

Patterns of Intelligence

CHAPTER 28

INTRODUCTION TO THE STATISTICS OF EVOLUTION

So far we have not gotten into any actual mathematics; we have only referred to mathematics. That is about to change. This is where the real debate occurs or as we say in America: "it is where the rubber meets the road."

Let me explain, as simply as possible, several of the many reasons the theory of evolution is nonsense.

First, **macro**evolution requires changes be made to the DNA of a "parent species." These changes must include: new nucleotides, changed nucleotides and/or deleted nucleotides. But above all, it must have "new nucleotides."

There is no way for evolutionists to avoid the "new nucleotides" issues if the "first living cell" DNA or RNA is going to become human DNA. The many, many steps (i.e. intermediate species) would have each required many, many new nucleotides.

Creating a new species from an old species would require many changes to the DNA of the "parent species." These changes are called "mutations." **All mutations must be totally random**, by the definition of evolution, because they reject the intelligence of God.

The three key mutation issues in deleting, modifying and adding nucleotides to DNA are as follows:

The "location of the mutation" issue (i.e. where on the DNA is the mutation),

The "type of mutation" issue, and

The "which nucleotide ends up at that location (if any)" issue.

First, is the "location of the mutation" issue, meaning: exactly "**where**" on the DNA of the "parent species" are the nucleotides that will be changed, added or deleted by evolution (to create the new species)?

For example, if a DNA strand has 2 billion nucleotides, and we numbered these nucleotides from #1 to #2,000,000,000, and if we made a random mutation, then at which of the 2 billion nucleotide locations would there be a change, addition or deletion? This is the "**location of the mutation**" issue.

Evolution has no intelligence, thus **whenever evolution picks a location** for a mutation, the location is totally random, meaning it can be **anywhere** on the DNA. Every nucleotide has an equal chance of being mutated.

Randomness (i.e. mutations) does a very, very poor job in choosing the correct location for a mutation because evolution has no clue where the mutation should happen, nor does evolution care because it has no direction and no intelligence!!

For example, suppose the new species needed a change to a nucleotide in location #1,543,233,212, but suppose the change (i.e. mutation) occurred in location #982,908,143. That mistake does not "fix" the incorrect nucleotide, *plus* it damages a good nucleotide that we didn't want to change!!

As we try to change a nucleotide in the chosen location, a vast, vast number of errors will occur before we accidentally change the correct nucleotide.

The location issue turns out to be the most important issue in this discussion, as will be seen below.

Second, for each mutation in a location, what is the "type of mutation" that will occur. These are the three "types of mutations":

Type 1) A mutation can *change* an existing nucleotide (e.g. an 'A' can be changed into a 'G');

Type 2) A mutation can *add* a nucleotide (e.g. a 'T' can be added between two existing nucleotides);

Type 3) A mutation can *delete* an existing nucleotide (e.g. a 'C' can be deleted).

Third, for type 1 and type 2 mutations, what nucleotide will result at that location from the mutation, an A, C, G or T? This is the "which nucleotide ends up at that location" issue. Of course, if there is a deletion, there will be no nucleotide at that location and we are concerned about which type of nucleotide was deleted.

We can summarize some of this with examples:

- 1) Will a mutation (at a random location) *change* an existing nucleotide, and if so, what will the new nucleotide be (on the DNA), or
- 2) Will a mutation (at a random location) *insert* a new nucleotide into the DNA and what will the new nucleotide be, or
- 3) Will a mutation (at a random location) *delete* an existing nucleotide on the DNA and which type of nucleotide was deleted.

As a more complete example, the new species may need a nucleotide *changed* from an 'A' into a 'T' in location #1,543,233,212. But the mutation may *delete* a 'G' in location in #982,908,143!!

Not only has this not fixed the nucleotide in location #1,543,233,212, but a perfectly good nucleotide at location #982,908,143 was deleted, thus possibly damaging the functionality of the DNA!!

This is not a good thing to happen to the new species because the deletion has likely damaged the functionality of the DNA and has certainly not fixed it.

Every time evolution creates a new species, **several new highly sophisticated genes must be created** (note that the nucleotides in a gene are clustered together, but statistically, randomness does not cluster mutations).

Furthermore, the old "morphing of the embryo" algorithms (which are part of the DNA sequence) need to have **incredibly precise changes** made to them, as we saw above.

Changing the old "morphing of the embryo" algorithm is like changing the compiled code of an incredibly complex computer program, but with the changes being made totally randomly.

"Randomness" and "precision" (which requires intelligence) do not yield the same results!!

Let us dig deeper into these concepts before giving you a test.

THE "PRIME DIRECTIVE" OF THE POST-DNA DEBATE

The "Prime Directive" of Evolution: If evolution were true, scientists should be able to look at two animals (which have a parent-child relationship on the phylogenetic tree) and easily demonstrate how the DNA of the parent species could randomly mutate into the DNA of the child species.

That is so important I am going to repeat it because it is central to the post-DNA evolution debate:

The "Prime Directive" of Evolution: *If evolution were true, scientists should be able to look at two animals (which have a parent-child relationship on the phylogenetic tree) and **easily demonstrate** how the DNA of the parent species could randomly mutate into the DNA of the child species.*

The reason it has to be "easy" is because evolution claims it has happened many millions of times, **with few or no failures**, and something highly improbable is not likely to happen a single time in a few million years timeframe. Thus, evolution must be shown to be "easy," meaning very accurate every time.

As mentioned, there must be very, very few errors in this process or there would be **billions of "dead" animals** which were **born as mutated forms of valid animals** but had flawed mutations to their DNA such that they could not mate with any other animal.

This is the "prime directive" of the post-DNA evolution debate. Scientists must demonstrate how easy it is to take existing DNA, **randomly** mutate it and then end up with new and improved intelligence on the new DNA!!

This is the **heart and sole** of **macro**evolution after the discovery of DNA.

The mutations to create a new species have to occur in **pinpoint locations** on the DNA, the **correct type of mutations** must occur and the **correct nucleotides** must end up (or be deleted) in the correct locations on the DNA.

The key word is "**randomly**"!! How do you "**randomly**" make incredibly **precise** changes to existing DNA in order to create new and improved DNA?

This is the oxymoron of oxymorons. It is equal to the phrase: "randomly precise."

The word "randomly" means exactly the opposite of "precise," yet with evolution "random" mutations must be incredibly "precise." The concept of "randomly precise" (or "random precision") is the quintessential oxymoron.

In short, evolutionists must demonstrate and prove how an animal with perfectly good DNA (the "parent" species) can have its DNA randomly mutated and end up with a new and improved species (the "child" species).

The "child species" are always considered to have superior DNA to the DNA of the "parent species," meaning the DNA of the child species is always an **improvement** (not just a change) over the DNA of the parent species. This makes the claims of evolution more absurd.

APPLYING THE THREE KEY MUTATION ISSUES

Now let us apply the three key issues related to mutations to the issue of improving the DNA of a parent species to test the feasibility of the "prime directive" of evolution.

According to evolution, **every location** on the 2 billion nucleotide DNA (assuming the parent species has 2 billion nucleotides) must have the same probability of being chosen as the **location** of the mutations because the new child DNA will likely have many changes scattered throughout the parent DNA and evolution doesn't have a clue **where** to make the changes, what kind of changes to make or what nucleotides need to end up in each location.

For example, let us say that we want to *change a specific nucleotide*. We must *first* pick a "**random location**" on the DNA (e.g. nucleotide #45,119,004), then the

mutation must *change* that nucleotide to a new nucleotide (the new nucleotide must randomly end up being an A, C, G, or T).

Because every nucleotide has the same chance of being changed, and we know which nucleotide needs to be changed (i.e. #45,119,004), note that there is a **one in 2 billion chance** that the correct nucleotide will be "changed" because every nucleotide has the same probability of being changed and there is only one nucleotide (out of 2 billion nucleotides) we want to change and we know where it is (**but evolution doesn't know where it is because evolution is stupid, by definition**)!!

Before going on we need to clarify an issue. Evolution (i.e. a mutation) may *change* a nucleotide, at a certain location, but it may turn out that the "old" nucleotide and the "new" nucleotide are the same nucleotide (i.e. an "old C" may be converted into a "new C"), meaning there is **no net change to the DNA** made by this mutation. In other words, even though there was a change, the old and new nucleotides were coincidentally the same so there was no net change. This possibility will come up later in this discussion.

As another example of a mutation, a random mutation, such as a *deleted nucleotide*, must *first* pick a *random location* on the DNA (e.g. nucleotide #1,633,099,415), then the mutation must delete that nucleotide (the nucleotide that was deleted might have been an A, C, G, or T).

Note that there is a **one in 2 billion chance** that the correct nucleotide will be deleted because every nucleotide has the same probability of being chosen for deletion!! This is an example of the "location" issue combined with deleting a nucleotide.

It turns out that the "location" issue is far more important than the reader might think. Examples below will demonstrate the importance of the "location" issue.

Remember, the three key variables in a mutation are "location of the mutation," "type of mutation," and "resulting nucleotide," meaning which nucleotide will end up at that location (i.e. or lack thereof in the case of a deletion).

Every random mutation has a one in 2 billion chance of choosing the correct location (1 in 2 billion) for the mutation, a one in three chance of picking the correct type of mutation (1 in 3) and a one in four chance in ending up with the correct nucleotide (1 in 4), excluding deletions.

2 billion times 3 times 4 equals 24,000,000,000.

That means **every mutation has a probability of one in 24,000,000,000** of being what evolution wanted (i.e. one in: 2 billion times 3 times 4), if the parent species had DNA of 2 billion nucleotides!!

And if you make 1,000 mutations, every one of these mutations has a one in 24,000,000,000 chance of being the correct mutation (i.e. in the correct location, the correct type of mutation and the correct nucleotide ending up in that location, if any)!!

These three variables totally annihilate the theory of evolution from a statistical standpoint!! No statistician on earth would support the theory of evolution if they understood the issues and kept an open mind. Unfortunately, there are very few open minds in science.

Before going on, let us again state the "Prime Directive" of the theory of evolution because it is so very important:

*If evolution were true, scientists should be able to look at two animals (which have a parent-child relationship on the phylogenetic tree) and **easily demonstrate** how the DNA of the parent species could **randomly mutate** into the DNA of the child species.*

We must never lose track of this key directive of evolution. And we must never lose track of the claim that all child species are *improvements* over the parent species.

Evolutionists must prove this is possible by: first, randomly picking the "location" of each mutation, second, randomly picking the "type" of mutation (i.e. addition, change or deletion) at that location and third, randomly picking the "new" nucleotide (if any) at that location.

It is time for some training tests. Break out a pen and some paper and let's see how you do.

Gulp, now that we know the basics, let the mathematics begin!!

Note: the reader might be thinking that "evolution has no direction."
This, and other issues, will be discussed in a future chapter.