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Response to "No Replacement of Darwin
A Review of *Replacing Darwin—The New Origin of Species*"

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Abstract

I am grateful to Frello for his review, particularly for its length and detail. Ironically, Frello has actually done me a great favor; his review ends up bolstering my original claims.

Keywords: *Replacing Darwin*, mitochondrial DNA, mtDNA, genetics, species, speciation, testable prediction

Introduction and Overview

Frello's review is the third in his published attempts to find a flaw with the biological elements of young-earth creation (YEC) science. The first two (Frello 2017a, 2017b) helped advance the origins debate by revealing the deficiency (for documentation, see Jeanson 2017a and Jeanson 2017b) of his best anti-YEC claims. The current attempt is directed at my recent book, *Replacing Darwin* (Jeanson 2017c).

Frello's review of *Replacing Darwin* is much longer than his first two criticisms of my published work. His book review also contains many specific scientific claims. To ensure the thoroughness of my rejoinders, I will be responding to his review point-by-point. To do justice to Frello's claims, I will be quoting his review extensively. After responding to each of his specific points, at the conclusion of this response I will reflect on the implications of his objections for the specific claims that I made in *Replacing Darwin*.

Frello's General Claims

Frello begins his critique by incorrectly summarizing my book:

Biogeography, Taxonomy, Genetic diversity and Speciation are the main topics, which, according to Jeanson, ToE [Theory of Evolution] either fails to explain or which can be explained without reference to evolution.

In fact, my book made three points (the focus of parts I, II, and III in *Replacing Darwin*), which I will relist as follows:

1. The question of the origin of species is, fundamentally, a genetic question, and Darwin wrote *On the Origin of Species* before the field of genetics was even born. Therefore, when Darwin argued for evolution long before any genetic data were available, he took a massive scientific risk.

2. Darwin's arguments from non-genetic data were very effective in 1859, but irrelevant in the modern era. Modern creation science endorses migration as an explanation for biogeography; it endorses the formation of new species; and its expectations for the patterns and groupings of life have matured dramatically. In other words, in non-genetic fields of science, the origins debate is back to square one.

3. In the most important field of science (genetics) on the question of the origin of species, YEC science outstrips evolution. Not only do genetic data contradict evolution and confirm YEC science, but the YEC model is making testable, falsifiable predictions in genetics. In other words, the modern YEC model meets the gold standard of science; evolution does not.

Since Frello chose to side-step a direct confrontation of the main claims of my book, we are left with lesser disputes. To ensure thoroughness in our exchange over these lesser quibbles, I will now respond to the specific objections he raises, in the order that he raises them. We'll discover that his initial avoidance of my central conclusions foreshadows a deeper flaw in his analyses.

Frello's Claims About Biogeography

Frello begins his specific criticisms by focusing on the subject of biogeography. In *Replacing Darwin*, my most extensive discussion of biogeography is in Chapter 4. Yet Frello has little to say about this chapter.

Instead, Frello quotes from the Afterword: "Migration fits the current geographic distribution of species." Frello then tries to summarize the conclusions of *Replacing Darwin* on the question of biogeography: "[Jeanson] thinks migration *from Eurasia* to the rest of the world can explain the current distribution of animals" (emphasis mine).

Not surprisingly, Frello finds fault with this biogeographic conclusion. Frello says of my position, "This is a bold assertion." Then Frello lists several examples of biogeographic distributions (Australian marsupials, New World primates, and Malagasy

primates) that he thinks create problems for the model described in *Replacing Darwin*. From these three examples, Frello reaches a bold conclusion: "Jeanson fails to account for biogeography, while the topic is among Darwin's original arguments in favor of evolution."

Among the various sections of Frello's critique, this section on biogeography is his strongest. He uses a very clever strategy to engage this element of my book. Let's consider Frello's strategy and assertions carefully, and in detail, to understand their overall significance for the biogeographic claims that I made in *Replacing Darwin*.

Let's begin by reviewing in more depth what I actually wrote in my book. Since some of Frello's criticisms aren't very transparent in their reasoning, this larger picture helps explain Frello's strategy. A wider context also reveals where Frello's criticisms miss the mark. In *Replacing Darwin*, Chapter 4 contains the most extensive discussion of the question of biogeography. But it is preceded by an in-depth discussion of the scientific method, which sets the context for the biogeographic discussion. In the section on scientific methodology, I demonstrate that science is, fundamentally, a process of elimination. It begins with the statement of a hypothesis, proceeds to the identification of competing hypothesis, and concludes with the performance of every conceivable scientific test in an attempt to eliminate one or more hypotheses.

Following this discussion, I narrate how the scientific method was applied to the question of biogeography—but specifically in the context of 1859. On the creationist side, advocates argued for the fixity of species' geography and ancestry. Darwin countered these claims with evidence in support of common ancestry and migration.

One of the specific tests that Darwin used was a novel, probabilistic experiment. I illustrated his approach with modern species. For example, I asked why, for some groups of species, their morphology and physical appearance seems to track with geographic distribution. In other words, for some groups of species, geography seems to predict morphological and physical similarity. For instance, among the great apes, the two species of gorillas (both reside in Africa) look more like one another than either looks like the species of orangutans (orangutans are strictly Asian). Conversely, orangutan species look more like one another than any look like gorillas.

Under the hypotheses of the fixity of species geography and of the fixity of their ancestry, you might predict that geography and morphology should be randomly distributed. In other words, there should be little to no correlation between the two. Specifically, you might expect one species of orangutan to exist in Africa alongside a species of gorilla, and the same to

be true in Southeast Asia. By chance, the species with the most morphological similarity might occasionally share the closest geographic proximity. But the more frequent the occurrences of morphological and geographic correlation, the harder it is to maintain the fixity hypotheses.

Frello seems to partially adopt this strategy in his three biogeographic challenges to *Replacing Darwin*. Some of his strategy seems to be simply mocking, and his three biogeographic examples are notably shallow on data, charts, figures, and graphs. Yet his challenge involves statements like "What a coincidence!" which implies a probabilistic component.

To be fair, I never provided mathematically-detailed, probabilistic calculations in the main text of *Replacing Darwin*. So we can grant Frello a partial pass for his own lack of rigor in his scientific challenges to my book.

However, the purpose of Chapter 4 was simply to narrate the science of 1859, not lay out the modern biogeographic scientific paradigm in all its detail and controversies. Yet Frello wants to confront the modern creationist view head-on with supposedly contradictory data.

I anticipated the style of Frello's objections in the way that I designed the structure of *Replacing Darwin*. Specifically, I purposely tried to keep the main text free of overly-technical tangents, unresolved scientific debates, and quibbles over minor issues. Instead, I moved these aspects of the science of the origin of species to the Endnotes. Part of my reason for doing so was to catch less-than-rigorous critics of my work. In my experience, critics of creation science tend towards condescending and hasty responses. This strategy of the critics often results in logical errors that invalidate the critic's points. By putting technical details in the Endnotes, I gave myself a means for catching hasty reviewers in the act. On the question of biogeography, I kept the main text largely focused on the 1859 debate over biogeography, and I shoved the modern debate to Endnote 19 of Chapter 4. Specifically, Endnote 19 reveals that the 21st century debate is very different than the 1859 debate:

> The fossil record and other historical data add layers of complexity to the discussion of migration—according to both modern creationists and evolutionists. For examples from modern creationists, see the following: K. P. Wise and M. Croxton, "Rafting: a Post-Flood Biogeographic Dispersal Mechanism," in R. L. Ivey, ed., *Proceedings of the Fifth International Conference on Creationism* (Pittsburgh, PA: Creation Science Fellowship, 2003), p. 465–477; D. Statham, "Phytogeography and Zoogeography—Rafting vs Continental Drift," *Journal of Creation*, 2015, 29(1):80–87.

Had Frello engaged the Endnotes and these papers, he would have found himself with very different perspective on the question of biogeography. Not only do these references document challenges for the evolutionary explanation for biogeography, they lay out in great detail a much more comprehensive model for creationist biogeography.

However, even my Endnotes section doesn't do justice to the full details of the modern biogeography research program. Unlike the 19th century, the 21st century debate is multidisciplinary. It involves the fields of plate tectonics, radiometric dating, geologic sedimentation, historical climatology, paleontology, biological migration, genetics, and the like. Currently, neither the creationist position nor the evolutionary model has a consistent, comprehensive, discipline-wide explanation for biogeography (i.e., see Chapters 7–10 of my book which reveal just a few of the shortcomings of the evolutionary positions in many of these fields). In other words, if Frello wants to take up the topic of biogeography and have a debate, he must synthesize data from plate tectonics, radiometric dating, geologic sedimentation, historical climatology, paleontology, biological migration, and genetics—something he never attempts to do. (See discussion further on in this response, especially discussion of Frello's errors in attempting to make sense of modern genetic data.) This is Frello's first unscientific step.

If Frello's first unscientific step stems from his antiquated views of the scientific scope of the question of biogeography, his second unscientific step stems from his antiquated perspective on biogeographic hypotheses. For example, in 1859, the creationist hypotheses were the fixity of species' geography and ancestry. As I described earlier, modern creation science endorses migration as an explanation for biogeography, and it endorses the formation of new species. This dramatically alters the nature of the biogeography debate.

For example, let's contrast the simplicity of the 1859 debate with the complexity of the 2018 debate. Even without considering the morphology-geography correlations that we just discussed, the pre-1859 hypothesis that species' geography is fixed quickly runs into problems (detailed in Chapter 4). If we concede that species migrated, then the hypothesis of the fixity of species' ancestry would likely propose that species should migrate stochastically to their current locations. Non-random distributions (i.e., correlation between morphology and geography) would reject this hypothesis and argue for common ancestry (at appropriate statistical cutoffs). These are the hypotheses that Frello seems to consider. And these hypotheses would be appropriate to consider—if we were living in 1859.

In contrast, the 21st century debate is much more complex. Modern creationists invoke even more hypotheses than the creationists of 1859. Specifically, in some cases (i.e., the New World primates or Malagasy primates), modern creationists might indeed invoke common ancestry![1] Frello doesn't seem to recognize that the identification of the "kinds" is still a work in progress, rather than a settled question (*Replacing Darwin* makes this point clear, as does the Lightner *Answers Research Journal* paper that Frello himself cites). Other hypotheses include historical contingency (i.e., effects of the ice age on land connections among continents, which might explain the partial endemism of marsupials to Australia), biological function (i.e., differential migration rates), competition among "kinds" (i.e., this a subset of explanations under the category of biological function), and differential extinction among "kinds". If Frello wants to debate the question of biogeography in 2018, he's going to have to design scientific tests that consider and eliminate each of these hypotheses before he can conclude that his evolutionary hypothesis is correct.

Instead, Frello concludes "Jeanson fails to account for biogeography, while the topic is among Darwin's original arguments in favor of evolution." In light of the discussion above, Frello's bold statement makes a fundamental scientific error: Stating untested hypotheses as fact. For Frello to conclude that the evolutionary explanation for biogeography is correct, then Frello must scientifically eliminate all of the modern YEC hypotheses for biogeographic distributions. Since Frello fails to do so, his critique of creationist biogeography fails to meet the standards of science and, therefore, technically qualifies as pseudoscience.

Frello's Claims About Taxonomy

Frello's claims about taxonomy seem to primarily revolve around the contents of Chapter 5 in *Replacing Darwin*. Frello begins by correctly articulating a key distinction that I discuss at length in Chapter 5: "An important difference between the theory of evolution and creationism is the interpretation of the biological taxonomical hierarchy. According to the theory of evolution, all levels of the hierarchy reflect common descent. According to creationism, no level above the created 'kinds' (in vertebrates more or less the family-level) reflects common descent."

Unfortunately, in the very next sentence, Frello proceeds to misrepresent my position: "According to Jeanson (Chapter 5), common descent is not needed to explain the nested hierarchies." Actually, I said that both creation and evolution predict the existence of nested hierarchies:

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[1] This is based on my own unpublished analysis of mitochondrial DNA data for these primates, as well as of changes in taxonomic classification of these primates through the years.

The creation and design model predicts with equal force each of the biological evidences we examined. Thus, by the standards of the scientific method, the evidences that Darwin used to argue for universal common ancestry fail—because Darwin's evidences fail to eliminate competing explanations. (Jeanson 2017c, 140)

This may seem like a distinction without a difference. But I deliberately phrased my conclusions in this way because of my discussion of the method of inductive reasoning from Chapter 4. Furthermore, this distinction forms the basis for one of the major points of my book—points which Frello side-stepped (see documentation above). Frello's misrepresentation is a significant foreshadowing of the direction of his arguments—both the arguments that we've already discussed, and the arguments that Frello raises specifically in this section (see discussion below).

Leaving Frello's misrepresentation aside, let's explore what Frello can do with the data in Chapter 5. Frello successfully followed some of my analogy between designed things and the hierarchy of biological life: "[Jeanson] uses the analogy of vehicles to explain how such a nested hierarchy would result from design as well. For example, in vehicles the Family level could be cars, pickups, SUV and the like. The Order level would include tractors, the Class level would include military tanks, and the Phylum level would include airplanes. This Phylum would be 'Powered Vehicles'. Another Phylum could be 'Unpowered Vehicles' exemplified by a hang-glider. All these belong to the Kingdom of 'Vehicles'… Jeanson's corresponding examples in animals are Family: Horses; Order: Odd-toed ungulates (horses, rhinos and tapirs); Class: Mammals; Phylum: Chordates. Kingdom: All animals."

Why does Frello find fault? Frello's first objection: "However, in designed objects, many of the smallest parts are exactly the same: the same kind of batteries, wires and LEDs are used in different devices. The same kind of artificial polymers and metal alloys are used as well." Frello thinks my analogy breaks down upon close inspection.

However, Frello hasn't applied this objection consistently. His description of the supposed uniqueness of the design realm matches the biological realm equally well. For example, in living things, "many of the smallest parts are exactly the same." For instance, large swaths of life are based on the same chemistry (e.g., nucleotides, amino acids, carbohydrates, etc.). The genetic code is nearly universal. In fact, the near-universality of the genetic code is one of the most commonly cited evidences to justify *universal evolutionary common ancestry*. Is Frello now rejecting the "evidence for evolution" that his colleagues frequently cite? I doubt it. In other words, Frello has lobbed a self-defeating criticism.

At the same time, Frello has uncovered an additional line of evidence that strengthens my original analogy between the design realm and the biological realm.

Frello continues: "Also, more complex parts follow this pattern. The use of diesel engines vs. gasoline engines vs. electrical engines does not follow any reasonable taxonomy of vehicles. The problem goes further than just the common use of these things. One model of airplane, ferry, and car could use an upholstery constructed of, say, 10% rayon and 90% nylon. Another model of airplane, ferry, and car could use an upholstery constructed of, say, 90% rayon and 10% nylon."

Once again, Frello's description of the supposed uniqueness of the design realm matches the biological realm equally well. Specifically, the "more complex parts" among species also "follow this pattern." For example, anytime the evolutionary model invokes "convergent evolution," it is implicitly acknowledging a biological part or feature that does not follow the expected ("reasonable") taxonomy. For instance, despite the obvious outward similarity, marsupial moles and placental moles are *not* classified together. Instead, marsupial moles group with creatures like kangaroos, and placental moles group with creatures like llamas. As another illustration, despite their outward resemblance, echidnas and hedgehogs belong to very different taxonomic categories. Based on their modes of reproduction, echidnas group with the platypus, and hedgehogs group with elephants. Finally, in the biological realm, "the problem goes further than just the common use of these things." One type of equid can be covered with black and white stripes (e.g., zebras). Another lacks stripes altogether and is covered in a solid color (e.g., horses). One type of cat has orange fur with black stripes (e.g., tigers); another has white fur and black spots (e.g., snow leopard). In other words, Frello lobs another self-defeating criticism—while simultaneously revealing an additional line of evidence that supports my original analogy.

Thus, Frello's summary claim that "When it comes to living organisms, a corresponding violence of the hierarchical pattern would hardly be possible" is demonstrably incorrect. The "problems" that Frello finds in my analogy are actually common features of the biological realm. Frello's criticisms again serve to strengthen my analogy instead of weaken it.

To his credit, Frello tries to differentiate the biological realm from the design realm with specific biological examples: "When you look at, for example, structure of the cell membrane, it follows large taxonomical groups. Any protein sequence from the GenBank database is unique to the species or genus it comes from." But his choice of examples is,

once again, short-sighted. Vehicle body types (i.e., the structure of vehicles) follow large taxonomical groupings. Vehicles have VIN numbers that are unique. Specific differences in the biological realm find an echo in the design realm. Consequently, for the third time, Frello's criticisms serve to strengthen my analogy instead of weaken it.

Frello isn't finished in his attempt to dismiss my analogy between design and biology in the realm of nested hierarchies. He says, "Another objection to Jeanson's model is that there is no 'natural' hierarchy of vehicles. His major groups are 'Powered' and 'Non-powered'. But why not 'Military' and 'Civilian' (historically that would make more sense), or 'For transportation of people' and 'For transportation of goods'? Or why not use 'Powered' vs. 'Non-powered' as the main categories, including washing machines in the Kingdom 'Powered devices', while furniture, hand-tools and bicycles is placed in the Kingdom 'Non-powered devices'."

The same objections and questions could be leveled at biology. I could just as easily assert, "There is no 'natural' hierarchy of" species. Why not group creatures based on appearances rather than reproduction? For example, why not group echidnas and hedgehogs together, rather than hedgehogs and elephants? Why not group all moles together, instead of grouping marsupial moles with kangaroos, and placental moles with llamas?

Frello thinks he has an answer to this type of rejoinder: "Evolution immediately suggests a natural hierarchy: that based on descent. Today descent is mostly evaluated by comparing DNA-sequences for at least two reasons: DNA is the ultimate source of variation; and the details of information in DNA is much larger than in any other group of characters." But then Frello immediately undercuts his own argument. He concedes, "Not all genes suggest the same phylogeny." Which is it? Does descent naturally suggest a hierarchy? Or does it need multiple corrective factors before a "natural" hierarchy emerges?

Putting Frello's contradictions aside, his argument fails for no other reason than "descent" has an analogy in the design world. Take any common car. Each car has a history of "descent." In fact, each one has a history of "descent with modification." Consider just how many updates have been done to the Chevrolet Camaro or the Ford Mustang. You could justifiably claim that these cars have *evolved* over the years. Just when consumers think that the designs of these cars cannot be modified or improved any more, the next model emerges. At this risk of excessive repetition, I'll say it again: Frello's criticisms serve *strengthen* my analogy instead of weaken it. This fourth instance should make the strength of my analogy clear.

Frello lobs one final objection: "To put the argument to the limit, look at a motor glider and a normal glider (aircrafts). They are virtually identical. However, according to Jeanson's system, the motor glider belongs to the phylum 'Powered vehicles' while the normal glider belongs to the phylum 'Non-powered vehicles,' and as such, they should be more different than an electrical bicycle and a joint strike fighter (both belonging to the same phylum). What could be more ridiculous? Biological hierarchies, based on evolution, would never end up in such self-contradicting nonsense."

Once again, the biological realm readily supplies examples that refute Frello's claims. Any example of "convergent evolution" would immediately display the "self-contradicting nonsense" that Frello derides. For example, are hedgehogs closer to giraffes, elephants, manatees, and tigers? Or to echidnas? Because they are classified in very different mammalian groups, hedgehogs and echidnas "should be more different than" a zebra and a bat. (Zebras, bats, and hedgehogs are all placentals.) Yet, by all appearances, hedgehogs and echidnas "are virtually identical."

To be sure, Frello might object to this example. He might say, "Oh no, just look a little deeper. Go beyond the superficial similarities, and examine the stark differences inside—at the level of reproduction." In other words, Frello might ask us to "look under the hood" of these creatures to see the justification for their current biological classification. I'd respond by inviting him to "look under the hood" of motor gliders and normal gliders to see why they fall into such different classification categories. Thus, for the fifth time, Frello's criticisms serve to strengthen my analogy instead of weaken it.

As a side note, I find it revealing that Frello had nothing to say about the other points I raised in Chapter 5. For example, I pointed out that both evolution and design predict the existence of so-called "transitional forms" and of "homologous" structures. Scientifically, this means that the existence of "transitional forms" and of "homologous" structures cannot be used as evidence for evolution over against design. I also pointed out the deficiency of anti-design arguments from "vestigial" structures and organs. Finally, I highlighted a positive argument for common ancestry within vertebrate families—the Darwin-inspired comparison between breeds and species. Since Frello had nothing to say about any of these arguments from Chapter 5, I assume he concedes them. Given the prominent role that "transitional forms," "homologous" structures, and anti-design arguments typically play in origins debates, this is remarkable. Frello's behavior advances the origins debate by leaps and bounds.

Frello's Claims About Genetic Diversity

Frello's claims about genetic diversity presumably represent his response to Chapters 7–10 of my book, where I spend the most time discussing the impact of modern genetic discoveries on the origins debate. In this section of his critique, Frello's arguments vary. Some become very convoluted—almost to logical absurdity; others are clever, but shallow. At least one argument displays very disconcerting instances of misrepresentation. I will attempt to follow his logic and work through each of his examples slowly.

Sadly, Frello's opening claim represents an example of the logical absurdity category. Let's walk through it line by line. "According to Jeanson, most of the genetic variation within 'kinds' existed before speciation, and can be explained as original created variation." At best, this claim is ambiguous. To which "genetic variation" is Frello referring? Chapters 7 and 10 of my book are focused on mitochondrial DNA (mtDNA); Chapters 8–9 are focused on nuclear DNA and its impact on population genetics.

This ambiguity is critical to resolve. If Frello is referring to genetic variation in the mtDNA, he has misrepresented me. In fact, Chapter 7 shows that mtDNA differences within kinds are the result of mutation, not the direct result of God's creative acts during the Creation Week. If Frello is, instead, referring to nuclear DNA, then, yes, in *Replacing Darwin* I showed multiple lines of evidence that "most of the genetic variation within 'kinds'" was imparted at Creation.

Frello follows his ambiguous statement about my claims with a clear description of the evolutionary explanation for all genetic diversity, mitochondrial or nuclear: "The theory of evolution agrees that genetic diversity existed prior to speciation, but ascribes it to accumulation of mutations over past eons." (In my book, I say the same thing: "according to evolution, the ultimate cause of genetic change is mutation" [Jeanson 2017c, 243].)

Then, Frello appears to clarify his original ambiguity—to his detriment: "Jeanson uses great apes as one example among others (Chapter 10)." Presumably, Frello means that I use great apes as an example of his summary statement of my view that "most of the genetic variation within 'kinds' existed before speciation, and can be explained as original created variation." The trouble with Frello's logic is that Chapter 10 of *Replacing Darwin* is about mtDNA, not nuclear DNA. In Chapter 7, I explicitly show that the creation model ascribes mtDNA diversity to mutation. Even worse, Chapter 10 doesn't even discuss mtDNA patterns in the great apes.

Frello then states: "[Jeanson] excludes humans from the [great ape] family, as humans are not part of the great ape 'kind'. Jeanson relies on the nuclear genome in his analysis." Here, Frello's attempt to summarize my views goes far afield from *Replacing Darwin*. Again, Chapter 10 is about mtDNA, not nuclear DNA. Furthermore, I excluded humans from the great ape family because putting them in the same family failed to make accurate predictions (technically, *retro*dictions) of the data. And this was true for both human and great ape mtDNA (Chapter 7) and nuclear DNA (Chapter 8)—not nuclear DNA alone, as Frello erroneously implies.

Frello's next sentences twist his logic even further: "However, if you compare homology between nuclear genomes from humans, chimps, gorillas, and orangutans you have no choice. If homology between nuclear genomes reveals relationship, chimps are closer related to humans than to gorillas and orangutans (Prado-Martinez et al. 2013). If homology between nuclear genomes has nothing to do with relationship, Jeanson's calculations are worthless. What is it?" Let's attempt to understand this paragraph of Frello's in steps.

What does Frello mean by "homology"? Here, Frello seems to be using it as a synonym for *percent relative genetic identity*—which includes both identical sequences and mismatched sequences. This makes the best sense of his statement, "Chimps are closer related to humans than to gorillas and orangutans." So let's go with the assumption that "homology" actually means *percent relative genetic identity*.

What does Frello mean by "If homology between nuclear genomes reveals relationship"? Let's translate his sentence in light of my previous paragraph: "If *percent relative genetic identity* between nuclear genomes reveals relationship." Now let's remove the "if": Frello is saying that *percent relative genetic identity* between nuclear genomes reveals relationship.

But to whom is Frello attributing this claim? Surprisingly, Frello seems to be attributing this to *me*. His logic appears to be as follows:

1. Jeanson assumes that *percent relative genetic identity* reveals genealogical relationships.
2. At the genetic level, chimpanzees are relatively closer to humans than to gorillas and orangutans.
3. Therefore, Jeanson should accept common ancestry among humans and the great apes.
4. Since Jeanson doesn't accept this common ancestry, he must therefore reject the claim that *percent relative genetic identity* reveals genealogical relationships.
5. Since Jeanson is thus forced to reject the claim that *percent relative genetic identity* reveals genealogical relationships, all his genetic "calculations are worthless."

Let's compare the assumptions of this 5-step logical series to what I actually claimed in the book.

Do I assume that *percent relative genetic identity* reveals genealogical relationships? No. In fact, I argue for the *opposite* conclusion. In Chapter 5, I deal with the question of whether the fact of nested hierarchies (*percent relative genetic identity* is a form of nested hierarchy) is automatically evidence of common ancestry. (Evolutionists believe this is so.) By revealing that the design model also predicts the fact of nested hierarchies, I show (scientifically) that nested hierarchies are agnostic on the question of common ancestry. Because the competing hypothesis (design) cannot be eliminated by the fact of nested hierarchies, nested hierarchies say nothing about common ancestry. In Chapters 7 and 8, I extend this logic to the realm of genetics—specifically, to the realm of mtDNA (Chapter 7) and the realm of nuclear DNA (Chapter 8). In other words, in *Replacing Darwin*, I argue that the fact of *percent relative genetic identity* does *not* reveal genealogical relationships because two competing (and opposite) hypotheses predict the existence of *percent relative genetic identity*.

Frello has begun his claim with an assertion that has the logic of *Replacing Darwin* completely backwards.

Since Frello has misrepresented what I claimed, let's review what I actually propound in Chapters 7 and 8. The focus of these chapters is the *absolute* number of DNA differences among species, not the *relative* number of DNA differences among species. In other words, the central question that Chapters 7 and 8 try to answer is about the *number* of DNA differences, not the *pattern* of DNA differences.

From the absolute numbers of DNA differences, I used measured mutation rates to examine which model (creation or evolution) accurately predicts (technically, *retro*dicts) the number of DNA differences among species. In other words, I applied the gold standard of science to accept or reject competing scientific hypotheses. I found that creation meets this standard, but evolution does not.

Returning to Frello, it should be obvious that his paragraph (and his five logical steps that I listed above) are a straw man, not a summary of my book. Therefore, Frello's claims in his paragraph cannot count as a rebuttal to *Replacing Darwin*.

Let's continue working through Frello's accusations, line by line. His next paragraphs read as follows:

> Though data from the GenBank database could be used to test Jeanson's idea that the majority of genetic variation within families is due to original created variation, he makes no attempt to do so. To illustrate how this could be done, I have used information about differences in 15 nuclear genes in cats (Johnson et al. 2006). Cats are among the

'kinds' that, according to the Bible, were present at the Ark in only one pair. Therefore, a maximum of four alleles[1] of each gene could be present in this original pair. This should be traceable in the current variation within the cat family.

Fig. 1 shows the sum of differences found in these 15 genes.

To squeeze these results into four groups (the squares) reveals that at least 79 mutations must have occurred. According to creationism 4400 years has passed since the Flood, so there is a maximum of 4400 generations (no cats start breeding before they are two years old on average) between the most distantly related species. 79 mutations in 4400 generations in a sequence of 8696 nt correspond to 1 mutation in 500.000 nt per generation. In humans, according to Jeanson, the corresponding number is 1:40 million (78 mutations per generation per genome, 3.1 billion nt). Cats would have to have an almost 80 times higher mutation rate than humans. At best an extremely bold prediction.

Frello's endnote above refers to a clarifying definition (endnote 1), which reads as follows: "Allele: One of two or more versions of a particular DNA position."

Let's start by identifying where Frello's claims and representations of *Replacing Darwin* are correct. In these paragraphs, he clearly and unambiguously states the genetic compartment to which he refers—the nucleus ("15 nuclear genes"). He also correctly identified my explanation for the origin of the DNA differences in this nuclear DNA compartment as, "the majority of genetic variation within families is due to original created variation."

But then Frello's argument commits a common genetic mistake. In his endnote, he (correctly) defines an allele as "One of two or more versions of *a particular DNA position*" (emphasis mine). But then he contradicts himself in the paragraph above: "a maximum of four alleles[1] *of each gene* could be present in this original pair" (emphasis mine). By definition, genes consist of more than one DNA position. So which is it? Is an allele a version of a particular DNA position? Or a version of a gene that contains hundreds to thousands of DNA positions? Frello can't have it both ways.

In fact, his argument rests on his (erroneous) adoption of the second definition—that alleles are different versions of genes. Under this definition, he misrepresents my explanation for nuclear DNA differences. In fact, in one of my published papers (Jeanson and Lisle 2016) that I refer to at least 15 times in *Replacing Darwin*, I explicitly addressed Frello's error:

> If an allele is defined in terms of a gene unit, then generating "allelic" diversity by mutating just one

gene per mutational event produces little diversity. Instead, if an allele is defined as a single genomic position, independent of its relationship to a gene, then enormous allelic diversity can be generated by mutation…As an aside, allelic diversity need not arise via mutation. Again, if we use the genomic position definition of an allele rather than the gene unit definition, other mechanisms besides mutation can generate allelic diversity. For example, a single gene typically spans thousands of nucleotides, and SNVs [SNVs=Single Nucleotide Variants] might be distributed throughout the gene—for example, at 90 of the nucleotides within the gene. If we allow for the genomic position definition of alleles, every single one of these 90 SNVs may have existed in a heterozygous state in each of the individuals of the pairs brought on board the Ark.

Expanding this single gene example across the entire genome reveals a tremendous potential for allelic diversity on the Ark. In just two diploid individuals, four genome copies exist. Since only four DNA base-pairs exist, virtually every possible *genomic position* allele (i.e., far more than 4–28 *gene unit* alleles) could have been present at the time of the Flood, if the individuals were heterozygous. (Jeanson and Lisle 2016, 99) [emphases in original paper]

In other words, every single one of the nuclear DNA differences in Frello's graph could have existed in a heterozygous state in the felid ancestor on board the Ark—because my model defines alleles in terms of *DNA position*, not individual *genes*. Thus, Frello's (apparent) claim—that a maximum of four versions of each gene could be present in this original pair—is incorrect.

Conversely, my model has no need for the mutation rates that Frello claims; in fact, in theory, it has no need for mutations in this example at all. Frello has made a common genetic error, which nullifies his conclusion.

Thus, on the question of *relative* DNA differences and *absolute* DNA differences, Frello is unable to generate a rebuttal to my claims. His best attacks represent scenarios he invents that have nothing to do with my published work. Yet this section of his critique is one of the closest that he comes to engaging my central claims. Once again, Frello's avoidance of—and silence on—my central claims indirectly reveals their strength.

Multifunctionality of mitochondrial genes

In his critique, Frello returns to the topic of homology and spends an entire section on it titled "Multifunctionality of mitochondrial genes." In this section, Frello again employs a clever strategy. So let's work through his sentences slowly. First, Frello says, "A related topic is the fact that whenever genes are present in larger groups of species, such as mammals, all animals, or even all eukaryotes (organisms with a cell nucleus), the homology of the genes resemble the homology of the anatomy."

Again, what does Frello mean by "homology"? His next sentence reads, "mtDNA has no known function related to anatomy or physiology, yet the homology between mtDNA reflects that of anatomy throughout the biological system." In this context, "homology" again seems to refer to some type of nested hierarchy, be it genetic, anatomical, or physiological.

His next sentence suggests that this interpretation is correct: "Jeanson's solution is to ascribe additional functions to the mitochondrial genes (Chapter 7)." In Chapter 7, I discuss the nested mtDNA hierarchy among living Perissodactyl and Artiodactyl species. I then describe the usual evolutionary explanation for this fact: "As we observed in chapter 5, evolutionists see this pattern as evidence of common ancestry" (Jeanson 2017c, 171). And then I describe the creationist explanation, referring the reader to a lengthy paper I published in 2013 [Endnotes 19 and 20 below refer to this 2013 paper]:

As in chapter 5, the mtDNA hierarchy shows strong parallels with the hierarchy present within the Linnaean classification system.[19] Since this system is based on biological function, the parallel between the mtDNA hierarchy and the Linnaean categories suggests that the mtDNA hierarchy has something to do with function. In other words, the creation/design model predicts the fact of mtDNA nested hierarchies as much as evolution does.

More specifically, I have taken these design expectations one step further and derived a very detailed, testable model on mtDNA genome function.[20] For mtDNA differences among species within families, my model treats these as functionally neutral changes—the result of mutation over time. However, with respect to the differences between families—those mtDNA positions that are identical among species within a family but different to species outside of the family—my model views these as having been created. Thus, my model predicts that these mtDNA differences play a functional role specific to each family. (Jeanson 2017c, 171)

What could be objectionable about this explanation? Frello: "Such function should discriminate marsupials from other mammals, beetles from butterflies, squids from oysters and all the numerous groups of singled celled eukaryotes from each other. What he actually suggests is several functions of each gene. With no shred of evidence!"

Since my functional explanation is derived from taxonomies based on anatomy and physiology, let's explore Frello's logic in these fields first. For example, traditional taxonomy proposes that

anatomical and physiological function in marsupials distinguishes them from other mammals. Does it? Marsupials are *defined* by their unique (and very functional) reproductive mode. As another example, traditional taxonomy proposes that anatomical and physiological function in beetles distinguishes them from butterflies. Again, these creatures are *defined* by their unique, functional anatomy and physiology. The same logic applies to squids and oysters.

Surely Frello agrees with this. If he doesn't, he has to deny one of the most foundational fields of biology. So why does he object to the explanation of function in the genetic realm? In my 2013 paper, I explicitly laid out (testable) ways in which this functional explanation could be realized. For example:

Modern protein sequences might still perform the same basal metabolic function traditionally ascribed to them (i.e., participation in the electron transport chain), but the sequence might be optimized metabolically for the specific organismal context in which each protein is found. (Jeanson 2013, 496)

Is this hypothesis implausible? Does Frello disagree with the fact that proteins might have an optimal chemistry? Does he reject the basic principles of protein chemistry? Frello should specify exactly why chemical optimization is not a plausible way to distinguish species defined by their anatomy and physiology.

Another example of a way in which my hypothesis of molecular function could be realized is as follows (again, a quote from the 2013 paper):

Alternatively, each protein might be connected in a genetic network to pathways specifying taxon-specific traits (Lynch, May, and Wagner 2011). The phenomenon of protein "moonlighting" (Jeffery 2003) raises the possibility that the traditional metabolic functions of each mitochondrial protein are just one of many functions for each protein. For example, the electron transport chain protein cytochrome b ("CYTB") might participate, not just in basal energy transformation, but also in DNA transcription as a transcription factor, similar to the findings for the glycolytic enzyme glyceraldehyde-3-phosphate dehydrogenase ("GAPDH") (Kim and Dang 2005). This protein "moonlighting" hypothesis is consistent with the observation that the protein clusters found in this study transcend Linnaean classification categories—categories which sometimes separate (rather than cluster) species that share a functional trait. For example, bony fish, amphibians, birds, and most reptiles share the reproductive strategy of laying eggs, but these species are divided into separate Linnaean classes. In contrast, the ATP6 sequence comparison in this study joined species from Actinopterygii, Amphibia, Aves, and Reptilia into a vertebrate sub-cluster (Fig. 2). Hence, the clustering patterns I observed might be explained in part by functions shared by multiple taxonomic categories. (Jeanson 2013, 496–497)

I repeated this scenario in *Replacing Darwin*:

Since the 1970s, the advances in molecular biology have upended the overly simplistic and early views of protein function. For example, evidence is accumulating for the phenomenon of protein "moonlighting."[22] Rather than perform a single function in a cell, proteins perform an unexpected number of additional functions. As an illustration, some proteins that were classically thought to catalyze a single metabolic reaction now appear to function in information flow as well. Conversely, the proteins encoded by mtDNA genes might also moonlight and function in additional subcellular processes. (Jeanson 2017c, 173)

For the record, Endnote 22 references the following (mainstream) scientific review papers, which contain many references to primary literature on moonlighting proteins:

C.J. Jeffery, "Moonlighting Proteins: Old Proteins Learning New Tricks," *Trends Genet,* 2003, 19: 415–417.
D.H.E.W. Huberts and I.J. van der Klei, "Moonlighting Proteins: an Intriguing Mode of Multitasking," *Biochim. Biophys. Acta,* 2010, 1803: 520–525.

Does Frello reject these papers? Has he written up a peer-reviewed denial of their observations? Has he done experiments that call into question the results described in these papers? What basis does Frello have for calling the results cited in Jeffrey (2003) and Huberts and van der Klei (2010) "no shred of evidence"?

Leaving these data aside, I clearly stated that my functional explanation for *mitochondrial* proteins was, at present, a *hypothesis*:

To date, moonlighting has not been documented for proteins encoded by mtDNA. However, this phenomenon has also not been rigorously tested. Once these experiments have been performed, we can directly compare the predictions of the evolutionary model to the creationist one. (Jeanson 2017c, 173)

Hypotheses that have "not been rigorously tested" are, almost by definition, without much supporting evidence. Otherwise, they wouldn't be hypotheses.

Conversely, this means that Frello's implicit claims about the *lack* of multi-functionality in mitochondrial proteins is *equally* without evidence. Where are the published papers that disprove protein multi-tasking? Where are the experiments that reject my hypothesis and confirm his? Frello appears to be (1) denying published literature and (2) deftly changing my hypothesis into a claimed theory. Neither of these actions constitute a rebuttal of my claims.

Frello, however, thinks he's found a fatal flaw:

I am not sure Jeanson actually has realized what a challenge he has given himself. Let's take the mitochondrial protein 'Cytochrome oxidase subunit 1' or just 'Cox1' as an example, starting with the dog family (Canidae).

Jeanson has to suggest, and ultimately identify, one or more function(s) of the Cox1 protein that can explain why this gene can be used to discriminate between *Canidae* and other families in the suborder *Caniformia* (such as bears and seals). He has to repeat this process (with either the same or another function) and explain why Cox1 can be used to discriminate between *Caniformia* and the suborder *Feliformia* (e.g. cats and hyenas). *Caniformia* and *Feliformia* are suborders of the Carnivore order, *Carnivora*, and Jeanson has to make the same explanations about the discrimination of *Carnivora* from other orders of placental mammals. Then the process should be repeated, comparing placentals, marsupials and monotremes, which together form the class Mammals. Next level is to compare Mammals with other classes of tetrapod vertebrates such as birds and crocodiles. Next, the tetrapods should be compared to other vertebrates such as bony fish and sharks. Vertebrates is a subphylum of the phylum *Chordata*, so vertebrates should be compared to invertebrate subphyla within the chordates for example, the tunicates. Chordates then should be compared to other phyla, for example, arthropods or mollusks. We could extend the investigation to other kingdoms: plants or fungi, or to the plethora of single celled eukaryotes, who also have mitochondria.

Every single level can be recognized by their Cox1 protein sequence. On every level, homology within the group is as high or higher as it is when species within the group is compared to species outside the group. Jeanson suggests that this complicated pattern reflect function.

Instead of starting with the wolf, we could start with the ladybird (insects), the thale cress (plants), the portobello (fungi) or even the malaria parasite (single celled eukaryote).[2] All have their own version of the Cox1 protein. The task of suggesting function to all these levels of living organisms is overwhelming.

It is not enough to suggest one specific function. Jeanson still has to explain why the function in question reflect the hierarchical structure of taxonomy. If we, for example, accept that Cox1 has influence on fur-color, why then, is Cox1 from wolf more homologous to that of a leopard, than to that of a horse?

This aspect of Frello's concerns can be summarized succinctly: In a sense, it's the "problem" of classification. Since this fact may not be obvious at first pass, let's restate Frello's "challenge,"

substituting anatomical or physiological features for genetic ones:

I am not sure taxonomists have actually realized what a challenge they have given themselves. Let's take skull shape as an example, starting with the dog family (Canidae).

Taxonomists have to suggest, and ultimately identify, one or more function(s) of skull shapes that can explain why this anatomical features can be used to discriminate between Canidae and other families in the suborder Caniformia (such as bears and seals). Taxonomists have to repeat this process (with either the same or another function) and explain why this function can be used to discriminate between Caniformia and the suborder Feliformia (e.g. cats and hyenas). Caniformia and Feliformia are suborders of the Carnivore order, Carnivora, and taxonomists have to make the same explanations about the discrimination of Carnivora from other orders of placental mammals. Then the process should be repeated, comparing placentals, marsupials and monotremes, which together form the class Mammalia. Next level is to compare mammals with other classes of tetrapod vertebrates such as birds and crocodiles. Next, the tetrapods should be compared to other vertebrates such as bony fish and sharks. Vertebrates is a subphylum of the phylum Chordata, so vertebrates should be compared to invertebrate subphyla within the Chordates e.g. the Tunicates. Chordates then should be compared to other phyla, e.g. arthropods or mollusks. We could extend the investigation to other kingdoms: Plants or Fungi, or to the plethora of single celled eukaryotes, who also have or lack skulls.

Every single level can be recognized by their skull shape (where skulls actually exist) or by their lack of skulls. On every level, homology within the group is as high or higher as it is when species within the group is compared to species outside the group. Taxonomists suggests that this complicated pattern reflects function.

Instead of starting with the wolf, we could start with the ladybird (insects), the thale cress (plants), the portobello (Fungi) or even the malaria parasite (single celled eukaryote). All have their own unique physical traits. The task of suggesting function to the physical traits at all these levels of living organisms is overwhelming. It is not enough to suggest one specific function. Taxonomists still have to explain why the function in question reflect the hierarchical structure of taxonomy. If we e.g. accept that skull shape has influence on diet, why then, is the skull shape from wolf more homologous to that of a leopard, than to that of a horse?

In reality, my "problem" of finding functions for mitochondrial proteins is as simple to solve as the

"problem" of finding functions for anatomical and physiological features of species. By Frello's logic, we can't possibly (1) use the skull of the wolf to create a nested hierarchical pattern/the Linnaean classification system and, simultaneously, (2) identify a function for the wolf skull. According to Frello, if we tried, we'd have to find 1.6 million functions for the wolf skull—in order to distinguish it from the 1.6 million species on earth.

It should be obvious that no taxonomist is worried about this "problem." Wolf anatomy and physiology makes for (1) very clear, nested taxonomic categories and (2) readily assignable function. Why? First, the function of the wolf skull is readily distinguishable from the heads of the other 1.6 million species alive on earth (at least, from those species with heads) because it is a complex shape. Every skull is complex because each consists of multiple dimensions (length, width, and height). Second, the specifics of each skull in each of these dimensions are what imparts distinguishing functions to the skulls of animals around the globe. Third, the shape and function of the wolf skull is used *in combination* with the other features of the wolf to identify its particular taxonomic placement. Together, these three factors make simultaneous taxonomic placement and assignment of function very straightforward.

A similar logic holds at the genetic level. For example, when organisms are built during development, genes control this process. Furthermore, this process can be described, not in three dimensions, but in *four*—the three spatial dimensions, and the time dimension. Since proteins are molecules, and since the cell represents an enormous space relative to the size of molecules, the number of possible places for genes to act exceeds our comprehension. Furthermore, since genes tend to act at sub-second speeds, and since even rapidly-developing creatures like *Caenorhabditis elegans* still require hundreds of thousands of seconds to develop (humans require tens of millions of seconds), the number of possible times for genes to act exceeds our best comprehension. (The times and places at which a gene—or a gene product—acts represent some of the seminal parameters delineating a gene's function.) If we expand our exploration to consider all the physical and temporal ways we can *combine* the actions of genes, the number of possible permutations becomes nearly impossible to count. The potential functional space to be explored likely exceeds the actual functions that cellular molecules realize. Furthermore, these functions are surely determined— at least in part—via the sequences of the genes themselves. Thus, (1) using mitochondrial sequences to create a nested hierarchical taxonomy, while simultaneously (2) finding distinguishing molecular functions for these same sequences is straightforward.

The functions for these sequences might not yet be discovered. But Frello's theoretical objections pose no real hurdles to my hypothesis.

Frello takes his criticism a step further: However, Jeanson's problems don't stop here. This is just the function of the proteins. The proteins are coded by genes. The majority of differences on the gene-level (the DNA-sequences), are so-called silent or synonymous substitutions. These are differences between two protein-coding DNA-sequences that do not result in a difference at the protein level. If creation is true, and the differences between proteins are functional, the synonymous substitution must be functional as well. Otherwise, why would they reflect the taxonomy? Jeanson should suggest what those functions could be and how they can be so important that they outnumber the non-synonymous substitutions.

Here, the deliberately-designed structure of my book comes into play again. The answer to Frello's objection is in the Endnotes—specifically Endnote 47 of Chapter 3. This Endnote references about 10 papers that were published in *Science*, *Nature*, or *Cell* that describe functions for the "silent substitutions." Thus, Frello's objection has already been answered in *Replacing Darwin*.

Frello's next criticism: "However, Jeanson's problems don't stop here. About one third of the mtDNA in animals does not encode proteins but are so-called tRNA, rRNA or the D-loop (also called the control region). What anatomically relevant functions can be attributed to these regions?"

Again, the structure of my book catches Frello in less-than-rigorous review. Had he consulted the the ~10 mainstream, peer-reviewed papers that I listed in Endnote 47 of Chapter 3, Frello would have found a functional connection between the "silent substitutions" and tRNA molecules. Furthermore, with respect to rRNA variants and D-loop variants, my previously published hypotheses apply equally well: These variants might represent metabolic optimization, and/or they might be cellular multi-taskers. The potential and actual answers to Frello's questions are readily available.

Conversely, let's put the challenge back to Frello: What experiments can Frello cite to support his hypothesis that these differences are *non*functional? If Frello is not careful, his strongly worded denunciation of my hypothesis ("no shred of evidence!") might quickly fall back on his own position.

Frello's next criticism: "The function of the various mtDNA sequences is well known. It is therefore Jeanson, who has the burden of proof. I challenge him to suggest relevant functions, and explain how they fit the pattern outlined above. Until he does so, I will claim that he cannot."

Again, in *Replacing Darwin*, I wrote:

> To date, moonlighting has not been documented for proteins encoded by mtDNA. However, this phenomenon has also not been rigorously tested. Once these experiments have been performed, we can directly compare the predictions of the evolutionary model to the creationist one.

In other words, yes, the classic biochemical functions of mitochondrial proteins are well known. But how do we know that these classic biochemical functions are the *only* functions for these proteins? How do we know that (apparently, according to Frello) sequence differences among mitochondrial proteins from separate "kinds" are functionally *neutral* (instead of metabolically optimized)? Until Frello can supply evidence that favorably answers each of these questions, Frello is engaging in yet another self-defeating criticism.

Selection

In the section discussing "Selection," Frello begins by making his focus clear: "Jeanson makes a number of other analyses on the mtDNA." Then Frello's next sentence contains two statements that are so far from what I wrote, that it's difficult to overstate the level of misrepresentation: "In all cases, he fails to include selection, though this can be shown to be a very real phenomenon."

What follows is a lengthy list of quotations that represent just some of the instances in which I (1) obviously embrace selection as a real phenomenon and (2) include an extensive analysis of selection. First, I explicitly endorse natural selection—so much so that it forms a part of the model for the origin of species that I defend in the book:

> To clarify, the model of preexisting genetic diversity [the model I defend in *Replacing Darwin*] invokes multiple mechanisms as this second step [of the speciation process]—*natural selection*, migration, genetic drift, etc. (Jeanson 2017c, 245, emphasis added)

Second, it should be clear to readers of *Replacing Darwin* that I analyze selection in great depth. In fact, with respect to mtDNA, the analysis of selection formed perhaps the strongest and most central argument in my book.

For example, consider this discussion of selection and mtDNA in Chapter 7. After showing that evolution fails to predict (technically, retrodict) the absolute number of mtDNA differences among humans and chimpanzee, among modern humans and Neanderthals, and among various modern ethnolinguistic groups, I consider how the evolutionary model might bring these failed predictions into agreement with reality:

> Perhaps the explanation involves natural selection.

At first pass, this might seem plausible. After all, mtDNA encodes proteins with critical functions in the cell. If you interrupt basic metabolism, cellular death is sure to result. Surely most of the thousands of mtDNA mutations that have occurred over the last several million years of evolutionary time were lethal to the possessors of these mutations. Consequently, natural selection would surely have eliminated these mutations (and individuals) from the mtDNA pool.

How might we evaluate the natural selection hypothesis? The scientific community has a long-established practice of dealing with scientific controversies. We've already discussed in chapter 4 how to advance a scientific debate towards resolution. The scientific method operates like a process of elimination. When two hypotheses offer competing explanations for the same phenomenon, one must be eliminated before scientific inferences can be made.

Naturally, this logic assumes that two competing hypotheses actually make *testable* predictions. We assumed as much in our discussion of the history of genetics (chapter 2–3) and in our discussion of Darwin's arguments from biogeography. For example, Mendel was successful as a scientist because he inferred rules that made testable, accurate predictions about the mathematical ratios of traits among offspring in each pea plant generation. As another example, in our discussion of whether DNA or proteins were the substance of heredity, we observed that both of these hypotheses made testable predictions. If proteins were the substance of heredity, their chemical elimination in the experiments of Avery and colleagues should have eliminated the transforming ability of the heat-killed smooth cells. The same prediction follows from the hypothesis that DNA is substance of heredity. Conversely, if species were created in their present locations, then you might expect the fauna on islands to possess more terrestrial species. You wouldn't expect the native fauna to be so skewed towards aquatic and aerial species. In other words, the hypothesis of the fixity of species' geography makes testable predictions.

Hypotheses that fail to make predictions do not qualify as science. As evolutionists maintain to this day:

"Science is…a process of acquiring an understanding of natural phenomena. This process consists largely of posing hypotheses and testing them with observational or experimental evidence. …Scientific research requires that we have some way of testing hypotheses based on experimental observational data. *The most important feature of scientific hypotheses is that they are testable*" [emphasis his].[53] [The reference cited in Endnote 53 is: D.J. Futuyma, 2013. *Evolution* (Sunderland, MA: Sinauer Associates, Inc., 2013), p. 634–635.]

The importance of this fact to the evolutionary community is manifest in the way in which it has been applied to creationist ideas:

"Science differs in this way [see quote above] from creationism, which does not use evidence to test its claims, does not allow evidence to shake its a priori commitment to certain beliefs, and does not grow in its capacity to explain the natural world. Unshakeable belief despite reason or evidence (i.e., faith) may be considered a virtue in a religious framework, but is precisely antithetical to the practice of science."[54] [The reference cited in Endnote 54 is: D.J. Futuyma, 2013. *Evolution* (Sunderland, MA: Sinauer Associates, Inc., 2013), p. 634.]

In other words, since the most important feature of a scientific hypothesis is that it is testable, the seeming un-testability of the existence of God, of the supernatural creation of various creatures, and of a global flood a few thousand years ago has typically removed creationist ideas from the realm of science.

Some evolutionists have even taken the criticism of the creation model one step further. They have summed up creationist views in a short phrase: "God did it." Besides rejecting this phrase as unscientific, they have denounced it as *anti*-scientific. For example, let's say that you were testing a potential anti-cancer drug in the lab. If you were laboring over a confounding experimental result, "God did it" wouldn't seem to reveal an answer. At least, it wouldn't lead to discoveries on how the natural world operated. Rather, testable hypotheses would be the only scientific way forward toward a solution. In light of this historical practice, we can revisit the evolutionary explanation of natural selection. The elimination of thousands of mtDNA mutations by natural selection might seem plausible. But to be scientific, this explanation would have to make testable predictions. For example, the mtDNA mutation rate in the most divergent African people groups (San peoples, Biaka peoples, etc.) has not yet been measured. Can the evolutionary explanation of natural selection *predict* what this rate will be? In other words, before the rate is actually measured, will evolutionists publish a guess as to what it will be? If not, is the evolutionary explanation scientific?" (Jeanson 2017c, 184–185)

In addition to exploring the role of selection in the context of humans and great ape species, I also analyzed the role of natural selection in other species. For example, in the section in which I explore other vertebrate mtDNA mutation rates, I show that the evolutionary model fails to make sense of modern mtDNA differences among species. Again, I consider how the evolutionary model might bring these numbers into alignment:

What could possibly explain these vertebrate results? Could natural selection reconcile the evolutionary predictions with reality? If so, what testable predictions does this model make? For example, the mtDNA mutation rate has not yet been measured in tens of thousands of other vertebrate species. What predictions does the evolutionary model make for these? (Jeanson 2017c, p. 195)

At the end of Chapter 7, I summarize the stark implications of my analyses of the role of natural selection in mtDNA differences among species:

Recall from chapters 4–6 the central mechanism of evolution—descent with modification. Though Darwin had no knowledge of genetics, his scientific descendants have put his mechanism in concrete genetic terms. In modern evolutionary theory, DNA mutations are the driving force behind evolutionary change. To be sure, natural selection filters out certain DNA mutations and non-randomly shapes and sculpts the DNA sequences that we observe today. But mutations are at the heart of evolutionary change.

Yet, in this chapter, we observed that the mutation rate was not predicted by the evolutionary model. Instead, it was the 6,000-year timescale that made accurate retrodictions and even made *pre*dictions. In other words, in the branch of genetics that is most relevant to the evolutionary model, it's actually the creationists who have taken the lead. (Jeanson 2017c, 205)

In the context of mtDNA, my analysis of selection has sobering implications for the evolutionary model.

My analyses of selection weren't limited to mtDNA. In Chapter 8, I analyzed the role of selection in explaining nuclear DNA differences. With respect to human-chimpanzee nuclear DNA differences, I showed that the evolutionary model again fails to account for what we see between these species— evolution *under*predicts the differences we see between humans and chimpanzees. Could natural selection play a role? I answered this question by putting the nuclear DNA results together with the mtDNA results:

For human-chimpanzee comparisons on the evolutionary timescale, neither the mtDNA compartment (see chapter 7) nor the nuclear DNA compartment led to successful predictions.

Together, these failed predictions made the evolutionary explanatory challenge more acute. Consider the contrast in results between the mtDNA and nuclear DNA predictions. First, the two genetic compartments differed in the magnitude of their failed predictions. The mtDNA predictions (Figure 7.3) were over an order of magnitude higher than the actual number of differences; the nuclear DNA predictions (Figure 8.3) were only 50% different

from the real result. Second, these failed predictions differed in the direction of the error. The evolutionary timescale vastly *over*predicted mtDNA differences (Figure 7.3), but *under*predicted nuclear DNA differences (Figure 8.3).

This contrast constrained the explanatory options for the evolutionary model. Consider the most likely evolutionary explanation for the mtDNA discrepancy. Given the massive number of predicted differences—differences that exceeded the length of the mtDNA genome—I anticipate that evolutionists will invoke natural selection to reconcile prediction with fact. Yet, in the realm of nuclear DNA, natural selection is excluded from the discussion, almost by definition. Since the nuclear DNA predictions *under*estimated the actual level of DNA differences, elimination of mutations via natural selection would only make this discrepancy worse—it would reduce the number of predicted differences even more. This presents a conflict for evolution. When does natural selection play a role? When does it not? Can the evolutionary model *predict* when natural selection sculpts the genome and when it doesn't? Or will natural selection always be an idea that is retrofitted to any result as needed—a "natural selection did it" type of explanation? (Jeanson 2017c, 214)

In other words, I analyzed the role of selection in *both* genetic compartments, and I found that the evolutionary model had a seemingly intractable scientific problem to solve.

I also analyzed the role of selection in explaining yeast nuclear DNA differences:

With respect to other species, mutation rates and divergence times run into additional problems. For example, among yeast species, the current mutation rate over the 15 million-year evolutionary time of divergence predicts[45] far too many mutations among yeast species (Figure 8.18). Just like we observed for mtDNA, the number of predicted mutations actually exceeded the yeast genome size. This result raises again the questions of what role natural selection plays, when it plays its role, and how much of a role it plays in each compartment. If nothing else, it demonstrates that evolutionary divergence times do not consistently predict mutation rates.

If divergence times do not predict the mutation rate, what does? If evolutionary divergence times do not make accurate predictions in genetics, should they be accepted as scientific?" (Jeanson 2017c, 227–228) [The reference cited in Endnote 45 is to methodological details of the calculations used to create Figure 8.18]

In light of these extensive quotes from *Replacing Darwin*, let's consider again Frello's claim that "In all cases, [Jeanson] fails to include selection, though this can be shown to be a very real phenomenon."

Has Frello not read *Replacing Darwin*? Our discussion of his objections to other parts of my book suggests that this is not the case. For example, Frello's analysis of Chapter 5 (see section titled "Frello's Claims about Taxonomy" above) suggests that Frello has actually paid attention to some parts of *Replacing Darwin*. Frello's critique contains an extensive restatement of content from Chapter 5, and this content is largely unique to this book (i.e., it's not found in this level of detail in my published papers). Frello must have read at least Chapter 5 to make the detailed accusations that he does. Has Frello not read Chapters 7 and 8?

Could Frello have failed to understand what I wrote in Chapters 7 and 8? Perhaps. But notice that the foundation for my biggest challenges to the evolutionary model comes from a standard of science that *evolutionists* have proposed. I quote an *evolutionary textbook* to support my contention that scientific models should make testable predictions. It's hard to imagine that Frello is unfamiliar with textbook evolutionary science.

Why might Frello misrepresent one of the central points of my book so badly? Recall that Frello's critique began by side-stepping the three main claims of my book. The biggest claim—and most fundamental scientific reason for my contention that science has *replaced* Darwin instead of just *rebutted* Darwin—comes from my discussion of testable predictions in Chapters 7 and 8. If Frello wants to undermine my book, he *must* deal with the discussion of testable predictions in these chapters. Unfortunately, his main response seems to this discussion seems to be either ignoring it or misrepresenting it.

If ignoring and misrepresenting is Frello's best strategy for rebutting the most critical sections of *Replacing Darwin*, then my book must be on solid scientific footing. Why else would Frello avoid a more traditional route of rebuttal? Why doesn't he find and publish an error in my calculations? Why doesn't he point out a key hypothesis that I have missed? Better yet, why not point out *failed* predictions that my model has made? Perhaps unintentional on his part, his strategy exposes the deficiency of scientific arguments *against* my book. This is a helpful discovery, and Frello has been instrumental in revealing this fact.

Let's now consider the remainder of Frello's criticisms under the section titled "Selection." Frello attempts to illustrate his erroneous claim (i.e., "[Jeanson] fails to include selection, though this can be shown to be a very real phenomenon") with some examples. At this point, it should be clear that this will be a fruitless task. An incorrect claim is going to be very difficult to justify, regardless of how creative the examples are.

So why might Frello proceed with examples? Let's

consider what he says, and then consider the backstory to our exchange. Frello begins by re-introducing the concept of synonymous mutations: "To understand this you have to know that most mutations in protein coding genes fall into two categories: synonymous mutations that do not alter the resulting protein, and non-synonymous that do alter the protein. Due to the way DNA is translated into protein, about 21% of all mutations are synonymous (See Chapter 3, especially Table 3.1 and the appendix)."

Then Frello tries to use synonymous mutations to justify a role for selection. His main example is a comparison of mtDNA differences among modern humans, to mtDNA differences between modern humans and Denisovans: "I compared two of the most different Human mtDNAs (GenBank numbers EF184607 and FJ168742) and counted the non-synonymous and synonymous differences in the protein-coding genes. 35 of 55 = 64% were synonymous. If more distant mtDNA sequences are compared (Modern Human: KC345974 and Denisovan: FR695060) 85% are synonymous. This tells us that non-synonymous mutations are under stronger selection than synonymous. Selection is thus important, and Jeanson should include it."

For the sake of argument, let's accept all the data that Frello just presented without question. Does it help Frello's case? His main point is that "Jeanson should include [selection]." As the extensive quotes from *Replacing Darwin* have already revealed, I do (in fact) include selection. And I challenged evolutionists to *scientifically* show *how* selection should be included by *making testable predictions.* I wonder if Frello will ever meet this challenge. He certainly doesn't here. Therefore, his claims thus far are not science. In fact, technically, Frello's claims could be termed pseudoscience.

Now let's resume the question of whether Frello's data is legitimate. Actually, I don't need to. Frello anticipates this objection and takes it up himself:

Jeanson doesn't accept the mtDNA sequences from Neanderthals and Denisovans. He claims that the sequences are unreliable, partly because the DNA has been degraded or contaminated. I have urged him to confront the relevant scientists, but he refuses to do so for reasons I don't think are valid (Frello 2017; Jeanson 2017b). If mtDNA from Denisovans is unreliable, the mistakes in the sequence should be expected to be randomly distributed, when counted as synonymous vs non-synonymous substitutions. A short look at the results mentioned above show that this is far from the case. To dismiss Denisovan mtDNA as unreliable is thus unfounded.

Unfortunately, Frello's paragraph here is, again, dangerously close to misrepresentation. If you read his quote without reading *Replacing Darwin*, you

might think I deftly avoided the subject of Denisovan DNA and other ancient humans (Neanderthals, etc.). In reality, *Replacing Darwin* contains an extensive discussion of DNA from ancient humans like Denisovans, Neanderthals, and the like. I already alluded to it above; it follows the discussion of the failed evolutionary predictions for human-chimpanzee mtDNA differences:

These evolutionary predictions improve little if we narrow our focus to living and extinct members of the genus *Homo*. For example, Neanderthals are classified within the *Homo* genus, and a Neanderthal mtDNA sequence has been published. Evolutionists put the split between the Neanderthal and modern human lineages about 400,000 to 700,000 years ago.[48] Treating them as members of the same species,[49] we can use a coalescence calculation to predict how many mtDNA differences should exist today between Neanderthal sequences and sequences from living humans. At a mutation rate of one base pair per 76 to 419 years, a minimum of 955 mtDNA differences (1 mutation per 419 years * 400,000 years = 955) and a maximum of 9,211 mtDNA differences (1 mutation per 76 years * 700,000 = 9,211) would arise. Today, only 213 mtDNA differences separate Neanderthals and modern humans.[50] (See also Figure 7.4, which uses more precise calculations based on previously published work.[51]) Again, the evolutionary timescale predicts mtDNA differences far in excess of what is observed. The discrepancy between predictions and reality is less than what we observed for the human-chimpanzee calculations. But it still fails to capture actual differences. (Jeanson 2017c, 181–182)

[Endnotes 48–51 reference several technical papers and one clarifying comment about treating Neanderthals and modern humans as separate species]

Furthermore, the analysis of the role of natural selection (that I referenced above) was a *direct commentary* on the Neanderthal calculations that I just cited (i.e., just look at the page numbers I listed for the quotes from *Replacing Darwin*).

Let's try to take the spirit of Frello's criticism and construct a more realistic objection. Let's say Frello concedes the problems for evolution that I just described. Wouldn't Neanderthal and Denisovan DNA present a problem for the creation model? Aren't there too many mtDNA differences between modern and ancient humans to explain them all in 6000 years? My book answered this objection:

You may have noticed that I have said nothing about the YEC predictions for Neanderthal DNA. I did so deliberately. The explanation for these differences follows from what I just discussed. When Neanderthal and modern human sequences are visualized together in tree format, the Neanderthal sequences branch off

of the sub-Saharan African lineages (Figure 7.12).[75] From the YEC perspective that I've just outlined, it would appear that this lineage derived from ancient Africans. Since some African people groups might mutate their mtDNA faster than non-African people groups do, Neanderthal DNA might simply represent a hyper-mutating lineage—which eventually went extinct.

Alternatively, for technical reasons that I elaborate elsewhere,[76] the Neanderthal sequences might be too degraded to be reliable. In short, when I perform DNA sequence analyses in the lab, I tend to throw away DNA sequences that are older than a year. Despite storing them at −20°C, being 12 months removed from their normal cellular environment appears to do irreversible damage to DNA. How much more so when DNA sequences sit in fluctuating temperatures and environmental conditions for thousands of years. (My evolutionary colleagues disagree with my assessment regarding DNA degradation—which is why I still made predictions for Neanderthal DNA under the evolutionary model.)

Regardless of the actual explanation for Neanderthal sequences, the way to investigate these hypotheses is clear. It's the same method we would use to investigate any hypothesis. If someone thinks that they have an explanation for Neanderthal mtDNA, I would ask them what testable predictions their hypothesis makes. The hypothesis of an ancient timescale fails to make accurate predictions. My explanation of DNA degradation stems from the successful match between the predictions of the YEC timescale and mtDNA differences among modern humans. This may seem mundane. But can any other explanation do better? (Jeanson 2017c, 192–194)

[Endnotes 75–76 both reference a technical paper that I published previously]

In other words, *Replacing Darwin* (1) contained a detailed discussion of ancient human DNA and (2) insisted that explanations for ancient human DNA conform to the gold standard of science: They must make testable predictions. My model does; Frello's doesn't. Therefore, my model represents a scientific explanation; Frello's, something less than science (i.e., pseudoscience).

Furthermore, Frello repeats an error that he published previously (see Frello 2017a for his initial claim; see Jeanson 2017a for refutation). He thinks that "If mtDNA from Denisovans is unreliable, the mistakes in the sequence should be expected to be randomly distributed, when counted as synonymous vs non-synonymous substitutions." The form of this argument resembles the form of similar argument that he published previously: "If [Jeanson's explanations for ancient DNA] were true, we should expect various Neanderthal mtDNA-sequences to be

at least as different from each other as each of them are from mtDNA from modern humans. This is far from being the case."

Since Frello's logic is the same, both in the previous case and the current one, I'll paraphrase my answer from our previous exchange: Frello never gives a scientific justification as to why, "if mtDNA from Denisovans is unreliable, the mistakes in the sequence should be expected to be randomly distributed, when counted as synonymous vs non-synonymous substitutions." I could just as easily assert that if the hypothesis of DNA degradation were true, the mistakes in the sequence should be expected to be non-randomly distributed, when counted as synonymous vs non-synonymous substitutions. What data could Frello cite to reject my claim? He cites none to justify his own. Frello assumes that the processes which degrade DNA always force these degrading sequences towards equal numbers of synonymous and nonsynonymous substitutions. How does he know that this is true? I could just as easily assume that the processes which degrade DNA preferentially force these degrading sequences towards synonymous substitutions. How could Frello prove me wrong? Thus, this particular objection of Frello's is speculation stated as fact.

Just for sake of argument, let's say (1) that the Denisovan sequence is reliable and accurate and (2) that the Denisovan sequence has more synonymous mutations than modern human sequences do. Would this fact falsify my explanation for mtDNA? As I described above (see *Replacing Darwin* quotes), Denisovan sequences might represent a type of hyper-mutating sequence—one in which natural selection might indeed play a role. Again, as I mentioned above, I fully embrace natural selection as a real phenomenon. The only question is when it plays a role. At high levels of mutation, a role for natural selection wouldn't surprise me at all. But the only way we can know when to invoke it (and when not to) is by evaluating the testable predictions that flow from models that include or omit selection. Frello has yet to make a scientific argument for his position; his critique of my claims under the section titled "Selection" have yet to enter the realm of science.

Under normal circumstances, my response to this section of Frello's critique would end here. But since this section is explicitly tied back to our previous exchanges, it's worthwhile to dwell briefly on the significance of Frello's latest critique for our prior discussions. We'll soon see that Frello has, again, aided my position by his behavior.

Let's review the ground he and I have covered in previous exchanges in the *Answers Research Journal*. In both exchanges, the central subject matter was the reliability and significance of ancient

human DNA sequences. Frello's first objection (Frello 2017a) to my treatment of the topic turned out to be pseudoscientific in nature and deficient in its scholarship (see Jeanson 2017a for documentation). Then, instead of correcting his mistakes or offering a scholarly rebuttal, Frello changed the subject to confronting the preeminent evolutionary biologists who are researching ancient DNA (Frello 2017b). I responded by pointing out the contradictory and self-refuting nature of Frello's claims (Jeanson 2017b). In his current (third) critique of my work, Frello again makes no attempt to correct any of his previous errors or offer a scholarly reevaluation of my rejoinder. Instead, he changes the subject (again) to the synonymous versus non-synonymous mutations question—which, as we just observed, is yet another example of non-science or pseudoscience.

Thus, Frello's latest actions help advance our continuing exchange. By his silence, he is conceding all the points I have made prior, which makes his objections on my treatment of ancient DNA even harder to maintain.

Frello's Claims About Speciation

I'll let Frello open this section with an extensive quote so that we can follow his logical flow:

Jeanson deals with this in several ways (Chapter 6). First, he notices that the number of breeds of horses, dogs etc. is much larger than the number of species within the relevant family. Jeanson concludes that speciation within a biblical timeframe is unproblematic. He makes no calculations to support his claim. This is rather strange, because a method for doing so is right in front of his eyes: The mtDNA that he uses in other arguments.

As soon as such an analysis is made, the problems appear. A few calculations on mtDNA from dogs will illustrate the problem. Between mtDNA from domesticated dogs and wolves, there are about 170 differences. The dog family falls into two large groups: One includes wolf, dhole and the African wild dog; the other includes various species of foxes[3]. The mtDNA from the two groups has between 2400 and 2600 differences between them. Not taking selection and differences in generation time into account, this means that the dog family is at least 15 times older than the domestication of dogs from their wolf ancestors. Taking selection into account will make this difference even larger. It should be noted that in the GenBank, mtDNA are missing from five genera (one of which is extinct) and several species of the dog family. Therefore it might be that the most different mtDNAs is yet to be identified. It also should be noted that the dog family is often used by creationists as an example of a biblical 'kind' and acknowledged as such by Lightner in her analysis of mammalian Ark

kinds (Lightner 2012, 151–204). [Frello's endnote 3 contains technical details to support his listed number of mtDNA differences.]

Frello's paragraph makes a number of logical and scientific errors. First, Frello misses an entire section of my book. I introduce the breed-species comparison at the end of *Chapter 5*. This is a telling omission, for reasons that follow. Second, at the end of Chapter 5, I show that my breed-species comparison comes from *Darwin himself*:

Lost amidst the popular arguments for universal common ancestry are more subtle hints on the scope of species' family trees. The popular arguments can be found in the later chapters of *On the Origin of Species*. The subtle hints were suggested in Darwin's opening arguments. The very first sentence of chapter 1 reads:

"When we look to the individuals of the same variety or sub-variety of our older cultivated plants and animals, one of the first points which strikes us, is, that they generally differ much more from each other, than do the individuals of any one species or variety in a state of nature."

Applying Darwin's observation today, we can quickly appreciate Darwin's point. For example, among horses, the "cultivated animals"—the different *breeds* (i.e., domesticated varieties within a single species)—possess tremendous variation in size, coat pattern, coat color, hair length, and body proportions (Color Plates 42–57). Donkey breeds are also strikingly diverse (Color Plates 58–62).

When you compare this diversity to the amount of variety among the one horse and three ass species in the wild, the diversity among breeds far outstrips the variety in the wild (compare Color Plates 29–32 to Color Plates 42–62). In more rigorous quantitative terms, we can easily reach the same conclusion. If we use the existence of a breed or species as a marker of diversity, far more diversity exists in breeds than in species. Over 850 breeds of horses and donkeys exist today,[17] yet only four species of these creatures exist in the wild.

In Darwin's day, the origin of these breeds was unknown. Yet Darwin saw the potential significance of discovering their origin:

"When we attempt to estimate the amount of structural difference between the domestic races [i.e., breeds] of the same species, we are soon involved in doubt, from not knowing whether they have descended from one or several parent-species. This point, if it could be cleared up, would be interesting; if, for instance, it could be shown that the grey-hound, bloodhound, terrier, spaniel, and bull-dog, which we all know propagate their kind so truly, were the offspring of any single species, then such facts would have great weight in making us doubt

about the immutability of the many very closely allied and natural species—for instance, of the many foxes—inhabiting different quarters of the world."[18]

Today, the origin of these breeds is uncontroversial. Both evolutionists and creationists accept that horse breeds trace to a common ancestor. Both positions accept that donkey breeds trace to a common ancestor.

If we accept the common ancestry of horse breeds (or donkey breeds), can we deny the common ancestry of wild horse and ass species? If breeds could vary so widely yet still have a common ancestor, why couldn't species — which have less variety than breeds — also have a common ancestor? (Jeanson 2017c, 144–145) [Endnote 17 references technical publications to justify the stated numbers, and Endnote 18 gives the documentation for the quote.]

Third, Frello takes exception to my morphological comparison of breeds to species and insists it should be based on genetics—despite the fact that the morphological comparison came from Darwin. Thus, Frello isn't really arguing against me; he's trying to take on the father of his own position.

Fourth, in *Replacing Darwin*, the breed-species comparison is first an argument *for common ancestry*—before it ever becomes an argument for a recent timescale. Thus, if Frello wants to reject the implications of the comparison for the timescale of speciation, he must also reject the implications for common ancestry. I have a hard time believing that Frello is willing to deny the common ancestry of zebras and horses.

Fifth, Frello again resorts to serious misrepresentation: "Jeanson concludes that speciation within a biblical timeframe is unproblematic. He makes no calculations to support his claim." In fact, the one chapter that Frello references (Chapter 6) has many calculations. *The entire chapter* is one long mathematical argument. (Since I would have to quote the entire chapter to justify this statement, I'll leave readers to investigate Chapter 6 for themselves.)

Let's reflect on what Frello has just done—and on why he might engage yet again in misrepresentation. His first instance of misrepresentation revolved around the foundational argument for my book— testable genetic predictions. Chapter 6 is not quite as foundational as Chapters 7 and 8, but it does present a strong argument—on Darwin's own terms, no less—for the recent origin of species. It seems that I'm beginning to see a pattern in Frello's behavior. Anytime the science becomes strong, Frello engages in misrepresentation rather than in direct confrontation of the relevant scientific facts.

Frello's misrepresentation continues in his very next paragraph. After trying to argue that, based on mtDNA, breeds and species are an invalid comparison (Darwin's own claims notwithstanding), Frello makes an additional point from Canid mtDNA:

Jeanson further argues that the variation in mtDNA within species or genera is way too small to represent the long time spans suggested by evolution. He doesn't include selection in his analyses, though he could easily convince himself that this is a very real phenomenon. As in the example in humans above, if the ratio of synonymous vs. non-synonymous substitutions is compared between individuals with high vs. low homology, the difference leaves a strong signal of selection in mtDNA.

This is basically a repetition of his argument under the "Selection" section of his critique. As such, it is another serious misrepresentation, as the quotes from *Replacing Darwin* demonstrate (see section above titled "Frello's claims about Genetic Diversity" and specifically the subsection titled "Selection") that I do indeed accept selection as a real phenomenon and included it in my analyses.

Frello's next paragraph is an ironic summary of his critique:

Jeanson uses mtDNA to track the speciation within a number of families and comes up with linear models of speciation in all the cases he evaluates. In his calculation of number of generations since the last common ancestor, Jeanson concludes that the time suggested by evolution is way too long to be accounted for by the differences within the species or genus in question. I have already pointed out that selection should be included in such calculations, but there is another objection that invalidates at least the non-human examples (fruit fly, water flea, and nematode), that is extinction. Jeanson makes no attempt to include extinction in his evaluation, though he appreciates that extinction is a very real phenomenon. This neglect leaves his analysis rather useless.

The first appearance in the fossil record of a genus or species need not be the last common ancestor of all modern members of that genus or species. That could appear much later if most other lines have become extinct.

Let's try to follow his logic in steps. His first sentence is a good summary of a large chunk of Chapter 10. But the rest of the paragraph seems to abruptly change the subject back to the mtDNA clock calculations of Chapter 7.

Since Chapter 7 is the fulcrum of my book, let's consider carefully what Frello adds to our discussion. He begins by repeating (again) his erroneous statement about my failure to include selection. Then he raises a new point about the role of extinction.

Frello begins his discussion of extinction by misrepresenting my analysis yet again: "Jeanson makes no attempt to include extinction in his

evaluation, though he appreciates that extinction is a very real phenomenon." He implies that I blindly take dates from the fossil record and force them through genetic calculations, and that I do so all the while ignoring the fact of extinction. This is revealing for a number of reasons. First, the evolutionary dates for my evolutionary clock calculations were based on published *genetic* data from *extant* organisms—not on fossils of extinct species. The premise of Frello's argument is false.

Second, the structure of my book reveals Frello's analysis to be less than rigorous. To find the source (genetics or fossils) for the dates for my evolutionary clock calculations, Frello would have had to read the Endnotes (see Endnotes 100–102 of Chapter 7).

Misrepresentations aside, let's take Frello's logic to its appropriate conclusion. For the sake of argument, let's grant him his point that "The first appearance in the fossil record of a genus or species need not be the last common ancestor of all modern members of that genus or species. That could appear much later if most other lines have become extinct." What might this later date be? Based on the calculations in *Replacing Darwin*, this date must be 6000 years ago. In other words, Frello's logic forces him to concede that species arose within the last 6000 years.

This is a fascinating way to end a critique from a PhD evolutionist.

Frello's Additional Points
Frello's comments on "Darwin didn't know genetics"
In this section, Frello objects to my first central claim, that Darwin took a risk when he penned a strong answer to a deeply genetic question—long before genetic data were available to test it.

Despite Frello's rhetoric, he is unable to avoid the force of my main point. His description of the evolutionary process is inescapably genetic:

> If traits are inherited; If there is variation in inherited traits; If some source of new hereditary variation exists; If part of the inherited variation influence survival and, more importantly, reproduction. Then we can conclude the following:
> Some hereditary traits, those that support reproduction more than the alternative traits, will spread in a population. Others will disappear. Hence, the combination of hereditary traits in the population will change over generations. This is evolution in its most basic form: Descent with modification.
> Darwin's bold idea was not only to suggest this process, but also to suggest that this process could go on forever, and that there is no limit to variation."

Did you count how many times heredity or inheritance showed up in Frello's description? For all his contrariness, Frello seems to concede the point of Part I of my book.

Yet Frello still tries to reject the point of Part I. Given his deeply genetic description of evolution, the only way Frello can avoid Part I of *Replacing Darwin* is via misrepresentation. His objection begins with an attempt at a restatement of the thesis of Part I: "Jeanson postulates that because Darwin didn't know genetics, there is good reason to question his theory." Is this really what I said? Before parsing what Frello meant in this ambiguous sentence, let's try to follow Frello's logic. Frello contends, "Knowledge of the details of heredity thus isn't necessary to suggest evolution!" Did I insist that hypotheses should not be *suggested* until tests are performed? No. By definition, hypotheses are untested. (As a side note, does Frello really think that Darwin just *suggested* a hypothesis? Or does he agree that Darwin attempted to—and successfully—persuaded the scientific community of his views in a decade or less?) Frello then concedes that genetics is a direct, independent, sufficient test of evolution: "When investigated, the genetic variation within and among species has to reflect the expectations that can be made from descent with modification. Otherwise, evolution would have been disproven." (Here, Frello seems to agree with me again on the importance of genetics to evolution.) Then Frello changes the subject: "Nevertheless, Jeanson's assertion that Darwin's theory was unfounded in his own times, fails." Where did I make this point in *Replacing Darwin*? And what does it have to do with the statement, "Jeanson postulates that because Darwin didn't know genetics, there is good reason to question his theory"? Was my logic that, because genetics was not a field of science in 1859, Darwin's theory was unfounded in his own times? No. It should be clear from Part II of my book that Darwin successfully used (in 1859) non-genetic data to argue for his thesis. Conversely, the point of Part I was that Darwin took a massive scientific *risk* in penning his work. Frello tries to refute Part I of my book by setting up a straw man, and then knocking it down.

As a side note, Frello does appear to try to insert a massive claim about the implications of genetics for evolution: "Darwin's bold idea was not only to suggest this process, but also to suggest that this process could go on forever, and that there is no limit to variation… The details of genetics has to be such that variation actually *is* endless! It has to be such that brand new traits actually *can* occur!" Frello cites no data or references to back up this sweeping claim.

Frello's remarks under "Strange quotes"
Let's walk through each of Frello's examples in this section.

Frello quotes me: "At the molecular level, major changes to the standard developmental pathway for vertebrae would be required to produce the

giraffe's signature structure [the long neck]." Then Frello objects: "Hardly." Does Frello *not* think that development must be altered to produce a change in the final anatomy? Does he think something other than the process of development controls the final anatomical forms of giraffes and okapis? If so, I'd like to hear his ideas.

Frello quotes me: "Could jellyfish become jaguars?" Frello obviously thinks this question is preposterous: "Why such a silly example. No biologist has ever suggested this. Evolution can only result in transformations that can be linked by multiple small differences. The theory of evolution does not state that all organisms can evolve into any other." However, Frello's claim does not stand up to close inspection. First, Frello takes a question asked of biology in general ("Could jellyfish become jaguars?"), and then tries to answer it with the fact of evolution—the very point in question in *Replacing Darwin*. This is very close to circular reasoning.

To logically evaluate the quote that opens the previous paragraph, let's consider the context of the quote in *Replacing Darwin*. The focus of Chapters 2–3 is the history of *genetics*, not the history of evolutionary thought. The question was not, "Could jellyfish become jaguars according to Darwin's theoretical constraints on evolution?" Instead, it was, "Did we have any *data* that answered the question of whether jellyfish could become jaguars?" The entire purpose of these two chapters was to show the reader the primitive understanding of genetics that existed for decades after Darwin wrote his book. I narrated the development of tools to understand the origin of species—not the development of the modern evolutionary synthesis. Frello is trying to ask and answer a question that is different from the one that he quoted from *Replacing Darwin*.

Second, had Frello looked at the Endnotes for Chapters 2–3 (the main chapters that try to answer the question in my quote), he would have discovered that my narration of the history of genetics— and the unanswered questions that swirled prior to the establishment of DNA as the substance of heredity—was based on a book written by a prominent evolutionist (Ernst Mayr). If Frello has a problem with Mayr's history, Frello would need to take up his objections with Mayr and his fellow evolutionists.

Third, Frello seems to have forgotten that the hypothesis of spontaneous generation (i.e., rotting meat spontaneously spawning fruit flies—an even bigger morphological change than jellyfish becoming jaguars) wasn't disproven until Pasteur's experiments (Berche 2012). This fact becomes even more significant when we realize that Pasteur was a contemporary of Darwin.

Fourth, Frello seems to have forgotten that, even as late as 1940, Richard Goldschmidt proposed his "hopeful monster" hypothesis (Dietrich 2003). If my question about jellyfish and jaguars had been answered and settled long before Darwin, why could an eminent scientist like Goldschmidt seriously propose something so drastic—long after the father of modern genetics (e.g., Mendel) died?

Fifth, biologists regularly observe morphological transformations *much bigger* than jellyfish to jaguars:

> Each generation, all traits are erased—only to be rebuilt again. This fact is a curious phenomenon in its own right. It's one thing to observe red hair appear and disappear on a family tree. It's something entirely different to discover that all traits—hair color, facial features, hands, legs, feet, etc.—are absent when sperm and egg meet, yet eventually appear in the adult. (Jeanson 2017c, 39)

This leads to a paradox:

> Consider some of the questions we have asked of species. Can a fish spawn a spider? Can elephants give birth to giraffes? Could butterflies sire birds? The differences between these pairs of creatures are striking—fins versus eight legs, trunks versus long necks, scaled wings versus feathered wings. The morphological changes required to transform one of these creatures into another are numerous. But none of these theoretical transformations are as profound as the transformations that occur during the process of development. For example, all of the species transformations listed above are between species with heads [spiders have fused heads], trunks, limbs, respiratory systems, digestive systems, and excretory systems. To go from a single cell to, say, an adult zebra, far more visible change is required. At fertilization, head, trunk, limbs, etc. are absent. (Jeanson 2017c, 40)

Thus, if Frello wants to merge my question with the mechanism of evolution, he has little basis for objection. Given millions of years, evolutionists are happy to accept that jellyfish could eventually become jaguars. From a morphological perspective, the main difference between evolution and development is one of time.

Frello's objection has little basis in scientific fact.

Frello also expresses his disdain for my reference in the Afterword to Michael Behe's work. Frello scoffs, insisting that "Michael Behe's central ideas of 'Intelligent design' and 'Irreducible complexity' have never been accepted by 'secular' scientists. His books has been heavily criticized in 'secular' scientific journals." Again, Frello seems to have missed the Endnotes of my book, which cite Behe's responses to the unscientific treatment he's received (see Endnote 1 of the Afterword). (This demonstrates that, in

fact, I'm well aware of the response of the 'secular' scientific community to Behe's work.) In fact, Behe's responses reveal his critics' claims to be empty.

In response to my claim that atheistic evolution is logically self-defeating, Frello retorts:

> If evolution is true all details in our anatomy are the result of mutation/selection through eons of time. Numerous small beneficial variations in our forefathers have been selected and added to beneficial variations in their ancestors. To what benefit would a variation in an eye be, if it didn't help survival and, ultimately, reproduction? None! How can a variation in the eye help survival? Only by giving a slightly more accurate picture of the world. Therefore, according to evolution, we can trust our senses because they are the result of natural selection. That they are not 100% accurate is understandable. Random variation cannot be expected to result in perfection.

> Jeanson is taking selection out of evolution, and then saying: Look, evolution doesn't work.

Here, Frello takes the self-defeating nature of atheistic evolution and, rather than solving this problem, Frello amplifies it. Let's uncover this error by asking some questions of Frello. To paraphrase Frello's logic, he basically asserts that, according to evolution, we can trust our senses because they are the result of natural selection. Since natural selection ultimately selects those things that increase survival and reproduction, and since our senses exist, our senses must be beneficial—they must have increased survival and reproduction in our ancestors, over and above those individuals that lacked senses.

But how does Frello know that natural selection ultimately selects those things that increase survival and reproduction? He doesn't discover this from some holy book or from divine communication. Frello reaches this conclusion, ultimately, from observations he makes with his senses. Thus, his argument in favor of trusting his senses assumes his senses to be trustworthy in the first place. Frello is still trying to make a circular argument.

Frello's concluding remark

Frello's final statement in his review is deeply ironic: "Would you trust an Atheist to teach your children about Christianity? If not—don't trust a creationist to tell them about evolution!" Yet Frello's entire critique begs readers to trust an evolutionist…to teach them and correct them about a creationist work. Taking Frello's logic to its full

conclusion, you might rightly conclude that Frello doesn't want you to believe a word he says. This is an intriguing way in which to end his extensive review of *Replacing Darwin*.

Summary and Conclusion

Despite writing a 4000+ word critique of *Replacing Darwin*, Frello deliberately side-stepped the three central theses of my book. Where aspects of these theses arose in Frello's review, he resorted to misrepresentation or non-science (pseudoscience) to object to my claims. This is a very helpful discovery. It shows that Frello has no rejoinder to the major thrust of my work, and it immediately underscores the strength of my conclusions. This is helpful progress in our debate over the relative merits of each origins position.

In addition, where Frello engaged sub-points in my book, his objections often revealed a conclusion opposite to his. By exploring lines of reasoning not included in *Replacing Darwin*, Frello actually ended up providing additional evidence in favor of the arguments in my book. For his part in (inadvertently) strengthening the evidence supporting *Replacing Darwin*, I'm grateful.

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