

# Patterns of Intelligence

## CHAPTER 29

### YOUR FIRST TEST QUESTION

Suppose a "parent species" has DNA with 2 billion nucleotides (we only count the nucleotides on one side of the DNA strand). Suppose the "child species" will also have 2 billion nucleotides, but 10,000 of the nucleotides will be different than on the "parent species" or "old species."

In other words, we will take an existing DNA strand (of the "parent species") and randomly **change** 10,000 of the nucleotides to create a new species (the "child species").

To keep things simple, we will assume no nucleotides will be added and none will be deleted. We will only deal with changed nucleotides in this example.

**Note:** Technically this will not create a new species because, by my own definition, a new species must have at least one "new" gene. But hang in there, this is a training exercise. Later we will deal with the "new" gene issue.

We will assume **we know which 10,000 nucleotides need to be changed** and we will call them the "**target nucleotides**" because these are the only nucleotides we want to change!! We will also call them the "**bad nucleotides**" because we want to change them to create a new species. We could list the nucleotide # of each of the 10,000 nucleotides we want to change, but we won't.

In other words, on the "**parent species**" these 10,000 specific nucleotides are "good nucleotides" because they are the correct nucleotides **for the "parent species."**

But on the "**child species**" these **same 10,000 nucleotides** need to be changed so we will call them "**bad nucleotides**" or "**target nucleotides.**" They are at very precise locations on the DNA and we know where these exact locations are!!

However, evolution is dumb and evolution has no clue where these locations are or what is supposed to be there or not be there!!!

Remember, every nucleotide on the **child DNA** (which is a copy of the parent DNA and will then be mutated) is either a "target nucleotide" (i.e. a "bad nucleotide" that we want to change) or a "good nucleotide" (that we don't want to change), relative to the new "child species."

On the DNA of the "child species," there are 10,000 "target nucleotides" or "bad nucleotides" and there are 1,999,990,000 "good nucleotides" that we don't want to change.

In an attempt to create this new "child species," suppose there are 200,000 random mutations (all of them are "changes" of a nucleotide) at random locations on the DNA strand of the "child species."

When making these 200,000 random mutations, remember that the "location" of each mutation on the DNA strand must be totally random and the new nucleotide at that location must also be totally random.

In other words, if we numbered the nucleotides on the DNA from #1 - #2 - #3 - #4 etc. to the end of the DNA at #2,000,000,000, the "location" issue means evolution doesn't know which nucleotides should be changed because evolution is clueless and stupid because, by definition, mutations are totally random, both in terms of location, type of mutation and resulting nucleotide (if any).

If "evolution" knew which nucleotides needed to be change then we would be dealing with intelligence, meaning "God," which is a forbidden word for evolutionists to utter or think about.

For example, when picking a location for a mutation, we essentially pick a random number from #1 to #2,000,000,000. An example would be: nucleotide #1,397,943,567. The nucleotide at this location might be a "bad nucleotide" or a "good nucleotide," randomness or evolution doesn't have a clue and doesn't care.

Every nucleotide has an equal chance of being chosen every time there is a mutation.

In fact, a single nucleotide could be changed two or three times, but we will ignore this possibility because it really messes up the statistics without justification.

And the new nucleotide put at each of those locations (considering only "changes") is also totally randomly chosen. That is the only way that evolution can work, otherwise we are dealing with intelligence.

With this background, let us talk about the 200,000 random mutations which will attempt to convert this "parent species" into a "child species."

As mentioned, to make things simple we will not consider deleting or adding any nucleotides to the DNA of the new species.

### **FIRST TEST QUESTION:**

Statistically speaking, if we randomly choose 200,000 nucleotides from the DNA, **at random locations**, and then mutated each nucleotide into a **randomly chosen nucleotide**; how many of these 200,000 mutations will affect one of the 10,000 "**target nucleotides**" or "**bad nucleotides**" that we **want** to change and how many will affect "**good nucleotides**" that we **don't want** to change?

Try to calculate the number, or take a wild guess, before reading any further.

[Write down your answer on a piece of paper before reading on.](#)

### **FIRST ANSWER:**

The number of "target nucleotides" that will be affected is one. That's right: 1 out of the 200,000 mutations will affect a "target nucleotide"!! The other 199,999 mutations will affect "good nucleotides" that we **do not** want to change!!

Here is how to calculate the 1 "target nucleotide" that is changed:

**Step 1:** Take 200,000 mutations and divide it by 2,000,000,000 total nucleotides and you get **0.0001**. This is the ratio of all nucleotides that will be affected by the 200,000 mutations.

**Step 2:** Multiply 10,000 (the number of "target nucleotides") times **0.0001** (the ratio or probability of a mutation affecting a random group of nucleotides; this will tell us how many nucleotides in this group will be mutated) and you get one.

One is the number of "target nucleotides" that will be affected by the 200,000 mutations!!

If you did computer simulations for this exercise 350 times, on average only '1' of the "target nucleotides" would be changed per simulation.

### **THE MOST DAMAGING QUESTION**

**The fact that only one "target nucleotide" is changed is not even remotely the biggest problem for evolution.**

For those who are bold enough, here is an even bigger question:

How much damage to the DNA of the new "child species" will be done by the 199,999 mutations which affected "good nucleotides"? Hint: these mutations, in the wrong location, could potentially **damage** many, many of these critical "good nucleotides?"

Try to calculate that number before reading on.

Evolution would have to take into account both the one mutation that affected a "target nucleotide" plus the **far more important** 199,999 mutations that affected "good nucleotides" each of which could potentially replace a "good nucleotide" with a "bad nucleotide!!"

In other words, how many of these 199,999 "good nucleotides" will be converted into "bad nucleotides" by these 200,000 random mutations?

The answer to this question will require a lot of explanation.

Let us start by talking about the third key issue, what "type of nucleotide" ends up at each location, an A, C, G or T? Remember: the "location of the mutation" on the DNA is the first key issue and the "type of mutation" is the second key issue.

The third key issue is "what type of nucleotide ends up at that location." Let us analyze the third key issue in detail.

### **WHICH NUCLEOTIDE WILL RESULT FROM EACH MUTATION?**

Suppose, for a specific "target nucleotide" you want a mutation to change a 'C' (a "target nucleotide") into a 'G' (the new "good nucleotide" for the new "child species"); as part of creating this new "child species."

However, mutations create random nucleotides; meaning randomness (i.e. evolution) could not care less what you want!! To convert a nucleotide into what you want would be using intelligence, and God is not allowed.

**Note:** The reader may have noted in the above histogram of real human DNA, that every permutation of four nucleotides was represented in the chart. This indicates that any permutation of four nucleotides can be found on human DNA. Remember also that 97% of human DNA is not understood by scientists and its function is unknown.

A random "change mutation" can change a 'C' into an 'A' or into a 'C' (yes, as noted above a mutation can change an "old C" nucleotide into a "new C" nucleotide, but it ends up being a 'C' nonetheless) or into a 'G' or into a 'T'.

Of these four options, only one of them is correct, the 'G' in this case. This means **25% (1 of 4) of all possible mutations are correct** (the 'G') and **75% (3 of 4) of all possible mutations are incorrect** (an 'A', a "new C," which is nothing but a

'C', and a 'T') even when they apply at the location of an existing correct nucleotide!!

Thus, when there is a "change mutation" there is only a 25% chance the mutation will leave a correct nucleotide at the location, regardless what was there before.

**Note:** As a side note it should also be observed that any nucleotide can be changed more than once. For example, suppose a 'C' "target nucleotide" was changed into a 'G' by the 3,391st mutation, which is what you wanted. However, there is nothing to "protect" this nucleotide from later being changed into an 'A', which you don't want!! For example, in the 159,102nd mutation the 'G' might be changed into an 'A', which you don't want.

The reason I mention this issue is because some evolutionists have claimed that if a nucleotide is changed into a good nucleotide, that it is somehow "protected" from being changed again by a later mutation. This is absolute nonsense, there is no such thing as "protecting" a nucleotide from being mutated. How would evolution know which nucleotides to protect or how would it protect such a nucleotide??

Let's get back to the 199,999 mutations which occurred in locations you didn't want to change (i.e. they affected "good nucleotides" which were already correct for the new "child species" because they didn't need to be changed).

For each and every one of these mutations, there is only a 25% chance a "good nucleotide" ended up as a "good nucleotide," using the above logic!!

For this to happen, for example, the mutation of an "old T" (which was a "good nucleotide") would have to be changed into a "new T" in order for the "good nucleotide" to remain "good." In other words, the mutation would not change the type of nucleotide at that location and the new nucleotide was also a "good nucleotide."

But with the other three options ('A', 'C' and 'G'), you have damaged a perfectly good nucleotide and converted a "good nucleotide" into a "bad nucleotide"!!

We definitely do not want to change any "good nucleotides" into "bad nucleotides," but 199,999 of the random mutations affected "good nucleotides" so we have to consider this possibility!!

When you do the math, you mutated 199,999 nucleotides that you didn't want to change, and 75% of these "good nucleotides" will be changed into a "bad nucleotide"!! This is because only one of four mutations (25%) will yield the nucleotide you want for the new species!!

And there is also a 75% chance that the one "target nucleotide" you changed will still be a "bad nucleotide" (i.e. there was only a 25% chance the "target nucleotide" was changed into what you wanted).

Thus, if you add 199,999 (the "good nucleotides" you changed) to 1 (the "target nucleotide" you changed), statistically: **200,000 times 75%** (or **150,000**) **of the nucleotides that were changed will end up being "bad nucleotides"** (all but one of which were originally "good nucleotides") *as a result of the 200,000 random mutations!!*

Note also that 9,999 of the original 10,000 "bad nucleotides" were **not affected** by the mutations, thus they remain "bad nucleotides."

***In summary, because of the 200,000 mutations, you went from 10,000 "bad nucleotides" to 159,999 "bad nucleotides (if the one "target nucleotide" was not fixed) or 159,998 bad nucleotides (if the one "target nucleotide" was fixed)!!***

I'll bet that is not what you were expecting!! You probably thought the number of "bad nucleotides" would drop as a result of the 200,000 mutations!! Nope, **the number of "bad nucleotides" skyrocketed from 10,000 to 159,999 or 159,998 "bad nucleotides"!!**

What is wrong with this picture? **You went backwards as you tried to "fix" the DNA to create a new species!!**

And this is always the case!! Attempting to "fix" DNA with random mutations always causes far, far more damage than it fixes!!!!

Remember, remember, remember, if evolution were true you could take the DNA of a parent species, apply random mutations to this DNA and end up with the superior DNA of the child species which evolution claims was created. But the mathematics doesn't add up!!

Let us formalize these concepts above by creating an axiom:

**The Axiom of Random Mutations:** For every mutation, whether it affects a "good nucleotide" that you don't want to change or a "target nucleotide" that you do want to change or a "new nucleotide" that you want to add; the probability that the resulting nucleotide will be a "correct nucleotide," meaning a "good nucleotide," is 25%. This means there is a 75% chance the wrong nucleotide will result.

I should mention that this axiom does not deal with the location issue, which is far more important. Remember, we only changed one nucleotide that we actually

wanted to change and 199,999 mutations changed nucleotides we did not want to mess with. This is typical of the "location" issue.

Note that deleted nucleotides were not discussed in the above axiom because there is no resulting nucleotide. But this does not mean deletions are not important, only that I won't discuss them. But remember that deletions have exactly the same issues with regards to **location** (i.e. you will almost always delete the wrong nucleotide).

What all of this means, is that for every random mutation, there is a 75% chance the mutated nucleotide will end up as a "bad nucleotide," whether it was originally a "good nucleotide," a "target nucleotide" (i.e. a "bad nucleotide") or a "new nucleotide"!!

**Do the math - the more mutations that occur; the more wrong nucleotides will result!!**

In other words, EVERY "change mutation," no matter what nucleotide you are talking about, results in a 75% chance you will end up with a "bad nucleotide" in that slot.

Thus, in addition to the "location issue" (meaning the probability you actually change a "target nucleotide"), 75% of all mutations, whether of the "target nucleotides" or of the "good nucleotides" will yield a bad or wrong nucleotide in that slot!!

Now let's use this axiom on the above example to simplify obtaining the answer.

You started with 2,000,000,000 nucleotides. Ten thousand (10,000) of these were "target nucleotides" or "bad nucleotides." 1,999,990,000 were "good nucleotides." You mutate or change 200,000 of these nucleotides.

Because of the "location" issue, you changed 199,999 "good nucleotides" and you changed one "target nucleotide."

By the Axiom of Random Mutations, you end up with 150,000 wrong nucleotides (75% of 200,000) on average!!!

Add these 150,000 wrong nucleotides to the initial 9,999 "bad nucleotides" that were not changed, leads to 159,999 "bad nucleotides" which resulted after the 200,000 mutations (assuming you did not fix the one "target nucleotide")!! This is the same number we calculated above.

Note also that the newly damaged nucleotides are randomly scattered over the entire DNA, meaning they will likely affect the critical and complex morphing of the embryo algorithm multiple times, many genes, etc. etc.

This is going to be difficult to comprehend, but try to understand this: it doesn't significantly matter how many "target nucleotides" there are, the results are the essentially the same!!

In other words, it doesn't matter if there are 10,000 "target nucleotides" or 100,000 "target nucleotides," the 200,000 mutations will always damage about 150,000 nucleotides by the Axiom of Random Mutations.

This is the real axiom: "Every time you mutate DNA the DNA will get worse."

You may have originally thought these 200,000 mutations would improve the new species, but in fact they were a giant step backwards in creating a new and improved species!!

You also probably thought that every one of the 200,000 mutations would change only "target nucleotides." But in fact they (statistically) only changed **one** of them!!

Also, you may not have realized that in this process you went from 10,000 "bad nucleotides" to 159,999 or 159,998 "bad nucleotides." That is not a good thing, especially when you were trying to fix the DNA!!

Now ponder this: *any attempt to "fix" these 159,999 or 159,998 "bad nucleotides" (which resulted **after** the first 200,000 mutations), with another 200,000 mutations, **will make things even worse!!***

This is obvious by the Axiom of Random Mutations.

In summary, you "may" have fixed one "target nucleotide," but you definitely ended up with at least 159,998 bad nucleotides!!

The combination of the "location issue" and the Axiom of Random Mutations is far more than enough to totally obliterate the theory of evolution and renders it far beyond scientific nonsense. It is always a fact that the more mutations you have the more damage is done to the DNA.

It is impossible, and I mean impossible, to blast a DNA strand with a lot of random mutations (both random in terms of location and random in terms of the final nucleotide at that location) and end up with better DNA. It is mathematical nonsense to think otherwise!!

Try it on computer programs. Take an existing computer program and try to turn it into a superior program by blasting it with random mutations of '0's and '1's in random locations. But instead of using individual bits use pairs of bits (e.g. '00', '01', '10', or '11') to simulate the base 4 nucleotides.

No superior computer program will ever be created by this process **even if you have no direction**!! The Axiom above has nothing to do with whether or not you have direction.

Randomness cannot create intelligence; in fact it always damages or randomizes any existing intelligence.

In the case of a computer program, one bad "bit" can destroy the entire functionality of the program.

In the case of a human being, a handful of mutations can destroy the human or give him or her a serious genetic disease.

Mutations are never good. Evolution is nonsense.