Patterns of Intelligence

Chapter 30

Applying These Numbers to "New Nucleotides"

In the prior chapter the new species did not involve any new nucleotides or new genes. Now let us consider this option.

Suppose we wanted to create a new species, meaning create new genetic material or create a new DNA structure, using evolution, meaning macroevolution.

Suppose the new species had 2 new genes, which were each 2,500 nucleotides long (which total 5,000 new nucleotides), and suppose the new species needed to add 5,000 new nucleotides to its morphing of the embryo algorithms. This is a total of 10,000 additional nucleotides.

This means we must add 10,000 new nucleotides to the DNA: 5,000 new nucleotides to create two new genes and 5,000 new nucleotides for technical changes (e.g. new nucleotides for the morphing of the embryo algorithms).

In the prior example we changed 10,000 nucleotides to the DNA and in this example we are adding 10,000 nucleotides.

Do you think the mathematics will be different?

The answer is 'no'.

We can look at the added nucleotides as going into "slots" between two nucleotides instead of changing existing nucleotides.

For example, let us look at the 2,000,000,000 nucleotides above and the 2,000,000,000 slots between the nucleotides. Thus we would have something like this:

Nucleotide #1
Slot #1
Nucleotide #2
Slot #2
Nucleotide #3
Slot #3
Nucleotide #4
Slot #4

and so on and so forth for 2 billion nucleotides. Thus the last 3 nucleotides and slots would be:

Nucleotide #1,999,999,998
Slot #1,999,999,998
Nucleotide #1,999,999,999
Slot #1,999,999,999
Nucleotide #2,000,000,000
Slot #2,000,000,000 (actually the "endpoint")

Now, instead of changing 10,000 of the nucleotides, we are putting 10,000 new nucleotides into "slots" because we are adding these nucleotides.

Actually, more than one nucleotide could be put into one slot. In fact, hundreds or thousands of nucleotides could be put into one slot, such as for one of the new genes.

We have almost the same mathematical problems with "slots" as we had with nucleotides. The key issue is still a "location" issue, but in this case the "location" issue is a slot instead of a nucleotide.

A nucleotide looking to be put into a slot will be put into a randomly chosen slot (the "location" issue applies to slots instead of positions), not necessarily the correct slot.

In other words, the concept of "location" is almost identical whether you are talking about nucleotide locations or slot locations!!

You also have the issue of putting the "right" new nucleotide or nucleotides into the correct slot(s). But evolution never knows where the right slot is or what the "right" nucleotide(s) is that goes into each slot. So evolution will always put new nucleotides into randomly chosen slots (the location issue) and will fill these slots with randomly chosen nucleotide(s).

Does adding new nucleotides help the statistical problems with the theory of evolution?

Obviously not. Adding new nucleotides has roughly the same problems as changing nucleotides, which we already discussed.

For example, consider an existing species which has perfectly good DNA (Where did the good DNA come from? Certainly not evolution!). Now suppose we have to change 10,000 of these nucleotides (at random locations with randomly chosen nucleotides) and we need to add 10,000 new nucleotides (at random locations with randomly chosen nucleotides).

This scenario effectively has the same probability issues whether changing 20,000 nucleotides or adding 20,000 nucleotides or some combination thereof!!

The only difference is that when we talk about changing nucleotides we are talking about "location" issues and when we talk about adding nucleotides we are talking about "slot" issues. But "slots" are a type of "location" issue. The only difference is that multiple nucleotides could go into one slot. But this would be rare indeed, so we can ignore this possibility.

This example is exactly why I say that macroevolution is scientific nonsense.

The devastating "location" issues apply almost equally to "changed" nucleotides (location issues), "added" nucleotides (slot issues) and "deleted" nucleotides (location issues).

In addition, the 75% failure rate created by the "which nucleotide at that location or that slot," for changed and added nucleotides, will always guarantee that 75% of all changed or new nucleotides will be the wrong nucleotide.

The end result is total nonsense. The entire DNA strand would be splattered with wrong nucleotides.

The location issue and the Axiom of Random Mutations totally obliterate the theory of evolution.

A Very Critical Point Regarding Genes

Another fatal problem with evolution is that random locations of mutations are usually fairly evenly scattered across the entire DNA. But the needed changes (such as a new gene) are usually clustered in one or more different places on the DNA. Let me quickly explain why I mention this.

Given any consecutive sequence (i.e. "cluster") of 1,000 nucleotides (Note: on a two billion long DNA strand there would be 2,000,000 consecutive clusters), it is unlikely more than two of the mutations would occur in this cluster. The reason this is significant is that evolution claims that evolution has no "direction," yet evolution claims random mutations is how new genes were created.

But in order to create new genes, many mutations must appear in the *same cluster* of nucleotides. But computer simulations demonstrate the absurdity of this claim. It would take a massive number of damaging mutations before enough mutations could occur in one cluster to create a new gene. The DNA would literally be destroyed before a single new gene could be formed. But even if there were enough mutations inside a cluster, then the issue of the probability of viable permutations [to create a viable gene] issue comes into focus.

These things are precisely why it is ludicrous beyond imagination to claim that humans were created by macroevolution (they obviously weren't created by microevolution). While macroevolution might have created 2 or 3 of our single-celled ancestors, to claim that thousands of our highly complex "ancestor species," on our phylogenetic tree, developed by macroevolution is insanity beyond comprehension.

This is why I keep saying that the discovery of DNA in 1953 destroyed the theory of evolution.

For example, we assumed above that there were 10,000 new species between the "first living cell" and Adam and Eve (or whatever the first humans were named by evolution). This means there would have been at least 10,000 examples of macroevolution, sequentially, on the same planet and on the same evolution line. Many of these would have involved improving the morphing of the embryo algorithms for the new species to create a more complex species.

This is scientific nonsense far beyond comprehension especially when considering how many thousands of large and highly clustered, complex genes would have had to be created during this time period by macroevolution (i.e. purely random changes to DNA both in terms of location, types of mutations and which nucleotides ended up at each location).

It is bad enough to expect a relatively small gene (e.g. for a bacteria) to be created by macroevolution, but to think that a large and complex set of genes for a mammal was created by macroevolution is exponentially many times more absurd.

To claim this would be as insane as saying that an explosion in a book factory, one that published children's reading books, would yield the most advanced physics book on the planet earth, complete with graphics and binding. The claim would be far beyond inane.

For example, this is what Elder Russell M. Nelson has said, both at BYU (this talk was published in the Ensign) and in General Conference (which was also published in the Ensign):

> "Through the ages, some without scriptural understanding have tried to explain our existence by pretentious words such as *ex nihilo* (out of nothing). Others have deduced that, because of certain similarities between different forms of life, there has been a natural selection of the species, or organic evolution from one form to another. Many of these people have concluded that the universe began as a “Big Bang” that eventually resulted in the creation of our planet and life upon it.

> To me, such theories are unbelievable! Could an explosion in a printing shop produce a dictionary? It is unthinkable! Even if it could be argued to be within a remote realm of possibility, such a dictionary could certainly not heal its own torn pages or renew its own worn corners or reproduce its own subsequent editions!
>
> We are children of God, created by him and formed in his image. Recently I studied the scriptures to find how many times they testify of the divine creation of man. Looking up references that referred to create, form (or their derivatives), with either man, men, male, or female in the same verse, I found that there are at least fifty-five verses of scripture that attest to our divine creation."
> Russell M. Nelson, “The Magnificence of Man,” Ensign, Jan. 1988, 64
> A similar quote was given in the April, 2012 General Conference

Note the phrase: "such a dictionary could certainly not heal its own torn pages or renew its own worn corners or reproduce its own subsequent editions." The fact that the human body, and the bodies of many animals, can heal themselves, and have children, is yet another testimony of the creation.

What Elder Nelson is asking is this: Could an explosion in a printing factory create a male and female dictionary that could mate and have a "baby" dictionary that could grow and have new words, with their definitions, which neither parent dictionary had in their pages??

Of course not!!

Could Evolution Have Occurred in Small Chunks?

Sometimes scientists claim that evolution, from one species to another, occurred in many small chunks rather than one large chunk.

How do small chunks overcome the massive statistical problems of macroevolution?

Whether you are talking about evolution taking a long time or evolution occurring in small chunks, spreading out evolution does not affect its probability.

It is as absurd as saying that you can take an existing computer program and make it into a far superior program by making a small number of mutations (by exclusively using random number generators, not programmers), many times, and that the end result of these many new programs, (which each had small random changes) will end up being many functional computer programs.

Furthermore, evolution would claim that each and every intermediate computer program would be an improvement over the prior intermediate computer program and each rendition would have at least one new feature.

All of this is nonsense because it does not help the mathematical problems even remotely. The location, type of mutation and resulting "nucleotide" (or resulting bits) are not affected by using a large number of "small" mutations or by using a very slow processor.

For example, let us say that someone claimed that evolution used 50 generations of small evolutionary changes to create a new child species from a parent species.

How does this fix the "location" issue? All it does is spread the "location" issue over 50 small iterations. Each iteration has its own "location" issues.

How does this tactic fix the "type of mutation" issue? How does this fix the "which nucleotide ends up at that location" issue?

The statistics issues are identical whether it takes 50 generations of a small number of changes or 1 generation of a large number of changes. The only difference is that the statistical absurdities of evolution are spread out into 50 small absurdities instead of 1 large absurdity.

The math doesn't change by stopping and starting the program 50 times!!

Hopefully, the reader will study the prior chapter and this chapter until they fully understand the total absurdity of the theory of evolution.