

Patterns of Intelligence

CHAPTER 32

SHOULD WE EVEN TALK ABOUT "TARGET NUCLEOTIDES"

An evolutionist might say this: "Let's not talk about target nucleotides, rather let us just mutate the DNA and see if we end up with a better species, we don't know or care what we will end up with so we don't care about target nucleotides."

While this might seem like a viable question, it is not. I will give four reasons why target nucleotides are important.

FIRST ANSWER - MALE AND FEMALE ALIGNMENT

First, let us think about a new species where the parent species has both a male and female. Many of the ancestors of humans (if evolution were true) would have had both a male and female in their species.

In order for a "new species" to be created, the mutations to **both** the male sperm DNA and the female egg DNA must "align" so the male and female can mate and have viable offspring which can in turn have viable offspring.

In addition, the "correct" male sperm must be the one to connect with the female egg and it must happen in the same timeframe and location (i.e. they must mate).

Note that the "set" of mutations (which includes the location issue, the type of mutation issue and the nucleotide at that location issue) to the male and female must be identical, though the mutations would not have to occur in the same order.

(Yes, I know there are slight differences between male and female DNA, but these differences can be ignored in this discussion and only "common" DNA segments need to be considered. And I know it is more complex than this, but fine-tuning the discussion will likely make the statistics worse, not better.)

For example, each gene must be in the same location on the DNA of both the male and female DNA. The morphing of the embryo algorithms, and many other things, must be in the same location, and in the same order, on both the male and female DNA (actually the morphing of the embryo algorithms are different for a male and female, but let us ignore this and other distracting issues).

Let us assume the male has the necessary mutations before the female and that the male is a "new species."

The female now needs to have exactly the same mutations as the male so that they can mate and have viable offspring that are fertile (i.e. so the new species can have viable offspring), though as already mentioned her mutations do not need to occur in the same order as his!!

In other words, **the female now has "target nucleotides"** because her nucleotides must match those of the male so that they can mate and have offspring!! **The new and changed nucleotides on the male DNA become the "target nucleotides" of the female!!**

Remember, both the male DNA and female DNA must align before they can mate and have viable offspring that are fertile. This cannot happen until the female DNA aligns with the male DNA. Thus, the new male DNA becomes the "target nucleotides" of the female DNA.

Of course, if the female DNA mutations are completed first, then her DNA becomes the "target nucleotides" of the male DNA.

The point is that if a species has both a male and a female, in order for evolution to create a new species the "target nucleotide" issue is unavoidable!! You have two "animals" which must have the same DNA. There is no way around this.

You have to consider the probability that both sets of ending mutations are identical. You don't have to worry about the order of the mutations on the male or the female!! When all is said and done, the male and female must have the same set of mutations!!

The "probability" issue becomes the probability of having two "sets" of identical mutations, independent of the order of the mutations on the male and female.

For example, suppose you have two identical computers with identical software, meaning they both have the same complex computer program. Suppose you randomly mutate the bits of the computer programs, on each computer, independently (e.g. you use a different "seed" numbers and different random number generation algorithms) and simultaneously, in order to create a new and improved program.

What are the chances both computers will end up with the same new and improved program **even without any preconceived notion about what you wanted to end up with (i.e. there were no "target bits")?**

The answer is ZERO (i.e. far, far less than: 10^{-80}) because the set of "mutations" are independent of each other and yet must be identical in the end. The two sets of mutations will not be the same no matter what order the mutations occur.

SECOND ANSWER - CLUSTERS OF MUTATIONS

Second, if you are going to create a new species from an old species, very precise mutations must be made to multiple genes; at least one new gene needs to be created from scratch (by definition); incredibly precise changes need to be made to different sections of the "morphing of the embryo" algorithms (wherever they are), etc.

It doesn't matter where these changed and new genes are etc., but they must be somewhere. Well, it probably does matter but we will pretend it doesn't matter.

These new and changed nucleotides must be in incredibly precise locations (because they are clustered in many cases). For example, all of the nucleotides in a new gene must be in roughly the same location on the DNA. Fixes to the morphing of the embryo algorithms must be in exact locations. Etc.

However, random mutations will be evenly scattered across the entire spectrum of the DNA. That is the way that randomness works for the location variable for a new species!!

Random mutations are not precise, yet to create a new species the vast majority of the necessary mutations will be clustered in many different places on the DNA. But this is not the way that randomness operates. Randomness is generally spread out somewhat evenly across the entire DNA. Try this with computer simulations and you will know what I am talking about.

This is the second reason we must reject the theory of evolution even if we didn't have a specific new species in mind.

THIRD ANSWER - PROTEINS, MORPHING OF THE EMBRYO

Third, have you ever seen the nucleotides that form a "protein" which is used inside the cell? The section of DNA that creates a protein is called a "gene." It is much easier to look at a protein than a gene. Some genes can actually be used to create many different proteins.

When you think of a "structure made of proteins" think of a bicycle made of Lego® building blocks in the sense that a set of proteins can attach to each other (at very specific points), to create a highly complex structure which is made up of individual proteins (each individual protein is made of amino acids) which are bound together and form a very specific shape.

The "binding issue" is very critical because only specific types of proteins can bind to each other (or repel each other, etc.). Thus, to get a specific shape, very specific proteins must be in exact locations.

An [outstanding book](#) was largely written on this very issue ([The Edge of Evolution - The Search For the Limits of Darwinism](#) by Dr. Michael J. Behe). Read that book if you don't believe my summary.

If you took this section of DNA (i.e. a gene) and started to randomly mutate it, the "protein" it creates would very quickly become unusable!! A single wrong nucleotide, in the wrong location, could destroy the entire function of the shape and binding sites (or repel sites) of the protein.

The [set of proteins](#) could become a pile of unrecognizable, worthless garbage (rather than a highly functional and sophisticated shape), frequently after [the first mutation to a single gene](#) (i.e. the shape of this single, mutated protein could destroy the entire structure of the set of proteins).

Let us again think of a bicycle. Suppose you blindfolded a person and put every individual part of the bicycle in a pile. Suppose the blindfolded person then took several of the individual parts of the bicycle and individually started twisting and breaking these parts of the bicycle.

What are the odds the parts of the bicycle will fit together and a person would be able to ride the bicycle after this exercise? The odds are pretty slim. The shape of the individual parts of the bicycle represent the individual proteins which are used to create a structure in the cell.

Here is the key: only very rare and very specific combinations (technically "permutations" because the order of the nucleotides on the DNA is critical) of nucleotides will create a gene that will create a functional protein that will fit into a protein structure.

The point is that even if you have no "target nucleotides," almost all types of mutations will damage the functionality of the protein structure almost immediately because very, very few permutations will create something viable for a specific protein structure. Furthermore, in many cases contiguous protein structures must be compatible with each other (either because they fit together or have some other structural relationship).

Also, some proteins do not form structures at all. Some proteins have tasks which involve supervising the construction of a protein structure. Some proteins are used for communications. And so on. These complex proteins can easily cease to be able to fulfill their function with a single mutation.

Also, can you imagine randomly mutating the "morphing of the embryo" algorithms on the DNA!! Who knows what you would end up with, but you would know one thing - the animal would quickly be so deformed by mutations it would die immediately after birth or more likely long before birth.

And I suspect a significant percentage of the DNA (e.g. close to 97%) is part of the "morphing of the embryo" algorithm for a complex species. There is very little, if any, margin of error in these nucleotides!!

For example, if more than three-fourth of the DNA was the "morphing of the embryo" algorithm, and there are 20,000 mutations; roughly 15,000 of these mutations would affect the "morphing of the embryo" algorithm, which is very sensitive to errors due to its complexity and the fact that parts of the algorithm affect many, many layers of the asymmetric cell divisions.

Thus, even if you have no direction, when you randomly mutate the highly precise nucleotides in a gene or the morphing of the embryo algorithms, and many other sections of DNA, you will do massive amounts of damage very, very quickly!!

Thus, you cannot just brush-off the "target nucleotide" issue because only an incredibly small percentage of permutations of DNA (i.e. unique ways to order the nucleotides on the DNA) will yield a viable animal. Plus, in many cases these sections will be clustered together!!

FOURTH ANSWER - NO NEED FOR COMPUTER PROGRAMMERS

Fourth, I wish there were a way to graphically demonstrate "intelligence" on a DNA strand. Well, to some degree there is, but I don't have the time, money or the computer horsepower to do the calculations. A histogram is nice, but there are better ways to demonstrate intelligence (such as color coding the histogram for certain situations).

Think of human DNA as a huge, gigantic, highly sophisticated computer program.

Actually, there is no computer program on earth which is even remotely as sophisticated as the algorithms on human DNA which control the morphing of the embryo, the genes, etc.!! You can see that by the above discussions. DNA does something totally unique!!

A compiled computer program is composed of "bits" called '1's and '0's. Thus, if you change a "bit" you know what the outcome will be (the opposite of what it started out to be).

Do you think you could improve the intelligence in any highly sophisticated computer program by randomly changing the "bits" on the compiled code??
Absolutely not!!

Never, never would the code improve by randomly changing the bits with a random number generator which would randomly choose where (i.e. the location issue) the bits were changed, deleted or added.

If highly complex computer programs could be written in this way, as evolution implies, **all computer programmers could be replaced** with "random number generators" which could write new and improved computer programs by *randomly* choosing:

- 1) Where on the old, compiled computer code each mutation to the program will occur (the "location" issue), and
- 2) Whether the mutation will be a deletion, addition or a change.

Computers are much faster than computer programmers!!! You wouldn't need people to design the new programs, just let "evolution" design and write the new and improved program.

Computers are almost infinitely faster than programmers or evolution, plus computer programs are always very, very simple compared to human DNA; thus if evolution could work by randomness, it would be **much easier** to write new computer programs by using random number generators.

But it has never happened and it never will happen.

Even if you did this process 10 times on an existing computer program, and "chose" the best of the 10 "new" programs (i.e. to simulate natural selection) you would never end up with a better program.

Try writing a new and improved computer program using this technique!!

If this were a viable way of writing newer and more sophisticated computer programs with random number generators, corporations would immediately fire all of their programmers to make more money (i.e. they would have less salary and overhead expenses and thus they would make more profits if they had less programmers).

Trust me, many corporations care more about profits (i.e. the "bottom line") than their employees. Some corporations, every time they need to increase their "earnings per share" will simply lay off hundreds or thousands of their employees. Stockholders will always be more important than the employees!!

And programmers are generally near the bottom of the pecking order of the employees because there are so many of them (though they are not all equally talented).

Needless to say, no stingy corporation in history has ever fired a single computer programmer because using random number generators was a superior way to write new, complex computer programs from existing programs!!!

Even without direction, and even without any "target code," and even simulating "natural selection," the computer program will very quickly cease to function and will be irreparable due to the "mutations."

If it is impossible to use randomness to write better computer programs using high speed computers which operate very, very quickly; **even without any direction**; why would anyone expect you could create a better species of plants or animals by using random mutations which happen very, very slowly in a much more complex environment?

Computers are many, many, many quadrillions of times faster than evolution could ever be. Yet, no corporation would be so idiotic as to fire their computer programmers and replace them with random number generators.

As mentioned, the computer algorithms on DNA are far, far, far more sophisticated than any computer program ever written by a human!! Thus, DNA is far more sensitive to errors, though I suspect DNA is designed to survive some errors!!

In fact, no human being on earth can even remotely understand the "morphing of the embryo" algorithms on human DNA, as mentioned above.

But the "morphing of the embryo" algorithm is only part of the vastly complex network of what is on human DNA.

Yet, evolution claims human DNA was all the result of a long series of fortuitous accidents to DNA. What absolute nonsense!!

Do you think that you can go from dirt, water, lightning, etc. (i.e. the pre "first living cell" period) to human DNA by a long series of very slow, totally random mutations to DNA??

And while this is going on you must also accidentally create *millions* of other species, which are not on our ancestry path from the "first living cell" (e.g. turtles and guppies are not our ancestors)!! Each species would have highly sophisticated DNA strands, among their ancestor species, during the same time period human ancestor species were evolving!!

Zero randomly created, quality computer programs have ever been written. This should give you a clue about the absurdity of the theory of evolution.