Research

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The ENCODE Embroilment: Research on "Junk DNA" Verifies Key Predictions of Intelligent Design

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Section I. Why Are Biologists Lashing Out Against Empirically Verified Research Results?

Is the vast majority of the human genome useless junk or crucial for cellular function? Scientists are split over this question, with evolutionary biologists principally holding the former viewpoint, and molecular biologists the latter.

In our era of advanced biological research, one would think this an easily resolvable question, but when a powerful evolutionary paradigm is threatened by the findings of molecular biology, don't expect the establishment to quickly concede defeat. Indeed, the entire debate over neo-Darwinian evolution and intelligent design (ID) may turn on the outcome of this question.

Flotsam and Jetsam No More

For those who follow the debate over origins, the demise of junk DNA is old news. But that hasn't stopped leading evolutionary scientists from arguing that junk DNA refutes intelligent design.

For example, Francis Collins argues in *The Language of God* that our genome is full of "genetic flotsam and jetsam" (i.e., trash), making it "virtually inescapable"[1] that we share common ancestry with mice. But as I explained then, numerous functions had been discovered for noncoding DNA, and more have been found since, forcing a revolution in biological thinking. In a sign of the times, a 2010 *Nature* article heralded this new era of genomics, noting that "biology's new glimpse at a universe of non-coding DNA—what used to be called 'junk' DNA—has been fascinating and befuddling."[2] Many other scientific papers reporting functions for "junk" DNA have made similar remarks.

But no publication shook this debate so much as a 2012 *Nature* paper that finally put junk DNA to rest—or so it seemed. This major paper presented the results of the ENCODE (Encyclopedia of DNA Elements) Project, a years-long research consortium involving over 400 international scientists studying noncoding DNA in the human genome. Along with 30 other groundbreaking papers, the lead ENCODE article found that the "vast majority" of the human genome shows

biochemical function: “These data enabled us to assign biochemical functions for 80 percent of the genome, in particular outside of the well-studied protein-coding regions.”[3]

Ewan Birney, ENCODE’s lead analyst, explained in *Discover Magazine* that since ENCODE studied 147 types of cells, and the human body has a few thousand cell types, “it’s likely that 80 percent will go to 100 percent.”[4] Another senior ENCODE researcher noted that “almost every nucleotide is associated with a function.”[5] A headline in *Science* declared, “ENCODE project writes eulogy for junk DNA.”[6]

Bad News for Evolutionary Biology

This report was a game-changer in the debate over unguided evolution and intelligent design because, since the mid-1990s, ID theorists had been predicting that noncoding DNA would turn out to have function, and ID critics had been arguing that junk DNA drove a stake through the heart of ID.

For example, in 1998, ID-theorist William Dembski predicted function for junk-DNA:

> [Intelligent] design is not a science stopper. Indeed, design can foster inquiry where traditional evolutionary approaches obstruct it. Consider the term “junk DNA.” Implicit in this term is the view that because the genome of an organism has been cobbled together through a long, undirected evolutionary process, the genome is a patchwork of which only limited portions are essential to the organism. Thus on an evolutionary view we expect a lot of useless DNA. If, on the other hand, organisms are designed, we expect DNA, as much as possible, to exhibit function. And indeed, the most recent findings suggest that designating DNA as “junk” merely cloaks our current lack of knowledge about function. … Design encourages scientists to look for function where evolution discourages it.[7]

In 2004, pro-ID biologist Jonathan Wells argued that “The fact that ‘junk DNA’ is not junk has emerged not because of evolutionary theory but in spite of it. On the other hand, people asking research questions in an ID framework would presumably have been looking for the functions of non-coding regions of DNA all along, and we might now know considerably more about them.”[8]

But perhaps the earliest ID-prediction of function for junk-DNA came in 1994, when pro-ID scientist Forrest Mims submitted a letter to *Science* warning against assuming that “junk” DNA was “useless.”[9] *Science* wouldn’t print the letter, but that same year, anti-ID biologist Kenneth Miller published an article in a different journal making the opposite conclusion, namely that “the human genome is littered with pseudogenes, gene fragments, ‘orphaned’ genes, ‘junk’ DNA, and so many repeated copies of pointless DNA sequences that it cannot be attributed to anything that resembles intelligent design.”[10]

Contrast Miller’s assertion with a conclusion of *Discover Magazine* 18 years later in light of ENCODE’s 2012 breakthrough report: “The key point is: It’s not ‘junk.’”[11]

Evolutionists Strike Back

Defenders of the evolutionary consensus weren't going to take ENCODE's data sitting down. But this time, they found themselves in an unaccustomed position. Many proponents of unguided evolution take great assurance in knowing they stand in the scientific majority, which enables them to appeal to the consensus and dismiss challengers as "deniers." But in the post-ENCODE world, these scientists have found *themselves* challenging the consensus of an international body of leading molecular biologists who have discovered that the vast majority of human DNA has biochemical function.

How could they possibly oppose such empirically based conclusions? The same way they always defend their theory: by assuming an evolutionary viewpoint is correct and reinterpreting the data in light of their paradigm—and by personally attacking those who challenge their position.

For instance, multiple initial rebuttals from evolution defenders called ENCODE "hype"[12] and castigated researchers and science journalists for acting "irresponsibly" in favorably reporting on its findings.[13] In a post titled "The ENCODE Delusion," PZ Myers dismissed ENCODE's central claim that 80 percent of the genome has biochemical functions as "bull****," maintaining that evidence of biochemical activity in DNA and RNA "isn't function. That isn't even close." He called the ENCODE researchers themselves "fundamentally dishonest," and scoffed at Evan Birney, saying, "I don't think Birney has a clue about the biology."[14]

Another "consensus"-defending biologist, Nicholas Matzke, allowed that the ENCODE researchers weren't stupid, just ignorant: "I'm beginning to think that certain parts of molecular biology and bioinformatics are populated with people who are very smart, but who got through school with a lot of detailed technical training but without enough broad training in basic comparative [i.e., evolutionary] biology."[15] But University of Toronto biochemist and pro-evolution blogger Laurence Moran wouldn't even grant that the ENCODE researchers were intelligent: "I guess I'll just have to be content to point out that many scientists are as stupid as many Intelligent Design Creationists,"[16] he ranted.

Moran further lamented that "the creationists are going to love this," and he feared that ENCODE's results were "going to make my life very complicated,"[17] since "it's going to take a lot of effort to undo the damage caused by [ENCODE]."[18]

The vast majority of those defending ENCODE, however, are not pro-ID and have no motive to aid and abet "the creationists." ENCODE researchers responded the way you would expect someone to respond when the data is on their side: "Some people seek attention through hyperbole and mockery. We should stay focused on the issues."[19] They're driven by the empirical data. For example, University of Chicago geneticist James Shapiro praised ENCODE's results while simultaneously disavowing ID. He found that "the old idea of the genome as a string of genes interspersed with unimportant noncoding DNA is no longer tenable," since "ENCODE revealed that most (and probably just about all) of this noncoding and repetitive DNA contained essential regulatory information."[20]

Shapiro wrote papers in the mid-2000s predicting function for "junk" DNA, and he explained that his co-author was an ID proponent who held views he didn't share:

> In 2005, I published two articles on the functional importance of repetitive DNA with Rick von Sternberg. The major article was entitled "Why repetitive DNA is essential to genome function."
>
> These articles with Rick are important . . . for two reasons. The first is that shortly after we submitted them, Rick became a momentary celebrity of the Intelligent Design movement. Critics have taken my co-authorship with Rick as an excuse for "guilt-by-association" claims that I have some ID or Creationist agenda, an allegation with no basis in anything I have written.
>
> The second reason the two articles with Rick are important is because they were, frankly, prescient, anticipating the recent ENCODE results. Our basic idea was that the genome is a highly sophisticated information storage organelle. Just like electronic data storage devices, the genome must be highly formatted by generic (i.e., repeated) signals that make it possible to access the stored information when and where it will be useful.[21]

Clearly, some ID critics are embracing ENCODE's results. But most remain steadfastly resistant, most likely because ENCODE threatens to overturn some of the most prominent scientific arguments for an unguided evolutionary origin of the human genome.

What If ENCODE Is Right?

Earlier in 2014, *Science* reported on the arguments made by another leading evolutionary critic of ENCODE, University of Houston biologist Dan Graur. According to *Science*, "Graur's atheism inflamed his anger at ENCODE."[22] It's not surprising that Graur would become emotional over ENCODE given his blunt framing of the issue in a talk he gave in 2013:

> If the human genome is indeed devoid of junk DNA as implied by the ENCODE project, then a long, undirected *evolutionary process* cannot explain the human genome. If, on the other hand, organisms are designed, then all DNA, or as much as possible, is expected to exhibit function. If ENCODE is *right*, then *Evolution is wrong*.[23]

Graur's framing of the issue just might be correct. But to appreciate why ENCODE's critics are wrong, read the next sections of this article

Section II. Denying ENCODE Data Won't Change the Emerging Facts of Biology

As we've already seen, the ENCODE project found that 80 percent of the human genome is biochemically functional—with 100 percent functionality in sight—overturning the concept of junk DNA. Fearing the demise of a cherished argument, evolutionists immediately retaliated in their customary style—by becoming emotional and attacking the messengers. Even top journals like *Science* and *Nature* recognized the "anger," "rudeness," "intemperate griping,"[24] and "vitriolic . . . hyperbole and mockery"[25] levied by ENCODE's critics.

But what were the substantive responses to ENCODE from hardline evolution-defenders, and do their arguments hold up? Let's examine their top objection.

Response #1: It's Still Junk
The most common counterpoint has been that the ENCODE consortium may have detected "biochemical activity" for most of our genome, but that's very different from demonstrating that the activity has some necessary or important biochemical "function."

According to the central dogma of biology, DNA is transcribed into RNA, and then RNA is translated into protein. ENCODE found that the vast majority of our DNA is making RNA. But what if the process stops there and the RNA isn't doing anything useful? What if it's not junk DNA, but *junk RNA*?

Under this view, "all this extra transcription may simply be noise, irrelevant to function."[26] Or, as outspoken ENCODE critic Dan Graur argues, "transcription is fundamentally a stochastic [random] process," and ENCODE researchers are falling prey to the "human propensity to see meaningful patterns in random data."[27]

Aside from the fact that, even from an evolutionary viewpoint, it would seem colossally wasteful to expend cellular resources creating enormous amounts of RNA from over two-thirds of our genome if that RNA wasn't doing something beneficial, this rejoinder is factually false.

Transcription Isn't Random
ENCODE didn't merely study the genome to determine which DNA elements are biochemically active and making RNA. It also studied patterns of biochemical activity, uncovering highly non-random patterns of RNA production—patterns which indicate that these vast quantities of RNA transcripts aren't junk.

"By studying the *trans*-cellular patterning of biochemical signatures," writes John Stamatoyannopoulos, a leading ENCODE researcher at the University of Washington, "we gain telling insights into elements responsible for cell-selective regulation of transcript expression, the combinatorial patterns of transcription factors (TFs) that occupy them, and their likely genic targets."[28]

In other words, we find meaningful patterns of RNA production throughout the genome, creating an orchestrated army of bio-molecules that correlate with the activity of transcription factors—proteins that turn genes on and off. This suggests that our genome's biochemical activity is not just doing something, but doing something very important. And it's not hard to speculate what sort of tasks these RNAs might be doing, for RNA molecules can have all kinds of biochemical functions—including enzymatic properties and gene regulatory functions—whether or not they are translated into proteins.

The fact that DNA transcription is immense—and nonrandom—was confirmed in a 2013 paper that studied RNA transcripts in yeast. It found that while the yeast genome contains only about 6,000 genes, there were over 1.8 million unique RNA transcripts, which were "arranged in a remarkably complex, overlapping pattern across the genome."[29]

RNA Transcripts Specify Development

Clearly RNAs in yeast are encoding many protein sequences. Yeast, however, is only a single-celled organism; in multicellular organisms like animals, RNAs can have additional important functions. They can regulate gene expression and participate in RNA editing and RNA splicing—processes in which different pieces of RNA are stitched together and modified to create new RNA transcripts that in turn can yield additional types of proteins. Such RNA functions have been understood for some time. But a new revelation from ENCODE is that RNAs help specify how cells develop into a particular type.

Animals are composed of many different types of cells. Humans, for example, have nerve cells, blood cells, bone cells, skin cells, and so on. Different kinds of cells combine to form tissues, tissues interact to form organs, and organs coordinate to form an animal's body plan. The distribution of different types of cells is thus foundational to an organism's body plan. But what determines the specific type into which a given cell will develop?

ENCODE's results suggest that a cell's type and functional role in an organism are critically influenced by complex and carefully orchestrated patterns of expression of RNAs inside that cell. As Stamatoyannopoulos observes, ENCODE found that "the majority of regulatory DNA regions are highly cell type-selective," and "the genomic landscape rapidly becomes crowded with regulatory DNA as the number of cell types" studied increases.[30] Thus, as two pro-ENCODE biochemists explain, "Assertions that the observed transcription represents random noise . . . is more opinion than fact and difficult to reconcile with the exquisite precision of differential cell- and tissue—specific transcription in human cells."[31]

Stamatoyannopoulos further finds that repetitive DNA (often called "transposable elements"), which comprises over 50 percent of our genome, is active only in specific cell types. This non-random transcription of repetitive DNA into RNA suggests that transposable elements have functions whose importance are on par with other gene regulation mechanisms:

> In marked contrast to the prevailing wisdom, ENCODE chromatin and transcription studies now suggest that a large number of transposable elements encode highly cell type-selective regulatory DNA that controls not only their own cell-selective transcription, but also those of neighboring genes. Far from an evolutionary dustbin, transposable elements appear to be active and lively members of the genomic regulatory community, deserving of the same level of scrutiny applied to other genic or regulatory features.[32]

Opponents of ENCODE further assert that "there is currently no evidence that the majority of highly repetitive elements are functional."[33] But the vast majority of our genome—including repetitive DNA—is transcribed into RNA in nonrandom, cell-type-specific ways. That is evidence of some important function.

Individual RNA molecules then form networks in a cell, interacting with DNA, proteins, and other RNAs to control which genes are turned on and off, and which genes are expressed as proteins, thereby playing a crucial role in determining the cell's type. As Stamatoyannopoulos puts it, this complex system exudes function:

> More of the human genome sequence appears to be used for some reproducible, biochemically defined activity than was previously imagined. Contrary to the initial expectations of many, the overwhelming majority of these activities appear to be state-specific—either restricted to specific cell types or lineages, or evocable in response to a stimulus. . . . [B]iochemical signatures of many ENCODE-defined elements exhibit complex trans-cellular patterns of activity. . . . Together, these observations suggest that the genome may, in fact, be extensively multiply encoded—i.e., that the same DNA element gives rise to different activities in different cell types.[34]

These consistent and predictable cell-type-specific patterns of RNA expression, and stimulus-specific patterns of transcription, show that mass genomic transcription of DNA into RNA is not random, but has important functional purposes.

Non-Random Transcription of Endogenous Retroviruses

As a specific example of how ENCODE's data has helped reveal function for non-coding DNA, consider endogenous retroviruses (ERVs)—long cited by evolutionists as non-functional, parasitic DNA that supposedly refutes intelligent design of the genome. A 2013 paper in *PLOS Genetics* used ENCODE data to show that very high percentages of human ERVs are associated with open chromatin—strong evidence of transcription—*and* that the transcription occurs non-randomly, suggesting an important functional role:

> TEs [transposable elements] have contributed to the human genome nearly half of its active elements. Using DNase I hypersensitivity data sets from ENCODE in normal, embryonic, and cancer cells, we found that 44% of open chromatin regions were in TEs and that this proportion reached 63% for primate-specific regions. **We also showed that distinct subfamilies of endogenous retroviruses (ERVs) contributed significantly more accessible regions than expected by chance, with up to 80% of their instances in open chromatin.** Based on these results, we further characterized 2,150 TE subfamily-transcription factor pairs that were bound in vivo or enriched for specific binding motifs, and observed that TEs contributing to open chromatin had higher levels of sequence conservation. **We also showed that thousands of ERV-derived sequences were activated in a cell type-specific manner, especially in embryonic and cancer cells, and we demonstrated that this activity was associated with cell type-specific expression of neighboring genes. Taken together, these results demonstrate that TEs, and in particular ERVs, have contributed hundreds of thousands of novel regulatory elements to the primate lineage and reshaped the human transcriptional landscape.[35]**

We see from this that a great number of ERVs are found within open chromatin, strongly suggesting they are transcribed into RNA. Junk-DNA advocates respond that this isn't enough to show function because the transcribed DNA might just be producing "junk RNA." That's a weak response. As the paper states, ERV-based RNA transcripts are produced "in a cell type-specific manner" and are "associated with cell type-specific expression of neighboring genes." They further report "Thousands of LTR/ERV sequences are activated in a cell type-specific manner" and, strikingly, ERV transcription is highly enriched compared to other parts of the genome:

> [W]e observed that 1237 of the 2337 (52.9%) LTR7 repeat instances (a subfamily of the LTR/ERV class) were contributing to open chromatin in the human embryonic stem cell (ESC) line H7 when we would have only expected 60.5 (2.6%). This corresponds to a 20-fold enrichment and is highly significant (p<1.0E-100). We call such repeat subfamilies DHS-associated repeats (DARs) ... although LTR/ERV repeats constitute 13.5% of the repeat instances in the genome, they represent 25.0%, 54.6%, and 33.0% of the DAR instances in normal, embryonic, and cancer cells, respectively. ... LTR/ERV repeats have contributed a disproportionate fraction of cell type-specific accessible chromatin regions especially in embryonic and cancer cell lines. This is interesting given that network rewiring using ERV elements has already been described in ESCs [embryonic stem cells] and that it has been shown that stem cell potency fluctuates with endogenous retrovirus activity in mouse. ... [R]epeat subfamilies activated in a cell type-specific manner were also frequently associated with higher expression of neighboring genes.[36]

In other words, ERVs aren't merely massively transcribed—they are transcribed in a non-random, cell type-specific manner that correlates with the transcription of other functional genetic elements, including some that are important to embryological and developmental processes. Moreover, ERV transcription happens at a higher rate than other parts of the genome. All of this decidedly points towards their functionality.

No Accident

But how does transcription even begin to occur? It doesn't happen by accident. Transcription can't start without special stretches of DNA, called promoter sequences, which bind to special enzymes called transcription factors (TFs). And just any enzyme won't do—TFs must be able to recognize the specific DNA promoter sequence that they're keyed to unlock for transcription. Without that precise biochemical correspondence, transcription can't take place.

Once the right TFs bind to a promoter sequence, a molecular machine called RNA polymerase can then find the right place on the DNA to start converting the genomic message into a strand of RNA. The fact that the vast majority of the genome is transcribed suggests that these specified molecules—DNA promoter sequences and TFs—exist and are carefully matched throughout the genome.

If all that RNA is junk, why do these innumerable specified molecules exist throughout our cells?

Faulty Default Assumptions

For ENCODE-critics, however, none of this is enough. Their evolutionary mindset is wedded to the notion that organisms are poorly cobbled, junk-filled kluges. "If you don't know a function," Dan Graur argues, "assume as a null hypothesis that it doesn't have function."[37] His default assumption was dubious to begin with, but ENCODE provides empirical evidence that it is false. As a Nature summary puts it:

> Results from the ENCODE project show that most of these [non-coding] stretches of DNA harbour regions that bind proteins and RNA molecules, bringing these into

> positions from which they cooperate with each other to regulate the function and level of expression of protein-coding genes.[38]

Despite their bluster, critics have been unable to disprove what a leading ENCODE researcher stated in 2014: "There is not a single place in the genome that doesn't have something that you might think could be controlling something else."[39] If we're willing to follow ENCODE's experimental evidence where it leads, unhindered by evolutionary assumptions, evidence of important genomic function is everywhere.

Section III. ENCODE Critics: 'Evolution Proves Our Genome Is Junky ... Which Proves Evolution!'

The ENCODE project presented strong, experimentally derived evidence that the vast majority of our genome has important biochemical functions, but the specific functions of most of our six billion nucleotides have yet to be determined. Perhaps a hundred years from now molecular biologists will have these puzzles largely solved. But our present ignorance leaves enough ambiguity for some evolutionary biologists to hide out in the hope that the bulk of our genome may still turn out to be junk.

In the previous section, I showed that ENCODE critics are wrong in their main counterargument that research hasn't detected function throughout the genome. Continuing that discussion, we'll now examine four additional arguments from those who claim our genomes are largely junk DNA—and see why their circular logic doesn't hold up.

Response #2: The C-Value Paradox

Opponents of ENCODE often cite the "C-value paradox" as evidence that most DNA is junk.[40] According to this argument, the amount of DNA in an organism's nucleus (its "C-value") does not necessarily correlate with its overall complexity. For example, onion cells contain five times as much DNA as human cells, and humans have eight times more DNA than pufferfish. "Surely an onion doesn't need some 40 times more DNA than a fish," cries the ENCODE critic. "Much of that DNA must be junk!"

Appealing to the "onion test," junk defenders argue that if most onion DNA is useless, the same must be true for human DNA. As one proponent puts it:

> The onion test is a simple reality check for anyone who thinks they have come up with a universal function for non-coding DNA. Whatever your proposed function, ask yourself this question: Can I explain why an onion needs about five times more non-coding DNA for this function than a human?[41]

However, a number of observations and arguments mitigate the import of the C-value paradox and the "onion test."

First, we find a positive correlation between genome size and cell volume (and the size of a cell's nucleus), hinting at structural reasons for all that DNA.[42] Onions can have very large cells, and by this hypothesis, it's unsurprising that their genomes are also gigantic. Other correlations—like

a negative correlation between genome size and metabolic rates in various vertebrates—also hint at functional reasons for the C-value.[43]

A second response asks, *Who are we to dictate how much DNA an organism needs?* We are far from fully understanding the simplest bacterial genomes—much less our own. Evolutionists use this excuse to claim that most of our genome must be junk. But we might retort: "Why can't it be possible that onions are using most of their DNA?" Indeed, some single-celled protozoans—supposedly "simple" organisms—use massive amounts of non-coding DNA during their reproductive processes.[44]

Finally large-genomed organisms like the onion seem to have undergone genome duplications. This phenomenon, called polyploidy, shows that genomes can occasionally multiply in size, especially in plants.[45] Perhaps the onion genome was originally designed small, but ballooned through such natural duplications. That this may have happened in a few plant species that doesn't therefore mean that most DNA in most species is junk.

Some might find it surprising, and thereby persuasive, to learn that the onion has a huge genome, but the "onion test" is touted mostly for rhetorical effect. Logically speaking, it does not demonstrate that giant genomes are mostly junk, nor does it say anything about whether our own genome is junk-laden. The C-value paradox is a weak rhetorical argument that ignores empirically derived evidence showing mass genomic function.

Response #3: Very Little DNA is "Conserved"

After raising the C-value paradox, ENCODE critics often follow with a logical argument. "Only about 10 percent of our DNA is 'conserved," or has a similar sequence, compared to the genomes of other mammals," they point out. "This means that only about 10 percent of our genome is under selection to preserve the DNA sequence." They then reason: "Since natural selection is the only force that creates and preserves functional elements in our genome, it's impossible that more than about 10 percent of our genome is functional."

This argument was on display in a 2014 paper claiming that only 8.2 percent of human DNA is functional because only that percentage of our genome is "conserved" between humans and other mammals like mice and pandas.[46] But there's a glaring problem with this thinking: it *assumes* that all DNA sequences are the result of undirected mutation and selection to begin with, and that biological function only comes from natural selection. Throw out the assumption of an evolutionary origin of species and there's no reason to believe that only conserved DNA can be functional. After all, an intelligent agent could independently design functional genetic elements with widely divergent DNA sequences in the genomes of different species—no "conservation" required.

Only if we assume that strictly unguided evolutionary mechanisms produced our genome can we infer that such a small fraction of our genome is functional. Under this logic, when evolutionists cite the preponderance of junk DNA as evidence for evolution, they engage in circular reasoning.

Junk proponents seem blind to these flaws. A co-author of the 8.2-percent paper claimed, "our approach is largely free from assumptions or hypotheses."[47] But what about assumptions and hypotheses like unguided evolution?

Even worse, ENCODE critic Dan Graur called it "'idiotic' to suggest that a part of the genome could be functional if it didn't respond to pressure from natural selection."[48] He further charges that "what ENCODE researchers did not take into account . . . is that everything is shaped by evolution."[49] In Graur's evolutionary world, the possibility that some important functional genetic element arose from a cause other than natural selection is simply inconceivable.

There's another reason why the "sequence conservation" argument is unpersuasive. Whether or not one takes an evolutionary viewpoint, it's apparent that many differences between species *must* be encoded somewhere. If species have unique physical or biochemical traits, they should also have unique DNA sequences that encode those traits. As one paper correctly observes, non-conserved DNA "suggests taxon-related functions."[50]

In any case, ENCODE provides a nice empirical test of the evolutionary assumption that only conserved DNA can be functional: It finds evidence of mass functionality in "non-conserved" (i.e., unique) DNA sequences. As one lead ENCODE researcher explains: "Most elements defined by biochemical signatures lacked strong evolutionary conservation."[51] Other ENCODE defenders argue that the research shows that "absence of conservation cannot be interpreted as evidence for the lack of function."[52]

Response #4: Mutational Load

The average person has between 70 and 150 mutations compared to his parents.[53] Natural selection effectively "weeds out" extremely harmful mutations, but it doesn't work efficiently enough to prevent slightly deleterious mutations from accumulating in the population. How can the human population tolerate so many mutations—such a high "mutational load"—without facing a disastrous crash?

Standard evolutionary thinking answers this question by inferring that we can tolerate all those mutations because our genome is mostly junk. If the vast majority of our genome isn't doing anything, then most mutations will land in inconsequential locations and have a neutral (i.e., neither good nor bad) effect. Thus, humans can tolerate a high "mutational load" without facing major problems.

ENCODE-critic Dan Graur is a major proponent of this argument. In his view, "Mutational load considerations lead to the conclusion that the functional fraction within the human genome cannot exceed 15%."[54] According to Graur's argument, if every element of a genome is functional, then every possible mutation stands to be non-neutral, and thus could have a potentially deleterious effect. But if only a small portion of the genome is functional, then most mutations will occur in unimportant regions, and this spreads out mutations in a manner that greatly decreases the likelihood of experiencing a deleterious mutation. Given known mutation rates, Graur argues that only a small fraction of the genome can be functional or else our mutational load will become too great and our population will crash.

Graur's arguments require making certain assumptions about mutation rates, population sizes, and the percentage of mutations that are deleterious—assumptions which are dubious.[55] But even if we assume his arguments are correct, they still imply very important functions for all aspects of the genome. Under this view, in one sense much of the genome is "junk" because it isn't important for encoding genetic elements that have specific selectable functions. But in another sense under Graur's view the "junk" actually has an exceedingly important purpose: It allows the population to endure a much larger "mutational load" (i.e., experience mutations) before it crashes. Thus, even if Graur is right that most of the genome isn't "biochemically functional," he'd be wrong to say that the rest of the genome has no purpose; its purpose is to diminish the likelihood that organisms will experience deleterious mutations. Thus, even if Graur is right, it implies that the entire genome—both the portions that encode biochemically important genetic elements and those that do not—have important functions.

One *Scientific American* article restates the "mutational load" argument as follows:

> The third reason for accepting the reality of junk DNA is to simply think about mutational load. Our genomes, as of other organisms, have undergone lots of mutations during evolution. What would be the consequences if 90% of our genome were really functional and had undergone mutations? How would we have survived and flourished with such a high mutation rate? On the other hand, it's much simpler to understand our survival if we assume that most mutations that happen in our genome happen in junk DNA.[56]

But this argument fails to recognize that not all functionally important DNA operates in the same way. Specifically, proponents of the "mutational load" argument assume that non-coding DNA responds to mutations similarly to protein-coding DNA.[57] But different types of functional genetic elements may tolerate mutations in different ways. As two ENCODE-defending scientists point out, "protein-coding. . . sequences may have structure-function constraints and therefore mutational patterns different from those"[58] in much non-coding DNA. They further observe:

> Like words, [non-coding] regulatory sequences have *more relaxed* structure-function constraints than protein-coding sequences, which encode analog devices with strict chemical requirements. Indeed this is well supported by comparative analysis of gene promoters, *which nobody disputes are functional*, but where. . . function can be retained. . . in the absence of any recognizable primary sequence conservation.[59]

In 2020, three scientists writing in the journal *Genome Biology and Evolution* specifically responded to Dan Graur and other ENCODE-critics who had claimed the "mutational load" limits the proportion of functional DNA in the genome. They noted that proponents of "mutational load" arguments use models that wrongly assume that there could potentially exist a person with no deleterious mutations in their genome:

> Our approach is different from previous work that compared mean fitness at mutation-selection equilibrium with the fitness of an individual who has no deleterious mutations; we show that such an individual is exceedingly unlikely to exist. We find that the

> functional fraction is not very likely to be limited substantially by mutational load, and that any such limit, if it exists, depends strongly on the selection coefficients of new deleterious mutations.
>
> […]
>
> By comparing the population mean fitness at mutation-selection equilibrium to that of an individual who possesses no deleterious mutations, Graur (2017) reached the conclusion that, for likely values of the human per-base deleterious mutation rate, the functional fraction must be small.
>
> In this article, we present a different approach to analyzing mutational load and the human functional fraction. We do not take the fitness of an individual with zero deleterious mutations to be a meaningful value, because in a finite population of realistic size such an individual will never exist. Instead, we consider the fitness of the fittest individual likely to exist in a finite population. We conclude—while making no claims about the actual functional fraction as determined by comparative studies—that a mutational load argument is unlikely to set a low limit on the functional fraction of the human genome, and that any attempt to set such a limit must take into account the fitness effects of new deleterious mutations.[60]

Because no individual can exist with zero deleterious mutations, the maximum realizable fitness by the "fittest" person in a population is not ideal: "A main point of this article is that no individual with the theoretical maximum fitness, given the fitness model, will ever exist in a real population."[61]

Additionally, the scientists note that mutational load arguments against a highly functional genome are heavily dependent upon selection coefficients of new deleterious mutations. Only for very high values of selection coefficients is any meaningful limit imposed on the proportion of the genome that is functional (*f*). They thus note that "when considering the likely maximum realized fitness in a finite population, the limit to *f* [the fraction of the genome that is functional] is by no means low." They therefore conclude that "an argument from mutational load does not appear to be particularly limiting on *f*."[62]

More to the point, like the other junk-DNA arguments we've examined here, this one doesn't address ENCODE's direct experimental results showing function for non-coding genomic regions. Rather, it infers junk based upon evolutionary considerations.

Like the "conservation" objection, the "mutational load" argument assumes that random mutation and natural selection are the only forces that shaped our genome. If our species was originally designed—but isn't necessarily designed to live forever—then our genome could be largely functional and still experience a high "mutation load."

Response #5: Shift the Burden of Proof

In Section I, we saw how ENCODE-critic Dan Graur approaches genomics by adopting the default assumption that unknown genetic elements are junk: "If you don't know a function,

assume as a null hypothesis that it doesn't have function."[63] This strategy tries to shift the burden of proof from those claiming the genome is junk-filled to those claiming the genome is functional. It's a rhetorical strategy designed to let the pro-junk view win whenever there is ignorance, or a gap in our knowledge of genomic functionality. One might call it "junk of the gaps." Such reasoning is common among junk DNA defenders.

In a 2015 paper, Brunet and Doolittle argue that one study which found over 100 functional transposable elements (TEs) didn't offer evidence whatsoever that TEs may be generally functional class. Why is this the case? Because, according to them, we haven't detected specific functions for the rest of the millions of TEs in our genome:

> Their 100 positive cases represent only about 0.0003% of that multitude. Surely even the most optimistic and up-to-date estimate of proven contributions to organismal fitness would not yet reach 1%. It seems premature to imagine that a function for TEs as a class has been found![64]

Implicit in their argument is Graur's default assumption that we must assume something is junk until a specific function is found for every example. Under such reasoning, the conclusion that our genome is junky reflects mere assumptions, not data.

Normally in science, inferences are allowed to follow from the specific case to yield predictions for a general case. But for ENCODE critics, numerous specific examples of genetic function don't permit predict other scientists to infer that the genome is largely functional. This isn't how science is supposed to work.

For example, imagine what would happen if Isaac Newton had a default assumption that apples fall upward. Never mind that he once observed an apple falling and hitting the ground. Until he observes every apple falling downward, he's going to assume that they fall upward. And since he's only observed a few apples fall to the ground out of the millions and millions of apples that grow on trees each year, he's not allowed to infer that apples fall to the ground.

Such an assumption—which prevents us from making reasonable inferences from the data we have—stifles scientific advancement. Yet this is exactly how ENCODE-critics approach the genome.

Under their view, when we find function in one case, we are not allowed to suspect function in another. But what does the raw data say? The raw data always implications function. Non-functionality is always an outgrowth of our evolutionary assumptions, not the result of some research study.

Thus, where are the papers that look at genetic elements and empirically discover they are *not* functional? Such papers are virtually impossible to find. When we scrutinize specific genetic elements, we almost always find evidence of function. Indeed, Brunet and Doolittle admit that TE sequences "may vary relatively little between organisms within a species," providing the exact type of sequence conservation which, under other circumstances, is supposed to indicate evidence of an important selectable function.

Indeed, one paper using ENCODE data reported that 80% of endogenous retroviruses in the human genome are associated with open chromatin—strong evidence of transcription, suggesting some functional role.[65] But Brunet and Doolittle dismiss simply this evidence because of their default assumptions. Their objection is circular and it amounts to saying (paraphrased): "The human genome is full of junk because we assume the human genome is full of junk."

Breaking the Circle

A few months after ENCODE's results were published in 2012, junk-DNA advocate Sean Eddy published a paper promoting these sorts of objections:

> ENCODE's publicized interpretation would require that such nonconserved regulatory sequences account for 80-95% of the genome, far outnumbering evolutionarily conserved regulatory sequences. Given the C-value paradox, mutational load, and the massive impact of transposons, the data remain consistent with the view that the nonconserved 80-95% of the human genome is mostly composed of nonfunctional decaying transposons: "junk."[66]

Aside from the fact that ENCODE provides strong empirical evidence that most of our DNA is functional (see the previous section), we might pose the following questions to Eddy:

- What if the C-value has functional importance, and the "paradox" only pertains to the few species whose genomes have ballooned compared to their aboriginal design, but doesn't mean their DNA isn't functional, and doesn't say anything about whether other genomes (including ours) are full of junk?
- What if species were intentionally designed with important and diverse functional genetic elements, but weren't intended to live forever, such that seeking "conserved" sequences or studying the "mutational load" won't reveal how much of the genome is functional?
- What if "transposons"—i.e., repetitive DNA—are actually important functional control elements in the genome (again, see the previous section), which we've mistakenly identified as selfish, junk DNA?

These arguments for junk only work if one assumes an evolutionary viewpoint. If one must assume an evolutionary view to conclude that the genome is full of junk, one cannot argue that junk demonstrates an evolutionary view.

Two biochemists from down under, John Mattick and Marcel Dinger, agree that the case for junk DNA is based upon circular logic. They argue:

> [T]he conclusion of lack of conservation of most of the human genome is largely based on a circular comparison with the rate of evolution of [repetitive DNA] . . . which are assumed to be largely non-functional and therefore evolving "neutrally." ... If the first assumption is incorrect, and increasing evidence suggests that it may be, the derived conclusion of nonfunctionality of the rest of the genome is also incorrect.[67]

They conclude that ENCODE's empirical evidence for functionality is the ultimate test: "differential expression (including extensive alternative splicing) of RNAs is a far more accurate guide to the functional content of the human genome than logically circular assessments of sequence conservation."[68] Bottom line: good evidence trumps bad theory.

A Great Divorce

Critics like Dan Graur charge that ENCODE is guilty of "divorcing genomic analysis from its evolutionary context"[69]—and that's exactly right. ENCODE's empirically based finding that the vast majority of our genome is functional has withstood theoretical, evolution-based objections from critics. Maybe a divorce from evolutionary thinking is exactly what we need to liberate biology from bad evolutionary assumptions and explain what's happening inside our cells.

Section IV. Post-ENCODE Posturing: Rewriting History Won't Erase Bad Evolutionary Predictions

While many evolutionists adamantly maintain—even in the face of the ENCODE consortium's compelling experimental results—that the vast majority of the human genome is junk, some Darwin-defenders have tried hedging their bets by embracing ENCODE's research. This camp attempts to revise history by claiming that evolutionary biology expected all along to find what ENCODE found: mass functionality in our genome.

Others in this compromising camp are more forthright. They don't deny evolutionary biology's bad predictions about junk DNA, and they admit that new models are needed to accommodate ENCODE's data. In other words, they accept ENCODE's conclusions, but admit they can't explain them in evolutionary terms.

After an introduction to ENCODE in section I, sections II and III covered four objections from evolutionists who reject ENCODE, and showed why they failed to refute the project's findings. This final installment will assess two more responses from evolutionists—ones who accept ENCODE, but now struggle to comprehend a junkless human genome in the post-ENCODE world.

Junky Predictions

Before examining those cunning evolutionary biologists who now pretend they never predicted our genomes would be junk-filled, it's important to document what evolutionists were saying prior to ENCODE's breakthrough papers in 2012 which showed the vast majority of our genome is functional.

The April 17, 1980 issue of *Nature* published papers by influential biologists arguing that evolution predicts our genomes should be full of junk DNA. The first article, "Selfish Genes, the Phenotype Paradigm and Genome Evolution," by W. Ford Doolittle and Carmen Sapienza, maintained that "Natural selection operating within genomes will inevitably result in the appearance of DNAs with no phenotypic expression whose only 'function' is survival within genomes."[70]

A second paper, “Selfish DNA: the ultimate parasite,” was by Francis Crick, who won the Nobel Prize for determining the structure of DNA, and the eminent origin-of-life theorist Leslie Orgel. They concluded, “much DNA in higher organisms is little better than junk," and “it would be folly in such cases to hunt obsessively for” its function.[71]

Fifteen years later, the junk-DNA paradigm was alive and well, as *Scientific American* reported:

> These regions have traditionally been regarded as useless accumulations of material from millions of years of evolution … In humans, about 97 percent of the genome is junk.[72]

Numerous similar examples exist, but we’ll revisit one more—what prominent Columbia University philosopher of science Philip Kitcher wrote in his 2007 Oxford University Press book *Living with Darwin*. Citing the “masses of genomic junk” that “litters the genome” Kitcher pronounced that “The most striking feature of the genomic analyses we now have is how much apparently nonfunctional DNA there is.”[73] In his view, “From the Darwinian perspective all this is explicable,” but “if you were designing the genomes of organisms, you would certainly not fill them up with junk.”[74]

Response #6: Just Kidding—We Anticipated Function!

When ENCODE’s findings were published in 2012, many evolutionists reacted harshly to the conclusion that virtually our entire genome is functional (see *Salvo* 31, 32, and 33). Others, however, have seen the writing on the wall for junk DNA, and realized that they better switch their bets—or at least place some new ones.

For example, a 2014 paper in *Biology & Philosophy* initially claimed that “junk DNA seems at odds with the view that the genome is … the work of an intelligent force or designer,” but then argued that a junkless genome “is compatible with evolution by natural selection,” because “we could expect natural selection to evolve lean genomes.”[75] Under this posturing, whether our genome is full of junk or devoid of it, evolution wins.

But first prize for betting on both horses goes to Richard Dawkins. In his 1976 book *The Selfish Gene*, Dawkins famously argued that “a large fraction”[76] of our genomes is useless parasitic DNA, and that Darwinian evolution explains why:

> The true ‘purpose’ of DNA is to survive, no more and no less. The simplest way to explain the surplus DNA is to suppose that it is a parasite, or at best a harmless but useless passenger, hitching a ride in the survival machines created by the other DNA.[77]

Again in 2004 he railed against “creationists” on the basis of our junk-laden genomes:

> [C]reationists might spend some earnest time speculating on why the Creator should bother to litter genomes with untranslated pseudogenes and junk tandem repeat DNA.[78]

As recent as 2009, Dawkins adopted the incredible position that “the greater part (95 per cent in the case of humans) of the genome might as well not be there, for all the difference it makes.”[79]

In September 2012, however, Dawkins changed his tune dramatically. Just one week after ENCODE's results were published, in a debate against Britain's chief rabbi, Dawkins declared that ENCODE's results are precisely what Darwinism predicts:

> There are some creationists who are jumping on [ENCODE] because they think it's awkward for Darwinism. Quite the contrary, of course, it is exactly what a Darwinist would hope for—to find usefulness in the living world.[80]

He went on to say that, "whereas we thought that only a minority of the genome was doing something, namely that minority which actually codes for protein. And now we find that actually the majority of it is doing something." Under Dawkins newly reformed view, "the rest [of the genome] which had previously been written off as junk" is now understood as "the program" that's "calling into action the protein coding genes."[81]

It's as if Dawkins' decades of arguing that our genome is full of junk never happened.

History is Not Easily Rewritten

While some evolutionists now try to erase their history of pro-junk arguments, others try to mitigate their embarrassment by highlighting the occasional suggestion, mined out of the annals of scientific literature, that some rare bits of the junk might end up being functional. For example, University of Guelph evolutionary biologist T. Ryan Gregory is an ENCODE-critic,[82] but he has been dug up some a nice little collection of quotes from evolutionary scientists who are purportedly predicting or finding some function for non-coding DNA.[83] Presumably he did this just in case ENCODE turned out to be right.

Many of Gregory's quotes don't really support his case. They simply show biologists finding *experimental* evidence of function for noncoding "junk"—just like ENCODE did – *not* predicting it before the fact due to some scientific model (which is what ID did). To be sure, many of the biologists who made these discoveries are evolutionists, but they made their discoveries by spending time in the lab studying how the cell works, not on the basis of evolutionary theory.

Gregory, however, aims to make a stronger argument, as he co-wrote in a scientific paper:

> [I]t is simply not true that potential functions for noncoding DNA were ignored until recently. In fact, various early commenters considered the notion that large swaths of the genome were nonfunctional to be "repugnant", and possible functions were discussed each time a new type of nonprotein-coding sequence was identified…[84]

His "repugnant" quote comes from a paper that discovered much of our genome is repetitive DNA[85]—long cited as "junk" in our genome.[86] It's true that those *particular* authors didn't think the repetitive DNA was "trivial," but their paper was published in 1968, *before* the term "junk" DNA was even coined.[87] Indeed, soon thereafter, this paper on repetitive DNA was being cited by another paper in *Science* that has proven foundational for evolutionary biology in establishing the pro-junk-viewpoint. That latter paper (published in 1969) made the astounding suggestion that "99 percent of mammalian DNA is not true genetic material"[88]—i.e., junk. In 1972, Susumu

Ohno, the Japanese evolutionary biologist who coined the term "junk DNA," made a similarly striking prediction: "At least 90% of the mammalian genomic DNA appears to represent 'nonsense' DNA base sequence of various kinds."[89]

Thus, while it's true that some scientists have proposed various functions for noncoding DNA, evolutionary theorists by and large predicted that the vast majority of the genome would be functionless. The typical attitude is canonized in various editions of Douglas Futuyma's evolutionary biology textbooks, published from the 1970s into the 2000s. His first edition, written just a few years after the concept of junk DNA was conceived, anticipated that repetitive DNA would have no function:

> [O]ther features may well be neutral, having no function whatever. The most extreme, still hypothetical, example is that of the highly repetitive short sequences of DNA that may never be transcribed into RNA. **These** may have a function … **but I would not be surprised if they did not**.[90]

Futuyma's second edition, published in 1986, likewise claimed our genome is full of transposable, repetitive DNA sequences which "do not exist because they serve the organism" but rather are "ignorant DNA" or "selfish DNA … and may be viewed as parasites."[91] The third edition, published in 1998, again stated these repetitive elements generally "do not provide any adaptive to the service to the organism" because they are "selfish DNA" or "parasites, much like viruses, of the genome in which they reside."[92] This viewpoint was still heavily promoted in Futuyma's 2005 textbook, where he wrote:

> Because natural selection consists only of differential reproductive success, it results in 'selfish genes' and genotypes, some of which have results that are inexplicable by intelligent design. We have seen that genomes are brimming with sequences such as transposable elements that increase their own numbers without benefitting the organism.[93]

As late as 2009, Futuyma's textbooks still claimed "In eukaryotes, the vast majority of DNA has no known function, even though as much as 80 percent may be transcribed."[94] While Futuyma often includes caveats allowing that some small portion of this DNA might turn out to be functional, his view is typical of the evolutionary community: it's mostly junk.

Pro-ID biologist Richard Sternberg offers a forceful reply to Gregory's style of argument:

> As someone who has studied the concept of "junk DNA" for over twenty years, I am dismayed by … a half-truth and a false fact that … goes something like this: "No one ever asserted that junk DNA is without function … it was long suspected that these sequences have important roles in the cells."[95]

Sternberg acknowledges that a few evolutionary scientists speculated that some junk might accidentally acquire a useful function. Even Crick and Orgel suggested that "occasionally" this might happen, but still predicted "most sets of repeated sequences will never be of use."[96] Their

view—common among evolutionary theorists—stands in great contrast to ENCODE's recent findings, as Sternberg explains:

> [T]he view expounded by Orgel and Crick …, and Doolittle and Sapienza … has been considered by many cellular and molecular biologists to be the correct explanation for much of genomic DNA until very recently. So the oft-read claim on the web that the term "junk DNA" never implied developmentally "non-functional DNA" is one that is made either out of ignorance or disingenuousness.[97]

Indeed, it's difficult to put much stock in Gregory's claims that evolutionary biologists by-and-large anticipated function for non-coding DNA when he himself is a prime example of an evolutionary scientist who ardently advocates the view that our genome is overwhelmingly junky. A March, 2015 article in the *New York Times*, "Is Most of Our DNA Garbage?," the prominent science journalist Carl Zimmer praised Gregory's research and noted that he "champions an idea first developed in the 1970s but still startling today: that the size of an animal's or plant's genome has essentially no relationship to its complexity, because a vast majority of its DNA is -- to put it bluntly -- junk." According to Zimmer, "Where some look at all those billions of bases and see a finely tuned machine, others, like Gregory, see a disorganized, glorious mess."

Zimmer goes on to explain that Gregory not only thinks that there's much junk DNA in our cells, but also lots of junk RNA:

> But to Gregory and others, [the view that most noncoding RNA is crucial] is a blinkered optimism worthy of Dr. Pangloss. They, by contrast, are deeply pessimistic about where this research will lead. Most of the RNA molecules that our cells make will probably not turn out to perform the sort of essential functions that hot air and fire do. Instead, they are nothing more than what happens when RNA-making proteins bump into junk DNA from time to time.

Zimmer concludes by saying Gregory believes the prevalence of junk DNA is strong evidence for evolution:

> The blood-drenched slides that pack Gregory's lab with their giant genomes only make sense, he argues, if we give up thinking about life as always evolving to perfection. To him, junk DNA isn't a sign of evolution's failure. It is, instead, evidence of its slow and slovenly triumph.[98]

Zimmer quotes other evolutionary biologists asserting that most of our genome is junk, which is no surprise since his own evolutionary biology textbook, co-written with biologist Douglas Emlen, adopts and promotes the standard evolutionary view that our genome is full of junk:

> Over half of the genome is composed of neither genes, nor vestiges of human genes, nor regulatory regions. Instead, it is made up of parasite-like segments of DNA, known as mobile genetic elements, with the capacity to make new copies of themselves that can then be reinserted into the genome. Some mobile genetic elements originated as viruses

> that integrated their genes into the genome of their host. The origins of other mobile genetic elements are more mysterious. Once they become established in their host genome, mobile genetic elements can proliferate into thousands of copies and take up large amounts of space.[99]

The quotes from evolutionary scientists listed in this present article only scratch the surface of a huge body of literature. Again and again, evolutionary scientists have stated or predicted that our genome is primarily useless junk. Occasional caveats from evolutionary scientists, allowing that some small amount of the "junk" might be functional, do not mitigate the widespread, longstanding evolutionary viewpoint that our cells are full of junk DNA. We now know that on this point, evolutionists were wrong. Evolutionary biology inspired, created, and promulgated the now-false "junk DNA" paradigm.

We now return to the central question raised section I: *Is the vast majority of the human genome useless junk, or is the vast majority of the human genome crucial for cellular function?*

In answering this question, it's important to clarify what the different camps are, or are not, saying. ID proponents and ENCODE defenders, who take the latter view, aren't saying the genome must have *zero* junk. And ENCODE's evolutionary critics, who take the former view, aren't saying that *all* non-coding DNA must be junk. Nonetheless, there's a titanic difference between the two viewpoints. In fact, if evolutionary scientists hadn't long-predicted that our genomes would be mostly functionless junk, we wouldn't be having this conversation.

Why does ID tend to predict function for junk DNA? This is simple: *Designers tend to design things for a purpose, so if something was designed it probably has a function.*

Response #7: Live in Limbo

Other evolutionists handle ENCODE's results in a more admirable manner. Instead of trying to rewrite the history of evolution's predictions, they acknowledge the evidence now supports mass functionality in the genome, and even concede that evolutionary models didn't anticipate this result. They are content to live with ambiguity until evolutionary model are developed to explain ENCODE's data.

For example, lead ENCODE researcher John Stamatoyannopoulos admits that, "new models of evolutionary conservation are needed"[100] to explain why so much human DNA is functional. Similarly, in a *Nature* article titled "Celebrate the Unknowns," Philip Ball reflects upon ENCODE's implications:

> [T]he current picture of how and where evolution operates, and how this shapes genomes, is something of a mess. … But we are grown-up enough to be told about the doubts, debates and discussions that are leaving the putative 'age of the genome' with more questions than answers. Tidying up the story bowdlerizes the science and creates straw men for its detractors. Simplistic portrayals of evolution encourage equally simplistic demolitions.[101]

Aside from Ball's admission that ENCODE leaves evolutionary genomics in "a mess," don't miss his last two sentences. In referencing "detractors" who make "demolitions" of "simplistic portrayals of evolution," he's referring directly to proponents of intelligent design (ID) who point out that ENCODE refutes evolutionary models which predicted a junk-filled genome. Now that those predictions have failed, the best way to save evolution from ENCODE is to disavow those models by calling them "simplistic" or "straw men."

Ball is being honest that ENCODE's data wreak havoc upon old evolutionary models, and that evolutionists cannot, presently, explain ENCODE's results. What he's not telling is that those old models that predicted junky genomes were not "straw men" or fringe hypotheses, but were well-accepted proposals and direct consequences of evolution-based population genetics math.

ID Phobia

Evolutionists who accept ENCODE's results have tried to comprehend why other biologists steadfastly would challenge the project's experimentally demonstrated conclusions. They concur that a major force driving anti-ENCODE attitudes is fear of lending credence to intelligent design.

In his retrospective on ENCODE, Philip Ball acknowledges an "anxiety that admitting any uncertainty about the mechanisms of evolution will be exploited by those who seek to undermine it."[102] Likewise, pro-ENCODE biochemists John Mattick and Marcel Dinger observe that "resistance to [ENCODE's] findings is further motivated in some quarters by the use of the dubious concept of junk DNA as evidence against intelligent design."[103] Writing in a slightly different context, eight biologists published a *Nature* article in 2014 recognizing that scientists self-censor criticisms of neo-Darwinism because, "haunted by the spectre of intelligent design, evolutionary biologists wish to show a united front."[104]

It's disturbing that scientists oppose empirically-based research results or suppress their own doubts about the neo-Darwinian paradigm simply because they don't like the perceived alternative—ID. And we should be disturbed: these admissions show that evolutionary biology is in an incredibly unhealthy state, where devotion to the paradigm trumps the evidence. A 2003 paper in *Science* observed that "the term 'junk DNA' for many years repelled mainstream researchers from studying noncoding DNA,"[105] but even now that junk DNA has finally been overturned, evolutionary dogmatism is still hindering scientific advancement.

Indeed, ID phobia is admitted not only by ENCODE proponents, but also by pro-junk ENCODE-critics. The journal *Science* explained how University of Houston biologist Dan Graur opposes ENCODE because he doesn't like its ID-friendly implications:

> Graur's atheism inflamed his anger at ENCODE. He perceives an echo of intelligent design in the consortium's "80% [of the genome is functional] claim," which he takes to imply that most of the genome exists because it serves a purpose.[106]

But the most blunt summary of why scientists oppose ENCODE came when Graur declared: "If ENCODE is right, then Evolution is wrong."[107] With ENCODE's empirical data now showing

that the vast bulk of the genome has an important purpose, we can safely say that the fears of ENCODE critics are entirely justified.

Future Forecast

Since 2012, research has continued to uncover additional specific functions for non-coding DNA, making the case for ENCODE grow stronger and stronger with each passing month.[108] Eventually, the evolutionary holdouts will be unable to deny that virtually our entire genome is functional. Or so you'd like to think.

Evolutionists who believe their paradigm stands only if ENCODE falls have invested careers, reputations, and deeply held worldviews on the view that humans were created by purposeless processes that filled our genomes with useless DNA. Thus, after famously saying, "If ENCODE is right, then Evolution is wrong," Dan Graur's action plan was, in his own words: "Kill ENCODE."[109] Human nature may never allow such critics to concede defeat. For them, too much is on the line. Win or lose, they're going down fighting.

The good news, however, is that most scientists aren't evolutionary ideologues. Rank and file biologists know compelling empirically-based experimental data when they see it, and because they see it in ENCODE, they will build (and may have already built) a new consensus that rejects "junk DNA" and views ENCODE-critics as a footnote—perhaps one that cautions against putting the paradigm before the evidence.

Some of these biologists now explore what they call "post-Darwinian"[110] models of evolution, often adopting the same critiques of Darwinism made by ID proponents. They still seek unguided material evolutionary explanations of life, and are resistant to design. But that resistance is weakening. Indeed, widespread fears about aiding intelligent design show that many biologists understand how ENCODE's results represent a major coup for ID. As William Dembski eloquently put it some 14 years pre-ENCODE:

> [D]esign is not a science stopper. Indeed, design can foster inquiry where traditional evolutionary approaches obstruct it. Consider the term 'junk DNA.' Implicit in this term is the view that because the genome of an organism has been cobbled together through a long, undirected evolutionary process, the genome is a patchwork of which only limited portions are essential to the organism. Thus on an evolutionary view we expect a lot of useless DNA. If, on the other hand, organisms are designed, we expect DNA, as much as possible, to exhibit function. … Design encourages scientists to look for function where evolution discourages it.[111]

If scientists had embraced an ID paradigm when Dembski wrote those words in 1998, how much more advanced would molecular biology—unhindered by evolutionary assumptions—be today? We may never know for sure, but this much is clear: ID boldly predicted ENCODE's results, and evolutionary biology didn't. This puts ID in a strong position to lead science forward into a post-Darwinian world.

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