paul Nelson and Jonathan Wells, "Homology in Biology: Problem for Naturalistic Science and Prospect for Intelligent Design," pp. 303-322, in John Angus Campbell and Stephen C. Meyer, *Darwinism, Design, and Public Education* (East Lansing, Michigan: Michigan State University Press, 2003.**
  Paul Nelson and Jonathan Wells reexamine the phenomenon of homology, the structural identity of parts in distinct species such as the pentadactyl plan of the human hand, the wing of a bird, and the flipper of a seal, on which Darwin was willing to rest his entire argument. Nelson and Wells contend that natural selection explains some of the facts of homology but leaves important anomalies (including many so-called molecular sequence homologies) unexplained. They argue that intelligent design explains the origin of homology better than do mechanisms cited by advocates of neo-Darwinism.

- **Stephen C. Meyer, Marcus Ross, Paul Nelson, and Paul Chien, "The Cambrian Explosion: Biology's Big Bang," pp. 323-402, , in John Angus Campbell and Stephen C. Meyer, *Darwinism, Design, and Public Education* (East Lansing, Michigan: Michigan State University Press, 2003.**
  Meyer, Ross, Nelson, and Chien show that the pattern of fossil appearance in the Cambrian period contradicts the predictions or empirical expectations of neo-Darwinian (and punctuationalist) evolutionary theory. They argue that the fossil record displays several features -- a hierarchical top-down pattern of appearance, the morphological isolation of disparate body plans, and a discontinuous increase in information content -- that are strongly reminiscent of the pattern of evidence found in the history of human technology. Thus, they conclude that intelligent design provides a better, more causally adequate explanation of the origin of the novel animal forms present in the Cambrian explosion.

- **William A. Dembski, "Reinstating Design Within Science," pp. 403-418, , in John Angus Campbell and Stephen C. Meyer, *Darwinism, Design, and Public Education* (East Lansing, Michigan: Michigan State University Press, 2003.**
  Dembski argues that advances in the information sciences have provided a theoretical basis for detecting the prior action of an intelligent agent. Starting from the commonsense observation that we make design inferences all the time, Dembski shows that we do so on the basis of clear criteria. He then shows how those criteria, complexity and specification, reliably indicate intelligent causation. He gives a rational reconstruction of a method by which rational agents

decide between competing types of explanation, those based on chance, physical-chemical necessity, or intelligent design. Since he asserts we can detect design by reference to objective criteria, Dembski also argues for the scientific legitimacy of inferences to intelligent design.

- **Frank J. Tipler, "Intelligent Life in Cosmology,"** ***International Journal of Astrobiology*****, 2 (2): 141-148 (2003).**
  This paper by Tulane mathematician and cosmologist Frank Tipler observes that teleological explanations are live possibilities within physics. Tipler also contends that the universe is set up to permit the existence of life, and that the universe seems guided by an ultimate goal inherent it. The implication, as Tipler writes, is that the evolution of life has been guided by that goal, rather than being entirely random.

- **David L. Abel, "Is Life reducible to complexity?,"** ***Fundamentals of Life*****, Chapter 1.2 (2002).**
  This article suggests that explaining the functional complexity in life requires a force that can make choices: "Progress in understanding the derivation of bioinformation through natural processes will come only through elucidating more detailed mechanisms of selection pressure 'choices' in biofunctional decision-node sequences. The latter is the subject of both 'BioFunction theory' and the more interdisciplinary 'instruction theory'. … Life, then, is not only not reducible to complexity; it is not even reducible to FSC! Life is a symphony of dynamic, highly integrated, algorithmic processes yielding homeostatic metabolism, development, growth, and reproduction (ignoring the misgivings of those few life-origin theorists with mule fixations!). But as Yockey argues, it remains to be seen whether such highly sophisticated algorithmic processes can exist apart from the linear, segregatable, digital, FSC instructions observed at the helm of all known empirical life." The author argues that "The key to life-origin research lies in uncovering the mechanisms whereby these productive algorithmic programming choices were made and recorded in nucleic acid." He compares the processes that generated life to those that generate computer programming: "Selection is exactly what is found in computer algorithms. Correct choices at each successive decision node alone produce sophisticated software. RSC strings are pragmatically distinguished from FSC strings by virtue of the fact that RSC strings are almost never observed to do anything useful in any context. FSC strings, on the other hand, can be counted on to contribute specific utility."

- **David K.Y. Chiu and Thomas W.H. Lui, "Integrated Use of Multiple Interdependent Patterns for Biomolecular Sequence Analysis,"** ***International Journal of Fuzzy Systems*****, 4 (3): 766-775 (September 2002).**
  Citing the work of William Dembski, the opening paragraph of this article reads: "Detection of complex specified information is introduced to infer unknown underlying causes for observed patterns. By complex information, it refers to information obtained from observed pattern or patterns that are highly improbable by random chance alone. We evaluate here the complex pattern corresponding to multiple observations of statistical interdependency such that they all deviate significantly from the prior or null hypothesis. Such multiple interdependent patterns when consistently observed can be a powerful indication of common underlying causes. That is, detection of significant multiple interdependent patterns in a consistent way can lead to the discovery of possible new or hidden knowledge."

- **H-A Becker, H Saedler, WE Lönnig, "Transposable Elements in Plants," in** ***Encyclopedia of Genetics*****, Sydney Brenner and Jeffrey A. Miller (chief eds.) (Academic Press, 2002), pp. 2020-2033.**

This peer-reviewed entry in the *Encyclopedia of Genetics* (published by Academic Press and edited by Sydney Brenner and Jeffrey Miller), reviews the roles of transposable elements (TEs) in plants. Can mutations induced by TEs help explain plant diversity? The article is skeptical that TEs can explain many complex features, and it favorably cites the concept of irreducible complexity as developed by Michael Behe:

> It was no less a person than Charles Darwin himself who provided the following test for his theory (Darwin, 1859): "If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous successive, slight modifications, my theory would absolutely break down." However, Darwin stated he could "not find out such a case." Yet, the question whether the situation has changed in the interim of some 150 years of biological research is answered in the affirmative by several biologists. Michael J. Behe (Behe, 1996, 2000), has refined Darwin's statement by introducing and defining his concept of "irreducibly complex systems," specifying:
>
> > By *irreducibly complex* I mean a single system composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease function.
>
> Behe and like-minded researchers are convinced that they have detected several such systems at the biochemical level (origin of the cilium, the flagellum, blood clotting, vesicular transport, and further examples, see Behe, 1996, 2000). Lönnig (1998), suggests that irreducible complexity may also be found at the anatomical level (in combination with biochemical systems) in angiosperms as, for instance, in the trap mechanism(s) of *Utricularia* and several other carnivorous plants.

Peer-reviewed publications such as this show that core ID arguments such as irreducible complexity are gaining traction in the scientific community.

- **Richard Sternberg, "On the Roles of Repetitive DNA Elements in the Context of a Unified Genomic–Epigenetic System,"** ***Annals of the New York Academy of Sciences,*** **981: 154-188 (2002).**
  This paper by ID-friendly evolutionary biologist Richard Sternberg explores functions for repetitive elements in our DNA, often called 'junk DNA.' The paper opens by noting that repetitive DNA elements have often been viewed as "junk" but that they indeed can have "functionality":

  > Repetitive DNA sequences comprise a substantial portion of most eukaryotic and some prokaryotic chromosomes. Despite nearly forty years of research, the functions of various sequence families as a whole and their monomer units remain largely unknown. The inability to map specific functional roles onto many repetitive DNA elements (REs), coupled with the taxon-specificity of sequence families, have led many to speculate that these genomic components are "selfish" replicators generating genomic "junk." The purpose of this paper is to critically examine the selfishness, evolutionary effects, and functionality of REs.

Sternberg is heavily critical of how the neo-Darwinian model of evolution led to the development of the “selfish DNA narrative” which was designed to bolster a neo-Darwinian view:

> The selfish DNA narrative and synthetic approaches are explicit extensions of neo-Darwinian evolutionary theory to the domain of genomic data interpretation. … The neo-Darwinian influence that led to the selfish DNA narrative is, then, primarily the subordination of genomic systems, and investigations of chromosomal structure/function, to evolutionary scenarios. … [T]he success of the selfish DNA narrative may rest in its role as a “worldview hedge,” as a means of affirming neo-Darwinism no matter what intricacies of the chromosomes and genome are discovered.

Citing and reviewing the work of many scientific studies, Sternberg then lists a variety of functions that have been uncovered for REs:

- satellite repeats forming higher-order nuclear structures
- satellite repeats forming centromeres
- satellite repeats and other REs involved in chromatin condensation
- telomeric tandem repeats and LINE elements
- subtelomeric nuclear positioning/chromatin boundary elements
- non-TE interspersed chromatin boundary elements
- short, interspersed nuclear elements or SINEs as nucleation centers for methylation
- SINEs as chromatin boundary/insulator elements
- SINEs involved in cell proliferation
- SINEs involved in cellular stress responses

After reviewing these many functions for repetitive elements, Sternberg concludes that the “standard neo-Darwinian framework” of thinking has led to wrong assumptions about REs, and failed to anticipate their functions. Citing to Jonathan Wells book *Icons of Evolution*, Sternberg concludes that the “selfish DNA narrative” has itself become an icon that needs to be rejected:

> The objective of this paper was to remove the subject of RE functionality from the standard neo-Darwinian framework in which the topic is usually discussed. Given all that we know of REs, the selfish DNA narrative may explain aspects of the origin of these sequences, but it certainly fails to capture the diverse roles of these elements in chromosomes and during ontogenesis. Not only that, but the selfish DNA narrative appears to be refractory to any type of falsification. Inferred evolutionary effects of REs also appear to be just-so stories. As unpalatable as this may be for most readers, it would seem that the selfish DNA narrative and allied frameworks must join the other “icons” of neo-Darwinian evolutionary theory that, despite their variance with empirical evidence, nevertheless persist in the literature.

Sternberg’s paper thus represents another example of an ID-paradigm leading researchers to anticipate function for non-coding junk DNA, showing intelligent design to be a fruitful heuristic which can guide research.

- **Michael J. Denton, Craig J. Marshall, and Michael Legge, "The Protein Folds as Platonic Forms: New Support for the pre-Darwinian Conception of Evolution by Natural Law," *Journal of Theoretical Biology*, 219: 325-342 (2002).**
  These researchers reach a conclusion that is thoroughly teleological and non-Darwinian. The authors look to laws of form embedded in nature as possessing the power to guide the formation of biological structures. The intelligent design research program reflected here is broad yet certainly recognizable, positing design as a feature programmed into nature.

- **Wolf-Ekkehard Lönnig and Heinz Saedler, "Chromosome Rearrangement and Transposable Elements," *Annual Review of Genetics*, 36: 389-410 (2002).**
  This article examines the role of transposons in the abrupt origin of new species and the possibility of a partly predetermined generation of biodiversity and new species. The authors' approach is non-Darwinian, and they cite favorably the work of design theorists Michael Behe and William Dembski, acknowledging that some biological systems are irreducibly complex.

- **Stuart C. Burgess, "Reliability and safety strategies in living organisms: potential for biomimicking," *Proceedings of the Institution of Mechanical Engineers, Part E: Journal of Process Mechanical Engineering*, 216 (1): E02600 (2002).**
  Biological organisms have elegant and sophisticated examples of reliability and safety strategies that may be mimicked to produce better human-engineered systems. In this peer-reviewed paper, ID-friendly engineer Stuart Burgess reviews over 32 reliability and safety strategies of organisms ranging from the design of deep-sea fish body structures to the self-healing of human skin. Burgess emphasizes the supremacy of natural systems over human-engineered systems:

  > "[T]he human heart can function as a self-maintaining subsystem for 75 years or more. During this time it beats the order of 2.5 billion times and pumps the order of 150 million litres of blood. This performance is superior to any man-made pump working in similar conditions, and indeed, it is very difficult to design a man-made replacement heart with anywhere near the same capability as a living heart."
  >
  > "However, the fail-safe systems in engineering are relatively simple compared with those found in nature."

  He begins with discussion of similarities between biological and engineering systems. Tables 1 and 2 provide a list of analogous systems and processes, respectively. Then the paper turns to discussing the reliability strategies of nature. For example, Burgess examples "planned inspection," where birds engage in flight feather inspection. Burgess also discusses the use of a minimal number of parts or simplicity in the engineering of organisms to reduce the risk of failure. He notes that "simplicity is a design goal that must be carefully defined by design engineers."

  Next, Burgess outlines 15 safety strategies used in nature. One example he gives is visual warnings, giving the example of poison color codes; the engineering example he gives is warning signs. Burgess notes "Since human beings are biological systems, it is worth taking particular note of the warning signals used in nature. The natural warning patterns and sounds used in nature may provoke an instinctive and fast reaction within humans. If this is indeed the case, then the warning signals used in nature may be more effective in engineering systems than randomly chosen warning signs." He again organizes these safety strategies by those commonly used in engineering and then transitions to those occasionally used in engineering.

The goal of this study is to emphasize that because engineered systems are similar to biological systems, it is worthwhile to examine how biological systems work in order to design higher reliability in engineered systems. It mentions that the extensive use of reliability strategies in nature supports continued and increased application in engineering. Burgess concludes by predicting that as engineering develops, the application of biological dependability and safety techniques will likely become more common and some of the technologies used by biological organisms will find their way into human engineered designs.

- **Douglas D. Axe, "Extreme Functional Sensitivity to Conservative Amino Acid Changes on Enzyme Exteriors,"** ***Journal of Molecular Biology*****, 301: 585-595 (2000).**
  This study published by molecular biologist Douglas Axe, now at the Biologic Institute, challenges the widespread idea that high species-to-species variation in the amino-acid sequence of an enzyme implies modest functional constraints. Darwinists commonly assume that such variation indicates low selection pressure at the variable amino acid sites, allowing many mutations with little effect. Axe's research shows that even when mutations are restricted to these sites, they are severely disruptive, implying that proteins are highly specified even at variable sites. According to this work, sequences diverge not because substantial regions are free from functional constraints, but because selection filters most mutations, leaving only the harmless minority. By showing functional constraints to be the rule rather than the exception, it raises the question of whether chance can ever produce sequences that meet these constraints in the first place. Axe himself has confirmed that this study adds to the evidence for intelligent design: "I concluded in the 2000 JMB paper that enzymatic catalysis entails 'severe sequence constraints.' The more severe these constraints are, the less likely it is that they can be met by chance. So, yes, that finding is very relevant to the question of the adequacy of chance, which is very relevant to the case for design." See Scientist Says His Peer-Reviewed Research in the Journal of Molecular Biology "Adds to the Case for Intelligent Design".

- **Solomon Victor and Vijaya M. Nayak, "Evolutionary anticipation of the human heart,"** ***Annals of the Royal College of Surgeons of England*****, 82: 297-302 (2000).**
  This article argues that intelligent design is recognizable in the human heart, stating: "Comparative anatomy points to a design and a Designer. Surgeons, anatomists and anyone studying the human form and function have an unsurpassed opportunity to ponder over the wonders of creation and contemplate the basic questions: where did we come from? why are we here? and where are we going?"

- **William Lane Craig, "The Ultimate Question of Origins: God and the Beginning of the Universe,"** ***Astrophysics and Space Science*****, Vol. 269-270: 723–740 (1999).**
  This paper by philosopher William Lane Craig, titled "The Ultimate Question of Origins: God and the Beginning of the Universe" and published in *Astrophysics and Space Science*, that the "discovery during this [20th] century that the universe began to exist … calls into question the universe's status as metaphysically necessary, since any necessary being must be eternal in its existence." He argues that "Unless we are to assert that the universe simply sprang into being uncaused out of nothing" then some cause external to the universe is necessary to explain the origin of the universe. Craig notes that the "Standard Big Bang Model" is "the best explanation of the evidence which we have" and says this suggests "origin ex nihilo" of the universe, and

requires “a supernatural cause of the origin of the universe.” He elaborates on what the cause of the universe requires:

> For as the cause of space and time, this entity must transcend space and time and therefore exist atemporally and non-spatially, at least sans the universe. This transcendent cause must therefore be changeless and immaterial, since timelessness entails changelessness, and changelessness implies immateriality. Such a cause must be beginningless and uncaused, at least in the sense of lacking any antecedent causal conditions. Ockham’s Razor will shave away further causes, since we should not multiply causes beyond necessity. This entity must be unimaginably powerful, since it created the universe without any material cause.

He concludes “we are brought, not merely to a transcendent cause of the universe, but to its personal Creator.” He summarizes his argument thusly:

> 1. Whatever exists has a reason for its existence, either in the necessity of its own nature or in an external ground.
> 2. Whatever begins to exist is not necessary in its existence.
> 3. If the universe has an external ground of its existence, then there exists a Personal Creator of the universe, who, sans the universe, is timeless, spaceless, beginningless, changeless, necessary, uncaused, and enormously powerful.
> 4. The universe began to exist.
> From (2) and (4) it follows that
> 5. Therefore, the universe is not necessary in its existence.
> From (1) and (5) it follows further that
> 6. Therefore, the universe has an external ground of its existence.
> From (3) and (6) we can conclude that
> 7. Therefore, there exists a Personal Creator of the universe, who, sans the universe, is timeless, spaceless, beginningless, changeless, necessary, uncaused, and enormously powerful.
>
> And this, as Thomas Aquinas laconically remarked (1911), is what everybody means by God.

- **Solomon Victor, Vljaya M. Nayek, and Raveen Rajasingh, “Evolution of the Ventricles,” *Texas Heart Institute Journal*, 26: 168-175 (1999).**
  This article concludes that “there is a design in the evolution of the venous connections of the heart, pectinate muscles, atrioventricular valves, left ventricular tendons, outflow tracts, and great arteries.” But the version of “evolution” it presents is decidedly non-Darwinian, as it notes that evolution appears to be goal-directed by a designer: “One neglected aspect in the study of evolution is that of anticipation. Fish atria and ventricles appear to have a built-in provision for becoming updated to the human 4-chambered structure. This transformation is achieved in stages: the truncus yields the great arteries, appropriate shifting takes place in the great arteries, the left ventricle decreases in sponginess and increases in the size of its lumen, the chordopapillary apparatus becomes more sophisticated, the coronary circulation undergoes changes, and the ventricular septal defect closes.” The article closes by stating, “This evolutionary progression points to a master design and plan for countless millennia.”

- **William A. Dembski, *The Design Inference: Eliminating Chance through Small Probabilities* (Cambridge: Cambridge University Press, 1998).**
  This book was published by Cambridge University Press and peer-reviewed as part of a distinguished monograph series, Cambridge Studies in Probability, Induction, and Decision Theory. The editorial board of the series includes members of the National Academy of Sciences as well as a Nobel laureate, John Harsanyi, who shared the prize in 1994 with John Nash, protagonist of the film *A Beautiful Mind*. Commenting on the ideas in *The Design Inference*, well-known physicist and science writer Paul Davies remarked: "Dembski's attempt to quantify design, or provide mathematical criteria for design, is extremely useful. I'm concerned that the suspicion of a hidden agenda is going to prevent that sort of work from receiving the recognition it deserves." Quoted in Larry Witham, *By Design* (San Francisco: Encounter Books, 2003), p. 149.

- **R. Kunze, H. Saedler, and W.-E. Lönnig, "Plant Transposable Elements," in *Advances in Botanical Research*, 27: 331-470 (Academic Press, 1997).**
  This peer-reviewed chapter from an academic book on plant research favorably references Michel Behe's concept of irreducible complexity. After noting that "some major problems have to be solved for gene duplications to be of fundamental evolutionary significance," it cites to Behe's 1996 book *Darwin's Black Box* to justify the question: "What could be the selective advantage of the intermediate ('still unfinished') reaction chains?" The authors further state that "examples of 'irreducibly complex systems'" are found in biology.

- **Michael Behe, *Darwin's Black Box: The Biochemical Challenge to Evolution* (New York: The Free Press, 1996).**
  In this book Behe develops a critique of the mechanism of natural selection and a positive case for the theory of intelligent design based upon the presence of "irreducibly complex molecular machines" and circuits inside cells. Though this book was published by The Free Press, a trade press, the publisher subjected the book to standard scientific peer-review by several prominent biochemists and biological scientists.

- **Charles B. Thaxton, Walter L. Bradley, Roger L. Olsen, *The Mystery of Life's Origin: Reassessing Current Theories* (New York: Philosophical Library, 1984; Dallas, Texas: Lewis & Stanley Publishing, 4th ed., 1992).**
  In this book Thaxton, Bradley and Olsen develop a seminal critique of origin of life studies and develop a case for the theory of intelligent design based upon the information content and "low-configurational entropy" of living systems.

- **Stanley L. Jaki, "Teaching of Transcendence in Physics," *American Journal of Physics*, 55 (10): 884-888 (October 1987).**
  This article from the *American Journal of Physics* seeks to help educators understand how they can teach students about the evidence for transcendence in the universe. The article assumes that a transcendent realm exists beyond the universe and that the universe can plausibly be said to reflect design.

- **Granville Sewell, "Postscript," in *Analysis of a Finite Element Method: PDE/PROTRAN* (New York: Springer Verlag, 1985).**
  In this article appearing in a 1985 technical reference book, mathematician Granville Sewell compares the complexity found in the genetic code of life to that of a computer program. He recognizes that the fundamental problem for evolution is the "problem of novelties" which in

turn raises the question “How can natural selection cause new organs to arise and guide their development through the initial stages during which they present no selective advantage?” Sewell explains how a typical Darwinist will try to bridge both functional and fossil gaps between biological structures through “a long chain of tiny improvements in his imagination,” but the author notes that “the analogy with software puts his ideas into perspective.” Major changes to a species require the intelligent foresight of a programmer. Natural selection, a process that is “unable to plan beyond the next tiny mutation,” could never produce the complexity of life.

- **William G. Pollard, “Rumors of transcendence in physics,” *American Journal of Physics*, 52 (10) (October 1984).**
  In this peer-reviewed paper, nuclear physicist William G. Pollard notes that Big Bang cosmology requires some kind of transcendent reality. Pollard argues that the scientific justification for this transcendent domain can be found in quantum mechanics because universal laws and constants are finely-tuned to permit the existence of advanced life, which point to an intelligent source, a mind, as designing the universe.

- **Robert Broom, “Evolution: Is There Intelligence Behind It,” *South African Journal of Science*, XXX: 1-19 (October, 1933).**
  Robert Broom was a British-South African medical doctor who was one of the founders of the field of palaeoanthropology. In 1933, he published an article in the *South African Journal of Science*, titled “Evolution — Is There Intelligence Behind It?” where he argued that an “intelligent foreseeing agency” is necessary to explain the origin of many animals, and concludes:

  > Lamarckism and Darwinism seem to fail completely, and one feels that mutation is quite out of the question if it is the result of pure accident, and only conceivable if an intelligent agency is behind it. (Broom, 1933a)

  Likewise, in his book *The Coming of Man: Was It Accident or Design,* Broom writes, “One feels driven to the conclusion that some intelligent power has played a part in the evolution” and argues that intelligent design is found throughout vertebrate history: “Many see nothing in it but a succession of fortuitous mutations which, by the selection of the blind forces of. nature, have resulted in the evolution of a Shakespeare and a Newton from a fish. I fancy I can trace intelligence behind it all” (Broom, 1933b:11, 207). This makes it clear that Broom promoted an intelligent design-based view of evolution regarding the origin of the human species.

Category 2: Further Mainstream Scientific Publications: Peer-Edited or Editor-Reviewed Publications Supportive of Intelligent Design Published in Mainstream Scientific Journals, Scientific Anthologies, Conference Proceedings, Publishers, Etc.

- **William A. Dembski, Winston Ewert, and Robert J. Marks II, "A General Theory of Information Cost Incurred by Successful Search," pp. 26- 63, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  This paper provides a general explanation of a methodology for measuring "active information," or the amount of information that is added to a random search to aid in finding a search target. This foundational paper is theoretical, aiming to establish mathematically that without active information being added, a search can perform, on average, no better than a random search:

  > When a search with probability q of success displaces a baseline search with probability p of success where q > p, conservation of information states that raising the probability of successful search by a factor of q / p (>1) incurs an information cost of at least log(q / p). Conservation of information shows that information, like money, obeys strict accounting principles.

  In other words, a "natural" search -- one that operates blindly -- cannot, on average, find the target any faster than a random search working without active information. To increase the probability of finding the target, "active information" must be added. This "conservation" of information operates in a law-like fashion that would prevent unguided mechanisms, like Darwinian processes, from improving the search. This is the essence of Dembski's "No Free Lunch" theorem. As Marks explains in the introduction to the volume, a search can be simplified "only by access to some source of information." That source, of course, requires intelligence. This methodology can then be applied to real-world situations, as it allows them to measure the extent to which computerized simulations of evolution are generating new information, or simply using information introduced by the programmer, not generated by the program.

- **Winston Ewert, William A. Dembski, and Robert J. Marks II, "Tierra: The Character of Adaptation," pp. 105-138, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  In this paper, Ewert, Dembski, and Marks apply the sort of methodology developed in their first paper ("A General Theory of Information Cost Incurred by Successful Search"). This study investigates Tierra, one of the earliest computerized simulations of evolution, developed by Thomas Ray in 1989. According to Ray, Tierra is capable of modeling the evolution of complexity, as supposedly occurred in events like the Cambrian explosion. As Ewert, Dembski, and Marks explain, in Ray's mind "once evolution (whether biological or artificial) has produced a Cambrian explosion, the rest of evolution should proceed easily." They observe, however, that after 20+ years of people using Tierra, the widely agreed conclusion "is that Tierra did not produce a Cambrian explosion or open-ended evolution." They observe that "Tierran evolution can be characterized as an initial period of high activity producing a number of novel adaptations followed by barren stasis," and thus ask why Tierra stopped producing new features. They explain:

> A closer look at Tierran evolution reveals an important characteristic of the adaptations. Tierra started with a designed ancestor to seed the population. In other words, it presupposed something like an origin of life and was concerned with the development of complexity after that point. The ancestor provides initial information to Tierra. Adaptations primarily consist of rearranging or removing that information. Open-ended evolution requires adaptations which increase information. However, such adaptations are rare in Tierra. Tierra's informational trajectory is reversed from what evolution requires. It is dominated by loss and rearrangement with only minimal new information instead of being dominated by the production of new information with minimal cases of removal or rearrangement of information. Long term evolutionary progress is dependent on the generation of new information.

Does Tierra actually produce new information? Ewert, Dembski, and Marks studied the workings of Tierra in detail and found:

> In a majority of the cases we see that evolution proceeded by deleting instructions. There are some new instructions inserted, but these are much smaller than the changes in other areas. As a result, we can clearly see that Tierran evolution is dominated by information-reducing mutations. ... The interesting behaviors produced by Tierra are created mostly by rearranging the information seeded into the simulation by its designer.

Thus, they found that Tierra was in a sense front-loaded -- or intelligently designed -- to stably evolve:

> Tierra also derives some information from the environment in which it runs. Ray was concerned about the brittleness of machine code, and accordingly made specific design decisions. Additionally, the original instruction set was created by choosing exactly the instructions which were used in the ancestor. This results in the Tierra instruction set being specifically tuned to the problem it faces. This work has not attempted to investigate the implications of these decisions, but it is our opinion that the Tierran evolution is substantially assisted through them.

Nonetheless, they observe, "The author of Tierra sought to create a digital Cambrian explosion whereby the power of the evolutionary process was unleashed. It is agreed that Tierra did not succeed in accomplishing this feat. Rather, the evolutionary activity within Tierra dies after only a transitory period. No Cambrian explosion occurs."

- **George Montañez, Robert J. Marks II, Jorge Fernandez, and John C. Sanford, "Multiple Overlapping Genetic Codes Profoundly Reduce the Probability of Beneficial Mutation," pp. 139-167, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).** How rare are beneficial mutations? This paper attempts to address that crucial question, since its answer "determines both the speed and the direction of genetic change." The authors point out that "If beneficial mutations are extremely rare, this profoundly limits the *rate and range* of all forward genetic change." In addressing the rarity of beneficial mutations, they observe that "DNA sequences are typically 'poly-functional'," meaning that any given nucleotide "can contribute to multiple overlapping codes simultaneously." They observe that "overlapping protein-coding sequences" are now considered "typical," meaning that it's common for a single base pair to "affect multiple traits simultaneously and interactively." To address the rarity of beneficial mutations, they perform computer modeling on functional DNA sequences that contain multiple overlapping codes, and describe the likelihoods of a given mutation being beneficial towards at least one code, or having a net-benefit, meaning it "is a mutation that improves more codes than it disrupts." They conclude that poly-functional codes will rarely incur universally beneficial mutations:

> [W]ithin all poly-functional nucleotide sites, essentially all "beneficial mutations" will at best be ambiguously beneficial, being beneficial at just one level, but simultaneously being deleterious at one or more levels. Therefore at any poly-functional nucleotide site, a "beneficial" mutation will almost always still consistently have deleterious effects, systematically eroding the total amount of information in the entire information system.

They conclude that "that increasing either the number of overlapping codes or the degree of optimization has negative effects on the probability of producing a beneficial mutation." Indeed, they argue that "The growing evidence for polyfunctional DNA therefore suggests that unambiguously beneficial mutations should be vanishingly rare," and "it is difficult to understand how poly-functional DNA could arise through random isolated mutations."

- **Granville Sewell, "Entropy, Evolution and Open Systems," pp. 168-178, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  In this article, Granville Sewell address the argument from defenders of Darwinian evolution that the second law of thermodynamics poses no problems for their model. They argue if entropy increases elsewhere in the universe, then it can decrease in open systems such as the Earth. Sewell calls this the "compensation" argument, and explains why it is seriously flawed:

  > It is widely argued that the spectacular local decreases in entropy that occurred on Earth as a result of the origin and evolution of life and the development of human intelligence are not inconsistent with the second law of thermodynamics, because the Earth is an open system and entropy can decrease in an open system, provided the decrease is compensated by entropy increases outside the system. I refer to this as the compensation argument, and I argue that it is without logical merit, amounting to little more than an attempt to avoid the extraordinary probabilistic difficulties posed by the assertion that life has originated and evolved by spontaneous processes. To claim that what has happened on Earth does not violate the fundamental natural principle behind the second law, one must instead make a more direct and difficult argument.

  Sewell elaborates that "the whole idea of compensation, whether by distant or nearby events, makes no sense logically: an extremely improbable event is not rendered less improbable simply by the occurrence of 'compensating' events elsewhere. According to this reasoning, the second law does not prevent scrap metal from reorganizing itself into a computer in one room, as long as two computers in the next room are rusting into scrap metal -- and the door is open. (Or the thermal entropy in the next room is increasing, though I am not sure how fast it has to increase to compensate for computer construction!)" He concludes: "The 'compensation' counter-argument was produced by people who generalized the model equation for isolated systems, but forgot to generalize the equation for non-isolated systems." His generalized model would be as follows: "If an increase in order is extremely improbable when a system is closed, it is still extremely improbable when the system is open, unless something is entering which makes it not extremely improbable."

Sewell's argument is not that the second law is necessarily a barrier to Darwinian evolution since, "Of course, one can still argue that the spectacular increase in order seen on Earth is consistent with the underlying principle behind the second law because what has happened here is not really extremely improbable...But one would think that at least this would be considered an open question, and those who argue that it really is extremely improbable, and thus contrary to the basic principle underlying the second law of thermodynamics, would be given a measure of respect, and taken seriously by their colleagues."

- **Andy C. McIntosh, "Information and Thermodynamics in Living Systems," pp. 179-201, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  This paper seeks to understand the origin of information in life, and proposes "an entirely different paradigm whereby the non-material message is accepted as being of an origin outside the area of physical investigation, but that its effect can readily be seen in the organisation of the molecular machinery in living organisms." In McIntosh's view, "Rather than the material and energy forming the information system as advocated by evolutionary philosophy, the non-material informational message expressed in the coded ordering of nucleotides is actually the mechanism of constraining the material itself." In his view, "Understanding the thermodynamics of this machinery shows that it is thermodynamically impossible both to form such machinery (abiogenesis) without intelligence, and that the laws of thermodynamics prohibit any formation of new machinery which is not there already or latently coded for in the DNA (evolutionary development)."

- **Jonathan Wells, "Not Junk After All: Non-Protein-Coding DNA Carries Extensive Biological Information," pp. 210-231, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  Citing numerous examples of functionality for non-coding DNA, in this paper Jonathan Wells argues that "the notion of 'junk DNA' is obsolete, and the amount of biological information in the genome far exceeds the information in protein-coding regions." Wells uncovers various lines of evidence in support of this claim.

  First, there are the conclusions of the ENCODE project which suggest that there is "widespread transcription of non-protein-coding DNA." According to Wells, this "suggests probable function; so does sequence conservation."

  This evidence, however, is somewhat circumstantial. Thus Wells observes as a second point that "[t]here is also direct evidence for specific functions of non-protein-coding RNAs." He gives many examples of how non-coding RNA performs specific functions in cells, including:

  - Regulating gene expression.
  - Alternative splicing, allowing the construction of many new transcripts. As Wells explains, "Alternative splicing plays an essential role in the differentiation of cells and tissues at the proper times during embryo development, and many alternatively spliced RNAs occur in a developmental-stage-and tissue-specific manner."

- Introns not only regulate gene expression, but “also encode many of the small RNAs essential for the processing of ribosomal RNAs, as well as the regulatory elements associated with such RNA-coding sequences.”
- “Non-protein-coding RNAs are essential for chromatin organization, and non-protein-coding RNAs have been shown to affect gene expression by modifying chromatin structure.”
- “Pseudogenes are transcribed into non-protein-coding RNAs that in some cases regulate the expression of the corresponding protein-coding genes.”

Wells also observes that the nucleotide sequence of DNA is not the only way that non-coding DNA can specify functions:

The genome functions hierarchically, and the order of nucleotides in protein- coding and non-protein-coding DNA constitutes only the first level of that hierarchy. The length of DNA sequences (even non-protein-coding ones) is a second level; chromatin organization is a third level; and the position of chromosomes within the nucleus is a fourth. There is evidence that DNA functions at the second, third, and fourth levels in ways that are independent of the precise nucleotide sequence.

He concludes that even as we find more and more functionality for non-coding DNA, other non-DNA-based sources of information are being discovered in living cells.

- **Donald Johnson, “Biocybernetics and Biosemiosis,” pp. 402-413, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
Can biology be studied through computer science? In this paper, computer scientist and chemist Donald Johnson argues that we can. He writes:

> Any serious origin-of-life or origin-of-species scenario must explain the origin of the required biological information. It is argued that each protein arises as the result of the execution of a genuine computer program. The creation of a functional protein via the mutation/selection paradigm lacks support from information science. Those who understand the reality of bioinformation, especially the prescriptive information of biocybernetics, will be able to incorporate that understanding into new models that will lead to a more complete understanding of life.

Johnson recognizes that “The vital nature of information in life has been downplayed by most materialists, since functional information has no feasible cause from physicality (though infeasible scenarios have been speculated).” However, “biology is an information science since all of the defining characteristics of biology are controlled by life’s information processing systems.” But life doesn’t just contain information, for “life uses common operating systems, programming languages, and devices.” Indeed, Johnson argues “[t]here are many components of life that can thus be classified as computers or components of computers,” such as the transcription/translation system.

Johnson also observes that life contains semiotic systems, which “is a system made of two independent worlds that are connected by the conventional rules of a code. … made of three distinct entities: signs, meanings and code.” Again the transcription/translation system provides a prime example, but “[s]ince information is non-material, there have been no feasible scenarios for production of semiotic systems from physicality.”

- **Jed C. Macosko and Amanda M. Smelser, “An Ode to the Code: Evidence for Fine-Tuning in the Standard Codon Table,” pp. 418-434, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  It’s well-established that the standard codon table (SCT) of the genetic code is finely-tuned in a way “that minimizes harmful effects of mutations and mistranslations while maximizing the encoding of multiple messages into a single sequence.” But how did this optimization arise? This paper argues that “external intelligence better explains the origin of the SCT.”

  According to the authors, Francis Crick’s “frozen accident” model, fails because “the SCT could have ended up with any arbitrary structure,” and thus they cannot explain the optimization of the code. Other models seek to explain the optimization through material mechanisms, such as chemical interactions “between amino acids and their respective trinucleotide codons.” These attempts have failed since “the preference for codon versus anticodon involvement appears random.” The authors also observe that materialistic explanations of the genetic code “do not explain the origin of the machinery that is responsible for converting mRNA information into amino acid sequences” and thus “theories for the origin of the coding machinery are abundant and are generally viewed as extremely speculative.”

  But just how finely-tuned is the genetic code? They propose that the SCT is optimized in multiple ways, which are both “optimal and are orthogonal, i.e. the optimality of one would not necessarily lead to the optimality of the others.” These include:

  > 1) similar amino acids are coded by similar codons thus minimizing the impact of errors, 2) the family/non-family symmetry minimizes mistranslations while maximizing tRNA usage efficiency, 3) the stop codons are related to commonly occurring amino acids in a way that optimizes second-layer codes, and 4) methionine is an optimal initiating amino acid due to its minimized energy for exiting the ribosome.

  Given this degree of fine-tuning, they calculate that if the SCT is the “best of all possible codes,” then natural selection can only work if there were a population of competing codes approaching 10^{84}. This, they observe, is “a ludicrous population size, considering that 10^{84} carbon atoms are a trillion, trillion, trillion times more massive than the earth.” They conclude intelligent design is the best explanation since “the general pattern of intelligence producing finely-tuned, optimized effects is well-known and well-studied,” and that an ID-based paradigm could have anticipated and accelerated the discovery of fine-tuning of the genetic code.

- **Michael J. Behe, “Getting There First: An Evolutionary Rate Advantage for Adaptive Loss-of-Function Mutations,” pp. 450-473, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  This paper elaborates on some of Behe’s arguments from his 2010 paper in *Quarterly Review of Biology*, in which he reviewed molecular mechanisms involved in adaptations in microorganisms documented in the literature. He found there that such adaptations almost always involved loss

or diminishment of function. In this paper Behe explores the implications of these observations for population genetics, and finds they pose a major challenge to Darwinian evolution.

Behe begins by observing that at the molecular level, far more mutations will cause loss-of function (LOF) than will cause a gain-of-function (GOF):

> It is very often possible to eliminate a molecular function by a variety of mutations. GOF mutations, on the other hand, are generally much more specific, sometimes being produced in only one way.

For example, Behe explores potential molecular mechanisms that can confer resistance to malaria in humans. One molecular mechanism involves creating a new binding site -- which Behe calls a GOF mutation. This requires very specific mutations. But other mechanisms work because they prevent production of a functional protein. Behe observes that there are many mutations that prevent the gene from functioning. This example helps explain why LOF mutations are far more common than GOF mutations. He concludes: “Because of the many ways in which a gene can be altered to lose function, the LOF mutation would have a rate several orders of magnitude greater than that of the GOF mutation for the duplicated gene.” What are the implications for neo-Darwinian evolution?

If different types of mutations (say, GOF mutations or LOF mutations) can confer some particular advantage on an organism, the LOF mutation is likely to become fixed before the GOF mutation since “LOF mutations always possess a rate advantage over GOF mutations if the respective selection coefficients are equal.” After reviewing various molecular adaptations observed in experiments reported in the literature, Behe argues: “Both experimental laboratory work over the past few decades and recent genomic studies of adaptation in natural populations attest to the importance, even dominance, of LOF mutations in short term evolutionary episodes.” His work helps make sense of this situation:

> The work presented in this paper helps show why this should be the case. Functional genetic elements such as genes and regulatory regions are built of multiple nucleotides, and a substantial fraction of mutations to these elements will cause them to lose their function. Thus the LOF mutation rate can be orders of magnitude greater than the nucleotide substitution rate. On the other hand, GOF mutations tend to be quite specific. So the rate for adaptive GOF mutations tends to be equal or very similar to the nucleotide mutation rate. As shown here, for some population size regions and for some values for the ratio of selection coefficients, the greater rate of mutation to the adaptive state for LOF versus GOF gives adaptive LOF mutations an intrinsic edge over adaptive GOF mutations.

This suggests that when Darwinian evolution is at work, it tends to diminish or destroy molecular functions rather than creating them. Behe closes with a quote from two biologists who observe that “there clearly are complex structures that are gained during evolution ... and we currently know little about how this process takes place.” The implication, of course, is that a process like Darwinian evolution, which tends to break or diminish functional molecular elements, is not a viable explanation for how these complex structures arose in the first place.

- **Jonathan Wells, “The Membrane Code: A Carrier of Essential Biological Information That Is Not Specified by DNA and Is Inherited Apart from It,” pp. 474-488, in Robert J. Marks II,**

Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C. Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).
In this paper, Jonathan Wells argues that "a genetic program is not sufficient for embryogenesis: biological information outside of DNA is needed to specify the body plan of the embryo and much of its subsequent development." Wells elaborates:

> Some of that information is in cell membrane patterns, which contain a two-dimensional code mediated by proteins and carbohydrates. These molecules specify targets for morphogenetic determinants in the cytoplasm, generate endogenous electric fields that provide spatial coordinates for embryo development, regulate intracellular signaling, and participate in cell-cell interactions. Although the individual membrane molecules are at least partly specified by DNA sequences, their two-dimensional patterns are not. Furthermore, membrane patterns can be inherited independently of the DNA.

Does this epigenetic information pose a problem for neo-Darwinism? Wells thinks it does:

> One could speculate that accidental changes in membrane patterns -- analogous to accidental mutations in DNA -- could provide the missing raw materials for evolution. Yet two- and three-dimensional information-carrying patterns are likely to entail more specified complexity than the one-dimensional information in DNA sequences, making beneficial "mutations" in such patterns much less probable than beneficial mutations in DNA. At the very least, calculations of the time required for evolution will now have to take into account these higher dimensions of biological information.

Thus, any viable model for the origin of biological information must explain not just the information in gene-coding DNA, but also the origin of the information in non-coding DNA, and the origin of epigenetic information. That, as even some evolutionary biologists are starting to acknowledge, is a tall order.

- **Douglas D. Axe and Ann K. Gauger, "Explaining Metabolic Innovation: Neo-Darwinism versus Design," pp. 489-507, in Robert J. Marks II, Michael J. Behe, William A. Dembski, Bruce L. Gordon, and John C Sanford eds., *Biological Information: New Perspectives* (Singapore: World Scientific, 2013).**
  In this paper, Axe and Gauger review the results of their own prior research, and the research of others, and examine six obstacles to Darwinian explanations of metabolic complexity. They suggest that a design-based paradigm offers the best solution to those obstacles.

  In discussing the first obstacle, the authors cite experimental work showing that duplicate genes are much more likely to be silenced, "Because gene expression is costly, it cannot be assumed that weakly converted enzyme functions isolated by laboratory selection would provide net selective benefit in wild populations." Intelligent design could provide a better explanation because such innovations require a goal-directed cause that looks beyond immediate fitness costs that go along with preserving a non-advantageous duplicate gene.

  The second and third obstacles pertain to the fact that "billions of years might be necessary" for features to generate arise that require "rare mutations or rare combinations of mutations" in order to function. They review their own research which suggests that multiple mutations would be required for even modest protein-to-protein conversions to occur. They conclude:

“enzymatic innovations requiring more than two specific mutations in a spare gene (provided by a duplication event) are implausible in neo-Darwinian terms.” Some goal directed process is required that can generate these complex adaptations.

The third problem found that producing even one new protein could strain the probabilistic resources of the Darwinian mechanism. But to produce metabolic complexity would require “multiple enzymatic innovations.” In their view, “This poses a severe challenge for neo-Darwinism. Mechanisms that have been proposed in attempts to meet this challenge, such as retrograde evolution, or serial duplication and recruitment do not match the actual distribution of protein domains across and within pathways.” Again, a goal-directed process seems necessary to solve this problem since “Useful innovations tend to require the simultaneous solution of multiple new problems, which means they tend to be compound innovations.” Like the fifth problem, they note that many simultaneous mutations would be required to produce new protein folds – leading to a similar obstacle, and solution.

The sixth problem is a novel one. Some proteins are necessary for their own production, leading to what Axe and Gauger call “causal circularity.” This presents something of a chicken-and-egg problem for Darwinism:

> [I]n order to conceive of an evolutionary origin of biotin biosynthesis, we must suppose that prior to this origin either A) cells were making their membranes without biotin, or B) cells had an abiotic source of biotin.

The authors realize that life itself presents such an obstacle: “Since life is a prerequisite for all biosynthesis, any biosynthetic product that is necessary for life in its present form is also necessary for its own biosynthesis in modern life. So causal circularity exists for all essential biosynthetic products.” Yet again, only a complex process, capable of working in a top-down fashion to coordinate multiple parts, can solve this problem. As a goal-directed process, intelligent design stands apart from unguided Darwinian evolution, and can uniquely provide the kind of innovative solutions necessary for complex life.

- **A. C. McIntosh, “Functional Information and Entropy in Living Systems,” *Design and Nature III: Comparing Design in Nature with Science and Engineering*, Vol. 87 (Ashurt, Southampton, United Kindom: WIT Transactions on Ecology and the Environment, WIT Press, 2006).**
  This paper explores the proper way to measure information and entropy in living organisms. Citing the work of Stephen Meyer, the author argues that random mutations cannot increase order in a living system: “[R]andom mutations always have the effect of increasing the disorder (or what we will shortly define as logical entropy) of any particular system, and consequently decreasing the information content. What is evident is that the initial information content rather than being small must in fact be large, and is in fact vital for any process to work to begin with. The issue of functional complexity and information is considered exhaustively by Meyer who argues that the neo-Darwinist model cannot explain all the appearances of design in biology.” McIntosh continues, explaining that only teleology -- intelligent design -- can explain the increases in information that generate observed biological complexity: “Even within the neo-Darwinist camp the evidence of convergence (similarity) in the suggested evolutionary development of disparate phylogeny has caused some writers to consider ‘channelling’ of evolution. Such thinking is a tacit admission of a teleological influence. That information does not increase by random changes (contrary to Dawkins’ assertion) is evident when we consider in

the following section, the logical entropy of a biochemical system." He concludes that goal-directed processes, or teleonomy, are required: "There has to be previously written information or order (often termed teleonomy') for passive, non-living chemicals to respond and become active."

- **Jonathan Wells, "Do Centrioles Generate a Polar Ejection Force?" *Rivista di Biologia / Biology Forum*, 98: 71-96 (2005).**
  Molecular biologist Jonathan Wells writes in the Italian biology journal *Rivista di Biologia* that the cell may be viewed and studied as a designed system with engineered machines. Showing the heuristic value of intelligent design, he writes: "Instead of viewing centrioles through the spectacles of molecular reductionism and neo-Darwinism, this hypothesis assumes that they are holistically designed to be turbines. … What if centrioles really are tiny turbines? This is much easier to conceive if we adopt a holistic rather than reductionistic approach, and if we regard centrioles as designed structures rather than accidental by-products of neo-Darwinian evolution. If centrioles really are turbines, then fluid exiting through the blades would cause them to rotate clockwise when viewed from their proximal ends." Wells hypothesizes that such approaches may lead to understandings of the workings of centrioles, perhaps even uncovering some causes of cancer.

- **Scott A. Minnich and Stephen C. Meyer, "Genetic analysis of coordinate flagellar and type III regulatory circuits in pathogenic bacteria," *Proceedings of the Second International Conference on Design & Nature*, Rhodes, Greece, edited by M.W. Collins and C.A. Brebbia (Ashurst, Southampton, United Kingdom: WIT Press, 2004).**
  This article underwent conference peer review to be included in this peer-edited volume of proceedings. Minnich and Meyer do three important things in the paper. First, they refute a popular objection to Michael Behe's argument for the irreducible complexity of the bacterial flagellum. Second, they suggest that the Type III Secretory System present in some bacteria, rather than being an evolutionary intermediate to the bacterial flagellum, probably represents a degenerate form of the same. Finally, they argue explicitly that compared to the neo-Darwinian mechanism, intelligent design better explains the origin of the bacterial flagellum. As the authors explain, "In all irreducibly complex systems in which the cause of the system is known by experience or observation, intelligent design or engineering played a role in the origin of the system."

- **William A. Dembksi, "The Logical Underpinnings of Intelligent Design," pp. 311-330, in William A. Dembski and Michael Ruse, eds., *Debating Design: From Darwin to DNA* (Cambridge, United Kingdom: Cambridge University Press, 2004).**
  In this article, Dembski outlines his method of design detection. He proposes a rigorous way of identifying the effects of intelligent causation and distinguishing them from the effects of undirected natural causes and material mechanisms. Dembski shows how the presence of specified complexity or "complex specified information" provides a reliable marker of prior intelligent activity. He also responds to a common criticism made against his method of design detection, namely that design inferences constitute "an argument from ignorance."

- **Walter L. Bradley, "Information, Entropy, and the Origin of Life," pp. 331-351, in William A. Dembski and Michael Ruse, eds., *Debating Design: From Darwin to DNA* (Cambridge, United Kingdom: Cambridge University Press, 2004).**

Walter Bradley is a mechanical engineer and polymer scientist. In the mid 1980s he co-authored what supporters consider a seminal critique of origin of life studies in the book *The Mystery of Life's Origins*. Bradley and his co-authors also developed a case for the theory of intelligent design based upon the information content and "low-configurational entropy" of living systems. In this chapter he updates that work. He clarifies the distinction between configurational and thermal entropy, and shows why materialistic theories of chemical evolution have not explained the configurational entropy present in living systems, a feature that Bradley takes to be strong evidence of intelligent design.

- **Michael Behe, "Irreducible Complexity: Obstacle to Darwinian Evolution," pp. 352-370, in William A. Dembski and Michael Ruse, eds., *Debating Design: From Darwin to DNA* (Cambridge, United Kingdom: Cambridge University Press, 2004).**
  In this essay Behe briefly explains the concept of irreducible complexity and reviews why he thinks it poses a severe problem for the Darwinian mechanism of natural selection. In addition, he responds to several criticisms of his argument for intelligent design from irreducible complexity and several misconceptions about how the theory of intelligent design applies in biochemistry. In particular he discusses several putative counterexamples that some scientists have advanced against his claim that irreducibly complex biochemical systems demonstrate intelligent design. Behe turns the table on his critics, arguing that such examples actually underscore the barrier that irreducible complexity poses to Darwinian explanations, and, if anything, show the need for intelligent design.

- **Stephen C. Meyer, "The Cambrian Information Explosion: Evidence for Intelligent Design," pp. 371-391, in William A. Dembski and Michael Ruse, eds., *Debating Design: From Darwin to DNA* (Cambridge, United Kingdom: Cambridge University Press, 2004).**
  Meyer argues for design on the basis of the Cambrian explosion, the geologically sudden appearance of new animal body plans during the Cambrian period. Meyer notes that this episode in the history of life represents a dramatic and discontinuous increase in the complex specified information of the biological world. He argues that neither the Darwinian mechanism of natural selection acting on random mutations nor alternative self-organizational mechanisms are sufficient to produce such an increase in information in the time allowed by the fossil evidence. Instead, he suggests that such increases in specified complex information are invariably associated with conscious and rational activity, that is, with intelligent design.

- **Granville Sewell, "A Mathematician's View of Evolution," *The Mathematical Intelligencer*, 22(4) (2000).**
  Mathematician Granville Sewell explains that Michael Behe's arguments against neo-Darwinism from irreducible complexity are supported by mathematics and the quantitative sciences, especially when applied to the problem of the origin of new genetic information. Sewell notes that there are "a good many mathematicians, physicists and computer scientists who...are appalled that Darwin's explanation for the development of life is so widely accepted in the life sciences." Sewell compares the genetic code of life to a computer program -- a comparison also made by computer gurus such as Bill Gates and evolutionary biologists such as Richard Dawkins. He notes that experience teaches that software depends on many separate functionally coordinated elements. For this reason "[m]ajor improvements to a computer program often require the addition or modification of hundreds of interdependent lines, no one of which makes any sense, or results in any improvement, when added by itself." Since individual changes to part of a genetic program typically confer no functional advantage (in isolation from many

other necessary changes to other portions of the genetic code), Sewell argues that improvements to a genetic program require the intelligent foresight of a programmer. Undirected mutation and selection will not suffice to produce the necessary information.

Category 3: Humanities Publications: Peer-Reviewed Publications Supportive of Intelligent Design Published in Academic Journals, Books, or Conference Proceedings within Philosophy, Theology, History, or other Humanities Disciplines.

- **Michael C. Rea, *World without Design: The Ontological Consequences of Naturalism* (Oxford University Press, 2004).**

- **William Lane Craig, "Design and the Anthropic Fine-Tuning of the Universe," in *God and Design: The Teleological Argument and Modern Science*, pp. 155-177. (Neil Manson ed., London: Routledge, 2003).**

- **Michael Behe, "Reply to my Critic: A Response to Reviews of *Darwin's Black Box: The Biochemical Challenge to Evolution*," *Biology and Philosophy*, Vol. 16, 685–709, (2001).**
  In this article published in the mainstream journal Biology and Philosophy, Michael Behe defends his views supporting intelligent design as stated Darwin's Black Box.

- **Del Ratzsch, *Nature, Design, and Science: The Status of Design in Natural Science* (State University of New York Press, 2001).**

- **William Lane Craig, "The Anthropic Principle," in *The History of Science and Religion in the Western Tradition: An Encyclopedia*, pp. 366-368 (Gary B. Ferngren, general ed., Garland Publishing, 2000).**

- **Michael Behe, "Self-Organization and Irreducibly Complex Systems: A Reply to Shanks and Joplin," *Philosophy of Biology*, Vol. 67(1):155-162 (March, 2000).**
  Michael Behe defends his arguments for irreducible complexity against the criticisms of various Darwinian scientists.

- **William Lane Craig, "Barrow and Tipler on the Anthropic Principle vs. Divine Design," *British Journal for the Philosophy of Science*, Vol. 38: 389-395 (1988).**

- **William Lane Craig, "God, Creation, and Mr. Davies," *British Journal for the Philosophy of Science*, Vol. 37: 168-175 (1986).**