

Letter To The Atheists

Part Two

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47. The Origin Of Life

Let us turn our attention to the origin of life on Earth. How did it come about in the first place? The writers of the Bible consistently claim that YHWH is the Creator of life. This sounds like an extraordinary claim, but I have already presented extraordinary evidence for it, showing how the story of Jacob's life in Padan-Aram contains many analogies to molecular biological processes including transcription and translation, as well as concepts such as selection and mutation.

However, let's consider the alternative, assumed by much of the scientific establishment, that life on Earth somehow arose by itself. First of all, what do I mean by "life"? It's difficult to define precisely, and there is disagreement over what is living and what is not. Since I want to avoid falling into a word trap and debating the definition of the word "life" rather than the idea behind it, let's put an exact meaning aside, and look at what life on Earth has in common.

One thing that seems common is the cell. But even the simplest of cells are actually very complex. A typical single-celled bacterium, for example, has a membrane and maybe also an outer wall, to keep itself separate from the outside world while still allowing certain materials in.

Another common feature of life on Earth is the DNA (deoxyribonucleic acid) molecule. Even the lowly bacterium has a circular DNA double strand which contains a blueprint for itself. Most cells also use the core biological processes of transcription and translation, where a DNA sequence is transcribed into a messenger RNA (mRNA) strand, and then the mRNA strand is converted by a ribosome into a protein.

A key requirement for life on Earth is the ability to reproduce or replicate. The bacterium can duplicate itself, in a process called "binary fission." It also has a built-in system for producing energy, and an internal transportation system to pass materials around the cell and in or out of its environment.

These are all complex features. If life came about all by itself, obviously it can't have started out being anywhere near as complex as even the humblest of single-celled organisms we see today. How did it happen? How did non-living chemicals become living organisms?

Scientists don't know for sure, because no human was around at the time to observe it. However, various ideas have been suggested. One of the most popular ones is called "RNA World." In this hypothesis, RNA (ribonucleic acid) molecules arose before DNA became prominent. There are several reasons why proponents of this idea think RNA helped life to get started.

First, some of the core cell machinery uses a lot of RNA, including the ribosome. Since RNA is quite similar to DNA, they argue that much of the initial machinery was made out of RNA strands, and then some of it was later replaced by DNA, which is more stable. Second, certain RNA strands can act as catalysts. This means they can dramatically increase the reaction rate of a chemical process, which is necessary for

many of the processes critical to life. Third, short strands of RNA can act like miniature machines, much like proteins do.

In the hypothetical RNA World, pieces of RNA perhaps floated around in some liquid, or were sandwiched together in clay or ice or something else, and gradually formed into longer strands. At some point, these clumps of RNA acquired membranes, forming a simple “protocell,” and the protocell somehow acquired the ability to replicate, and eventually to store coded information and translate that information into useful proteins or some primitive equivalent.

The real question for this or any other hypothesis on the origin of life is, how could these things happen, so that we arrive at the equivalent of the first living cell? It’s one thing to tell a story of how it could have happened, but quite another to show that it’s actually feasible. There are enormous hurdles along the way.

Let’s conduct a thought experiment in the laboratory of our mind, so we can gain a better understanding of the kind of challenges nature would face in getting anywhere close to the cell as we know it.

Everyone deserves to know what those hurdles are and whether nature really can overcome them on its own – especially atheists, because atheism is committed to the assumption that life arose by itself, without any supernatural interference.

I think it’s also a good idea, at least once in a lifetime, to carefully examine the basis of our own worldview and assumptions, to see if they stand up to deeper scrutiny. This is true just as much for believers as it is for atheists; and I think now is the perfect time to carefully examine the assumption that life came about on its own.

In our thought experiment, we will create a simple “protocell,” a very basic version of a cell with just a few critical features. We will start by giving it a simple membrane that keeps any inner machinery separate from its environment.

Inside our protocell, we will place a molecule that has the potential to store information. It will probably be an RNA molecule, but it might be DNA or maybe something more primitive, so we will simply call it the “master molecule” – for reasons that will hopefully become clear in a short while. To begin with, the master molecule doesn’t contain any useful information.

In a real cell, each unit of a DNA or RNA strand is called a “nucleotide.” We could think of a strand of RNA as a string of beads on a necklace, each individual bead representing a nucleotide. To help us shift away from our thought experiment and back to real biology later on, I will also stick with the term “nucleotide” to describe an individual unit making up the master molecule. In other words, the master molecule can be thought of as a string of nucleotides.

We’ll also assume that each nucleotide can be one of four bases, just as RNA uses the four bases adenine (A), cytosine (C), guanine (G) and uracil (U) – although there’s no reason to suppose a primitive protocell would use the same ones. In any case, if the master molecule is like a string of beads, then we could think of each individual bead as containing one of the letters A, C, G or U. We will start with a “blank” master molecule, which I suppose means that each nucleotide is the same letter, so

there isn't any useful information in the initial sequence of letters, just as blank digital media might start out full of 0's before any meaningful information is stored in it.

We will also grant our protocell the ability to replicate – that is, to duplicate itself in its entirety. This feature isn't coded for in the master molecule, which we have assumed to be blank. The ability to replicate and build a membrane need to be intrinsic chemical features of the protocell somehow. We will leave these processes unexplained for now, and just assume the protocell can do them.

Furthermore, we'll assume that during replication, errors sometimes occur. As a result, the sequence of nucleotides in the master molecule of a replicated protocell might differ slightly from that of the original. In evolutionary terms, this would be the equivalent of a mutation.

Finally, let's assume we have just the right environment for a virtually unlimited number of these protocells to come about through replication. We don't want our thought experiment to hit any space or resource constraints.

I have made a lot of important assumptions here, and I haven't explained how these features came about. In a sense, I have already given the race to life an unfair advantage. I have done this for the sake of pressing on with my main arguments. For the moment, let's just assume the protocell has these features, and get on with unleashing it into the environment of our thought laboratory, so we can watch as it replicates to become thousands, then millions, then billions, and then trillions of protocells. What happens? Do we get anything interesting?

What we find is, all of the protocells look essentially the same. This is because, to evolve into anything even slightly different, the master molecule must become more than just a place to store information. It also has to become a laboratory of innovation, and a primitive factory where new machinery can emerge. This is why biologists favor RNA molecules in the origin of life. RNA sequences have the potential to store information, and certain sequences can also perform other useful functions.

For our growing colony of protocells, a slightly better membrane or a more efficient replication process might evolve. However, we have assumed these things are purely chemical in nature to begin with, rather than being controlled by the master molecule, for reasons that will become clear in a little while. This means there aren't any blueprints stored away in the protocell for building a membrane or anything else. To begin with, the protocell must somehow manage without them.

Innovations requiring a blueprint therefore need to evolve in the master molecule, because as well as being the source of any new machinery that can help the protocell to survive, the molecule can also act as the protocell's memory bank, the place where blueprints can be stored. This is why I called it the "master molecule." It's where the real evolutionary action needs to happen.

Now, we have already granted our protocells one tool of evolution – the ability of its master molecule to mutate whenever replication happens. Incidentally, it's worth keeping in mind that mutation isn't really a tool or feature as such, but rather, it's the result of occasional copying errors in the replication process.

Another useful tool would be natural selection. If mutations can eventually produce a useful new function from the master molecule, one which can give a protocell a survival edge, the offspring of that protocell could perhaps inherit that advantage, and eventually their offspring could become dominant in the colony as a whole. But in order to find such an advantage in the first place, our colony of protocells has to perform what I call a “natural search.”

To explain what I mean by this, let’s suppose the master molecule in each new protocell is able to store a number in digital form, but it only has room for a sequence of six digits from 0 to 9. In other words, it can store a number ranging from 000000 to 999999. Each time a protocell replicates, the number is copied over to the new protocell, with one digit changed, the equivalent of a mutation.

For example, let’s start with a protocell storing the number 000000, which we will assume contains no useful information, so is “blank.” After replicating, the protocell copy might be storing the number 020000, because one number has mutated in the replication process. In turn, a copy of the copy might have the number 027000. A copy of the copy of the copy might have 027300, and so on.

Now, let’s say that the number 123456 would somehow give the protocell a survival advantage. How long would it take our colony of protocells to produce one with the number 123456 in it? It might happen very fast, but it could also take a while. However, as our colony grew larger and produced a greater variety of numbers, we could expect the 123456 sequence to be found more quickly.

This is a very simple example of what I mean by a “natural search.” The colony of protocells isn’t actively searching for the number 123456. It doesn’t particularly care for our thought experiments, and individuals in the colony are just getting on with the business of being imaginary protocells. But collectively, the colony is engaging in the equivalent of a search for the number, new generations producing mutated numbers until one protocell happens to hit on the sequence that will help it to survive better.

This is why I call it a “natural search.” I’m using the word “search” in the same sense that evolutionary theorists use the word “selection” in “natural selection.” Individuals aren’t deliberately searching or selecting. It’s a natural process that can take place in large populations.

For natural selection to apply to our colony of protocells, they first have to perform some natural searches, to find new functions that give some protocells an advantage. If the master molecule consists of RNA, then the protocell colony isn’t searching for numbers like 123456, but for RNA sequences that can perform some useful function, either on the master molecule itself, or in the protocell. Instead of the numbers 0 to 9, we can think of RNA sequences as made up of the “letters” A, C, G and U which represent the chemical bases used in RNA.

Incidentally, how many nucleotides in length do we make the master molecule in each protocell? What is its storage capacity? We didn’t specify this at the beginning of our experiment. For example, if we make it just 10 nucleotides in length, it can store the equivalent of 10 letters made up of A, C, G and U, ranging from AAAAAAAAAA to

UUUUUUUUUU and every variation in-between, such as CAUGGCAAUC. There are over a million possible variations.¹

However, this tiny length probably isn't enough to store or produce any useful new functions. As we increase the storage capacity of our protocells, we also increase the number of variations available to our colony in a natural search. Each time we add one nucleotide of storage capacity, we multiply the number of potential variations fourfold. For example, if we go from 10 to 11 nucleotides, we go from about one million to about four million possible variations. If we add another nucleotide we have about 16 million possible variations.²

The problem here is, as we continue to add more nucleotides to the master molecule, the number of possible variations quickly gets out of hand, so that by the time we reach a length of just 150 nucleotides, there are more variations available than there are atoms in the universe!³

This means, if we wanted to find a specific RNA sequence that was 150 letters long using a natural search, even if we were somehow able to stuff every atom in the universe with a protocell, we would still have a very hard time finding the sequence.

To put our protocell storage capacity into some kind of perspective, there are about 3 billion "letters" in a human DNA molecule, and several million in the DNA of a typical bacterium. Therefore even a 150 nucleotide storage capacity for our protocells would be pitifully small compared to a real cell.

However, storage size isn't our main concern, because we can always add more nucleotides. What matters is, for our colony to come up with the first useful new function by itself, the length of the nucleotide sequence which makes up the function needs to be small enough that our colony doesn't have to search for it using all the atoms in the universe – which, for obvious reasons, might be a bit impractical. Even though this is simply a thought experiment, we still want it to have some relevance to the real world.

A natural search is probably the only way our colony of protocells can acquire many new functions and RNA sequences, assuming we don't put them in ourselves, since the process of natural selection can't really begin until nature has something useful to select from. In other words, some basic functions probably need to come into existence from scratch, rather than evolve out of already existing functions, because in the primitive RNA World, there aren't many functions around in the first place!

Now, in the language used by biologists, the complete genetic sequence of an organism is called its "genome," and this is stored mainly in the DNA molecule. But at the moment, the nucleotides in each master molecule of our rapidly growing protocell colony don't actually code for anything. Therefore, the protocells don't really have a genome as such. At best, all they have is a potential one.

Until they evolve the kind of machinery I'll discuss shortly, all that can happen to our protocells is, certain bits and pieces of the master molecule might possibly mutate

to become little RNA machines. But to even begin getting close to cells as we know them, our protocells need the equivalent of a language or code.

In a real cell, the language of DNA is called the “genetic code,” and it is quite elegant. Three nucleotides in a row (such as AAA or AGC) make up one “codon,” and one codon usually represents an amino acid. For example, the AAA codon translates into an amino acid called lysine, and GGG codes for glycine.

Since three nucleotides make up one codon, and DNA uses four bases (A, C, G and T), there are 64 possible codon variations, ranging from AAA to TTT.⁴ This means the genetic code has room to code for 64 different amino acids. However, only 20 are actually coded for directly in a DNA sequence, with a few more included later in the system. Many amino acids are represented by more than one codon. For example, the codons GGG, GGC and GGA all code for glycine.

As you may recall, a DNA sequence is copied, or “transcribed,” into an mRNA strand. The mRNA strand is then read, or “translated,” by a ribosome, turning the codons into a chain of amino acids – so if the ribosome encounters a GGG, GGC or GGA codon, glycine gets added to a chain of amino acids that will make up a protein.

Why does our genetic code only use 20 amino acids, when it has room for 64? At first, biologists thought this was inefficient, and referred to it as “degenerate.” But it turns out to be a very clever system. It reduces the likelihood of producing the wrong amino acid. Coders and engineers call this “redundancy.”

Let’s say the third nucleotide in a GGG codon is accidentally mutated and becomes GGC. The redundancy of the genetic code means the same amino acid will still be produced, because both GGG and GGC code for glycine. In other words, the redundancy is a feature, meant to reduce errors. Furthermore, research has shown that, compared to a million other coding schemes, our genetic code is optimal for minimizing errors in many ways.⁵

Of course, our hypothetical protocell couldn’t start out with a genetic code, because that would be cheating even more than we have already done by giving it the ability to replicate. However, at some point it will need some kind of genetic code, if it’s going to begin storing information in the master molecule that can then be read and translated into something else.

Incidentally, I will use the words “language” and “code” interchangeably from now on, because both contain the properties we need, to turn data into something useful.

In a living cell, ribosomes and “transfer RNA” (tRNA) molecules do the job of turning coded information in an mRNA strand into a protein. If our protocells are going to evolve into anything that resembles a cell, they will need machinery equivalent to a ribosome. However, ribosomes as we know them are very complex machines, built out of multiple RNA strands and proteins that, in the language of DNA, require tens of thousands of nucleotides worth of data to construct.

One of the reasons biologists think some kind of RNA World must have existed in the past, is because the core of a ribosome seems to be made primarily out of RNA,

rather than proteins. Biologists interpret this as evidence that the primitive ribosome was made entirely of RNA. But is there an alternative explanation? For example, could this be a design feature? If so, why would it be this way?

The ribosome is the machine that makes proteins. If ribosomes stopped working in a cell, proteins couldn't be made; and if ribosomes were made out of proteins, the cell would die, since it couldn't make any new ribosomes.

However, since they are made primarily out of RNA, in an emergency scenario where the old ribosomes stopped working, the cell may still be able to put together new ones, and thus continue with protein production. In other words, that the core functions of a ribosome are made primarily out of RNA is perhaps an emergency fail-safe system to prevent the cell from dying if old ribosomes stopped working.

Basing the ribosome on RNA also solves a chicken and egg problem. If ribosomes were built out of proteins, and proteins built by ribosomes, which does the cell build first? It couldn't build proteins without ribosomes, but it couldn't build ribosomes without proteins. Therefore, it builds the core of a ribosome out of RNA strands instead, avoiding the dilemma.

In addition, if certain amino acids aren't available from the environment, this could disrupt the availability of proteins, but would have less effect on the construction of ribosomes, which are essential for making any proteins at all.

In other words, the construction of ribosomes primarily out of RNA could be a smart feature, designed to reduce the possibility of a cell dying, and to give it more flexibility at times when certain resources aren't available.

Whatever the case, in our thought experiment we can't simply gift ribosomes to our protocells. This would be cheating. However, this is what some researchers do. When creating "artificial" cells, they add in components such as ribosomes that have been extracted from living systems, because they know cells need to be able to read and translate information.⁶

The same is true for our protocells. If they are going to be able to read and translate information from the master molecule, they will need something equivalent to a ribosome. Of course, it would be much more primitive than a ribosome as we know it, but it must still be able to read the master molecule, and translate the information into something useful for the protocell.

However, this creates several dilemmas for our protocell experiment, and by extension, for any naturalistic theories on the origin of life.

First of all, if master molecules don't contain any coded information, there would be no need for a ribosome to evolve to do any translating. The master molecules might contain sequences of RNA that do interesting things, but these sequences wouldn't be coded proteins.

Second, if master molecules did contain information worth reading, if our protocells lacked the machinery to read and use the information, it wouldn't give the protocell any survival advantage and so would be mutated away.

We might choose to insert the complete works of Shakespeare into one particular master molecule, but unless the protocell can access the information and do something useful with it, Shakespeare's works would gradually mutate away into oblivion over many replication cycles, because our protocells don't care about great literature. It has no survival value to them.

Third, a protocell can't store or translate coded information in its master molecule without a genetic code, a language in which to read the information. But it wouldn't evolve a genetic code unless there was useful information written down; and if it's not useful, it would be mutated away. Without a genetic code, a GGG sequence in the master molecule wouldn't code for anything. It wouldn't be a codon for the glycine amino acid, it would just be three guanine (G) nucleotides.

In our own cells, tRNA molecules are the little machines that store the genetic code. Each of the amino acids used to make proteins has a corresponding tRNA molecule that carries it to the ribosome. For example, one particular tRNA molecule has, at one end, an "anticodon" that matches up with a GGG nucleotide sequence, and at the other end, it carries a glycine amino acid.

If a ribosome encounters a GGG codon while reading an mRNA strand, this type of tRNA molecule finds its way into a binding site in the ribosome, pairs up with the GGG codon, and the glycine amino acid it carries gets added to a chain. This is how GGG codes for glycine. Codons are simply instructions letting the ribosome know which amino acids are to be added to a chain. But without something like a ribosome and a genetic code stored in tRNA molecules, GGG is just GGG. It doesn't code for anything.

To sum up these three dilemmas: in the hypothetical RNA World, information can't be encoded in the master molecule, since there is no genetic code in which to encode it. RNA sequences have no reason to evolve protein-building equipment such as a ribosome, since there is no encoded information to extract from the master molecule. And even if there was, without the equivalent of a ribosome and a genetic code to translate the encoded information into something useful, the information would be mutated away.

This is why many theorists tend to skip over the precise details of how something like a master molecule, complete with the language to encode information, and the equipment to decode that information, actually came to be. They chalk it up to incredible luck, or brush it off with a little storytelling.

Fortunately, we don't need to rely on theories or stories. There is a way to put all of this to the test. To begin with, an engineer could design a minimally functional equivalent of a primitive ribosome. We don't want evolutionary theorists saying it evolved out of an even simpler ribosome, so ask the engineer to make it as simple as possible.

Presumably it would be very crude in comparison to a real ribosome. It just has to be capable of reading a sequence of nucleotides, and building something physical based on the sequence, in a consistent manner. We won't quibble if there is a slightly

simpler design available. We just want something that consistently translates information in nucleotides into something physical and potentially useful for the protocell.

For example, let's say our primitive ribosome can read a guanine (G) nucleotide, and then somehow attract a specific amino acid to itself, which begins to form a chain. It can also read an adenine (A) nucleotide, attracting a different amino acid which can be added to the chain as well. Keeping it fairly simple, let's say it completely ignores uracil (U), another base used by RNA, and it breaks the chain of amino acids when it encounters a cytosine (C) nucleotide.

In other words, this primitive ribosome uses a very simple genetic code. It can only process a couple of amino acids, while the human genetic code handles at least twenty. The machinery for this primitive ribosome may be crude, but the important thing is, it does something roughly similar to a real ribosome.

An engineer can design it and tell us the minimum number of parts required, and what those parts would need to do. Biologists can then tell us the precise RNA strands that would be needed for the whole thing to actually work in a protocell.

I suspect this is vastly more difficult to achieve in real life than it might sound on paper. Think about what we need our primitive ribosome to do. First it has to somehow connect to the master molecule. Then it has to move along the molecule one nucleotide at a time. It has to know which amino acid corresponds to which nucleotide base. It has to attract the relevant amino acid somehow, then add it to a growing chain of amino acids, and then break the chain when it encounters a cytosine (C) nucleotide. Think of the chemistry and engineering required to get our primitive ribosome to do any one of these things, let alone all of them together!

An intelligent engineer may be able to design this, but what we're really interested in is whether nature could do it by itself. Evolutionary theorists might say that natural selection could allow it to be built in a gradual manner, but nature can only select from what is available at the time. If our protocells don't yet have even the crudest ribosomes, then protein-based machinery can't be built for natural selection to test out. All nature can do is wait around until a new function mutates in and then somehow comes out of the master molecule.

As our imaginary colony grows to include enormous numbers of protocells, useful RNA sequences might perhaps mutate in a few master molecules now and then. The critical question is: could they eventually form a primitive ribosome, given enough time? I would suggest the answer is no. There are three reasons why I would argue it's actually impossible for them to do this.

The first reason is the set of dilemmas I posed earlier. Without coded information, there would be no need for a ribosome to evolve. If RNA sequences are already acting directly like primitive proteins, they wouldn't need to invent anything like a ribosome. And with no ribosome, there would be no need for a genetic code. And with no genetic code there would be no coded information.

In other words, coded information, a ribosome and a genetic code all need to be in place for proteins to be made, and proteins are a critical part of cellular life as we know it.

In the primitive ribosome I described a few moments ago, I bypassed the need for codons altogether, and had one nucleotide such as guanine (G) represent one amino acid. This presumably makes the whole thing easier to evolve early on, but it creates an enormous problem later, because how do we switch from a system where a single nucleotide represents an amino acid, to one where three nucleotides do?

If we alter the genetic code, we substantially change the meaning of any coded information previously stored away. For example, let's say we have a GGG sequence stored away in a master molecule. In our primitive ribosome, one G represents glycine, so the GGG sequence would code for three glycine amino acids.

But in the human genetic code, a GGG sequence represents one glycine amino acid. In other words, the different genetic codes would produce very different proteins. Altering the code would substantially change the meaning of any genes stored in the master molecule. It can't evolve without essentially breaking the proteins that have already evolved. This is why Francis Crick called the genetic code a "frozen accident." Nature must have hit upon a good code early on, since most organisms use roughly the same genetic code, with some fairly minor variations.

The second reason I don't think RNA sequences could form into ribosomes by themselves is an even more formidable obstacle. In an animal or plant cell, ribosomes are assembled in a giant manufacturing center called the "nucleolus." The pieces are assembled in the right order at the direction of control mechanisms and sequences that are written into the cell's blueprint.

Our protocells don't have a ribosome manufacturing center. Even if the necessary RNA pieces to make a ribosome somehow all evolved, were available in a protocell, and luckily assembled themselves into the equivalent of the first primitive ribosome (despite not having any reason to, since there was no information that needed decoding), what would hold all of the pieces together in this arrangement for its offspring? How would future generations know how to build the ribosome? There would be no blueprint, no "How To Make a Ribosome" manual.

Many theorists suggest that the primitive ribosome was self-replicating and self-assembling. It could somehow make a copy of and assemble itself. I suppose if we could get one or more of these into a protocell, then assuming the protocell was able to divide, and the ribosome was also able to self-replicate at roughly the same rate, new protocells would presumably also contain these ribosomes.

This would solve the problem of how our protocell puts together a ribosome. In short, it doesn't. The ribosome puts itself together all by itself.

The idea of a self-replicating, self-assembling ribosome sounds great in theory, but I think it would be very difficult and perhaps even impossible to achieve in reality. It would be the equivalent of designing a complex machine comprised of many parts,

that could replicate itself using only its own parts as a blueprint, that was then able to assemble those parts into the same form after each replication.

If theorists think this is easy, maybe they should first ask engineers to design a machine that not only acts like a primitive ribosome, but is also self-replicating and self-assembling, so we at least have proof of concept. Then biologists can tell us the exact RNA sequences that would be needed to make this machine at the molecular level. Personally, I suspect a self-replicating, self-assembling ribosome is actually impossible.

But wait a minute. Living cells are self-replicating, so why can't this be true of primitive ribosomes? The critical difference is, cells have access to detailed blueprints encoded in the DNA molecule, and they have all of the machinery they need to make copies of themselves. The cell's ability to self-replicate requires a lot of equipment and information! This is why the genomes of self-replicating organisms are typically millions or even billions of nucleotides in length.

In other words, a self-replicating, self-assembling ribosome would be an engineering miracle, which I suspect even human engineers may find impossible to design. But if they could actually achieve this, they would be showing us the exact level of engineering knowledge required, and the size of the blueprints needed, to create such a machine. They will have also created something that nature itself isn't using, since ribosomes in real cells are built by machinery other than itself, and so they are neither self-replicating nor self-assembling.

But if the first ribosome was neither of these, and instead came about through a lucky arrangement of RNA sequences, this arrangement would break down in later generations, because the blueprint for putting it together couldn't be written down. It would be like one of those good ideas you've had, that you forgot the next day because you didn't write it down.

However, the third reason why RNA sequences couldn't build a sustainable ribosome is perhaps the most formidable challenge of all. It's to do with the process of mutation itself. Mutations are necessary for new RNA sequences and useful functions to evolve, but in the RNA World, mutations would also destroy those things.

Cells as we know them employ several error correcting strategies when dividing, to minimize copying errors and therefore bring the rate of mutation down substantially. But we can't just give our protocells this ability, for the same reason we can't just gift them with ribosomes. If we did, that would be intelligent design, the opposite of the idea that life arose by itself.

A useful RNA sequence might evolve, and give a protocell an immediate survival advantage, but without error correcting, this advantage will be mutated away in later generations. Natural selection might help, but if the mutation rate is too high, which is very likely without error correcting to reduce it, any small innovations will be swept away faster than natural selection can keep up.

This paradox is acknowledged by biologists, and is often called the "error catastrophe" problem. It is usually framed in terms of the length of a functional

nucleotide sequence. Without error correcting, its length would be very limited, because in larger molecules, mutations would eventually destroy the information content for subsequent generations. But paradoxically, the maximum size available without error correcting would be too small to encode an error correcting process.

In other words, the error correcting code would take up more nucleotides than would be available to encode this information in a stable manner. Ideas have been suggested to help solve the dilemma, but they are theoretical, and other biologists have pointed out that the mechanisms proposed still suffer from loss of information.

Furthermore, in real cells, error correcting is performed by machinery made out of proteins. But these protein machines can't begin to evolve without ribosomes and a genetic code to make the proteins. All of these emerging functions will be mutated away without error correcting to preserve them.

Many origin of life theorists recognize that error correcting is one of the first problems nature has to solve, because without it, protocells can't hold on to any newly evolved advantages. For this reason, researchers hope to find a suite of RNA sequences that could perhaps perform error correction quickly and efficiently, without any need for complex proteins. I suppose they might exist, and come to be intelligently designed in a laboratory setting.

But whatever the case, without error correcting functions, emerging RNA sequences that could potentially be useful would be destroyed by mutations in later generations. This would make the evolution and long term sustainability of a complex machine such as a ribosome impossible.

Furthermore, until researchers have found this magical suite of RNA sequences that provide error correcting, we can't know how likely or unlikely the whole suite is to emerge without somehow mutating away.

Let me sum up the three reasons why I think a ribosome would never emerge out of RNA sequences from the master molecule, no matter how many protocells we had or how much time we allowed. First, RNA sequences have no need for a ribosome or a genetic code, and they don't have foresight, so they wouldn't even begin to assemble a ribosome.

Second, even if protocells did assemble a primitive ribosome, they would have no way to pass on the blueprint to future generations. The idea that they might be self-replicating and self-assembling sounds great on paper, but would be an engineering miracle in real life.

Third, there would be no way to keep any of these things around for the long haul without error correcting functions. Mutations would rip them apart faster than natural selection can preserve them.

Now, if a ribosome can't emerge on its own out of RNA sequences in the master molecule, could it have perhaps evolved out of the protocell's replication process? In our thought experiment, we granted protocells the ability to replicate, mainly to get the show started. But now it's time to give more serious consideration to how they actually do this.

If replication involves fairly simple chemistry that is somewhat independent from the rest of the protocell, then the process probably wouldn't have much to offer in the evolution of a ribosome, which would need specific functions and machinery.

However, if the process of protocell replication is controlled somehow by the master molecule, this is a very different story. The control sequence would be complex, and take up at least several thousand nucleotides worth of information. But where did this information come from?

This is why I was only willing to grant protocells the ability to replicate if it was a simple chemical process not controlled by the master molecule. If the process is governed by machinery and some kind of blueprint, then their existence would need explaining. If we just granted our protocells these things, this would clearly be intelligent design. But without them, how would the protocell replicate in the first place, to allow even a crude form of evolution to get started?

I suppose we might argue that the replication process could be entirely controlled by RNA sequences and machines. However, this presents us with two critical dilemmas. First, how would the RNA sequences know how, where and when to perform their functions? Would they be working to some kind of a blueprint? If so, how is the blueprint read and interpreted? Or do they all just happen to perform the same cascade of activity every time?

Again, this would need to be tested scientifically. Biologists and engineers could team up to tell us the precise RNA sequences that could perform this magical cascade which enables them to replicate themselves and build a protocell every time.

Personally, I think designing such a protocell is an incredibly tall order, and may even be impossible without endowing it with lots of machinery and blueprints, which would be evidence that intelligent design was required. After all, nature itself tells us that a self-replicating cell requires a genome, ribosomes and a genetic code. There is nothing in nature that equates to a protocell. Even a virus, which is perhaps closer to a protocell in some respects, isn't truly self-replicating, because it needs to hijack the equipment from a cell.

Either way, this is still nothing compared with the second dilemma for a replication process controlled by RNA sequences: what happened before the necessary RNA sequences evolved? How did the protocell replicate before this?

Evolutionary theorists argue that new functions usually evolve out of previously existing functions, but there aren't many functions around in RNA World, and besides, there can't be an infinite regress of simpler replication processes. That would be just as absurd as an infinite regress of creator gods. But without a self-replicating protocell, there can be no evolution. Indeed, the only way to evolve the RNA sequences needed to make a replicating protocell is to have lots of replicating protocells, so that RNA sequences can evolve. Clearly this is a problem!

What I have shown so far in this chapter is that naturalistic theories about the origin of life face several enormous dilemmas, and have to make several assumptions. If we wish to believe life arose on its own, we first need to assume that just the right

environment existed, and that the raw materials for life were available. It's one thing to create a chemical reaction in a laboratory under highly controlled conditions, but quite another to achieve it in a natural environment.

We need to assume that some kind of protocell existed, the forerunner of a cell, and that it had some information storage capacity, such as an RNA or DNA "master molecule," having the potential to contain genetic information.

We have to assume the protocell was somehow able to replicate. But the process couldn't be controlled by instructions or coded information in the master molecule, because that would require the existence of machinery to read and interpret the information.

We can assume that in the process of replication, mutations to the master molecule happened, allowing for variation and therefore the possibility of natural selection. We also need to assume that some parts of the master molecule emerged to act somewhat independently, and become little machines, but without any complex machinery like a ribosome to manufacture them.

These assumptions are necessary just to get things started. After that, we arrive at the real challenges, although each of the prior assumptions are huge challenges in themselves.

Without some kind of error correcting process while the cell is replicating, mutations will make the protocells unstable. Useful RNA sequences might emerge, assuming the master molecule is made of RNA, but the high mutation rate means they would be destroyed in later generations. Error correcting functions can't be arrived at either, because they will also be mutated away beforehand.

An origin of life theorist can make up a story about how "a simple error correcting process evolved and was able to confer an advantage on the early protocell," but this is devoid of any actual details. Engineers are better suited to tell us what such a "simple" process would actually involve, and what functions and equipment would be needed to do it. Then biologists can tell us which collection of RNA sequences could do the job, and demonstrate it in the real world.

Incidentally, in most cells as we know them, the separation between DNA and RNA provides the cell with an additional layer of stability. True, DNA can actually be altered by the cell, so it isn't just a read-only system as biologists initially thought. But deliberate changes made by the cell are highly regulated. Thus, the DNA molecule provides the cell with a stable blueprint for the equipment it needs, while disposable mRNA transcripts of DNA sequences are used to make proteins.

But protocells can't be granted this luxury. They aren't anywhere near as sophisticated. The entire system is unstable. If RNA machines evolve directly from the master molecule, then when they come out of it to perform their functions, they may end up breaking the molecule. If they somehow cut themselves out of the master molecule before the replication process begins, the duplicated master molecule won't have them in! But if they are separate from it, or self-replicating, then what

mechanism enables them to later create a blueprint for their own construction that can be written into the master molecule?

Another enormous challenge for our protocells is to evolve something like a ribosome. Without these, proteins can't be made and our protocells wouldn't even evolve into anything resembling bacteria, let alone creatures like birds and butterflies.

But how could a ribosome come about? Without a ribosome and a genetic code, there can't be coded information. But without coded information and a genetic code, there is no need for a ribosome to evolve.

Even if a ribosome fortuitously emerged in a lucky protocell, how would future protocells know how to build it? Cells rely on blueprints to build machinery, but our protocell would have no way to write up the blueprint for a ribosome to pass on to its offspring.

If the ribosome was self-replicating, it would be a miraculous invention. The machine would need to move along a sequence of nucleotides one at a time, attract a specific amino acid corresponding to the nucleotide, build a chain of amino acids, and break the chain when encountering another specific nucleotide. Furthermore, it would need to be able to build an exact duplicate of itself, without referring to a blueprint.

Origin of life researchers have made self-replicating RNA strands, but this is still a world away from designing a self-replicating protocell with a primitive ribosome that hasn't been extracted from actual cells, which would be cheating. If and when they finally achieve this, it will demonstrate the sheer amount of chemical, biological, engineering and coding knowledge needed to design even a "simple" self-replicating protocell.

But it's much easier just to assume the protocell was able to replicate, store information, read that information and translate it into something useful, without giving the details of how it acquired all of these abilities, other than glib stories. All of these things are assumed to have happened because, after all, life exists.

Of course life exists. The critical question for all of us is whether it arose by itself, or whether some kind of intelligence designed it. The dilemmas faced in the origin of life would be much more easily solved if there was a chemist, physicist, engineer and computer programmer behind them. It's easy to say that life came about on its own, but far from easy to demonstrate how the complex machinery for even the simplest cell came together.

I have also bypassed other critical features of the protocell, which I will briefly mention here. For example, how does it get access to the raw materials needed to build the things we have been talking about?

Humans have it easy. We only have to eat food, drink water and breath air, and that is the job of survival sorted out, at least in a basic sense. Our cells, organs, and the bacteria that live in our body all do the hard work of turning those inputs into useful energy and components. What they do every moment of every day makes humans look like lazy sloths by comparison.

Obviously a protocell couldn't be anywhere near as complex as our own cells, but it would still need processes to access raw materials, and turn them into energy or building blocks. Little RNA machines may be able to do some pretty interesting things, but could enough of them evolve quickly enough to create a system of metabolism, before being mutated away? And how do they even begin to do any of this, without the ability to convert raw materials into energy in the first place?

Furthermore, many chemical processes in living cells require a catalyst, something that dramatically increases the rate of a chemical reaction. These are often in the form of proteins called "enzymes" (from the Greek word meaning "leavened"), but some RNA sequences can also act as catalysts, and this class of sequences are given a special name, called "ribozymes."

Without catalysts, many chemical processes would be painfully slow, and in many cases the cell would die long before the process was completed. Many of these processes require more than one ribozyme to act as the catalyst, so what would happen to the process before the required catalysts evolved? It would be mutated away, since only the addition of catalysts would make it useful.

The problem of explaining the origin of life was summed up by one synthetic biologist as being about finding the solution to four paradoxes.⁷ The first is the "tar" paradox, the tendency of organic matter to devolve into tar, or asphalt. The second is the "water" paradox, that every interesting chemical bond is unstable with respect to water. The third is the "entropy" paradox, that nature likes to break things up, but any theory on the origin of life has to assemble larger and larger building blocks that fight entropy. The fourth is the "destruction" problem, that RNA sequences acting as catalysts are more likely to be active in a destructive sense, rather than a creative one.

Most or even all of the dilemmas and paradoxes faced by the RNA World hypothesis are also faced by the alternative ideas put forward, with the exception of one – that is, the idea that the cell was actually designed.

In this chapter, I haven't disproved the idea that life arose by itself, and neither have I proved that it came about through design. What I hope to have demonstrated is that the many dilemmas only exist when we insist on looking at life from the assumption that it arose by itself.

Origin of life scientists often like to give the impression that they are on the verge of solving life's deepest mysteries. This certainly helps with publicity and funding. In reality, the reason there are so many hypotheses about life's origins is precisely because of the dilemmas I've highlighted. Even the "RNA World" hypothesis has been described by one biochemist, slightly tongue-in-cheek, as "the worst theory of the early evolution of life (except for all the others)."⁸

Since no human was around to witness the origin of life, we shouldn't be surprised that different ideas exist. But then, why shouldn't design also be a valid idea? The fact is, many complex processes are required in order to put together even the simplest living cell: replication, metabolism, error correcting, a genetic code, the

ability to store, read and interpret information using that code, encoded proteins, blueprints for machinery, and so on.

If humans were to try and put together such things from scratch, it would require a high degree of physics, chemistry, engineering and coding knowledge; and even our smartest and best scientists would struggle to emulate these things.

Yet even before they were able to break open the cell and explore its contents, many biologists already assumed they knew how it came about. It must have arisen by itself. Wasn't that a little presumptuous, more akin to a religious belief or ideology, rather than actual science? But we already know part of the reason why. At least when working for a scientific establishment, biologists have to accept the Naturalistic Assumption, which excludes a designer by default.

The English clergyman William Paley argued that if we came across a watch on a beach, we would assume it had not arisen by chance, because we would notice how complex it was, and how its parts worked together purposefully. He used this as an argument for the existence of God. He reasoned that, since the world exhibits greater complexity than the watch, life also cannot have arisen by chance.

Then naturalists like Charles Darwin came along and argued that complexity can be explained by natural selection and large amounts of variation, which later biologists attributed to mutations in the DNA molecule of organisms. They argued that what we see is merely the illusion of design.

But in the origin of life after it supposedly emerged from non-life, mutations and natural selection aren't adequate explanations. Mutations would break things before anything beneficial could gain a foothold, and nature can't select from things that don't exist. New functions can't be preserved unless they are stored in blueprints, but the blueprints can't survive unless the emerging cell can read and do something useful with the information. Evolution can't even get started, without multiple complex mechanisms already being in place.

On the other hand, intelligence combined with a high degree of physics, chemistry, biology, engineering and coding knowledge could conceive, design and create a complete working cell, with all of its metabolizing, replicating, coding, decoding and manufacturing features. Indeed, this is partly what origin of life scientists, using their knowledge and intelligence, are trying to do in their labs, even though they often use parts extracted from real cells.

In other words, at least in the origin of life, perhaps the best explanation is not that design is an illusion and life merely looks designed, but that life actually was designed after all.

1 4 to the power of 10, which mathematicians write as 4^{10} or 4^{10} , is 1,048,576. **2** $4^{11} = 4,194,304$. $4^{12} = 16,777,216$. **3** There are an estimated 10^{80} atoms in the universe, and about 10^{90} possible permutations of 150 letters in an RNA sequence. I use the mathematical term "permutations" here because order matters in an RNA sequence. **4** $4 \times 4 \times 4$ or $4^3 = 64$. **5** Freeland, Hurst, "The Genetic Code Is One in a Million", *Journal of Molecular Evolution*, 1998. **6** As an example, see "Biologists create the most lifelike artificial cells yet", *Sciencemag.org*, November 19, 2018. **7** These paradoxes are discussed by Steve

Benner in an interview with Suzan Mazur, the author of "The Origin Of Life Circus: A How To Make Life Extravaganza". Page 151. **8** Bernhardt, "The RNA world hypothesis: the worst theory of the early evolution of life (except for all the others)", *Biology Direct*, 2012.

48. The Nucleotide Shuffle

Let's now turn our attention to real cells. The entire genetic sequence of an organism is usually referred to by biologists as its "genome." The genome of an organism contains the blueprints for proteins, and these blueprints are stored in an encoded form within a DNA molecule. When the cell needs to make a particular protein, the blueprint for it is transcribed from DNA into a strand of mRNA, and then a machine called a ribosome reads this strand and translates it into a chain of amino acids. This chain is the protein, and it usually folds up into a shape that is useful to the cell. Most of an organism's body is made up of different proteins.

Now, let's imagine for a moment that a smart and enterprising young ribosome happened to stumble upon an idea for a better protein or a more efficient ribosome. Could it pass the idea on to others? Not really, because it is just one of several thousand ribosomes in a single cell. Even if it could somehow convince its peers to adopt the new process, the invention wouldn't be taken up by the next generation.

Our inventive ribosome would somehow need to convince the DNA bosses, sitting in their plush cellular offices, to write the blueprint for a better protein or ribosome into the DNA itself, so that the update could be pushed out to future generations. In the case of sexually reproducing organisms, it would have to be written into the DNA of sperm or egg cells, because this is what is passed on from generation to generation.

In other words, from an evolutionary point of view, the only changes that matter in the long run are those affecting the specific DNA inherited by future generations of cells.

Now, when the entire genome of a cell is copied, the sequence of nucleotides it passes on to the next generation might turn out to be a little different from what the original cell inherited. A mutation can happen, which may be the result of a copying error, or damage to the sequence from sources such as radiation.

A common form of mutation is when a letter gets switched for another letter, like a scribe getting a letter wrong while copying a document. Sometimes letters can also get accidentally removed or added. Less common mutations include duplication of one or more letters, like copying and pasting in a word processor. The DNA copying machine has a proofreading system to make sure these errors are minimized, but mistakes still sometimes get through.

Changes to the genome can also be made in more organized ways. For example, in a process called "horizontal gene transfer," bacteria are able to take DNA from their environment or from other bacteria, and transfer it between themselves. This allows replicating organisms to avoid something called "Muller's ratchet," where populations end up with genetic deletions that can't be reversed. Sexually reproducing organisms avoid this through a process of genetic recombination, where similar sections of DNA from father and mother are exchanged, creating variety while also preserving essential information.

Most mutations are either neutral, meaning they don't have any effect, or they are harmful. According to evolutionary theorists, mutations to the genome provide the raw materials for evolution. Sometimes a beneficial mutation takes place, which gives one particular organism a survival advantage over its fellow organisms. As a result, its offspring are more likely to survive and become predominant within the population. This, in essence, is what is meant by "natural selection." Nature tends to preserve the fittest and sift out the less fit, although "fitness" in biological terms isn't about whether creatures go to the gym or not, but is simply about survival or reproductive advantage.

Any advantage that might help an organism survive or reproduce better must ultimately be the product of a change to the DNA sequence in its genome, because this is what is passed on to future cells. For this reason, we could think of life as a game, where each organism comes with the equivalent of a barcode, the DNA sequence it is able to pass on to its offspring, who will inherit it with perhaps a small tweak here and there. Evolution is really just a game of nucleotides being changed a little bit from generation to generation. I'll call this game the "Nucleotide Shuffle."

As a result, some aspects of evolution simply become a math problem, because it is based on changes to sequences of information, and in some cases this can be modeled mathematically. All we need to do is look at sequences, and ask how we can get from one sequence to another through the shuffling of letters, and over what time frame. This allows us to see what evolution is truly capable of, and what its practical limits are, if any.

If we wanted to evolve, say, a sequence of random English letters into a specific line from a Shakespeare play, how could we do it? We could write a computer program to change one letter at a time. The program could do it very quickly if it knew the line of the play we wished to arrive at, and it was allowed to keep a letter once it matched up with the same letter used by Shakespeare.

But this isn't how evolution works. Evolution doesn't know the outcome beforehand. If it did, this would be directed evolution or intelligent design. Therefore, we would be cheating if we told the program what to find. Natural selection also assumes there are small, cumulative steps along the way, and that each step gives the organism a survival or reproductive advantage, or at least doesn't kill it off. But what advantage does a line of random text with a few altered letters have? What function does it serve?

Changing a random sequence of text into a line from Shakespeare using a computer program is perhaps a reasonable analogy for what evolution might look like with the benefit of hindsight, but we can't use it to show evolution is easy, since the initial random text has no function, the transitional sentences along the way have no function, and the program knew the outcome in advance, which evolution does not.

In the real world, a "sentence" in a genetic sequence used by the cell still has to make sense after a mutation, and each mutation still has to allow the sequence to maintain some kind of function. If it loses its function along the way, natural selection

will no longer help the sequence to evolve and the sentence could mutate into gibberish; and there are infinitely more potential lines of gibberish than there are lines from Shakespeare.

Now, in order to evolve a useful function from scratch, or *de novo* as biologists call it (from the Latin, meaning “of new”), nature has to perform at least some “brute force” natural searches. These are searches over the entire range of possibilities.

For example, suppose you were to buy a combination lock, manufactured with a random three digit unlock code, but then you carelessly lose the piece of paper with the code on it. You could take the lock back to the store, but instead, you decide it would be quicker to find the correct code yourself, since it’s only three digits long.

There are 1,000 possible sequences to try, ranging from 000 to 999. You decide to start with the lowest number and work your way up. What you are doing is a “brute force” search. Searches involving longer sequences are normally done with computers because of the sheer number of permutations involved, but in this simple example, you are doing it manually.¹

You might get lucky. The manufacturers might have set the default unlock code to 000, meaning you would find the correct sequence right away. But they might have set it to 999, laughing to themselves in their plush offices as they did so; in which case, you would have to go through 999 previous possibilities before you found the right one. If they set the default code to a random number, it would be impossible to say exactly how many tries it would take you to find the right code for any one lock. All we could say is that it would take between 1 and 1,000 tries.

However, if you happened to enjoy the process, and decided to spend the rest of your life finding the code to newly purchased combination locks by brute force searches, we could say that, on average, it would take you about 500 tries before you found the right combination for a lock. About half the time it would take you more than the average, and half the time it would take you less.

The point here is this: to find a beneficial mutation that gives an organism an advantage, nature has to “search” through lots of neutral or damaging mutations, much like searching for the correct sequence to a combination lock. When we understand this principle, we can estimate how long a particular change can take, or how many tries it will take nature. Let’s now test this out, as we evolve our very own protein from scratch.

¹ In mathematics, “permutations” are used when sequence order matters, and “combinations” when it doesn’t. Even though we are talking about a “combination lock,” what actually matters here is the number of permutations. Each digit has 10 possibilities, so there are $10^3 = 1,000$ permutations.

49. The Billion Year Experiment

We've established that evolution can be thought of as a game, involving the shuffling of nucleotides in the genome to be passed on to the next generation. This means we can run a thought experiment, to see how many organisms it would take to evolve a new protein within a specific evolutionary timescale.

Let's set up an imaginary bacterial colony in the laboratory of our mind, and have it run a natural search for a protein that bacteria use today. It doesn't really matter which specific protein it is. We just want it to evolve a protein to see how feasible this is, and how many bacteria it will take.

We're using bacteria here because they are single-celled organisms, and they don't take up much space in our thought laboratory, so we will have room for lots of them. Bacteria are also able to replicate very quickly, so we can get ridiculously large numbers of them very fast.

Now, if we're going to round off or simplify any numbers in this experiment, we'll aim to skew them in favor of evolution, so skeptics can't say we're making things more difficult for our imaginary colony than it needs to be.

Proteins used by bacteria today are over 250 amino acids long on average. Our goal will be to evolve a protein that is 240 amino acids in length, for two reasons. Firstly, because this is less than the average protein size currently used by bacteria, so it should be easier to evolve. Second, this number can be divided into lots of smaller whole numbers, which will be useful later on.

We can't tell our colony exactly what to look for in advance, because that would be cheating. On the other hand, we will need to allow a series of intermediate steps, because natural selection is supposed to work through the accumulation of small advantages. Each step gives the organism enough of an advantage that it is better at survival or reproduction somehow, and as a result, the advantage gets spread throughout the population at large.

Amino acids are coded for in the DNA molecule by three nucleotides, which for the sake of simplicity we'll refer to as "letters," so we can say that three letters are needed to code for one amino acid. The protein we're hoping to evolve consists of 240 amino acids, so its DNA sequence would be 720 letters long.

It's basically impossible for nature to find this exact sequence by performing a brute search, or even a fairly civilized search. There are just far too many possibilities to search through.

The "alphabet" of DNA consists of only four letters: A, C, G and T. If you wanted to write a two letter "word" in the language of DNA, you would have 16 possibilities: AA, AC, AG, AT, CA and so on through to TT. For three letter words, there are 64 variations ranging from AAA to TTT. For four letter words, there are 256 possibilities. Each time we add a letter, the number of possibilities grows fourfold.

This might not sound significant, but it is. As I said a few chapters before, by the time we reach 150 letters in a sequence, which I suppose would make it a "sentence"

rather than a “word,” there are more “sentence” variations than there are atoms in the universe.¹ Clearly then, a protein that takes up 720 letters of DNA can’t evolve all in one go. This is why we need to break up the process into a series of smaller steps.

Now, to perform this experiment, we will need to specify some things in advance. These can be changed, and they will probably affect the outcome. We will also need to make some initial assumptions, which will also affect the result, but whenever possible we will do our best to skew these assumptions in favor of evolution. We will talk more about these once the results are in. What I’m really doing here is creating a model for testing the evolution of a protein from scratch.

First, we’re going to hire a whole lot of bacteria cells for a long period of time – a billion years. This should be enough time for them to produce something at least mildly interesting. We’ll fire them if they don’t.

Second, we’ll assume each individual bacterium lives only an hour, and then replaces itself with another bacterium. This is a very simplistic version of how a bacterial colony works, but it skews the experiment heavily in favor of evolution. In reality, an individual bacterium can potentially live forever, but if it doesn’t replicate or replace itself, mutations can’t be tested by natural selection.

We will say that each cell, and then its replacement, fills one “slot” in our colony, and therefore the size of the colony – the number of slots – remains fixed over the entire length of our experiment. This is to prevent the colony growing exponentially, which although useful to begin with would quickly cause problems. For example, starting with just two bacteria cells, if the number of cells was allowed to double every hour, within about 270 hours the colony would contain more cells than atoms in the universe.² Clearly this would make us very irresponsible thought experimenters.

This is why we’ll assume a fixed colony size. Our experiment will run for a billion years, which is about 9 trillion hours, so one cell “slot” in our colony will be host to about 9 trillion bacteria cells over the whole period. If it helps, think of the experiment as being conducted in an imaginary hotel designed exclusively for bacteria. Each bacterium gets its own room. There are only ever a fixed number of rooms, and each hour, every cell in the hotel checks out of its room and its offspring checks in.

The third assumption we’ll make is that there is a mutation rate of about one in every billion base pairs. In other words, when genomes are duplicated and passed on to their replacement an hour later, one in every billion letters contains a mutation across the colony as a whole. In real life, some bacteria have higher mutation rates at times, but this also makes their genomes more unstable.

Fourth, we will allow 12 intermediate steps. What this means is, rather than requiring our bacterial colony to find the desired protein sequence all at once, which we already know is impossible, we will allow the colony to find it in stages, with each stage involving a natural search.

Allowing 12 intermediate steps means we can break up the desired 720 letter DNA sequence into 12 smaller blocks of 60 letters each. Once the colony finds the correct sequence of 60 letters in the first block, we will say that the first of twelve

“evolutionary milestones” has been reached on the way to our desired protein, and we will allow the colony to keep that block perfectly intact from then on.

We do this because we’re assuming that when an individual bacterium stumbles on the correct sequence for one block, this gives it some kind of advantage in terms of survival or replication. Each cell in the colony then adopts the block into their own genome, and moves on to finding the correct sequence for the next block.

This is a highly simplified way of imitating what natural selection needs to do, but since we’re creating a model of protein evolution from scratch here, I think it’s a reasonably good way of simulating the idea of small but significant advantages that accumulate over time.

In theory, the experiment could continue until the colony has found the right sequence for all 12 blocks, which means it has successfully evolved our desired protein. However, if it can find the first evolutionary milestone within the required timeframe of a billion years, we don’t really need to continue the experiment. We can just assume the remaining milestones could be reached if we allowed more time or enlarged the colony.

We will also assume that the correct sequence in a 60 letter block must be found perfectly. We can think of each block as the equivalent of a 60 letter combination lock, with each letter being either A, C, G or T. The exact unlock sequence must be found before the colony can move on to the next block, and the only way they can find it is by testing combinations until they hit upon the right one – what we’ve called a “natural search.”

When a bacteria cell replicates, passes on its genome to its replacement, and then conveniently dies, we will call this a “trial.” To keep things simple, we’ll come up with a single probability of a mutation happening in each trial. Since each letter has a one in billion chance of mutating, we’ll just multiply this by the length of the block we’re allowing for, to get the chance of a mutation occurring in one trial. For a 60 length block of letters, there would be roughly a 1 in 17 million chance of a mutation occurring in each trial. The math isn’t exact here, but it’s good enough for our purposes.

We’ll revisit these assumptions after we have conducted our experiment, but now that we have set everything up, the question we want to know is: how many bacteria does it take to find the first 60 letters, the first block, in our desired 720 letter DNA sequence, in the specified timeframe of a billion years?

What we’re trying to find out here is, how easy or difficult is it to evolve a protein under these assumptions? Would we need to fill every atom in the universe with our bacteria, suggesting it is impossible, or could we do it with much more modest numbers that fit within the evolutionary timescale, and that don’t require us to use whole galaxies for our thought experiments? Let’s look at the results.

1 There are an estimated 10^{80} atoms in the universe, and 4^{150} or about 10^{90} possible permutations of 150 letters of DNA code. **2** $2^{269} = 9.486 \times 10^{80}$ to 3 decimal places.

50. How To Evolve A Protein

Just before we look at the results, I need to point out that what we're doing in this experiment isn't actually the way most proteins are said to have evolved. In evolutionary theory, new things evolve mostly from older things. New functions are usually said to be adaptations of older functions, and the same is true of proteins. New ones are often said to have evolved from previous ones. However, some must have evolved from scratch, if life arose by itself, otherwise we get an infinite regress of proteins coming out of proteins, but never any actual beginning.

Anyway, let's calculate the results of our experiment. I will be talking about ridiculously large numbers here, but I will put them into some kind of context immediately afterwards, so they make more sense.

First, we need to know how many permutations our colony has to search through, to find the correct 60 letter sequence. There are 4 possible letters (A, C, G and T) for each nucleotide of DNA in our experiment, and 60 letters in a block, so the number of possible permutations is 4 multiplied by itself 60 times, or 4 to the power of 60, which is about 1.3 multiplied by 10 to the power of 36. We need to divide this number by two since, as in our combination lock example, if we repeated the experiment endlessly, on average our colony can expect to find the right sequence after trying half of the possibilities. This gives us an average of about 6.5 multiplied by 10 to the power of 35.

However, when an individual bacterium replicates, most of the time the block won't contain a mutation, since it's only 60 letters long. To find out how many actual trials our colony would need to run, we need to divide the average we calculated above by the simplified probability of the block containing a mutation, which we assumed to be about 1/17,000,000. When we do this, we get about 10 to the power of 43 trials, which is 1 with 43 zeros after it. This is how many bacteria cells we would need over the one billion year length of our experiment, to have a reasonable chance of finding the first 60 letter block in our desired protein.

Due to its size, this number is pretty meaningless unless we can put it into some kind of context. As a useful comparison, it has been estimated that the number of single-celled organisms on Earth is about 5 multiplied by 10 to the power of 30, and all the bacteria that has ever existed, assuming the ordinary evolutionary timescale, probably has an upper limit of around 10 to the power of 40, or 1 with 40 zeros after it.¹

In other words, our experiment as it currently stands would require a thousand times more bacteria than has ever supposedly existed on Earth, just to find a specific sequence of 60 letters coding for a chain of 20 amino acids, which is a small fraction of the size of a protein used by bacteria today!

Now, this doesn't really prove or disprove anything. Ultimately, it's just a mathematical model that is based on certain starting assumptions, and we can always adjust these to get a different outcome. However, the experiment is still useful,

because it gives us a better sense of what may be needed for nature to find a particular sequence of amino acids from scratch.

The experiment, at least in the way we have currently set it up, implies that finding a specific sequence of even just 20 amino acids *de novo* is virtually impossible within the ordinary evolutionary timescale, at least using a natural search. Yet bacteria today have thousands of proteins available to them, averaging over 250 amino acids in length, so either they evolved them in spite of our thought experiment, or they were given them.

If bacteria really did evolve at least some of their proteins from scratch, then obviously something must be wrong with our experiment. Maybe we simplified it too much. Let's first look at what we didn't factor in and see whether these could help us evolve our protein.

We have ignored the fact that some codons code for the same amino acid, and that some amino acids in a protein can be swapped out for different ones, but the protein can still often perform the same core function.

If we factored this built-in redundancy into our experiment, it would probably make the evolution of a protein easier. On the other hand, we wanted the end result to be a specific chain of amino acids with the same letters as a protein used by bacteria today, not just one with the same function but different letters or amino acids.

We have focused on one type of mutation, where DNA letters get switched. This is the most common type, but there are others. Sometimes letters get added or deleted, or sequences of DNA get duplicated. These types of mutation could help, but they could just as easily break any progress made towards our new protein, so in the long run they might not actually help. I guess it depends on the type of protein we're trying to evolve.

We have also ignored stop codons. These instruct the ribosome to stop making the protein. In the human genetic code, UAA, UAG, and UGA are stop codons. Stop codons could be a significant hindrance to long amino acid chains evolving. The longer a chain gets, the more likely it is that a random stop codon could appear in the sequence as a result of mutations, causing the evolution of our new protein to halt, at least until the stop codon mutates back into one that codes for an amino acid. If we factored these in, it could slow down protein evolution.

Could our assumptions also be part of the problem? We have assumed our colony is together for a billion years, and that once one of the cells arrives at an evolutionary milestone, all bacteria instantly adopt it, as a crude approximation of natural selection.

However, if the colony is dispersed at any time, it wouldn't be possible for all of the cells to adopt it. In reality, bacteria are living organisms that might prefer not to stay together in the same colony for a billion years. In other words, this assumption is heavily skewed in favor of evolution.

We also assumed a mutation rate of about one in every billion base pairs. We could increase this, to try and speed up evolution, but then our colony would have to work harder to preserve any gains it had achieved, which might not actually help us in getting to our desired protein. If the mutation rate were too high, this would make the genomes of our bacteria unstable for later generations, resulting in far higher cell deaths.

Built into our experiment is also the underlying assumption that things can only get better. We have allowed the colony to keep an evolutionary milestone once found, and we have shielded that milestone from any further mutation. This allows the protein to evolve in cumulative steps. In evolutionary theory, these intermediate steps are preserved because they usually give the organism a survival or reproduction advantage over their fellow organisms, and its offspring inherit this advantage.

However, I think the most significant assumption we made at the start of our experiment is the number of intermediate steps allowed. We needed these steps, so our colony had a chance to evolve the protein. I called them “evolutionary milestones,” to remind us that each step would need to make a significant difference to the survival or replication ability of a cell, so the step could be preserved by natural selection.

In our experiment, the protein we were aiming for consisted of 240 amino acids taking up 720 letters of DNA. We allowed the colony to try and find this sequence in 12 intermediate steps, by breaking up the sequence into 12 blocks of 60 letters each.

The colony only needed to find the correct sequence for the first block, because if it could successfully do this, we can assume it could also find the others, given more time or a larger colony.

However, in our experiment, the colony couldn't even find the first block of 60 letters of DNA, which would represent a sequence of 20 amino acids, even if we hired all the bacteria that has ever supposedly existed on Earth, suggesting that our desired protein couldn't evolve from scratch, based on these initial assumptions.

The solution, at least as far as our model is concerned, is to allow for more intermediate steps. If we allowed 16 steps, the colony would only need to find blocks of 15 amino acids at a time, consisting of 45 letters of DNA. To find a specific sequence of 45 letters would require trials numbering about 10 to the power of 34, about a million times less than the estimated number of bacteria to have ever lived on Earth, according to the evolutionary timescale.²

If we allow 24 intermediate steps, our colony would only need to find 10 amino acid blocks at a time, made up of 30 letters of DNA. To find one block would require trials numbering around 10 to the power of 25, which is just a minuscule fraction of all the bacteria that has ever supposedly lived on Earth.³

In other words, in this model of protein evolution, the evolution of our desired protein consisting of 240 amino acids is at least theoretically possible, if we allow it to happen in much smaller steps.

If nothing else, this experiment has served one useful purpose. It suggests that if nature has to evolve at least some lengthy proteins from scratch, it probably needs

to start with pieces much smaller than 20 amino acids in length, which could perhaps be building blocks for larger pieces. On the other hand, nature as we know it today prefers much longer proteins. As I said earlier, the average size of a protein in real bacteria is over 250 amino acids in length, because long proteins can perform functions that short ones can't do.

Incidentally, this is why taking a line of random English letters, and turning it into a line from a Shakespeare play one letter at a time, is a poor analogy for what evolution has to do when it comes to evolving a protein.

A single "letter" change probably gives no survival or reproductive advantage to an organism, and the built-in redundancy of the genetic code ensures that the effects of this change are often minimized anyway. But if there is no advantage, then natural selection won't preserve it. Changes that might confer an advantage probably need to be at the level of "words," "sentences" or "paragraphs" most of the time.

Therefore, in the story of how a real protein of 250 amino acids in length evolved, any analogy involving lines from Shakespeare would need to end with a 750 letter section of his play. It would also need to show the gradual change of words and sentences into different words and sentences, and demonstrate how each of the pieces making up the section of his play could still be read, understood and make sense at each evolutionary milestone along the way.

1 Whitman, W B *et al*, "Prokaryotes: the unseen majority", *PNAS*, 1998. **2** There are 4^{45} permutations of 45 DNA letters, or about 1.2×10^{27} . If we halve this we get 6×10^{26} . With a one in a billion mutation rate, the simplified probability of a mutation occurring in 45 letters would be 45 divided by 1 billion, or 0.000000045. Dividing 6×10^{26} by 0.000000045 gives us about 1.3×10^{34} . The exact numbers would be a little different, but what matters here is the size of the number. **3** There are 4^{30} permutations of 30 DNA letters, or about 1×10^{18} . Halving this gives 5×10^{17} . With a mutation rate of one in a billion, the simplified probability of a mutation occurring in 30 letters would be 0.00000003. Dividing 5×10^{17} by 0.00000003 gives us about 1.6×10^{25} , roughly the number of trials that would need to be run.

51. The Microprotein Love Story

According to evolutionary theory, evolution usually happens in small cumulative steps. Each one should give the organism a survival or reproductive advantage, otherwise the step is likely to be mutated away again.

In our protein evolution thought experiment, the small amino acid blocks we could successfully evolve are the cumulative steps, but they are not the final product. The protein we wanted to arrive at is 240 amino acids in length, but each block must be less than 20 amino acids long. At the same time, each block must have its own useful function in the cell, otherwise mutations could destroy it over time.

What use do smaller parts of a protein have? Biologists have several ideas. For example, proteins usually have regions in them called “domains,” typically about 100 amino acids in length. A domain can act somewhat independently, and tends to fold into its own particular shape. Since many proteins use similar domains, evolutionary theorists think that some proteins evolved by the shuffling and stitching together of different domains.

However, domains can't be the original building blocks of protein evolution, because a domain made up of 100 amino acids, which is 300 letters of DNA, is still far too long to be found by a natural search. Even if we ran an experiment in which we filled the universe with mutating bacteria, this wouldn't even begin to be enough.

Researchers have also discovered recurring “themes” found in a variety of proteins. These themes vary from 35 to 200 amino acids in length.¹ However, themes can't be the evolutionary building blocks of proteins either. They are still much larger than the 20 amino acid blocks in our experiment, making them pretty much impossible to evolve from scratch. You would still need to fill the universe with bacteria to have even a slight chance of one evolving.

There are also “microproteins” floating around in the cell, miniature proteins that have useful roles, and small amino acid chains called “peptides” that perform useful biological functions involving hormones and antibiotics. In other words, it's certainly possible for smaller amino acid sequences to have a function, and biologists speculate that some proteins were therefore “stitched together” from smaller ones by evolution.

What does “stitched together” actually mean? It would be romantic to imagine two shy microproteins bumping into each other in a quiet corner of a cell, falling in love and committing to stay together forever, or at least until the death of the cell.

But this isn't how evolution works. It's a game of Nucleotide Shuffle. In other words, a mutation first has to take place in the genome, with a sequence of letters shuffling into a slightly different sequence of letters. When biologists casually say “larger proteins were stitched together out of smaller proteins,” this sounds easy, but it doesn't explain how the process actually happens. Is there a genetic grandmother in each cell, knitting protein scarves for the cell to wear on those dark winter nights? The

idea of “stitching together” also sounds believable, because we understand this metaphor better than we understand the idea of a sequence of letters mutating.

Let’s see how nature could actually stitch together two microproteins. We’ll call the first one Alice and the second one Bob. We will presume, as does evolutionary theory, that Alice and Bob already have useful functions in the cell. They are transcribed and translated separately as little microproteins.

Let’s also assume they’re already close to each other in the genome. However, between them is Carol, a small sequence of nucleotides that doesn’t really do much, except keep Alice and Bob from meeting each other and perhaps enjoying a little cellular wining and dining together. Fortunately, Carol is only ten letters long. If we, or rather nature, could just make Carol disappear, perhaps the cell could treat Alice and Bob as one protein. They could finally be together, and who knows what might happen next?

Incidentally, evolutionary theorists have an elegant mechanism for making Carol disappear, called the “story.” When a story is evoked, any problem can disappear, just like that. Since letters in a DNA sequence have the potential to drop out as a deletion, theorists simply have to tell a story about the ten inconvenient letters being deleted, and their job is done. Carol is eliminated. Alice and Bob finally get to meet up, and the two microproteins can be “stitched together” into one.

Of course, engineers, computer programmers, mathematicians and other scientists might look at this and ask, “Wait a minute, what’s the actual chance of this happening, compared with all of the other things that could happen, such as Carol never going away, and perhaps even getting bigger and more interfering?”

If we factor in all of the other possibilities that could happen, the probability of Alice and Bob actually getting together is pretty low. But this vague language isn’t very helpful. How low is “pretty low”? We can’t know the exact figure, but we can make a rough estimate that will give us an indication of what “pretty low” means.

If Carol is made up of 10 random letters selected out of the four bases A, C, G and T used in DNA, there are about a million possible permutations of these 10 letters.²

However, we must also allow for the possibility that a letter might disappear or a new one might be added, otherwise we’ll never actually get rid of Carol. We don’t want her to change. We want her to go away. But this makes the math much more tricky, and I won’t work it out here. We could create a computer program to mutate one letter in a 10 letter sequence in a series of rounds, and to keep going until the whole sequence was eliminated. Unlike our previous experiment, what counts as a mutation here wouldn’t just be a letter change, but would also include the deletion or addition of a letter. We could then run this program a large number of times, to find the average number of mutations it would take before Carol disappeared altogether.

The answer we get would depend on the probabilities of a letter appearing or disappearing. However, if we had one guaranteed mutation every round, then let’s just say for the sake of argument that it takes an average of a million rounds before

Carol gets mutated out of existence. This is not in any way an exact figure, but it's good enough for our purpose. I'll show you why in just a moment. We could say it's a "One In A Million" event.

In reality, a 10 letter sequence in the DNA of a living organism isn't going to mutate every time it is duplicated. If it did, this would be an incredibly high mutation rate, meaning a stable genome couldn't be passed on, which would almost certainly result in the death of the offspring.

Therefore, let's also assume it takes a million copies of "Carol" before one mutation creeps in. This is still high compared to the mutation rate for most organisms, but my aim here is to keep the math as simple as possible. In this case, we can say that a single mutation is also a One In A Million event.

How many trials would we need to run in living organisms, in order to wipe Carol from the face of the genome for the sake of our Alice and Bob love story?

If we were evolving this sequence with a computer program, and one mutation occurred each round, we've assumed it might take a million rounds on average to eliminate a 10 letter sequence. But in an organism with a one in a million mutation rate, we'd have to run somewhere around a million trials just to get a single mutation.

Therefore, we'd need to run a million multiplied by a million trials in living organisms – that is, a trillion trials – before our 10 nucleotide sequence called "Carol" had a reasonable chance of being mutated away into oblivion.

I have kept the numbers as simple as possible in this example, because exact numbers don't really matter here. I'm just trying to show the magnitude of what is needed.³ I assumed the "Carol" sequence was small, just 10 nucleotides in length, and yet it could take a trillion generations of an organism just to get rid of Carol. We could call it a "One In A Trillion" event.

What happens if we were to add another 10 nucleotides to Carol? The number of possible permutations of the "Carol" sequence jumps from about a million to about a trillion, or by six orders of magnitude (i.e. six extra zeros), before we even factor in the probability of a mutation occurring.⁴

In other words, as the "Carol" sequence gets larger, or rather, the further apart our "Alice" and "Bob" microproteins are in the genome, the probability of them ever being stitched together by mutations also shrinks by orders of magnitude – which means it becomes very improbable, very fast.

The simple point I am making here is: when biologists and popular science writers say that "proteins were stitched together by evolution," it sounds easy. It sounds plausible. If your grandmother can stitch things together, why not evolution?

But when we look at what this actually involves, we see that even using very simplified math, the "stitching together" of two microproteins virtually next to each other in the genome is in the category of a "One In A Trillion" event, and the odds against this happening grow by orders of magnitude the further apart they are.

Think about the implications of this. It means nature first has to evolve the Alice and Bob microproteins, which I have shown is difficult and time consuming, but could

theoretically be done if they are small enough, and if we allow enough time. But then, for nature to arrive at the combined AliceBob protein, it would need to run another trillion or more trials, just to stitch the two microproteins together in the first place, assuming they were a mere 10 nucleotides from each other.

This might sound trivial, compared to the countless trillions of trials we talked about in the process of evolving a small block of amino acids, but nature has to go through all these trillion additional trials just to find out if Alice and Bob are even compatible. After all this, they might not even like each other! In that case, Carol would have “died” in vain. Evolution then has to find another microprotein for Alice to hook up with, if it wants to evolve larger proteins through this “stitching together” process.

But if Bob is the only microprotein in the local area of the genome, how is nature going to find Alice another date? The odds of being stitched up with anyone else drops dramatically, the further away the other microprotein is, at least through mutations.

Fortunately, biologists have an answer: magic wands.

1 Nepomnyachiy, Ben-Tal, Kolodny, "Complex evolutionary footprints revealed in an analysis of reused protein segments of diverse lengths", *PNAS*, 2017. See also the article "Protein archaeology: Understanding how proteins evolve" published by Tel Aviv University on December 17, 2017. **2** There are 4^{10} or 1,048,576 permutations. **3** Scientists often have to deal with ridiculously large numbers involving lots of zeros. When a zero is added to a number, they say the number increases by an “order of magnitude,” so the difference between 1 and 10 is one order of magnitude, and the numbers 10 and 10,000 differ by three orders of magnitude. This idea of “orders of magnitude” helps scientists to grasp the relevance of big numbers in relation to other big numbers. **4** There are 4^{20} or just over 1,000,000,000,000 (one trillion) permutations. A trillion has 12 zeros.

52. The Wands Of Serendipity

I spent the last few chapters getting into a little math, to give you a sense of what nature needs to do to evolve new protein sequences from scratch, or to stitch together smaller ones into larger ones. My purpose was also to heighten our intuition for what is and isn't possible in nature. I showed that we can get a rough estimate of how likely it would be for ten nucleotides in a sequence to be deleted from the genome of a real organism, through random mutations. Based on a few simple assumptions, we could consider it to be a "One In A Trillion" event.

This might sound rare, but we also need to put it into perspective. We just need a bacterial colony to perform a trillion trials, and it will likely happen at least once. In other words, a One In A Trillion event isn't necessarily a problem by itself. The problem is that it has to occur in the context of other low probability events.

Unfortunately, the probability of many of the things that are said to happen in evolutionary stories are almost impossible to calculate. Even so, it's useful to try and get a better sense of scale for the probability of a particular event, even if we can't get the numbers precisely right.

Now, when telling their stories, evolutionary theorists tend to credit nature with the ability to do extraordinary things, to explain how certain DNA sequences evolved. I will refer to these as "serendipity wands." They are like magic wands, but instead of magic, the power behind them is incredible luck. However, I prefer the word serendipity, even though it means basically the same thing, because "the wands of serendipity" has a nice ring to it.

The first serendipity wand is called "duplication." This is where just the right sequence of nucleotides gets duplicated right next to the original, often more than once, in just the right quantities. This wand is the equivalent of using the "copy" and "paste" functions in a word processor, with the pasted text placed next to the original. For example, if you were typing out directions for someone, and you wanted them to turn right three times, you could type "TURN RIGHT," then select the text, copy it, and paste it two times next to the original text.

In nature, duplicates are accidents, blips in the machinery that copies the cell's genome, and this is how many proteins are said to have evolved. A new protein supposedly starts out as an accidental duplicate of an existing one, and gradually the code for the duplicate protein mutates so that the protein somehow finds a new function.

Now, I don't think it's unreasonable to say that duplication happens from time to time. Maybe the copying machinery stutters, and spits out the same sequence of letters a few more times than it should, although we should be curious to know how these mistakes make it past the built-in error correcting processes, which we'll discuss in a later chapter. But this isn't the reason I call it a serendipity wand.

Evolutionary theorists say that duplication events are common. However, there is a certain amount of circular reasoning here. They argue this is the way many

proteins evolved, and so by definition, it must be a common event, because there are a lot of proteins. There are also a lot of repetitive sequences in the genome, so it is assumed they came about as a result of duplication events.

You will also find a lot of repeats of the word “the” in this letter, and their existence could be explained by the repeated stuttering of the copy and paste facility in my word processor. I suppose this is a possibility, but as the author of this letter, I know there is also a very different explanation.

I call “duplication” a serendipity wand because, in evolutionary stories, it isn’t about random sequences being duplicated. Instead, a specific sequence is “copied,” and then “pasted” exactly the right number of times. If you use copy and paste in a document, you don’t choose random letters and words. You first select the exact text you need. If you want someone to turn right three times, you can’t have your instructions say “TURN RIGHT, NRIGHT, GHT.” This wouldn’t make any sense.

You need to select the exact text “TURN RIGHT,” copy it, and then paste it exactly twice, right next to the original without any distracting or ambiguous text in-between, apart from spaces. If you pasted it just one extra time, the person following your instructions would find themselves right back where they started!

In the stories of evolving sequences as told by evolutionary theorists, the evolving item, whether a developing protein or something else, gets lucky because just the right sequence gets copied and pasted the right number of times. If even one extra letter is included or missed out in the copying process, the sequence could lose the desired function. The evolving sequence also gets lucky in that the duplicates somehow get past the mechanisms built into the system to prevent errors.

The second serendipity wand is called “translocation,” which is a term used by biologists. This is where genetic sequences are moved about through the genome, or perhaps even brought over from other organisms. On the other hand, if two sequences are very close, they can be brought together with a few convenient nucleotide deletions.

This wand is the equivalent of using the “cut” and “paste” functions in a word processor, except unlike the previous wand, you can cut the text from the same document or a different one, and paste the text into wherever you want it to be in your document. What’s more, the pasted text will just happen to follow on perfectly from the text that already existed in your document.

I think this is by far the most extravagant serendipity wand in evolutionary theory. I have already shown that to get ten nucleotides in a row deleted is the equivalent of a One In A Trillion event, and this was simply to get two sequences next to each other that were separated by those ten nucleotides. It might happen, although lots of other things are also much more likely to happen.

But what are the odds of any two specific sequences far away in a genome coming together, while remaining intact in the process? The probability decreases by orders of magnitude, the further away the two sequences are. Yet with the “translocation” serendipity wand as waved by theorists, it doesn’t matter. No matter

how far away, no matter how improbable, it can happen with a wave of the storytelling wand.

To be clear, certain pieces of the genome can definitely be moved about. But this usually happens for very specific reasons that involve strictly regulated control mechanisms and markers. In other words, it's one thing to say that translocation happens, which is true in certain limited circumstances. It's a completely different thing to say that specific sequence A gets moved to a specific region B of the genome, just because this is needed for an evolutionary story to work.

If a parcel was delivered to your door, and a friend said that "parcels get transported," you wouldn't consider it a good explanation for why it arrived on your doorstep. If the parcel was addressed to you, and contained gold bars worth a million dollars, you would probably find your friend's explanation a little lame.

Yet this is what evolutionary theorists do in their stories. Since parcels get "translocated" across the world all the time, this is apparently sufficient to explain how you got a parcel on your doorstep, addressed to you, containing gold bars worth a million dollars.

The third serendipity wand involves what I call "magical steps." To explain this one, let's take a closer look at how some proteins are said to have evolved, according to evolutionary theory. One way is through a process called "gene duplication."

The word "gene" usually refers to a genetic sequence that codes for a protein or perhaps an RNA sequence, although sometimes it is used more loosely to refer to any genetic sequence that does something useful.

In "gene duplication" a gene gets accidentally duplicated. The cell can still use the original sequence to make the protein, while the copy is then supposedly free to mutate; and somehow, the copy gradually finds a new function. This is the basic idea, which might sound reasonable on the surface, although it requires a whole lot of luck for the gene to be duplicated intact in the first place. But it also begs several questions.

First of all, if a new gene starts off as a duplicate of an old one, which one does the cell use to make the protein? If it only uses one of the genes, then the other doesn't get produced. But if it's not produced, it won't evolve through natural selection.

To explain why, it helps to think of mutations as designers in a factory, constantly tinkering with the design plans, and to think of natural selection as the factory testers, the ones who get to test each tweaked design before it gets rolled out for mass production, to see if the tweak is better, worse or the same as the previous design. Mutation is the tinkerer, and natural selection is the tester. According to evolutionary theory, you need both, in order for evolution to happen.

But a gene that doesn't produce a protein or something useful, can't be tested in the real world, and so isn't subject to natural selection. Rather than evolving into a sequence that does something different and useful to the cell, it is likely to lose its

information over time, becoming what is called a “pseudogene,” which usually has similarities to a known gene, but with some or even a complete loss of functionality.

However, let’s say that after the duplication of a gene, the cell produces both the original and the duplicate, because it can’t tell the difference. Let’s label the original gene A, and the duplicate gene A1. Gene A already has a function. According to evolutionary theory, duplicate gene A1 could eventually evolve into a new gene, which I will label as gene B, with a new or related function, through a series of evolutionary steps that I will imaginatively label as A2, A3, A4 and so on.

Ideally, each of the steps A2, A3 and so on should give the organism an advantage, so that natural selection can work cumulatively toward gene B. I suppose an individual step might be neutral, neither an advantage nor a disadvantage, and the gene might drift somewhat randomly towards the next step.

Individual steps probably shouldn’t be a disadvantage, because then natural selection would work against it. However, I suppose a temporary disadvantage might slip through the cracks once in a while, if an advantage is just round the corner. However, no step should break the gene, so that the protein it codes for loses its useful function, because then natural selection won’t have a need to preserve the sequence.

To sum up: each evolutionary step from duplicate gene A1 to new gene B needs to be viable. In other words, intermediate genes A2, A3 and so on should still have a function, and be turned into a protein by the cell, so that the function can be tested in the real world. If not, it can’t be tested and will probably devolve into a pseudogene. Many or all of the intermediate steps should also give the cell an advantage, so that natural selection can propel the evolving gene forward on the path to finding a new function.

However, in their stories, evolutionary theorists rarely spell out the exact mutational steps gene A1 would need to go through to become gene B, while also showing the effect each step would have on the organism. Admittedly, it’s probably difficult to do this, but surely it isn’t impossible, if this really is a major way in which new proteins evolve.

Scientists have the ability to knock out whole genes, and edit single nucleotides within a gene to test its effect on an organism. Evolutionary theorists can supply biologists with a viable functional and chemical pathway from gene A to gene B, and researchers could test this through many experimental rounds.

But obviously it’s much easier to simply assume it happened, and write, “gene A evolved into gene B through duplication followed by a series of mutations,” without any detailed proof or testing of the supposedly functional steps in-between.

This is why I call it a serendipity wand. In evolutionary storytelling, proteins find their functions almost by magic, going through a series of “magical steps” that might be discussed in vague theoretical terms, but are rarely spelled out in detail and then tested in the real world.

I call the people who write such things “evolutionary theorists,” because this is what they are. They often take valid processes such as horizontal gene transfer, which bacteria use to exchange genes, and then apply it universally, to any piece of the genome they want to move around. As long as scientific language is used and the story sounds plausible on the surface, when they wave the serendipity wands of duplication, translocation and magical steps, anything is possible.

53. The Story Of The Freezing Codfish

To see how the serendipity wands are waved by evolutionary theorists, let's look at the story of how certain Arctic codfish supposedly acquired the ability to produce an antifreeze protein in their blood – quite handy for a fish living in such a cold environment.

Researchers looked at seven related species of codfish.¹ Three of them had a working antifreeze gene. A fourth had the core of the gene, but it was mutated so it wasn't functional. The other three didn't have the gene, but they did have sets of related 27 to 30 nucleotide sequences that seemed to be duplicates.

One of these three species also had what the researchers considered to be the ancestor of the antifreeze gene, a tiny sequence of just 9 nucleotides, coding for three amino acids – threonine, alanine, alanine – that could have formed the basis of the antifreeze protein in the other species.

By comparing similar areas of the genome in the related species, the researchers constructed what they considered to be the evolutionary story of the antifreeze protein. According to the story, a 27 to 30 nucleotide sequence was somehow prone to duplication, and this is precisely what it did. It duplicated to become four copies next to each other.

Out of the midst of this came the threonine-alanine-alanine sequence, the core of the antifreeze property. This was also duplicated multiple times, so the evolving gene would have just the right chemical properties to prevent ice crystals from growing in the blood of the codfish. This was how the functional part supposedly evolved.

However, the emerging gene wasn't yet in a form that could be turned into a protein by the cell. For this, the gene would need a control sequence allowing it to be transcribed by ribosomes, and therefore manufactured. The control sequence somehow translocated its way over to the emerging gene, or the gene wandered over to a location where the control sequence was.

There also happened to be a sequence, one nucleotide away from the emerging gene, that could tag it for export from the cell and into the blood, exactly where it would need to go. According to the researchers, this export sequence didn't originate anywhere else in the genome. It just happened to be in virtually the right place at the right time. The nucleotide separating the export sequence from the gene was deleted, and the end result was a fully functioning antifreeze gene, ideal for the formerly freezing codfish.

Now, this was a fairly impressive piece of research, and certain people viewed it as a fish-slap in the face to the idea that intelligence was required to produce a protein.² However, there are three major problems with this codfish story, which should cause us to question whether it is even possible.

The first is the assumption that the lineage of species is correct and accurately reflects evolution moving toward the antifreeze gene. It assumes that the codfish species with the 9 nucleotide sequence was the source of the gene.

However, there are several clues that the real story might actually be the other way round. In one of the seven species they looked at, the antifreeze gene was almost intact, but contained mutations that inactivated it, likely because this species inhabited warmer water where antifreeze wasn't needed. Losing the function posed no threat to the survival of this species, so natural selection wouldn't need to preserve the gene. More likely then, in this species the sequence had become a pseudogene. It was losing information, devolving away from the antifreeze gene rather than evolving towards it.

If the order is wrong, it would explain why the so-called ancestor sequence, the threonine-alanine-alanine sequence of amino acids that forms the core of the antifreeze property, is present in one of the species without the antifreeze gene, along with the 27 to 30 letter sequences. In this scenario, it wouldn't be an ancestor but simply a remnant, with much of the original gene mutated away. According to the researchers, the 27 to 30 nucleotide sequences contained substantial variations, suggesting significant mutations, which would also be consistent with the idea that they are remnants of the antifreeze gene that had been mutated.

It would also elegantly explain why a sequence tagging a protein for export from the cell into the blood just happened to be in virtually the right place. It may simply be a remnant of the original antifreeze gene, still in the same place it had been in all along!

The news reports related to the research give us another clue as to what might be the real story. It turns out, the codfish on the opposite side of the world, in the Antarctic, also have this antifreeze ability, although they supposedly evolved it in a different way.

For evolutionary theorists, this is an example of what they call "convergent evolution," where the same function or feature is said to have evolved independently. However, perhaps it's evidence that both Arctic and Antarctic codfish had this antifreeze ability, but some Arctic ones lost it. Indeed, since evolutionary theory contains the idea of common descent, isn't it at least plausible that the assumed lineage is somehow incorrect, and that a common ancestor of both Arctic and Antarctic codfish had the antifreeze gene, but some species later lost it?

The second problem with the story is the extensive use of serendipity wands. The "duplication" wand is waved repeatedly, first so that multiple copies of the 27 nucleotide sequence are produced, and then again to make several perfect copies of the 9 nucleotide antifreeze sequence. In evolutionary storytelling, it doesn't matter how likely or unlikely this is, compared with the other things that could have happened. As long as it's not impossible, it is simply assumed to have happened.

Then the "translocation" wand is waved at least twice; once to get a control sequence from elsewhere, or to move the emerging gene to the control sequence;

and once more to get rid of the single nucleotide that separated the potentially functional part of the gene from the sequence that would export the protein into the blood – which by a stroke of yet more incredible serendipity, just happened to be in virtually the right place.

To give a comparison, the almost functional gene found the equivalent of a parcel on its doorstep, containing just the right mechanism to get the protein into the blood. Don't worry about probabilities. If it's not impossible, it must have happened. Three species of Arctic codfish now have their antifreeze protein because the mechanism to get it into the blood just happened to be there.

The “magical steps” wand isn't used in the codfish story. The researchers say this all happened in a non-coding region of DNA – that is, a region that doesn't code for proteins – so the emerging gene didn't code for a functional protein until all the parts came together. But if the gene didn't have a function while it was going through its “duplication” and “translocation” phases, it wouldn't be subject to natural selection. The implication is that these things must have evolved very fast, otherwise the emerging gene would be destroyed by mutations.

The third problem with the story is that the origins of the export and control sequences are vague. Where did they come from? Although the researchers suggest the emerging antifreeze gene might have somehow translocated over to a control sequence, they also provide evidence that both the control and export sequences didn't come from any existing protein-coding genes in the codfish genome, but originated *de novo*, which is a term used by biologists, meaning “of new.” In other words, the emerging gene might have found its way to a control sequence that wasn't even there before! ³

The bottom line is this: according to the evolutionary story told by these researchers, the antifreeze protein came about as a result of a series of seemingly improbable, serendipitous events. But this raises a vital question, highly relevant to our discussion of what evolution can actually do.

1 Zhuang *et al*, “Molecular mechanism and history of non-sense to sense evolution of antifreeze glycoprotein gene in northern gadids”, PNAS, 2019. See also the article “Study of Arctic fishes reveals the birth of a gene – from ‘junk’” published on the Illinois News Bureau by Diana Yates, February 11, 2019. **2** See the post “The evolution of ‘irreducibly complex’ antifreeze proteins in a polar fish (and a fish-slap at Behe)” at Jerry Coyne's blog whyevolutionistrue.com posted March 14, 2019. **3** See the section “Nongenic Origin of SP and Promoter Region” in the Zhuang *et al* paper. The export sequence is called a “signal peptide” (or “SP” for short), and the control sequence is called the “promoter.”

54. The Lottery Of Life

When it comes to seemingly improbable events, an important question we need to ask is: how many times in a row can serendipity be invoked, before our suspicions should be aroused that maybe something else is going on?

To illustrate, suppose you decide to enter the "One In A Million" lottery. The rules are simple. It is held once a week. It is one dollar a ticket, and there are a million tickets available. Each week there is one winner, who receives close to a million dollars.

If you choose to buy one ticket a week, the chance of you winning in any week is one in a million. But suppose you had a rich friend, whose name also happens to be Rich, for reasons I won't go into here. Rich offers you the following wager: "Before you enter the next lottery, pay me a thousand dollars. If you win the next two lotteries in a row, I will pay you ten million dollars."

Is this a good offer? To decide, you need to work out the probability of winning two of these lotteries in a row. If you buy one ticket each week, you have a one in a million chance of winning an individual lottery; but since you need to win two in a row for Rich to pay up, and each lottery is independent of the previous one, you have to multiply together the odds of winning each one separately. A million multiplied by a million is a trillion, so you would have a one in a trillion chance of winning both in a row.

For this reason, I think the offer from your so-called friend is bad, because it's incredibly unlikely you'll win two in a row. It's certainly not impossible, but it's unlikely to happen to you in your lifetime, if you only buy one ticket a week.

Notice that it's not merely a little more, but vastly more improbable, to win two "One In A Million" lotteries in a row compared with winning just one. Even so, these things do occasionally happen, even in lotteries with much worse odds of winning. People do occasionally win twice in a row.

If you could afford to buy a thousand tickets a week, you would increase your odds of winning one of these lotteries to one in a thousand, and so your chance of winning two in a row would be one in a million.

The key question, that also relates to the story of our freezing codfish, is: how many times could you win the "One In A Million" lottery in a row, before you could safely rule out serendipity? In theory, any number of sequential lottery wins is possible, but the odds shrink dramatically with each one we add to the sequence. Assuming you buy one ticket a week, winning two of these lotteries in a row is a One In A Trillion event. Three in a row would be a One In A Million Trillion event; and the odds shrink by a factor of one million with each extra lottery added to the sequence.

If you won it twice in a row, you would probably be amazed, but you might conclude that it was just incredible luck. If you won it three times in a row, I think you might start to wonder if something else was going on. Certainly, if you didn't, then other people would.

If you won it four times in a row, with a trillion trillion to one chance (a trillion trillion is 1 with 24 zeros after it), I suspect the authorities would be called. The odds of this happening by chance are so remote that fraud, foul play or some other form of intelligent design would be a much better explanation than extraordinary luck. At the very least, it would probably be investigated seriously. In other words, I think suspicions would be seriously aroused at either the third or fourth lottery win in a row.

Now, we need to be careful when making arguments from probability, because other factors have to be considered. For example, if you purchase one ticket a week, two sequential lottery wins might be a One In A Trillion event, but if you could somehow live long enough to enter it for a trillion weeks, then it becomes quite likely you'll win two in a row at some point in time. In other words, the solution here is lots of time. What may be improbable in the short term can become likely over a long enough stretch of time.

Alternatively, maybe you have a second rich friend who doesn't like Rich, your first rich friend, and who agrees to give you the money to buy up most of the available lottery tickets for the next two weeks, with the agreement that if you don't win both lotteries you owe him nothing, but if you do, you pay him five million dollars in return.

By purchasing most of the available lottery tickets for two weeks, it's highly likely you would win both lotteries, and your first friend Rich, who had assumed you wouldn't buy so many tickets, would have to pay you ten million dollars, leaving you with five million dollars after paying your second rich friend, plus the winnings from both lotteries. Your second friend had risked up to two million dollars of his own money, by giving you the money to buy up most of the lottery tickets over two weeks, but he had a very good chance of making his money back, plus an extra three million dollars.

Now, if nothing else, this might make a good movie plot. But it's also fair to say that serendipity no longer played a major role here. Your second friend helped to orchestrate a winning situation, so you didn't just get lucky. Then again, having these two rich friends, maybe you did.

In other words, probabilities do matter, as long as we also pay attention to the context. At the very least, they can help to indicate the point at which we can reasonably start to question the role of serendipity.

The story of the evolving antifreeze protein from the previous chapter is similar, in that the freezing codfish supposedly won the lottery multiple times in a row. They won it when several waves of the "duplication" serendipity wand multiplied the 27 or so nucleotide sequence, and then again when more waves of the wand duplicated the core 9 nucleotide antifreeze sequence multiple times.

It's difficult or perhaps even impossible to calculate the specific odds of each event, since we have to factor in all the other things that might have happened, as well as the chances of a mutation getting past the mechanisms that are supposed to minimize duplication errors.

The freezing codfish continued their streak of incredible luck when a tagging sequence just happened to be lying around in the right place, allowing the emerging protein to be secreted into the blood. What was it even doing there? The researchers say it didn't come from anywhere else in the genome, but evolved from scratch and just happened to be there.

I would suggest the odds of it evolving from scratch in just the right place are ridiculously small. However, if the order of species lineage is somehow incorrect, then maybe the tagging sequence was the remnant of a previously functional antifreeze gene. In this case, the chance of it being there would be high, although it's intriguing that this part remained intact while the functional part of the protein didn't, perhaps suggesting that the genome somehow preserved the tagging sequence just in case it was needed.

Our freezing codfish also won another huge lottery in a row when a control sequence supposedly translocated its way over to the evolving gene, or the other way round, apparently emerging *de novo*, just like the export sequence. Again, what are the odds? Unfortunately, they are impossible to calculate, but it's not sufficient to say "translocation can happen." This is like saying, "parcel delivery can happen." It doesn't explain the box of gold bullion on your doorstep addressed to you.

The other important factor here is, all of these things needed to happen quickly, since the gene couldn't be manufactured until it had all the necessary components – the antifreeze sequence, the control sequence to allow the protein to be made by a ribosome, and the tagging sequence to get it into the blood.

A protein needs to be produced in order to be tested in the real world, and for the functional gene to give the organism a survival or reproductive advantage, which could then help to preserve the sequence intact throughout succeeding generations. But if it took too long to become a useful protein, mutations would have degraded the sequence. Therefore it only had a small window of opportunity to become functional. A million years would perhaps be too long, but let's be generous and say a million years. Unlike colonies of hypothetical bacteria, schools of real fish take up a lot more space.

How many fish would be available for evolution to play with? Let's squeeze in a trillion freezing codfish together, each one living an average of a year and then replacing itself every year, doing this for a million years. That's a total of a million trillion codfish, or 1 with 18 zeros after it. This is a quite lot of fish. The important question is, will this allow nature to run enough trials to evolve all the right antifreeze components, and translocate them to the right place, in the required length of time? To keep things simple, if we say one fish has one mutation, then nature can run a million trillion trials.

Multiple copies of the 27 nucleotide sequence first need to be made, and then several copies of the 9 nucleotide antifreeze sequence. An individual duplication event might not be entirely rare, but we are talking about several such events in sequence here, all with exactly the right amount of genetic information being copied and pasted.

This is like winning the lottery at least six or seven times in a row. It is highly improbable. Furthermore, as the codfish researchers acknowledged, the evolving gene wasn't subject to natural selection, which meant nature didn't have any reason to preserve it during its development. It was therefore more likely to mutate away before arriving at its final form.

What about the presence of the control sequence, needed so that the protein could be manufactured by a ribosome? In a previous chapter I showed that bringing two microproteins together through the deletion of ten nucleotides is a One In A Trillion event, but the odds become orders of magnitudes worse as we space the two microproteins further apart. The genomes of codfish are typically over half a billion base pairs in length. The probability of an existing control sequence and the antifreeze sequence coming together in a genome of this size, at least through insertions, deletions and letter swaps, is so small as to be virtually impossible.

If there was a specific mechanism that could translocate a control sequence to just the right place, this would help immensely. But if the researchers knew of such a mechanism, they would have told us what it is. Translocation itself is not a mechanism. It's just a word that sounds more scientific than saying it got moved, which would then beg the obvious question: how did it get moved?

This is why I call translocation a serendipity wand. In evolutionary stories, specific sequences are said to have moved, often with little or no actual consideration for how likely or unlikely this is. It simply must have happened.

Finally, what are the chances of the tagging sequence, needed to tag the protein for export from the cell and into the blood, being just one nucleotide away in a genome that contains hundreds of millions of nucleotides? I'm not even sure what kind of lottery win this could be compared with. I suppose it would be like having multiple winning tickets turn up on your doorstep one morning.

My point is, from a mathematical point of view, I doubt any number of codfish could run enough mutational trials to achieve these things in the right sequence, let alone a million trillion of them.

However, from an evolutionary storytelling point of view, the fact that all of these things occurring in sequence are wildly improbable doesn't matter in the slightest. It must have happened because the antifreeze gene is here, and the lucky Arctic codfish are no longer freezing their scales off. I am suggesting that perhaps there are other explanations for why it is here.

What I have shown is that evolutionary stories usually contain many assumptions, and often rely on remarkable serendipity. Organisms seem to keep getting incredibly lucky multiple times in sequence, despite overwhelmingly unfavorable odds. This suggests it might not be serendipity after all.

In the case of the freezing codfish, I think the problem is that the researchers assumed evolution must have happened, and then lined up the species in a lineage based on their evolutionary assumptions. But the species with an almost functional antifreeze gene is evidence that this species is actually losing information, not gaining

it. The sequence appears to have devolved into a pseudogene, rather than being on the cusp of evolving into a gene.

The three species without the gene could have lost most of it because they no longer needed it, or maybe it wasn't there in the first place. But if the export tagging sequence really is present at the right location in these three species, and isn't just part of the storytelling, this would be evidence that they actually lost the functional part of the gene. In other words, this is devolution rather than evolution. Each of the seven species might have had the antifreeze gene, but some of them may have lost it because they found themselves in warmer waters where they no longer needed it.

Incidentally, by curious serendipity or intelligent design, the sticks that Jacob placed in the troughs are surprisingly similar to our serendipity wands. If you recall, while Jacob was working for Laban, he "took for himself a fresh stick from the poplar and almond and plane trees, and he peeled white peelings in them, to expose the white that was on the sticks." ¹ In the first part of this letter, I showed that what Jacob was doing with the sticks served as an analogy for how amino acids are put into ribosomes to create a protein.

The Hebrew words used here also seem to allude to a deeper meaning. The initial word used here for "stick" (*mql*) is singular, so even though it becomes clear from the account that Jacob has taken three sticks (the plural is used afterwards), I think the initial word is singular to remind us that one codon is actually three nucleotides attached to one another in a sequence. The ribosome reads one codon at a time.

In other words, we think of a codon as singular, even though it's really made of three building blocks. The same is true of a protein. We think of a protein as a single item, even though it's made up of a chain of amino acids.

The Hebrew words used to describe the sticks are very interesting. The word here translated as "poplar" (*lbne* in Hebrew, pronounced "liv-neh") is similar to the word for "Laban" (*lbn*), which means "white." It is a "duplication" of his name, but with a letter added, which can also happen in biological mutations.

The word translated "almond" (*luz*) is the word "Luz" in Hebrew, pronounced "lose," and is also the name of the place where Jacob had his dream of the ladder, which in the first part of this letter I suggested was an analogy for the double helix structure of DNA. If Jacob took a stick from Luz, we could say the stick had been "translocated" to where he was now. Jacob renamed Luz to Bethel, meaning "house of God," but biologists have replaced God with luck, mutations and serendipity wands.

The "plane" (*ormun*, pronounced "arm-own") is another interesting word. The Hebrew transliteration *ormun* would look and sound a lot like the word "amino" in amino acid if we could just shuffle the "o" to the end and switch the "u" for an "i."

"You can't do that," say skeptics. "That would be cheating!" Yes it would. But evolutionary theorists are allowed to do precisely this. New proteins supposedly evolve by duplicating out of old ones, and then amino acids and nucleotides shuffle around and change letters until a new function magically turns up.

Whatever you think of these ideas, we can say that the Hebrew words used to describe Jacob's three sticks serve as useful metaphors for the serendipity wands of "duplication," "translocation" and "magical steps" used by evolutionary theorists.

The word translated "fresh" (*lk*) to describe the sticks is pronounced in Hebrew more like "luck" or "lack" (but with the "ck" sounding more like the end of the word "ich" in German).

In a sense then, we could say that these are Jacob's Sticks of Luck, which would make them surprisingly similar to our Wands of Serendipity. The word (*lk*) also comes from an unused root word meaning to be new, which is similar to the term *de novo* (from the Latin, "of new") biologists use when they mean something came out of nowhere or was made from scratch.

If we can accept the possibility that the stories of Jacob and Laban are also meant to be metaphors for molecular biological processes (and I will present even more evidence for this a little later), which suggests God encoded this information in the story right from the beginning, then I think the Hebrew words used to describe Jacob's three sticks are meant to show that God knew in advance what many biologists would do with the discoveries they have made.

They would take away God's glory, and give it to luck – which would involve incredibly fortuitous duplications, virtually impossible translocations of specific sequences across the genome, and untested and vague magical steps involving nucleotides and amino acids, to transform one genetic sequence into another.

I don't wish to take away from the great research microbiologists have done in discovering how life works at such tiny scales. What they have achieved is nothing short of incredible. But just as Jacob peeled away the bark to expose the white on the sticks, we need to peel away the veneer of evolutionary storytelling by the men and women who work in their white lab coats, to expose their Wands of Serendipity – or as Jacob might have called them, the Sticks of Luck.

1 Genesis 30:37.

55. The Cellular Postal System

The protein we attempted to evolve in our earlier thought experiment faces another big challenge, which was also hinted at in the story of the freezing codfish: how to get the protein to a location where it will actually be useful.

Proteins are made in the main body of the cell, called the “cytoplasm” or “cytosol.”¹ But they often need to get to more specific locations inside or outside the cell. How can they do this? The answer is, there is a postal system and transportation network available for them.

Incidentally, there are two main types of cell found in nature. The one is called “prokaryotic” and the other is “eukaryotic.” I will explain the differences in the next chapter. The cells of plants, animals and humans are eukaryotic, and these are what I will focus on here.

A newly manufactured protein usually comes with one or more address labels in the form of amino acid sequences. Sorting by the postal system starts when a ribosome begins making a protein. As the protein emerges, another machine checks to see if it has a certain type of address label that biologists call a “signal peptide.” If it doesn’t, the protein continues to be made in the cytoplasm. If it has a different type of address label, it can be shipped to other places, such as the nucleus. However, without an address label the protein stays in the cytoplasm.

If a signal peptide is found at the start of the emerging protein chain, both the protein and the ribosome producing it are whisked away to a part of the cell called the “endoplasmic reticulum” (ER), which is like a mail processing center. Once there, the ribosome continues to make the protein, feeding it into the ER. Then the address label can be removed, the protein folds into shape, and certain bits and pieces are added to it, depending on its final destination, to help with stability.

Most of these proteins are then transported to the “Golgi apparatus,” the main sorting center for the protein postal system. Tiny transport molecules called “vesicles” act like a taxi service, carrying the proteins inside, traveling along filaments pulled by motor proteins until they arrive at the Golgi apparatus. Once there, proteins may get modified some more, before being sent on to their final destinations, depending on the address label. If they don’t have any specific destination tags, they can be secreted out of the cell.

There are various labeling systems in use by the cell. For a protein meant for the nucleus, the address label is around 6 to 20 amino acids long, and can be anywhere in the protein. One destined for the “chloroplast,” a miniature organ in plant cells for converting light into chemical energy, has a sequence 40 to 50 amino acids long at the beginning of the protein chain. Proteins bound for the ER processing center have a 16-30 amino acid signal peptide at the beginning. Some also have a second sequence, to indicate their destiny within a smaller compartment of one of the cell’s miniature organs.

Now, the whole system presents an interesting challenge for a newly evolving gene. How does it get an address label in the first place? Without one, the protein it codes for will be stuck in the cytoplasm, assuming it is even produced at all. The answer depends on how it supposedly evolved. There are four main theories about protein evolution.

The first is *de novo* evolution, where the protein evolves from scratch, as in the story of the freezing codfish. In that story, the antifreeze gene didn't have to do any hard work to get its address label. A signal peptide enabling it to be secreted into the codfish's blood just happened to be lying around, a mere one nucleotide away. Given that the codfish genome is over half a billion base pairs in length, this is either truly astonishing luck, or the evolutionary story is wrong. But how do other proteins that evolve *de novo* get their address labels? Do they all get just as lucky?

The second supposed method of protein evolution is by the "stitching together" of smaller proteins. Let's briefly return to the psychodrama of Alice and Bob, our two microproteins. In the latest episode of the drama, they find themselves working usefully in a eukaryotic cell, and as fate would have it, their genes have been mutated next to each other in the genome, so that they can be "stitched together" into one protein.

For a gene to be preserved intact in the genome, it needs to be produced at some point, and be useful to the organism in some way, so that natural selection can preserve it along with the organism.

But how can we be sure the newly combined AliceBob protein has a useful function to the cell? We can't. Evolutionary theorists simply have to assume the cell produces the new AliceBob protein, and that it has a function to perform which gives the cell a survival or reproduction advantage.

But the more relevant question for us right now is, what address label does the new AliceBob protein have? As individual microproteins, Alice and Bob were performing useful functions in the cell, which means they must have been produced by ribosomes. If they worked outside of the cytoplasm, they must have had their own address labels.

If they both worked at the exact same location and had the exact same address labels, then the new AliceBob protein would probably be posted to the same place. But if their work was in different locations, where would the new protein be sent? If it's sent to where Alice worked, Bob's place of work would notice his absence. If it's sent to where Bob worked, Alice's place of work loses a valuable employee.

Maybe the new AliceBob protein is sent to both locations. But what is the likelihood that the new much larger protein turning up at both places of work is an improvement, rather than a hindrance? Unfortunately, it's impossible to calculate the odds here. I will simply suggest that most of the time the combined AliceBob protein would be worse, and may even break the original function.

Either way, evolution faces a much bigger hurdle if the AliceBob protein is to be used in a different location from either Alice or Bob's place of work, because then a new address label has to evolve or be acquired somehow.

Since address labels are fairly specific, I would suggest it's close to impossible for AliceBob to evolve one *de novo*. If we take a short sequence of DNA coding for just 10 amino acids, this is 30 letters of DNA. There are roughly a million trillion variations of this sequence, which is 1 with 18 zeros.² But since mutations would be in the order of a One In A Million event for a specific sequence like this, the number of trials nature would need to run, just to evolve a specific address label consisting of 10 amino acids, would be something like a trillion trillion, or 1 with 24 zeros. This would be on top of evolving the functional part of the protein.

I suggest this would be far too impractical, and so probably wouldn't happen. While there may be some flexibility built into the address system, the situation would be closer to a "combination lock" scenario. Without a fairly specific and accurate address label, the AliceBob protein risks being labeled "return to sender" and destroyed. The postal system can't send it to locations that don't exist. And if AliceBob isn't useful, then natural selection can't save it from being mutated away.

In other words, if the AliceBob protein is to serve anywhere else besides where Alice and Bob originally worked, it will need to acquire a different address label. But there are no clear mechanisms in the cell that give newly evolved proteins new labels.

The third method of protein evolution is by gene duplication, where a gene somehow gets copied and pasted in its entirety, and then the duplicate gradually mutates into a new gene.

This method solves the problem of how it gets an address label, along with tags identifying it as a protein. They are copied from the original gene. Again, this is fine if the new protein works in the exact same location as the old one, but to be delivered somewhere else it needs a different address label. This is the real challenge.

The fourth method of protein evolution assumes a protein has two functions, a primary one and a secondary one. With this method, the secondary function is supposedly freer to evolve than the primary one, and may gradually evolve to become its own protein.

Many proteins do indeed have secondary functions, and even lots of functions. They don't just do one job. This method of protein evolution has been demonstrated for small proteins where functions can be interchanged because of the similarity of the structures, but whether this method can be extended to all or most larger proteins is a different question.

Either way, the key question for us is, how does a protein evolving through this method acquire its address label? If we call the original protein the parent, and the newly emerging one the daughter, I suppose it would be plausible for the daughter to inherit the same address label as the parent. But for the daughter to be used at a different location in the cell, it would need to acquire a different address label, and

there is no biological mechanism that allows for this, except through serendipity wands like “translocation.”

Incidentally, I’m not arguing that these methods of protein evolution are impossible. After all, if they weren’t designed, the existence of a vast library of proteins that organisms have available to them needs to be explained somehow. What I am suggesting is that these methods are a lot more theoretical than biologists like to make out.

My intention here has been to show that there is an additional layer of complexity nature has to deal with, when it comes to evolving a useful protein. It needs an address label to get it somewhere other than the cytoplasm. This makes a huge difference to what evolution can achieve.

From an evolutionary point of view, nature has only so much creative bandwidth to play with. Natural selection can only select from what is available at the time, and there are only a finite number of living organisms that have ever existed on Earth, meaning nature can run a fairly vast but still only a limited number of mutational trials.

It’s true that bacteria colonies can be measured in ridiculously large numbers with plenty of zeros in them, but they are still finite. Once we pass about forty zeroes in a number, we exceed the number of bacteria that are assumed to have ever existed on Earth in the evolutionary timescale. We reach a threshold of improbability that is measurable, at least approximately. In other words, if evolving something needs more trials than nature is capable of running, then it probably isn’t going to happen. This is the critical issue we are exploring.

The cellular postal system also poses an interesting riddle. If evolution built it from the ground up, then at some point it must have been simpler than the one used by all eukaryotic cells we know today, with their complex system of address labels and pathways, vesicles as taxis and filaments as highways.

But since the address label for a protein is already written into the genome, the postal system can’t easily evolve a different address system without large numbers of proteins suddenly being sent to the wrong place, which would probably result in chaos and the death of the cell. In other words, the core functions of the postal system must already be in place before a cell can function properly.

This sounds like a chicken and egg problem. Which came first, the postal system or the protein labels used by the postal system? Fortunately, evolutionary theorists have another magic wand to cover dilemmas like this. They call it “co-evolution.” The two evolved at the same time. Inventing a word doesn’t actually explain the phenomenon. It just labels it, making the problem seem to go away, and making it sound more believable to the general public.

Whatever the case, getting a newly evolved protein into a new or different place in the cell is an additional layer of complexity, because not only does the functional part of the sequence have to mutate into something useful, but an address label also has to evolve or be acquired, to get the protein to a place where it can be useful.

1 Technically, the “cytoplasm” is the cell substance between the membrane and the nucleus, while the “cytosol” is the fluid portion of the cytoplasm. **2** $4^{30} = 1.153 \times 10^{18}$, to 3 decimal places.

56. The Eukaryotic Advantage

Despite appearances, up until this point I have actually given evolution quite an easy time. I have shown that, under certain strict conditions, the information for small microproteins in bacteria could potentially evolve from scratch within a reasonable evolutionary timeframe, although how they acquire address labels is more problematic. But these are relatively simple problems compared with the next level of complexity found within cells.

There are two main types of cell – “prokaryotic” and “eukaryotic” – with a number of important differences between them. “Prokaryotes” are single-celled organisms, while eukaryotic cells are usually part of multi-cellular organisms, called “eukaryotes,” and their cells are much bigger than a prokaryotic cell.

Prokaryotes such as bacteria have a circular genome, with one or two “chromosomes” that contain the organism’s genetic information. Eukaryotes have genomes that are broken up into many linear chromosomes, allowing for a much larger information storage capacity. For example, this structure enables the human genome to contain over 3 billion pairs of nucleotides.

Eukaryotic cells also contain “mitochondria.” These convert oxygen into chemical energy, providing a power source for much of the cell’s activities, allowing them to do much more than prokaryotic cells.

Mitochondria contain their own DNA sequences, called “mitochondrial DNA” or mtDNA for short. Human mtDNA is made up of over 16,500 nucleotides in a circular, double-stranded DNA molecule, similar to those found in bacteria. This contains genes that make up what is called the “electron transport chain,” in which electrons are passed around to fuel proton pumps that create energy for the cell. The mtDNA also contains genes to make two major parts of a ribosome, and 22 genes for tRNA molecules that contain the genetic alphabet.

One evolutionary story of how mitochondria came to be goes like this: there was once a bacteria that invaded or was somehow engulfed by another prokaryotic cell, and gradually the invader merged with the host to become part of it, in a process biologists call “syntrophogenesis” or “endosymbiosis.”

How does one organism engulf or invade another, and get passed on with the offspring? If you swallowed a mouse, or one somehow managed to find its way into your gut, any future children you had wouldn’t have little mice in their gut.

On the other hand, trillions of bacteria live with us, often doing useful things. For example, lots of them live in our gut, helping with digestion, in a form of what is called “symbiosis,” where two or more different organisms live closely together in a helpful relationship. The important thing here is, our gut bacteria remain their own organisms. They are passed down from mother to baby, and this is usually beneficial for the baby.¹

However, mitochondria aren’t separate organisms. They are little organs (called “organelles”) in a cell. The blueprints for their manufacture are written into the

genome of an organism. The key question here is, how did a bacterial invader go from being an independent organism living in a host cell, to an organelle coded for by nucleotide sequences in the offspring of the host?

According to the evolutionary story, at first the invading or engulfed bacterium divided independently of the host cell, making many copies of itself, which would perhaps explain how it was able to get into the host cell's offspring. When the host divided, some of the invader's offspring found themselves in the daughter cells.

Next came the serendipity wand of translocation. The offspring of the invader fired off bits of their genome, and these were gradually incorporated into the host cell's genome, perhaps through the use of a DNA repair mechanism. A number of unspecified magical steps then occurred, assembling these bits over time into mitochondria by the host's genome. Evolutionary theorists assume that most or all of the invader's genome was translocated over to the host, but that most of it later mutated away, leaving only a tiny core of mitochondrial DNA that has been preserved by natural selection.

The evolutionary story skips over the exact step-by-step details of how this method of DNA acquisition can, over time, completely turn pieces of living bacteria into a cell battery. It would be like gradually salvaging parts from a shipwreck, only to find later that they have been assembled into a speedboat. The story also fails to tackle how all the parts acquire completely new address labels to assemble themselves at a specific place in the host cell, and how the host builds a blueprint to achieve this assembly.

Other research has challenged this story. Bacterial ribosomes are made up of about two-thirds RNA and one-third proteins, but this ratio is reversed in the ribosomes of mitochondria.² Plus, the link that supposedly connected mitochondria to bacteria isn't anywhere near as close as had been assumed.³

Furthermore, based on protein "superfamilies" – that is, groups of proteins that are assumed to be related – the code making up mitochondria couldn't have come from an individual bacterium, because half of the superfamilies aren't found in any one bacterium. However, they do occur in what is called the "universal common ancestor," the hypothetical ancestor of all organisms. As a result, some researchers argue that the mitochondria simply evolved in the more traditional manner.⁴

If mitochondria aren't engulfed or invading bacteria that turned into cell batteries after all, this shows how an evolutionary story can capture the minds of scientists, even if it turns out later to have been pure fiction.

But putting aside the exact way mitochondria are alleged to have evolved, and looking at them from a design perspective for a moment, why would they contain their own DNA molecules?

Since mitochondria are the powerhouses of the cell, their functions are critical. If they stop working, the cell dies. Their miniature DNA strand contains genes for their own version of a ribosome, which in turn produces many of the components needed to make power for the cell. This means mitochondria can repair and renew their own

machinery quickly and efficiently. They don't need to wait for the cell to send the components. Instead, they can manufacture them locally, saving critical time if anything goes wrong. This certainly makes for a good design feature.

Whatever the case, animal, plant and human life couldn't really exist without mitochondria. They provide the energy needed to support multi-cellular life. And this isn't the only "lucky" innovation for the eukaryotic cell.

In prokaryotic cells, the DNA molecule and the ribosomes are all in the main body of the cell. By contrast, eukaryotic cells – the cells of all plant, animal and human life – have an inner compartment called a "nucleus," which contains the DNA molecule and keeps it separate from the rest of the cell.

The nucleus is surrounded by a double membrane called the "nuclear envelope," which contains hundreds of channels called "nuclear pore complexes," or "NPCs" for short. Like cherubs guarding the entrance to Eden, NPCs control the entry and exit of large molecules through the nuclear envelope. The average NPC is built out of about 1,000 proteins that biologists call "nucleoporins." Many of these work together to form smaller units within the larger structure.

In an earlier chapter, I discussed how a sequence of DNA is transcribed, to create a strand of mRNA that provides the code to make a protein. I compared the DNA molecule to a library of books that couldn't be removed from the building. If you wanted to read a particular book, you needed to make a photocopy.

In eukaryotic cells, the "photocopy" of a DNA sequence is made inside the nucleus, as a strand of mRNA. The mRNA must then pass through one of the nuclear pore complexes and into the main compartment of the cell, the cytoplasm, before it can be translated into a protein.

To pass through the NPC, an mRNA strand is given the equivalent of a ticket that allows it to enter the central channel. Once it reaches the other side, it must give up its ticket, preventing it from re-entering the nucleus.

The presence of mitochondria, a nucleus and NPCs are defining features of eukaryotic cells. They are present in all plant, animal and human life. Clearly then, they are critical for creatures made up of more than one cell. Their core functions are virtually identical across the spectrum of eukaryotic life, with only fairly minor variations in species that are supposedly separated by a billion or more years of evolution.

Theorists assume these things must have evolved in or prior to what they call the "last common ancestor" of all eukaryotic cells, a particular ancestral cell that somehow bridged the gap between prokaryotes and eukaryotes.

The invention of a nucleus and nuclear pore complexes somewhat shields the DNA molecule from outside influences; but ironically, evolution needs this influence to produce large-scale changes. In other words, these new cell features should have put a substantial brake on evolution. Instead, what we see is an explosion of life based on this cell design. Either way, let's now turn our attention to building a nuclear pore

complex.

1 See the article "Like Genes, Our Microbes Pass from Parent to Child" by Martin J. Blaser, published at scientificamerican.com on March 1, 2015. **2** Sharma, *et al*, "Structure of the Mammalian Mitochondrial Ribosome Reveals an Expanded Functional Role for Its Component Proteins", *Cell*, 2003. See the "Introduction" section in particular. **3** See the article "Mitochondria's Bacterial Origins Upended" by Shawna Williams, published at the-scientist.com on April 25, 2018. **4** Harish, Kurland, "Mitochondria are not captive bacteria", *Journal Of Theoretical Biology*, 2017. See also the article "Overthrowing the Hegemony of the Culture of Margulis?" written by Susan Mazur, published at huffpost.com on August 22, 2017.

57. How To Build An NPC

Before we can build a nuclear pore complex (or “NPC”), let’s take a closer look at its structure, so we can understand the problem from an engineering perspective. To help you visualize these things, think of the nuclear envelope, the membrane of the cell’s nucleus, as a giant ball, into which we poke hundreds of holes spaced out evenly around it. We then fill the holes with NPCs, which act like channels to filter what gets in and out of the ball.

A typical human NPC is made up of about 1,000 proteins called “nucleoporins,” although there are only about 30 different types of nucleoporin. Some of them act as scaffolding, to keep the membrane of the nucleus curved and stable.

Around the central transport channel of an NPC are 8 identical spokes, made from 16 almost identical half-spokes. This means the channel is in the shape of an octagon. Research has shown that 8 spokes is the most efficient way of helping to transport very large molecules in and out of the nucleus.¹

If we were to cut an NPC open from top to bottom, we would see a central ring sitting between two outer rings, one facing down toward the nucleus, and one facing up toward the main compartment of the cell. The two outer rings act as a structural scaffold.

If we were to slice the NPC through the middle like a burger bap, the two halves of the bap would be mirror images of each other, which is why the inner core is called the “symmetric core.”

On the side of the NPC facing the nucleus, nucleoporins attach to the symmetric core and form what looks a little like a basket, so biologists call it the “nuclear basket.” It interfaces with the transcription machinery in the cell nucleus. On the side facing out, a different set of nucleoporins form filaments which assist transport through the NPC. These are referred to as “cytoplasmic filaments.”

The central channel has a barrier made up of several nucleoporins that contain stretches of repeated amino acid sequences, called “FG repeats.” This creates a kind of mesh that helps control what enters and leaves the nucleus.

Proteins called “karyopherins” recognize molecules that need to get in. When a molecule has an address label called a “nuclear localization signal,” it is helped through the NPC by a set of karyopherins that attach to the molecule and bind to the mesh. Energy for transport comes from what is known as the “Ran gradient.”

mRNA strands are produced in the nucleus, but the ribosomes needed to translate them into proteins are located in the cytoplasm, which is outside the nucleus. This means an mRNA strand needs to pass through an NPC. To indicate where it needs to go, the strand has an address label called a “nuclear export signal.”

While being transcribed in the nucleus, other proteins bind to the mRNA strand, to form what is called a “ribonucleoprotein complex” (or “mRNP”), that prepares the sequence for export. This is tagged with a “nuclear export factor,” a small protein that interacts with the mesh inside an NPC, helping the sequence through. It also serves as

a one-way ticket, because it is removed once the mRNP has made it to the other side, preventing it from going back into the NPC.

An interesting question we could ask here is: why are mRNA strands coding for proteins that are destined for the nucleus first of all exported, only for the proteins to be imported once they have been made? Wouldn't it be simpler just to make these proteins within the nucleus? Ribosomes are located outside the nucleus, so proteins couldn't be made without this step. But why aren't they also located in the nucleus, so at least some proteins could be made there?

I suspect this is for safety and quality control reasons. From a safety perspective, if proteins were made in the nucleus, there is a risk that faulty ones could damage or clog up the equipment that is critical for the healthy functioning of the cell.

Therefore, it makes sense that processes within the nucleus focus on storing and maintaining the information in chromosomes, and in transcribing some of this information in the form of mRNA strands, while more potentially dangerous functions, such as producing energy and building protein machinery, are done outside of the nucleus.

The export and import process can also provide quality control checks, to help ensure that mRNP sequences are in good shape before they are exported from the nucleus, and to make sure that only the right proteins are allowed in. Evidence indicates that the nuclear basket, which an mRNP needs to pass through to get into an NPC, can act as a hub for mRNA export quality control.²

In a living cell, nuclear pore complexes interact with other parts of the cell. However, for the moment, let's ignore this and think about what would be needed just to build one stand-alone NPC, one "hole" in the nuclear envelope.

First of all, we would need the raw materials, namely, the correct 1,000 or so nucleoporins. To help visualize one of these proteins, first picture a long balloon used by entertainers at children's parties, the kind that can be shaped into a man or a dog. Each balloon would be the equivalent of one amino acid, out of which proteins are built.

Now imagine several hundred of these balloons taped together to form one huge strand. The entire strand would visually represent one protein, one nucleoporin, and this would still be just one tiny piece of a nuclear pore complex. We would need about 1,000 of these strands of balloons to build an NPC. As a quick side note, I don't recommend trying to build a nuclear pore complex at children's parties.

In the microbiological world, proteins aren't as well-behaved as strings of long balloons. Different segments have properties that make them behave in certain ways. For example, some segments hate water. They are called "hydrophobic." Put them in water, and they will try to stay away from it, perhaps by hiding within other segments that love water, known as "hydrophilic." These and other properties, such as electrical charge and polarity, are part of the reason why some proteins can fold into shape almost by themselves, and why certain shapes are rigid enough to be used by cells as components for molecular machines.

In other words, building an NPC is far more complicated than simply twisting lengthy strings of long balloons around each other. We would also need to simulate the cellular environment in which an NPC is built, and the reactions to that environment by each amino acid in the protein sequence. I guess it could be done by smart human engineers, but it would be quite a feat, and would probably need to be done on a computer, in a virtual environment that simulated the conditions in a cell.

In addition, each piece would have to be fitted together in the right order, like a three-dimensional jigsaw puzzle in which certain pieces were repulsed by their environment, and some were attracted to it. In other words, for someone to build the equivalent of a stand-alone nuclear pore complex, it would be a formidable task requiring a lot of chemical and engineering knowledge.

Now, what is the story of how the nuclear envelope and NPC came about, according to evolutionary theorists? Nobody can be sure, because they weren't around to observe them evolving, but the story goes something like this:

Prokaryotic cells already had the ability to build a membrane, so perhaps another membrane accidentally mutated inside of a cell around the DNA molecule, forming what would eventually become the nucleus; or perhaps the development of an inner membrane was more gradual, evolving as an extension of the cell's own membrane. To begin with, it wasn't sufficient to shield the DNA molecule, but it somehow gave the cell a small survival advantage as it evolved.

Either way, a core scaffold co-evolved to support this new membrane, made up of proteins used elsewhere in the cell for membrane binding and tethering. Natural selection would then test out many different scaffold structures, and the one that worked best incorporated simple pores, which would gradually evolve into pores with basic gating mechanisms.

Since there is a symmetry to the NPC as we know it, multiple duplication events took place, where the structure of certain parts of the scaffold were duplicated, resulting in the symmetry we see today. Gradually the structure was improved on through natural selection, to include a more selective transportation system, until we arrive at our current NPC structure.

Stories like this perhaps sound convincing at first. Proteins are recruited from elsewhere. Functions get drafted in from one part of a cell to another. Sequences of code get duplicated. Throw in natural selection and vast amounts of time, and it almost sounds like the evolution of an NPC was inevitable.

But let's look at the details more carefully. First of all, the evolutionary story requires a complete or partial membrane to appear around the DNA molecule in one particular ancestral cell. For this to happen consistently in its offspring, some kind of control code is needed that regulates the construction of this new membrane from generation to generation, and calls up specific proteins in a particular order. But how can the control code organize the construction of this, and direct proteins to the right places, without new address labels for each protein?

Second, scaffolding is needed, to support the curvature of the membrane. Perhaps scaffold proteins were brought along by whatever events caused the new membrane to evolve, but how would these proteins get to their new places of work without new address labels? Indeed, how does the cell define the location of a place that didn't need to be defined before?

Third, the new membrane must be constructed carefully enough to allow transport in and out, so that the cell can not only continue to survive, but actually have a survival or reproduction advantage. If the new membrane lets nothing through, the cell dies, because the DNA molecule contains the blueprint for the cell's machinery. The membrane would effectively strangle the cell. On the other hand, if the new membrane let's everything through, evolution would likely discard it, unless it has some kind of useful function.

What about the nucleoporins that make up the NPC? Where could they have come from? Proteins are usually made up of one or more domains that fold into specific shapes. Research has shown that nucleoporins share a handful of similar domains, so biologists assume they evolved by the duplication and shuffling around of these domains from a smaller set of domains.³ Why the original domains would exist on their own at first isn't clear, and how whole sequences of code get shuffled around is also not clear; presumably a lot of the right type of copying and pasting would be needed.

Due to the symmetry of the NPC, multiple duplication events are assumed to have taken place during its supposed evolution. For example, nature could start with one half-spoke, and duplicate it seven more times to get the eight half-spokes. But that begs the question: what good is half a spoke on its own, before nature accidentally copied it another seven times? Evolutionary theory suggests it must have had a function, but these functions are rarely even explained, let alone scientifically tested.

To get eight whole spokes, nature could also duplicate all of the eight half-spokes at the same time. But this wouldn't arrange them into an octagon shape. If it did, this would imply nature knew that it was aiming for an eight-sided shape from the beginning, because the angles for each piece would need to be planned for in advance.

The point here is, duplication doesn't really explain the specific design of the NPC. Even after these alleged duplication events, nature still has to assemble the correct nucleoporins in the right order and shape.

Of course, according to evolutionary theory, nature doesn't have to figure out how to assemble 1,000 complex parts all in one go. It doesn't even need to start with 1,000 parts. It only has to make occasional tweaks, bring in or remove parts once in a while, and then test out slightly different designs through natural selection. We could think of evolution as a game of constant tinkering, played out over an almost endless series of rounds. The best tweaked design in one round goes on to compete in the next round.

But how exactly does nature get to play around with the design of an evolving NPC? The shuffling of nucleotides in a nucleoporin gene isn't really the answer, because nucleoporins share similar domains, with re-used fold structures. Furthermore, there are only about 30 choices of nucleoporin, but they are used multiple times in the NPC structure. Therefore, if the gene for one nucleoporin mutates, this may have a dramatic impact on the overall structure of the NPC.

The repeated use of only about 30 or so nucleoporins could actually be a design feature, meant to restrain changes caused by mutations. Too many mutations in any one nucleoporin would distort the shape of the NPC, perhaps even breaking it and thus killing the cell.

In theory, the way nature could test out alternative designs is by shuffling and tweaking parts of the blueprint that control how the NPC is put together consistently. But there doesn't seem to be a mechanism in the cell that allows pieces of the NPC to be shuffled around experimentally, like switching pieces in a jigsaw puzzle. There is only the serendipity wand of translocation; but this is often just a storytelling device rather than an actual mechanism. It's true that pieces of the genome can be translocated at times, but this usually happens in a strictly regulated manner by mechanisms following specific markers, pathways and blueprints.

Even if we allow for perhaps a virus or some other mechanism to do the job, this would still involve incredible serendipity. To test just one slightly different NPC design, an entire nucleoporin sequence would have to be cut or copied, and pasted into just the right place in the blueprint so the tweaked design could be made in the first place.

In other words, nature doesn't have an easy way of altering the design. And a similar problem exists for all of the complex structures found in the cell. Most proteins work alongside other proteins, and some of them form larger machines, called protein "complexes," which are often made from several, dozens or even hundreds of proteins. The nuclear pore complex is just one example.

What brings these proteins together in the right order? Clearly some kind of master blueprint needs to be in control of the process, so protein complexes can be built consistently and reliably, and so their designs can be passed down through the generations.

But how can these blueprints be improved on over time? According to classical evolution theory, they are tweaked through the game of Nucleotide Shuffle, the mutation of letters in DNA sequences.

From an evolutionary point of view, a cell is merely a vessel for the genome stored in a DNA molecule. A slightly mutated genome might be passed on to the offspring of an organism, and the offspring's cells are then built from it. If a mutation happens to give the offspring a survival or reproduction advantage, the mutated genome is more likely to be preserved than competing genomes. Or perhaps the organism just gets lucky.

Either way, nature doesn't have an easy way to piece together new protein complexes or try out alternative design plans. Evolutionary theorists talk about proteins and functions being "recruited" from elsewhere, but there is no cellular recruitment agency hiring proteins such as Alice and Bob who want to change careers. In other words, "recruitment" is just another serendipity wand, or another form of the "translocation" wand.

Besides, in the case of the NPC, there is yet another layer of remarkable complexity that has an enormous impact on its supposed evolution. Not only does it need to be assembled correctly, it also needs to be disassembled quickly when the cell goes through the process of division. This is critical, so the genome can be duplicated and passed on to daughter cells. In other words, while nature is supposedly evolving the NPC, it also has to figure out how to tweak both its assembly and disassembly at the same time.

The inner ring complex of the NPC is almost identical across all eukaryotic life forms, so it is assumed to be the core that holds the rest of it together. However, there is some flexibility in the size and shape of the outer ring complex, across different forms of life. Some also have wider or smaller pores, depending on the needs of the organism.

The way the NPC is put together, with its scaffold of similar building blocks, allows for this flexibility in the first place. It's almost as if nature had incredible foresight, by putting together a structure that could be adapted to suit the needs of a variety of creatures. But evolution has no foresight; so once again, in the evolutionary paradigm, this was all just incredible luck.

In the last few chapters, I have presented arguments implying that the features of eukaryotic cells pose a difficult challenge for evolution. However, in the next chapter I will present an intriguing line of evidence that suggests these features were deliberately designed after all.

1 Wolf, Mofrad, "On the Octagonal Structure of the Nuclear Pore Complex: Insights from Coarse-Grained Models", *Biophysical Journal*, 2008. **2** For more information, refer to the article "The Great Escape: mRNA Export through the Nuclear Pore Complex" by Paola De Magistris, *International Journal of Molecular Sciences*, 2021. See the "Remodeling at the Nuclear Basket" section in particular. **3** Devos *et al*, "Simple fold composition and modular architecture of the nuclear pore complex", *PNAS*, 2006. See "Evolution of the NPC" section in particular.

58. The Hebrew Tabernacle And The Eukaryotic Cell

As we have already discussed, eukaryotic cells contain power sources called “mitochondria,” as well as a “nucleus” which keeps the DNA molecule separate from the rest of the cell. Around the nucleus is a double membrane called the “nuclear envelope” which contains “nuclear pore complexes” (NPCs) restricting what can go in and out.

According to the story in the Bible book of Exodus, as the Hebrews wandered around the wilderness after coming out of Egypt, they were told by God to build a sanctuary that would later be called the “Tabernacle,” which they would carry around with them.¹ This turns out to have many intriguing similarities to the eukaryotic cell.

The Tabernacle was a large tent housing an inner tent called the “Tent of Meeting.” If we compare this to the eukaryotic cell, the inner tent would be the equivalent of the cell nucleus. The inner tent was divided into two rooms: the “Holy” and the “Most Holy.” Inside the Most Holy was the Ark of the Covenant, which contained two tablets of stone with the Ten Commandments on them, said to have been “written by the finger of God.”² Two poles were permanently attached to the Ark. The two tablets would correspond well to the genome of an organism contained within the DNA molecule, which is stored in base pairs. The two poles could correspond to the two strands of the DNA double helix.

Separating the Holy from the Most Holy was a curtain, beyond which only the high priest could enter once a year on the Day of Atonement. It was described as “a curtain of blue and purple and scarlet, of double and twisted linen, the handwork of a designer who will make its cherubs.”³

The Holy could correspond to the nuclear envelope, which separates the nucleus from the rest of the eukaryotic cell. For some reason, most translations don’t include the word “double” here, but it is there in the Hebrew, and the nuclear envelope is also a double membrane. The “blue and purple and scarlet” of twisted linen could represent the mesh of FG amino acid repeats within the central channel of a nuclear pore complex, helping to regulate what goes in and out of the nucleus.

In the Holy was a table and lampstand. Moses was instructed to “put the table outside the curtain and the lampstand opposite the table on the south side of the tabernacle,” and to “put the table on the north side.”⁴ Utensils for drink offerings were placed on the table, along with pieces of bread called the “showbread,” which Aaron and his sons were allowed to eat.⁵

The lampstand matches up well with the nuclear basket, the protein complex found on the inner side of a nuclear pore complex, and which might look somewhat similar to a lampstand. The table with its showbread and utensils would match up with the various proteins such as the karyopherins, associated with the outer side of an NPC, with the bread perhaps representing the energy for transport; although given that Aaron and the priests were allowed to eat it, instead of “Ran gradient” we could think of the bread as the “Aaron gradient.”

In human cells, each NPC has a central channel, around which are 8 identical spokes built from 16 half-spokes. There is also a central ring that sits between two outer rings, one facing the nucleus and one facing the cytoplasm.

The rear section of the Tabernacle, which was on the west side, sounds remarkably similar to an NPC. Its construction was described this way: "And you will make six panels for the sides of the tabernacle to the west, and you will make two panels as corners of the tabernacle in the sides. And they will be coupled from below, and together they will be coupled on top of it to one ring; so it will be for the two of them. They will be for the two corners. And they will be 8 panels, and joints of 16 silver joints, two joints under the one panel, and two joints under the one panel." ⁶

The Hebrew word here translated "corners" comes from a word meaning to "cut out," which would be a good choice if some kind of a hole cut out of the framework was being implied. Also, the exact phrase translated here as "two joints under the one panel" is repeated twice in the Hebrew, making them duplicates of one another. The 16 silver joints correspond well with the 16 half-spokes of an NPC that make up 8 spokes, which would then be represented by the 8 panels.

These panels formed the sides of the Tabernacle, yet they are somehow coupled to "one ring." There was also a middle bar in-between the panels, reaching from end to end.⁷ This would then correspond to the central ring of an NPC. Eight panels could then be coupled to form a "ring" above and below the middle bar, in the same way that the half-spokes in a human NPC are coupled to create two outer rings.

Within eukaryotic cells are mitochondria, the powerhouses of the cell. These contain their own circular DNA strands (called mtDNA), and they are 16,569 nucleotides long in humans. I would suggest that mitochondria are represented, in a cryptic manner, with the tribe of Levi and their families. The numbers associated with these families seem to imply circles and the length of mitochondrial DNA. To show this, first let me give some details about these families.

While Aaron and his sons served as priests in the Tabernacle, males from the tribe of Levi aged between 30 and 50 assisted the priests by carrying out various duties.⁸ The tribe of Levi consisted of three families: Kohath, Gershon and Merari. When the Tabernacle was to be moved, the priests, the sons of Aaron, were to cover the holy place and its utensils. The sons of Kohath were to carry those items, but they weren't allowed to touch or look upon the holy place. The sons of Gershon were assigned to carry the tent cloths and curtains for the rest of the Tabernacle, and the sons of Merari were assigned to carry its panels, frames, joints and bars.⁹

A census was taken of the males from a month old and upwards. There were 7,500 from Gershon, 8,600 from Kohath and 6,200 from Merari. While the total here is 22,300, the book of Numbers refers to it as 22,000. Also, some manuscripts of the Greek *Septuagint* put the number for Kohath at 8,300 instead.¹⁰

Moses and Aaron then registered those between 30 and 50 years of age, the age of service. There were 2,630 from the family of Gershon, 2,750 from the family of Kohath, and 3,200 from the family of Merari, making a total of 8,580.¹¹

They were also told to register all the Israelite males a month old and up, which came to 22,273. A ransom price of five shekels each was paid for the 273 who were in excess of the 22,000 Levites, for a total of 1,365 shekels.¹² The relevance of these numbers will become clearer in a moment.

The mathematical constant π is the ratio of a circle's "circumference" (the distance around the edge of a circle) to its "diameter" (the widest distance across). The "radius" is the distance from the center of a circle to its edge.

Historically, the smallest fraction that has been used to approximate π is $22/7$, which is also the equivalent of $858/273$. If we use this for π and take 1,365 as the radius of a circle, then the diameter of the circle would be 2,730 and the circumference would be 8,580, the same number as the sons of Levi who were of the age of service.

Since mitochondria are only found in the outer compartment of the cell (the "cytoplasm") if there was a correspondence with the Tabernacle to mitochondrial DNA, it would most likely be found in the numbers for Gershon (2,630) and Merari (3,200), who were assigned over the outer tent. This is indeed what we find. If we take the number 2,630 as the radius of a circle, then the circumference would be about 16,525, which is just 44 short of 16,569, the number of nucleotides in human mtDNA, which is circular.

The sons of Merari camped on the north side of the Tabernacle, the sons of Kohath on the south side, and the sons of Gershon on the west. These three camps formed a triangle around the Tabernacle. Moses and the priests camped on the east side, so that the four camps also formed a square.¹³

If we take the numbers 2,630 and 3,200 (associated with Gershon and Merari) as the smaller sides of a right-angled triangle, then the side opposite the right angle would have a length of just over 4,142. If we take this to be the side of a square, then the square's perimeter would be 16,568, just one digit short of 16,569, the number of nucleotides in human mtDNA.

Mitochondria, the powerhouses of the cells, produce "adenosine triphosphate," usually abbreviated to ATP. This is often referred to as the molecular unit of currency. It's the chemical providing the energy that drives many of the processes in living cells. A large amount of the ATP required to power eukaryotic cells is generated in a remarkable way, which involves shuffling protons and electrons around.

The main machinery that produces ATP is a protein complex called "ATP synthase," contained in the membrane of mitochondria. It is like a wind or water turbine, but powered by protons. The space between the double membrane acts as a barrier to protons, which are pumped into it with only one way to escape – through the ATP synthase machine. This flow of protons enables it to make ATP.

Even more remarkable is how protons are pumped into the intermembrane space. The process involves four protein complexes, collectively called the "electron transport chain." The first complex receives two high energy electrons which are then passed on, releasing a small amount of energy that is used to pump four protons

across the membrane. The second complex is similar but it doesn't pump protons. Both of these complexes pass their electrons to a carrier molecule, which then transports them to the third complex, where four more protons are brought across the membrane.

Electrons are then transported by another carrier to the fourth complex, where four electrons, four protons and a molecule of oxygen are converted into two water molecules, and another four protons are pumped into the intermembrane space, making it even more tightly packed with protons. Incidentally, this is why we breathe. It provides oxygen for the fourth complex in the electron transport chain.

I think this process is alluded to in the description of the Tabernacle after it was set up for the first time. The twelve chieftains of Israel made a special offering: "They brought their offering before YHWH, 6 coach carts and 12 oxen, a cart for two of the chieftains and an ox for one, and they brought them before the Tabernacle." ¹⁴ The 6 carts could represent 6 electrons, and the 12 oxen could represent the 12 protons that are pumped into the intermembrane space.

YHWH said to Moses: "Take them, and they will serve for the service of the tent of meeting, and give them to the Levites, as needed by a man for his service." ¹⁵ In the case of the electron transport chain, this is what keeps us and our cells alive, so is literally "needed by a man for his service" and for the service of individual cells.

Moses distributed the carts and cattle to the Levites: "He gave two carts and four oxen to the sons of Gershon, as needed for their service; and he gave four carts and eight oxen to the sons of Merari, as needed for their service." ¹⁶ The Levites were then cleansed with water, and offered two young bulls as offerings.¹⁷

The 2 carts and 4 oxen given to the sons of Gershon could represent two electrons received by the first complex and the four complexes of the electron transport chain. The 4 carts and 8 oxen given to the sons of Merari could represent the four electrons in the fourth complex, and the 8 subunits that make up the ATP synthase machinery. The two young bulls could represent the two electron carriers.

Now, while it could be argued that each of these things, when taken by themselves, could simply be coincidence, if we take the Tabernacle and the Levites who serviced it, and compare them to the way the eukaryotic cell works, a number of intriguing parallels can be found, that seem unlikely to be coincidence when taken together. Let me briefly recap the most significant correspondences.

The eukaryotic cell has an inner compartment (the nucleus) that houses the double-stranded DNA of the cell. The Tabernacle had an inner compartment (the Most Holy) that contained the two tablets of stone, written on by God's finger.

In the cell, a double membrane (the nuclear envelope) separates the nucleus from the outer part (the cytoplasm). In the Tabernacle, there were two curtains containing an area called the Holy that separated the Most Holy from the courtyard.

In human cells, the nuclear envelope is punctuated with nuclear pore complexes (NPCs) of 8 spokes built from 16 half-spokes, and a central ring that sits

between two outer rings. The rear section of the Tabernacle was made of 8 panels and 16 silver joints, joined above and below one ring.

Facing toward the nucleus in each nuclear pore complex is the nuclear basket, while facing outwards are karyopherins. In the Holy of the Tabernacle was a lampstand, and opposite it was a table of showbread.

Mitochondria are found in the cytoplasm, and contain their own circular strands of mtDNA consisting of 16,569 nucleotides in humans. The families of Gershon and Merari were assigned over the outer tent of the Tabernacle. Taking their numbers as the length of two sides of a right-angled triangle, the third side would be just over 4,142 in length. Using this as the side of a square, the square's perimeter would be 16,568, just one digit short of 16,569.

The electron transport chain consists of four complexes that shuffle six electrons to pump twelve protons into an intermembrane space, needed to power cells. The chieftains of Israel brought an offering of six wagons and twelve oxen before the Tabernacle, which was given "as needed by a man for his service."

I would suggest that the Tabernacle, which the Hebrews carried around in the wilderness, represented the eukaryotic cell, presumably to help us understand that the God of Israel was also the creator of life on Earth. I suppose this is why God told Moses: "Set up the tabernacle according to its manner which you were shown in the mountain."¹⁸ If the Tabernacle was meant to represent the eukaryotic cell, it would have been important for Moses to accurately copy the blueprint given to him! The idea that the Tabernacle represented something deeper is also found in the Christian New Testament, where the author of the book of Hebrews says that the Tabernacle and those serving in it were "a copy and shadow of the heavenly sanctuary."¹⁹

One final reason why the Hebrew Tabernacle makes a good representation of the eukaryotic cell, is that just as the nuclear envelope in the cell needs to be rapidly assembled and disassembled, the Tabernacle was also a tent that could be assembled and disassembled quickly.

Incidentally, to help you remember the type of cell the Tabernacle compares with, just remember that the Hebrews had to carry it around with them in the wilderness. In other words, "you carry it," and the type of cell it represents is a "eukaryote," which we also carry around in our bodies.

1 Exodus 25:8,9. **2** Exodus 31:18. **3** Exodus 26:31. **4** Exodus 26:35. **5** See Leviticus 24:5-9. **6** Exodus 26:22-25. **7** Exodus 26:28. **8** Numbers 8:19. **9** Numbers 4:3-15, 21-33. **10** Numbers 3:21-39. **11** Numbers 4:34-49. **12** Numbers 3:40-51. **13** Numbers 3:23,29,35,38. **14** Numbers 7:1-3. **15** Numbers 7:5. **16** Numbers 7:7,8. **17** Numbers 8:6-8. **18** Exodus 26:30. **19** Hebrews 8:5.

59. Correcting Errors And Repairing Damage

One of the most important things in a cell is the information stored within the DNA molecule. The cell needs this to access the blueprints for proteins and machinery. Preserving this information is therefore one of the cell's top priorities.

In the process of human cell division, the cell has to copy all of the 3 billion or so "letters" that make up the human genome. It does this at a very rapid rate, copying as many as 1,000 nucleotides a second, many times faster than a human typist.

The machinery that copies the genome is called "DNA polymerase." Due to the nature of the copying process, errors occur at a rate of about 1 every 100,000 nucleotides. This might sound low, but it would result in tens of thousands of mistakes creeping in every time the human genome was duplicated, which would be highly damaging to our offspring.

However, during duplication of the genome, two error correcting processes virtually eliminate these mistakes. The first is equivalent to proofreading each letter by its shape. If the shape of the letter isn't right, the copying machinery moves back a little, cuts out the wrong letter, and replaces it with the correct one.

The second is called "mismatch repair," where the old and new strands are compared, and incorrectly paired nucleotides are removed and replaced. Taken together, these two processes reduce the error rate to around just one in a billion nucleotides.

Earlier in this letter I put forward the hypothesis that the account of Jacob's life with Laban, as told in the book of Genesis, was also meant to serve as a series of analogies for various molecular biological processes. For example, Jacob's dream of the ladder represented the structure of DNA. His four wives represented the four bases used in DNA, and so on. Remarkably, we can also make parallels in Jacob's story to the two error correcting processes I have just described.

When Jacob and his family ran away from Laban, Jacob's wife Rachel stole her father's household idols. Laban chased after them, to find out why they had run away and why his idols had been stolen.

Jacob said to Laban: "With whom you find your gods, he will not live. Before our brothers, identify what is yours with me, and take it to you." ¹ Jacob didn't know Rachel had stolen the idols. She had hidden them in the saddle basket of the camel, and then sat on them.

Laban looked in the tent of Jacob, the tent of the two maidservants, and the tents of Rachel and Leah, "and Laban felt all of the tent, but did not find them." ² And "he searched, but he did not find the idols." ³ This could represent the first error correcting mechanism, which uses shape to find the error.

Jacob got angry, and said to Laban: "What is my error? What is my sin, that you chased after me, that you felt all of my belongings? What have you found, from all of the belongings of your house? Put it here before my brothers and your brothers, and they will correct between the two of us." ⁴

The word here translated “error” can mean error or transgression, and the word “correct” can also mean to reprove, but the Hebrew literally also means to correct. In other words, this would make a good analogy for mismatch repair, the second error correcting mechanism, where both strands are compared, and the new strand is corrected.

It’s also interesting that idols (*teraphim* in Hebrew, pronounced “tera-pheem”) would be used to represent errors, and they were stolen by Rachel, who I have previously suggested corresponds to one of the four DNA bases. Most of the creative mechanisms of evolution, which according to theorists are responsible for all life as we know it, are actually based on errors – from mutations, which are primarily copying errors or damage, to duplications, which are often just bigger copying errors. The serendipity wands of translocation and magical steps, as waved by evolutionary theorists, may or may not be based on error, but they are usually based on luck. In evolutionary theory, the idols of luck and error replace YHWH who claims to have created all things.

Now, a fair question we could ask at this point is: if these microbiological processes were actually designed, why include mechanisms to correct errors? Why not just make the copying process completely accurate in the first place?

I think there are two good explanations. First, copying has to take place with real molecular machinery, which places natural constraints on the system. A perfect copying system might be possible, but perhaps it would need extra equipment that wouldn’t fit easily into the microscopic space inside a cell.

Second, and perhaps a more important consideration, is that there are also time constraints. A cell needs to divide in a timely manner, so the organism can grow and survive. An extra error correcting step might increase the accuracy by additional orders of magnitude, or maybe a perfect copying system could be devised, but it could also increase the copying time by several orders of magnitude, severely hampering the growth of the organism and the renewal of its cells. In other words, I suspect the system may already be optimized to be as efficient as possible, within those time and space constraints.

Errors can also occur when proteins are being produced, but most organisms have processes to ensure only correct proteins are made. In an mRNA sequence, often referred to by biologists as a “transcript,” a stop codon tells the ribosome to stop making the protein chain. But sometimes a mutation or copying error can cause a stop codon to appear too early in the transcript. This could lead to the production of a faulty protein, which may be harmful to the cell.

However, a process called “nonsense-mediated decay” looks out for transcripts with premature stop codons. Another called “non-stop decay” looks for ones that lack a stop codon altogether, and therefore could get stuck in the ribosome. Yet another called “no-go decay” looks for transcripts that get stalled during the translation process. In each case, the faulty or incorrectly made protein is eliminated, to prevent it from causing cell damage.

Another type of fault that sometimes happens to a transcript is called “frameshift mutation.” In this, a letter gets accidentally added or deleted. But since transcripts are read by ribosomes in sets of three letters, a letter added or removed will often drastically change the meaning of the sequence, and produce a “nonsense” protein. For example, if we took the sentence THE CAT WAS FED, and added the letter R as a mutation before the letter C in CAT, since ribosomes read three letters at a time, the sentence would now read THE RCA TWA SFE D – which destroys most of the original meaning.

Remarkably, out of all the possible alternative coding structures that could have been used, the one used primarily in nature minimizes the effect of frameshift mutations. How so? Due to the structure of the genetic code, a frameshift mutation is more likely to result in a stop codon appearing within the transcript, triggering the “nonsense-mediated decay” process so that the faulty protein doesn’t get made. Even the specific choice of stop codons in the human genetic code – UAA, UAG and UGA – have been shown to be optimal for achieving this effect.⁵

The two cells that come about as a result of cell division are usually referred to by biologists as “daughter” cells. Another way that prevents errors from being passed on are called “cell cycle checkpoints.” They stop the cell from dividing until damage, faults or errors have been put right. These checkpoints ensure the daughter cells are preserved from damage.

For example, when bacteria are exposed to ultraviolet radiation that causes damage to their DNA, this triggers what is called the “SOS response,” which sets about to repair the damage. At the same time, it produces a protein that blocks cell division, so the genome isn’t passed on to the daughter cells until the damage has been repaired.

In eukaryotic cell division, each daughter cell receives one copy of a duplicated chromosome. Tiny filaments reach out and pull the duplicates to opposite sides, so they end up in different daughter cells. However, if a chromosome isn’t attached properly, a checkpoint signal prevents movement toward the sides. This ensures a potentially damaged genome isn’t passed on to the daughter cells.

We can find a striking analogy for cell cycle checkpoints in the story of Jacob and Laban. After they had gone through their “error correcting” ritual over the stolen idols, they both agreed to build a mound of stones as a witness between each other, that neither would pass to do harm to the other.

Laban said to Jacob: “If you mistreat my daughters, and if you take women besides my daughters, no man being with us to see you – God is a witness between me and you.” And again: “Look! this mound, and look! the monument which I have set between me and you. This mound is a witness and the monument is a witness, that I will not pass over this mound to you, and that you will not pass over this mound and this monument to me for bad.”⁶

After this, Laban departed, and angels of God came to Jacob, so he named the place he found himself in Mahanaim, meaning “two camps.”⁷ He also divided what he

had into two camps.⁸ This reinforces the idea that, in addition to the plain meaning that Laban was telling Jacob not to abuse his daughters, or God (and angels) would be a witness to it, the mounds they built between each other also represent cell cycle checkpoints, particularly before the division of the cell into two daughter cells, two “camps” as it were.

These checkpoints prevent the daughters from being “mistreated” in the sense of inheriting a damaged genome; and since I earlier suggested that Jacob’s four wives represented the four DNA bases, taking other women besides these could represent damaging additions to the genetic sequences that are passed on.

Now, even in the protective environment of the cell nucleus, thousands of nucleotides are damaged in each DNA molecule every day. Water degrades DNA over time, and chemicals and radiation also damage it. However, the cell has several DNA damage response systems. Without them, the genome of an organism would decay rapidly, and life would be impossible to sustain. These systems also tend to initiate a checkpoint which halts cell division until the repairs have been completed.

In cases where a single strand of the DNA double helix is broken, the cell can perform “base excision repair,” where the damaged nucleotide is removed and DNA polymerase machinery inserts the correct base, which is then chemically “glued” to the rest of the strand.

When more than one nucleotide needs to be removed, a process called “nucleotide excision repair” can be used, where the damaged section is removed and replaced with the correct sequence. In both cases, the other strand of the double helix is used as the template to identify the correct nucleotides.

Double-strand breaks, where both strands of the double helix have been broken, tend to be more serious and can even result in the death of the cell. These can be repaired in a process called “homologous recombination.” An undamaged section of similar DNA is used as a template. The damaged and undamaged strands exchange nucleotides, and then any gaps are filled in.

If this process can’t be used, the broken ends can still be joined together in a process called “non-homologous end-joining.” This almost always involves a loss of information, but at least the cell may still be able to function normally.

However, if more serious damage to the genome has occurred, the cell is likely to produce faulty proteins and machinery, and become a potential danger to the rest of the organism. In this case, the cell undergoes “apoptosis” or programmed cell death.

Incidentally, how does the cell know where to find a fault in a molecule consisting of millions or even billions of nucleotides? There are a number of mechanisms it uses, but one is particularly remarkable and worth describing briefly here. It turns out that the DNA molecule can also act like an electrical wire, and electrons can be sent down it in a process called “DNA charge transport.”

Repair proteins use this system to scan for mutations. They bind to the double helix and slide along it, sending out electrons down the DNA strand like engineers

testing the line. If the double helix isn't damaged, the electron reaches a second repair protein which then leaves the strand. But if there's a fault, this repair protein doesn't receive the electron signal and continues moving towards the damaged section.

With all of these error correcting and damage repair systems, cells clearly work hard to preserve the information they inherit. But this raises two important questions. First, how did the information in DNA molecules survive before these correction and repair systems supposedly evolved? If they really did evolve, there must have been a time when the systems didn't exist. But error correcting and damage repair are critical for viable genomes to be passed on to future generations of cells.

The second question is, how can these systems actually evolve in the first place? Think of the engineering wisdom required to design a system that can correct damage to just one nucleotide, as in base excision repair. At the very least, the system would need to be able to detect a fault, latch on to the double helix, cut out the faulty nucleotide, bring along the correct nucleotide, and glue it into place somehow.

Evolutionary theorists argue that some or all of these functions already existed in some form within the cell, so it's simply a question of recruiting these existing functions. For example, DNA polymerase, the machine which copies the genome, comes with the ability to cut out and repair an error. Maybe a more general damage repair system evolved from this.

But the real challenge for evolution is, how do all of the specific proteins and functions needed to perform base excision repair come together to form the new process? How do the proteins involved acquire new address labels, and how do the functions get new instructions? The process can't evolve in a gradual step by step manner. All of the steps I listed a moment ago need to happen in order to perform base excision repair. If any step is missed out, the repair won't take place.

Another intriguing question is, how did the shuffling of nucleotides, which evolution ultimately is, figure out how to send an electron down the DNA spiral, like an engineer testing a signal? And what happened before this system supposedly evolved?

Besides, an even bigger problem for evolution in general is, systems employed by the cell to protect its DNA molecule from damage and mutations places strong limits on what evolution can actually achieve.

For a directly relevant analogy, consider the field of "evolutionary programming." In this field, computer software is actually designed that can evolve programs. In these programs, modules, functions or lines of code can be switched on or off, or shuffled around, in an attempt to find more efficient versions of the program.

The rules written into the software determine how programs running within the software can evolve. However, the software itself can't mutate. If bits of the software were to do so, it would begin to fail along with the programs evolving within it. Similarly, the software can't change the computer's operating system, which governs what the software can do, without breaking itself.

In other words, evolving programs are restrained by the software designed to allow them to evolve in the first place; and the software itself is restrained by the computer's operating system.

We could compare the genome of an organism to a computer's operating system, and perhaps also the software in our analogy. Of course, a genome is far more advanced than software that humans write. After all, genomes contain a blueprint for the development of an entire organism, as well as blueprints for complex machinery, control sequences and individual genes.

The operating system used by cells is also very flexible. Rather than just being limited to switching things on or off, the cell can change how much of a gene is produced. It's an exquisite network of feedback and control. However, in many ways it operates according to the same principles used by computer programmers.

Programmers also use algorithms, which are sets of instructions to perform an operation or solve a problem, and they use loops to perform an operation until certain criteria are met. These must also be part of the genome's operating system, so that an organism made up of trillions of complex cells can be built out of code stored in a few billion nucleotides.

Programmers also use functions and modules, which are pieces of code dedicated to a specific task or sequence of tasks. We might think of genes and control sequences as being similar to these.

However, just as in evolutionary programming, where the rules of the software restrain how a program can evolve, the error correcting and damage response systems used by cells place limits on what evolution can actually do. These systems actively prevent unauthorized changes to the data in the genome, just as evolutionary programming software can't allow changes to itself.⁹

Replicating single-celled organisms such as bacteria tend to produce clones, which are copies of themselves. However, in sexually reproducing organisms there is a built-in system that allows for genetic variety. When producing new sperm and egg cells, called "gametes," genes are selected from the gene pool available to the two mating organisms.

In a process called "recombination" or "crossing over," genes between father and mother are exchanged, similar to the damage repair process of homologous recombination, but with a certain amount of randomness. This is a major way in which variations in a population are produced. Checkpoints are also present here too. If the genes to be crossed over aren't of the same length, the production of gametes is aborted.

Nature uses this system to produce variety. For example, the finches Charles Darwin observed on the Galapagos Islands had differing sizes of beaks. If hard seeds are all that are available to Darwin's finches in a particular year, ones with a combination of genes to produce a broad beak will survive, and the population will change to reflect this.

When food that requires a sharp beak is all that becomes available, finches with a combination of genes producing this beak will become dominant. This is natural selection at work, but nature is only selecting from an already existing gene pool which allows for variety. The creatures remain finches.

In other words, the sexual reproduction system allows for variation, which may be a major source of speciation, but the mutation protection systems used by cells actively work to prevent mutations, which according to evolutionary theorists is claimed to be the primary source of new functions and features.

Small-scale evolution is allowed, that changes beak size and shape, through the process of genetic recombination or "crossing over," but evolution that changes the software or operating system of an organism is actively prevented. In short, small-scale variation is built into the system, while large-scale evolution is blocked.

Furthermore, these mutation protection systems must have been in place from near the start of life on Earth, so that information in DNA could be preserved in the first place. This means large-scale evolution was blocked from the beginning!

By now it shouldn't be entirely surprising that we can also find an analogy for the biological process of crossing over in the story of Jacob. After splitting his camp into two, which represented cell division, Jacob selected a gift for his brother Esau.

"And he lodged there for the night, and he took a gift for Esau his brother from what had come into his hand: two hundred female goats and twenty male goats, two hundred female sheep and twenty rams, thirty suckling camels and their offspring, forty young cows and ten young bulls, twenty female donkeys and ten colts. And he gave the drove into the hand of his servants, the drove by itself. And he said to his servants: 'Cross over before me and put an interval between drove and drove.'" ¹⁰

Human genes contain regions called "introns" that don't code directly for proteins, and they are typically ten times bigger than the coding regions or "exons." The gift Jacob sent Esau is an analogy for one full human gene, the "two hundred" representing introns and the "twenty" representing exons. The other animals could represent address labels and sequences to mark it as a protein. The gene is treated as one "drove" in the biological process of crossing over, but it is really a collection of smaller "droves" separated by "intervals," the introns.

The account continues: "And the gift passed over before him, and he lodged that night in the camp. And he rose that night, and he took his two wives and his two maidservants and his eleven children and he crossed the ford of Jabbok. And he took them and he crossed them over the river, and he crossed over what was his. And Jacob was left alone. And a man wrestled with him until the ascending of the dawn." ¹¹

The Hebrew word here translated "ford" means "place of passing," and is related to the word here translated "crossed" (*abr*, pronounced "av-air"), which is used three times in the passage to describe crossing or passing over. In other words, the writer really wanted to emphasize the act of crossing over or passing something on. And the name of the river, Jabbok (*ibq*), contains three of the letters from Jacob's own name (*ioqb*), in a recombined order.

This is also what the “recombination” or “crossing over” biological process is all about. It’s about passing on genes from the parents to the next generation. Jacob is left alone on one side of the river, with his wives on the other, which also matches up with the idea of genes from the father and mother crossing over.

What about the unusual wrestling match that takes place immediately afterwards? Earlier I pointed out that this can remind us of the switch from thymine to uracil when going from DNA to RNA. However, in the context of biological crossing over, another form of wrestling is involved.

In normal cells, two copies of a gene are stored, one from the father and one from the mother, and they can be slightly different. These variations of the same gene are called “alleles,” and in the case of recombination, one allele becomes “dominant” and the other “recessive.” The dominant one is expressed, while the other is dormant. One isn’t really stronger than the other, the term just helps to determine which version of the gene gets used and which one gets stored as a backup.

The system of alleles also places another limit on what evolution can actually do. If genes between father and mother don’t match strongly enough, recombination can’t happen. Incidentally, the “homologous recombination” damage repair system uses the backup gene from the father or mother as a template for repair.

Jacob’s wrestling match serves as an analogy for the concept of dominant and recessive alleles. In the end, Jacob won. His genes became “dominant.” The account repeatedly tells us this all happened in the night, and the Hebrew word for “the night” (*lile*, pronounced “lah-yil”) is similar to the word “allele.” Curiously, even the Hebrew word here translated “wrestled” (*iabq*), which is used only in this account, seems to convey extra meaning. The word is similar to Jacob’s name (*ioqb*), except the Hebrew equivalent of “a” has become “o” and the “b” and “q” have been swapped. The two words (*iabq* and *ioqb*) would make a good analogy for alleles, genes that are structurally similar.

Let’s briefly recap the main biological analogies I have been able to make from the account of Jacob’s life with Laban. Jacob’s dream of the ladder represents the DNA double helix. The three flocks lying on the well represent DNA as an information storage medium for codons. Jacob’s four wives – Leah, Rachel, Bilhah and Zilpah – represent the four bases of DNA – adenine (A), cytosine (C), guanine (G) and thymine (T). They are paired into purines (A and G) and pyrimidines (C and T), just as Rachel is paired with her maidservant Bilhah and Leah with Zilpah. Jacob’s twelve children also come in pairs, representing a DNA sequence, or as Rachel put it as she named her son Naphtali, “the twistings of God!”

Jacob’s wages represent the process of “transcription” from DNA to mRNA, and the change from a thymine (T) base in DNA to uracil (U) in RNA. Jacob taking three sticks, peeling the bark, and putting the sticks into the troughs for the flocks to conceive represents the process of “translation,” where the “flock” of mRNA is converted by the ribosome “trough” into a protein. The “sticks” represent amino acids put into the ribosome to “conceive” a protein.

Jacob putting the stronger of the flock in and leaving the weaker out represents the splicing process where introns (regions of a gene that don't code for the protein) are left out, and also the biological concept of selection or survival of the fittest. Turning the faces of the flock represents protein folding. His complaint that Laban kept changing his wages ten times represents mutations.

When Jacob's family left, Rachel stole Laban's household idols, and Laban came and felt around in all of their tents, and then Jacob told him to put what he had found before them so it could correct between the two of them. These represent the two error correcting processes used when copying the genome before cell division.

The mounds Jacob and Laban built as a witness and boundary so they wouldn't pass to do bad to each other represent cell cycle checkpoints. Jacob then split his camp into two, gave a gift to his brother Esau, crossed his family over the ford of Jabbok, and wrestled with a man – which represent cell division, the exchange of genes in the biological process of crossing over, and dominant and recessive alleles.

At this point, I would like to make the hopefully obvious observation that this isn't coincidence or reading into the account. There is only one possible way I could make so many analogies in a story spanning a mere five chapters of the book of Genesis – Jacob's life with Laban was deliberately orchestrated by YHWH to match up with molecular biological processes.

God must have known in advance that humans would forget about him over time, as they have always done throughout history, and so he has provided skeptics and atheists thousands of years later with the extraordinary evidence they demand for his existence. This cluster of analogies is, in effect, the Signature of YHWH, the Creator of the heavens and the Earth and the creatures living on it; and he is the God of Jacob.

This "Signature" also serves as the ultimate error correcting and damage repair process. It corrects the fallacy that these biological processes came about by themselves as a result of endless luck and perpetual errors.

1 Genesis 31:32. **2** Genesis 31:34. **3** Genesis 31:35. **4** Genesis 31:36,37. **5** Naumenko *et al*, "On the optimality of the standard genetic code: the role of stop codons", 2007. **6** Genesis 31:50-52. **7** Genesis 32:2. **8** Genesis 32:7. **9** For a deeper discussion of mutation protection systems in the context of evolutionary theory, see DeJong, Degens, "The Evolutionary Dynamics of Digital and Nucleotide Codes: A Mutation Protection Perspective", *The Open Evolution Journal*, 2011. **10** Genesis 32:13-16. **11** Genesis 32:21-24.

60. A Brief Journey Into Complexity

Let's now take a brief journey around other complex aspects of cells. It begins from a nuclear pore complex, just in time to see its thousand or so parts disassemble with ease in front of our eyes. Think about the kind of exquisite control involved not only in assembling a machine made up of a thousand parts, but also in designing it to be disassembled easily, its parts moved, with some of them going on to serve a function in the process of cell division.

As we continue our journey, we arrive in the nucleus, just in time to see cell division take place. The genome of the eukaryotic cell is stored in many highly compact packages called "chromosomes." They line up in the middle of the cell as the nucleus disassembles. Before the cell divides, an exact copy of each chromosome is made, with each piece, called a "chromatid," joined at the middle. A complex structure called a "kinetochore" forms around each side of the middle. Spindles then emerge from two opposite sides of the cell. As the cell divides, the chromatids separate. The spindles attach to the kinetochores and pull the chromatids to opposite sides of the cell. New nuclei form around the two sets of chromatids, and finally the cell body is split, forming two daughter cells.

Let's take a closer look at one of the chromosomes. It consists of a thread of DNA, wrapped around little spools called "histones." Some of the histones have little tails which can be modified to activate or repress genes. When the cell is ready to divide, chromosomes form into a neat X shape, but most of the time they are more like a ball of noodles. Yet there is something remarkable about this noodle clump. There are no knots. It is not tangled. You can pull out a piece of the noodle and put it back in, without disturbing the structure. It is folded into a fractal shape similar to a "Hilbert curve," a shape that can fill a two dimensional space without ever overlapping. For chromosomes, this is also true in three dimensions.¹

Chromosomes have two regions, one for inactive and another for active genes. The non-tangled structure of the noodle allows pieces to be moved easily between the two regions. If evolutionary theorists are to be believed, apparently all by itself, nature found the perfect structure in which to store and manage huge amounts of genetic information in a microscopically small space.

What about the information stored in these chromosomes? When biologists looked at bacteria, which are single-celled organisms with prokaryotic cell structures, they found that gene sequences were continuous. However, when they looked at eukaryotic cells, they were surprised to find that gene sequences were usually broken up into regions which they called "exons" (the regions where proteins were expressed), separated by regions that didn't code for the gene, which they called "introns" (because they interrupted the expressed regions). Introns are typically about ten times longer than exons.

This system of introns and exons turns out to be incredibly useful. Exons can be pieced together in many different ways to create different proteins with differing

structures, called “isoforms.” The whole process is called “alternative splicing” and it allows for much more genetic diversity. In fruit flies, for example, about 50 genes can each make over 1,000 isoforms.

The process of creating an isoform is highly elaborate. A miniature machine called the “spliceosome” cuts out the introns from a genetic sequence, and then a cascade of proteins act as repressors or activators to determine which exons will be used in the required isoform.

Introns pose yet another formidable challenge to the evolution of a protein. If multiple isoforms depend on the structure of a particular gene sequence, that sequence can’t easily evolve without changing the isoforms produced from it. Evolutionary theorists suggest that introns were the result of an invasion by a parasite or genetic element that left its mark all over the genome, breaking up genes. But by incredible luck, cells didn’t die from their genes being broken up. The forces of serendipity combined with a large quantity of time just happened to turn this parasitic invasion into an elaborate system of splicing, where one gene sequence can actually produce multiple isoforms.

Within the genetic material of an organism are transposable elements, or “transposons” for short. These are sequences that can move around in the genome, earning them the nickname of “jumping genes.”

There are two main types. The first uses what could be described as a “copy and paste” mechanism. The gene sequence is copied from DNA into RNA, and then pasted back into DNA somewhere else in the genome, by a machine called “reverse transcriptase.”

The second type uses a “cut and paste” mechanism. The sequence to be cut has markers on either side of it. “Transposase” enzymes bind to these markers and cut the relevant sequence out of the genome. They then paste it into another place that is also marked out in the genome. In other words, the cell already had the cut, copy and paste functions of a word processor well before humans invented them.

Almost half of the human genome is made up of transposable elements. As a result of evolutionary thinking, they were long thought to be mere junk DNA or genetic parasites. But then researchers found that the most common transposon, called “LINE1,” which makes up nearly a quarter of the human genome, is actually a critical regulator of the first stages of embryonic development. Its purpose is to work with other gene regulatory proteins to turn off and on programs and genes that are needed for the embryo to develop. Not quite so junk after all! ²

Incidentally, why are LINE1 elements so common in the human genome? The researchers suggested that these elements make the early stages of development far more robust. Since LINE1 is repeated thousands of times in the genome, it becomes virtually impossible for a mutation to disrupt the function of development. This makes sense, because if anything goes wrong in the incredibly complicated development of an organism, it could be fatal or highly damaging. It’s almost as if these were design features, built in to prevent mutations and therefore stop evolution from taking place.

Research has also shown that transposable elements stabilize the three dimensional folding patterns of the DNA molecule inside the nucleus.³

While transposable elements are critical for development, the organism doesn't want bits of its genome jumping around whenever it likes. This is why transposons can be suppressed by yet another layer of complexity, called "methylation." This is where a group of atoms in what is called a "methyl group" are added to a DNA segment, without changing the nucleotide sequence. They are like little flags attached to certain letters in the sequence. Methylation can switch genes off, and prevent them from being transcribed.

Markers such as these, along with histone tails and other modifications, come under the category of "epigenetics." These tweaks can change the meaning and interpretation of the coding sequence, without changing the genetic content. They are like comments or notes connected to a line in a book, but that don't change the line itself. They are yet another intriguing layer of complexity found within the cell.

If we wished to see an example of cellular complexity outside of a human cell, we would find it in the pond-dwelling single-celled organism *Oxytricha trifallax*. As single-celled creatures, populations of *Oxytricha* come about through replication of themselves. They also engage in a form of sex when they aren't busy munching on algae, but the purpose isn't to reproduce. It's literally to exchange DNA. This enables them to replace old genes and DNA parts.

The *Oxytricha* cell is ten times larger than a human cell. It contains two nuclei, one to house its active DNA, and one that serves as an archive of the genetic material it will pass on to the next generation. Unlike most other single-celled organisms, it stores its archive genome in thousands of scrambled, encrypted pieces. When it's time to mate, this genome is broken up into roughly 225,000 pieces, which are then massively rearranged to produce about 16,000 chromosomes, containing about one gene each. This is very different from the 46 chromosomes humans inherit from father and mother.

The scientists who researched *Oxytricha* described this process as a form of encryption and decryption.⁴ Curiously, almost half of the 225,000 pieces overlap, and they can be cut in different ways. Some of the genes are also scrambled in intriguing ways. Some contain sequences that are inverted, or regions that are partitioned into even and odd-numbered segments. The most scrambled gene is fragmented into 245 segments that assemble into a protein 1,300 nucleotides in length. There are also many nested genes that are weaved with each other in an elaborately tangled order. All of this implies massive scale and coordination in the rearrangement of its archive genome, in order to assemble its 16,000 chromosomes.

Why does *Oxytricha* go through this complex process for replicating itself, when most other single-celled organisms don't? I think the encryption of its genome probably makes it much harder for mutations to cause lasting damage over generations. To put it bluntly, its encrypted genome seems specifically designed to limit evolution. Perhaps also the remarkable nature of this humble pond-dwelling

creature is meant to serve as a lesson for us – that behind the seemingly simple hides incredible ingenuity, the mark of a designer.

My purpose for taking you on this brief journey into some of the deeper complexity found in cells is to show you that, as scientists explore further inside, life increasingly looks like the equivalent of advanced nanotechnology. As well as clever molecular machinery, it also uses the biological equivalent of highly advanced programs, ingenious information processing and storage, and smart encryption and decryption techniques.

I doubt this is what Charles Darwin expected to be in the cell when he came up with the theory of evolution. The finches he observed on the Galapagos Islands could access different food sources depending on the sizes and shapes of their beaks. But if they were to break themselves up into thousands of pieces and then assemble the pieces into a different functional arrangement, as does the pond-dwelling *Oxytricha* with its archive genome, or arrange into a three-dimensional Hilbert curve where nothing overlaps, as do our own chromosomes, then perhaps Darwin would have drawn very different conclusions about the development of life on Earth.

1 See the article “The Human Genome In 3 Dimensions” by Brandon Keim, posted at wired.com on October 8, 2009. **2** Percharde *et al*, “A LINE1-Nucleolin Partnership Regulates Early Development and ESC Identity”, *Cell*, 2018. **3** See the article “‘Jumping genes’ help stabilize DNA folding patterns” by Julia Evangelou Strait, posted at medicine.wustl.edu on January 23, 2020. **4** Chen *et al*, “The Architecture of a Scrambled Genome Reveals Massive Levels of Genomic Rearrangement during Development”, *Cell*, 2014.

61. The Layers Of Complexity

Life consists of multiple layers of complexity. When viewed in isolation, I suppose each layer is not impossible for human engineers to copy, although it would require an in-depth knowledge of chemistry, physics, engineering and coding to build the equivalent of, say, a nuclear pore complex or a ribosome.

But with each layer, the problems faced by nature are often very different. For example, to evolve a protein, a functional sequence must be found from a natural search of almost endless variations, or by smaller proteins being accidentally stitched together, or by genes being accidentally duplicated, or by domains and themes from existing genes being shuffled about somehow, or by some other method.

Then a potential new protein must acquire the equivalent of an address label, so it can be sent somewhere in or outside the cell. If a new gene is a duplicate of an old one, it will have the same label as the original. But how can it acquire a different address label?

This is a different type of problem compared with evolving a functional sequence, but the two problems need to be solved in conjunction with each other. We could refer to this as “parallel complexity.”

Just to begin the process of turning a gene into a protein, the gene also needs the right control sequences made up of “enhancer” and “promoter” regions, so that RNA polymerase machinery can latch on and transcribe the sequence. This, in itself, is a remarkably complex process. Enhancer regions can often be many thousands or even hundreds of thousands of nucleotides away from the gene, so the DNA strand is folded into a loop, to bring the enhancer and promoter regions together.

Then various transcription factors congregate near the binding site in high numbers, helping each other to latch on. Hundreds of mediator proteins join the party, forming into giant clusters, all helping RNA polymerase to do its job of copying the DNA strand.¹ This is a huge co-operative effort just to produce one mRNA transcript that can be converted into a protein. It would be incredibly challenging for human engineers to replicate this process.

So far in this letter I have focused on what we might call “upward complexity,” where sequences in DNA and RNA give rise to proteins, and proteins form multi-protein machinery and structures such as nuclear pore complexes.

However, a different form of complexity that I have hardly touched on is the process of development. Multi-cellular organisms go through various stages of development before arriving at their mature form, which involves many temporary processes along the way.

This is another form of parallel complexity, where nature has to get multiple stages of complexity to work in sequence over time. Since we spent a whole chapter looking at the nuclear pore complex, let's briefly look at how an NPC develops in the first place.

In early embryos, NPCs appear in some parallel stacked membrane sheets of the endoplasmic reticulum, or ER, which I have previously compared to a mail processing center. Biologists initially thought that the NPCs in the ER were storage compartments for nucleoporins, to be made available to the cell during early embryo development. But there was apparently no clear path for getting the whole NPC structure directly from the ER and into the nucleus. Researchers then looked at fruit flies, and discovered how it was done.²

During early development of the flies, parallel ER sheets containing NPC structures are highly interconnected in three dimensions; and the nuclear envelope, the membrane around the nucleus, contains openings. The openings and sheets line up, allowing the NPC structures from the ER to be inserted into the openings. Initially, the NPC structures are more like scaffolding, but once inserted, they can recruit other nucleoporins so they become fully working NPCs complete with transport controls. Without this mechanism, the development of the embryo would be slower. However, once the organism is more developed, other mechanisms take over the task of building NPCs.

Of course, this is just a minuscule fraction of the complexity that goes into turning one cell into an organism made up of trillions of cells. How does the shuffling of nucleotides come up with such intricate features? In evolutionary theory, new inventions usually come about because of things going wrong, such as the accidental addition, deletion or substitution of letters in the genome, the spluttering of copying mechanisms, cut and paste mechanisms going a bit crazy, parasites getting out of hand, large helpings of serendipity, and enormous amounts of trial and error by the population of organisms as a whole.

But how does the feature I have just described evolve in a cumulative manner? Either it works, or it doesn't. If nature evolves holes in the nuclear envelope that aren't filled, it will die, since the cellular transport system will no longer work. Of course, the magic wand of "co-evolution" is the standard answer given by theorists, but this doesn't actually provide the details. To build such a feature, I would suggest, requires vast engineering knowledge, and can't be achieved merely by tweaking nucleotides a bit at a time.

We have looked at parallel and upward complexity, but there is also what we might call "downward complexity," and in many ways this is perhaps the most remarkable of all. For example, in a previous chapter I discussed the electron transport chain, which shuffles around electrons, drawing off some of their energy, which is then used to pump protons into a confined space. These protons are then forced through the tiny equivalent of a turbine, producing the power for our cells.

What makes this all so remarkable, quite apart from the ingenuity of the system, is that protons and electrons are subatomic particles, both much smaller than an atom. How did evolution, which is ultimately the shuffling of nucleotides consisting of dozens of atoms in fairly fixed configurations, combined with huge amounts of trial and error, manage to figure out how to manipulate subatomic particles in such an

elegant way? There is a vast scale difference between an atom and an electron. Furthermore, the fairly strict chemistry of nucleotides doesn't allow much room for experimentation.

Some have speculated that the process arose naturally around deep sea vents in the ocean, and then somehow genes took over later.³ In this idea, perhaps tiny crevices in the rocks acted like cell membranes, and a certain flow of chemicals through the rocks provided energy, and perhaps even formed a simple electron transport chain. In other words, nature supposedly "invented" the electron transport chain through the interaction of chemicals, and then organisms "adopted" it later.

But this is just another example of evolutionary storytelling, which waves an enormous magic wand over the critical details of how an organism encoded the whole process into nucleotide sequences, amino acids, proteins and protein complexes. It is, after all, complex machinery and proteins that do the electron shuffling and protein pumping in an actual cell, not deep sea vents.

The vital details that are missing from the evolutionary story also highlight why the electron transport chain couldn't have evolved through cumulative selection. The chain requires several critical abilities. It needs to be able to receive donated electrons and then shuffle them through protein complexes. It needs to capture the released energy from the electrons. It needs to use that energy to pump protons into a confined space. Finally, an ATP synthase complex is needed, to take advantage of this accumulation of protons. Take away any of these abilities, the system fails and the organism dies.

These processes involve complex chemistry that is finely tuned. I accept there may be some room for flexibility. For example, it could be that not all four of the initial complexes are essential. Maybe one, two or possibly even three of them could be ditched. But if we wanted to design our own molecular process to shuffle electrons, and utilize their energy to pump protons into a confined space, there are probably only a limited number of ways to do it with a reasonably high degree of efficiency.

This is where chemists and engineers can help. They might find a simpler way, but even this would probably involve a lot of complexity. After all, we're talking about pumping protons and shuffling electrons here, and these are much smaller than atoms! In other words, in all probability, the process couldn't be dramatically simplified. At best, a slightly simpler version could perhaps be designed, but this still wouldn't account for the evolution of the process we see in real cells.

Unlike proteins, whose exact functions can often be difficult to determine, chemistry is very specific. If the electron transport chain really did evolve from a sequence of simpler versions, then unlike most evolutionary stories, those simpler versions could be put together and tested in a lab. But as I have said, even the simplest version would still be complex, because the process needs to pump protons and shuffle electrons, showing that cumulative evolution couldn't have happened.

In any case, the fatal point to the evolution of this process is that nature would have no way of easily tweaking it. Evolutionary changes take place in the DNA

blueprint of an organism, at the nucleotide level. It's a game of Nucleotide Shuffle. The mutation of a nucleotide can perhaps change an amino acid in a protein, which could change the chemical composition and structure of the protein, but there is no simple correspondence between changing a nucleotide that encodes a protein, and tweaking a chemical or chemical reaction at the atomic level. They are at two very different scales.

This is why saying that nature "invented" the electron transport chain and then an organism "adopts" it is equivalent to a fairy tale. An organism has no mechanism for taking a process happening around it, and turning it into multiple complex, specific sequences of nucleotides that become proteins, that in turn make up complexes that must be put together in sequence to even begin to build its own useful electron transport chain. Mutation followed by selection will not arrive at this, because it requires the invention of multiple specialized proteins that must be pieced together in very specific ways to create the chain.

To put the magnitude of the task into some perspective, nature must first evolve the proteins that make up at least one of the four complexes in the electron transport chain, which means it has to invent the ability to pump protons, shuffle electrons and utilize the released energy.

Perhaps, as is typical in evolutionary stories, nature invented them in some other context, and then managed to recruit them for another purpose, with multiple waves of the "translocation" or "recruitment" serendipity wand. Of course, the inventions would have had to be brought together all at once, because without all the abilities of an electron transport chain – receiving electrons, shuffling them around, and utilizing their energy to pump protons into a confined space – the chain would be useless.

Besides, all these activities would be pointless without something like an ATP synthase complex to benefit from the proton flow, so how do all of these complexes get fitted neatly together? Again, if the functions don't all come together, the system won't work. Cumulative improvements can't happen to a process that already requires a fairly strict set of chemical processes to begin with, and it can't be tweaked by shuffling nucleotides around.

There is variety in what can deliver electrons to an electron transport chain. For example, bacteria called "lithotrophs" (literally "eaters of rock") can eat other chemicals to get its electrons. Since the chain is widely used across all domains of life, from an evolutionary perspective it must have been invented very early on.

It is also used in other contexts, such as in photosynthesis, the process of converting light into chemical energy. Clearly then, there is some flexibility in the system. The system seems to be somewhat modular – that is, the process is a discrete unit that can be used elsewhere in other contexts.

When we see complex systems being re-used like this, maybe we should ask whether modularity could actually be a design feature. Perhaps instead of serendipity wands copying and pasting entire systems and using them elsewhere, maybe less luck

and more intelligence is really behind it, being able to do so precisely because the systems were designed to be modular in the first place; or at the very least, an intelligent hand would know precisely where to copy and paste.

Either way, I would suggest that evolution, as a game of Nucleotide Shuffle, can't solve the problem of subatomic particle manipulation by itself. But what if a different game is being played, not at the divine level, but maybe at the cellular level?

1 See the article "What Does It Look Like to 'Turn On' a Gene?" by Alla Katsnelson, Casey Rentz and Knowable Magazine, posted at the-scientist.com on May 3, 2019. **2** Hampoelz *et al*, "Pre-assembled Nuclear Pores Insert into the Nuclear Envelope during Early Development", *Cell*, 2016. **3** For example, see Chapter 1 of *Life Ascending – The Ten Great Inventions of Evolution* by Nick Lane; W. W. Norton & Company, 2009.

62. Did The Cells Do It Themselves?

An important question we could ask at this point is: what if organisms aren't relying on the game of Nucleotide Shuffle to evolve? Could nature be playing a more advanced game somehow?

Bacterial geneticist James A. Shapiro, discoverer of transposable elements in bacteria, recognized that classic evolutionary mechanisms such as mutations and natural selection weren't sufficient to explain the complexity of life. He proposed that cells somehow shape their own genome, perhaps intelligently – a process he called “natural genetic engineering.”¹

This is an intriguing idea, and in many ways I think it's superior to the game of Nucleotide Shuffle. It would be more like a game of “Sequence Shuffle,” where whole sequences of nucleotides are shuffled about, perhaps under the “intelligent” control of the cell.

If this were true, I suppose it could account for the serendipity wands of duplication, translocation and magical steps. These would no longer be based on incredible luck, but perhaps on a form of intelligent design, although the intelligence wouldn't be at the divine level, but at the cellular one.

Cells do have the ability to manipulate their own genomes to a certain extent. As I discussed earlier, transposons are sequences of genetic material that can be “cut” and “pasted” in combination with transposase enzymes and specific markers in the genome, or “copied” from DNA into RNA and then “pasted” back into DNA somewhere else in the genome by reverse transcriptase machinery.

Genes can be transferred between bacteria, and sometimes between other organisms, in a process called horizontal gene transfer. In eukaryotes, genes can often be spliced into pieces, and those pieces can be shuffled, to produce many different variations, a process known as alternative splicing. DNA can be repaired by adding nucleotides to the genome.

These and other mechanisms imply that cells at least have the potential to genetically engineer themselves. Could natural genetic engineering be the explanation for the variety of life we see today? Did the cells themselves engineer life as we know it?

There are three main reasons why I think not. First of all, the functions needed to manipulate the genome require sophisticated machinery, such as the ability to “cut,” “copy” and “paste” sequences. How did the cell acquire these?

If they evolved in the classical evolutionary manner, by mutations and natural selection, then there is no particular reason why mutations and natural selection couldn't produce everything else, without the need for the cell to intelligently engineer anything.

Another interesting question we could ask here is: if cells do their own genetic engineering, why didn't they develop the machinery to directly create new proteins or sequences?

“Cut and paste” or “copy and paste” functions are fine if you want to re-use information that already exists. But if a cell wanted to create part of a gene or other genetic sequence from scratch, it would be useful to have machinery equivalent to a keyboard, which allows someone to type directly into a word processor.

For example, if I wanted the sentence THE CAT SAT ON THE MAT to appear here, I can just type this sentence directly into a word processor using my keyboard, rather than having to search for, copy and then paste the individual words THE, CAT, SAT, ON, THE and MAT from elsewhere in the document. If all I could do was cut, copy and paste, and I hadn't used the word CAT before, I'd have to copy and paste the individual letters C, A and T. I'd also have to paste the word THE twice, and put them in just the right place for the sentence to have the desired meaning.

But despite supposedly evolving for several billion years, and despite having cut, copy and paste facilities, the cell doesn't appear to have evolved a mechanism to directly write up genetic inventions. In all that time, why hasn't it evolved the cellular equivalent of a keyboard? Maybe it's because the cell wasn't the author of those genetic sequences after all, and it had no need for this facility, or the ability to create it in the first place.

Either way, the lack of a keyboard implies cells can't do the kind of genetic engineering that could eventually produce frogs and princesses.

A second reason why I don't think natural genetic engineering is the answer, is that each potential tool in the cell's engineering toolkit has important limitations.

For example, the ability of the cell to cut, copy and paste sequences doesn't mean these features can be used at will. This is a common mistake made by evolutionary theorists. They take an idea that has been demonstrated to be true in a limited or highly specific context, and generalize the idea as being true in a much wider context that is often unproven. We could call this the “fallacy of generalization.”

Consider the concept of “translocation.” Just because certain sequences such as transposons have the ability to translocate across the genome through highly regulated mechanisms, it doesn't follow that the cell can translocate any sequence anywhere at will. This would be a fallacy.

Let's look at two more potential tools of natural genetic engineering, and their limitations. Alternative splicing is a feature of eukaryotic cells where exons from a gene can be pieced together differently, to make varying proteins. In theory, this could provide the cell with an opportunity to experiment.

The process seems to be regulated in a number of ways, involving proteins that act as silencers or enhancers, genetic and epigenetic markers, growth factors in the cell cycle, and the structure of the chromosomes.

The development of an organism also seems to play a major role in splicing regulation. When development is over, and if the cell isn't in the process of dividing, presumably it can focus on the business of being alive, and can perhaps respond and react to signals from its environment or other cells. However, it's not clear that the cell has any truly creative capacity to use the splicing equipment for experimentation.

Let's consider the DNA repair mechanism known as non-homologous end-joining, where broken ends of the DNA double helix can be repaired by adding DNA that isn't necessarily the same as the original.

From a natural genetic engineering point of view, this is seen as a potential toolkit for the cell, because it might be able to use this new information to build new things. However, it's not clear how the cell could know what to do with the new information, so in classical evolutionary thinking, this is simply treated as a mutational process. Either way, the repair mechanism is a feature meant for survival rather than for creative design.

A third reason why I don't think natural genetic engineering explains life as we know it, is that prokaryotic and eukaryotic cells both have their own unique limitations.

Prokaryotes are single-celled organisms such as bacteria. They can do lots of remarkable things such as swap genes, hunt for food together, and sometimes form what looks like a multi-cellular organism. They use ion channels to communicate with one another, which enables a kind of memory. They can regulate their own genes as a response to cell population density, in a process called "quorum sensing."

Bacterial colonies also have their own "pangenomes" or "supergenomes," which we could think of as a large library of genes, out of which an individual bacterium owns a smaller subset. The size of the supergenome has been estimated to be up to ten times bigger than an individual bacterial genome.²

Indeed, bacteria seem to defy the classic evolutionary mechanisms. They lose and gain genes at an order of magnitude faster than they duplicate them, so any supposed evolution doesn't happen by small changes, but by big leaps as a result of swapping genes. It's almost as if they were designed to rapidly adapt to their environment. They are, in effect, nature's little helpers.

We know that cells have built-in mechanisms such as error correcting, to limit mutations. Intriguingly, in situations where they are starving, bacteria switch off error correcting to a certain extent, meaning any genetic sequences they copy in this state are more prone to mutation. This is considered by natural genetic engineering proponents to be another potential toolkit for the cell. Perhaps by allowing more mutations, the colony as a whole can engage in a natural search for any protein variations that might allow at least some of them to survive. On the other hand, when the colony is starving, they would probably lack the resources needed to function normally, so perhaps bacteria have no choice but to shut down this form of error correction.

Either way, if they were capable of engineering their own genomes, surely they could make the proteins needed to survive. But if they have to rely on a higher mutation rate to search for genetic sequences that might keep them alive, this suggests any genetic engineering they can do is limited.

Eukaryotes, by contrast, are usually multi-celled organisms. Eukaryotic cells are much more sophisticated than prokaryotic cells. They usually have a nucleus, which

acts as a data management center, where millions or billions of bits of data are stored and processed. The main part of the cell, the cytoplasm, contains mitochondria that provide the power needed to sustain more sophisticated machinery and processes.

Animals, which are eukaryotes, go through a process of development. For humans, this means being a sperm and egg first, then an embryo. The blueprint for this must be stored in the genome. As we discussed earlier, LINE1 transposons are critical for development.

The evidence we have about cells in multi-cellular organisms indicates that they act in a highly regulated manner. They follow blueprints, algorithms and sequences. This is how a human sperm and egg can grow into a human adult with an extraordinary degree of consistency. Development is strictly controlled, otherwise we would see more people with ten heads and twelve legs, in disturbing natural genetic engineering experiments.

There is room for variety, through built-in systems like sexual recombination, gene expression, and epigenetic markers not directly coded for in the DNA blueprint. Cells and organisms can adapt and change to a certain extent, but they do it in highly regulated ways, based on feedback from the environment or other cells. However, the ability of an individual cell to create innovations is limited by being part of an organism.

Furthermore, if anything new is to be inherited by future generations, it must be made in the germline, the cells that pass on the genetic material to their offspring. This means a cell can't really test the effects of an innovation on the organism as a whole, but can only pass on the change, relying on natural selection to determine whether it was beneficial or not, which isn't really any different from classical evolutionary thinking.

Incidentally, one line of evidence used to support the idea of natural genetic engineering is the story, which I discussed in a previous chapter, that one day a cell engulfed or was invaded by another cell, and that over time the host was able to transform the cell invader into mitochondria, the cell batteries, in a process called "symbiogenesis" or "endosymbiosis."

If the story is true, it suggests that cells can indeed engineer their own genomes. After all, they were supposedly able to build themselves cell batteries out of pieces of genetic flotsam and jetsam! However, I have already explained why I think this is an evolutionary fairy tale, widely believed because mitochondria use circular DNA like bacteria do.

The story highlights the philosophical differences between the more traditional evolutionary theorists, who believe that mutations and natural selection, with some duplications, translocations and magical steps thrown in, are enough to turn genetic flotsam and jetsam into a cell battery, and the natural genetic engineering proponents who see this as an obvious form of intelligent design on the part of the host cell.

But perhaps the story is simply fiction. Maybe mitochondria weren't gradually pieced together from bits and pieces of another cell, but eukaryotic cells were equipped with mitochondria by some other means, such as outside design.

Whatever the case, when we ignore evolutionary storytelling and look at what we know cells are capable of – and we don't know they are capable of engineering batteries out of genetic bits and pieces – we can say that cells have a number of built-in mechanisms and programs to respond to other cells and their environment.

They contain genes, blueprints, algorithms and gene regulatory networks. They use these to build proteins, and machines made out of those proteins, and more cells in their image. They can regulate how and when sequences are cut, copied or pasted. Genes can be switched on or off, or their expression can be varied according to gene regulatory networks or external feedback.

It is remarkable and truly extravagant how the single-celled pond-dwelling *Oxytricha* breaks up its genome into nearly a quarter of a million pieces, and then rearranges them into 16,000 chromosomes. It is clearly following a plan, and not doing this at random. Some of its genes can probably be pieced together in different ways, so *Oxytricha* might make a good case for natural genetic engineering.

However, I would suggest that if the organism is making any choices about which genes to pass on, it is based on feedback from its fellow pond dwellers or the environment. The organism is likely programmed to respond and adapt in certain ways, based on outside signals. In other words, it seems that any engineering *Oxytricha* do is already built into their programming. They are designed to be flexible and adapt to their environment.

In summary, cells are incredibly complex and exquisite things, and yet they act much more like automatons executing their programming, rather than engineers creatively designing things. The fact that cells are pretty predictable allows biologists to perform repeatable scientific experiments on them in the first place. This also allows human parents to plan for the birth of an actual child, rather than a randomly shaped blob with an uncertain number of mouths to feed.

If intelligence is involved in the design of life, I'd suggest the same intelligence was also behind the origin of life, including all the functions and features needed for living cells to operate, which would require a top-down design approach. I will present a more thorough case for this in the next chapter.

I think James Shapiro was right to question the ability of mutations and natural selection to explain the complex things that happen in living cells. He recognized that there seems to be a kind of intelligence in the way cells adapt.

However, I would say that if the smartest human minds struggle to put together even a self-replicating protocell, and can barely mimic the incredible nanotechnology found within a cell, this highlights the level of ingenuity required to design such things, and suggests that the cells themselves weren't the inventors of the technology they use, and neither was the blind shuffling of nucleotides. In that case, it becomes time

to start asking one of the Forbidden Questions, the questions scientists aren't allowed to ask.

1 See James A. Shapiro's book *Evolution: A View From The 21st Century* for a detailed explanation of the concept of natural genetic engineering; FT Press, 2011. **2** Eugene Koonin, "The Turbulent Network Dynamics Of Microbial Evolution And The Statistical Tree Of Life", *Journal Of Molecular Evolution*, 2015.

63. The Forbidden Question

There are certain “Forbidden Questions” that scientists, particularly biologists, aren't allowed to ask if they want their careers to continue smoothly and the research funds to keep flowing. After all, whether they are consciously aware of it or not, their field adheres to the Naturalistic Assumption, the assumption that all things in nature must be explained without resorting to things that are outside of the laws and forces of nature.

This is assumed in scientific research and when scientists communicate with the public, and it takes on the form of an ideology, similar to a religious doctrine which must be accepted by its adherents. The problem is, adhering to an ideology can prevent scientists from seeing when the evidence is pointing in a different direction.

Since the Naturalistic Assumption has become a doctrine, by definition the evidence can't point to anything that doesn't have a natural explanation, even if that explanation is just a tall story. In fact, I would suggest that the presence of a story is an indication that the assumption of naturalism may be at fault.

This assumption also leads to false reasoning. Since many scientists believe they have to explain everything by means of natural causes, it creates the illusion that God doesn't need to exist, and therefore doesn't exist. After all, what is left for him to do? Everything God could have done, scientists insist nature can do on its own.

But if nature can't actually do it all by itself, then scientists have created a self-imposed illusion upon themselves, and by extension the general public who rely on them for information.

However, let's step back from the Naturalistic Assumption for a moment, and ask ourselves one of the Forbidden Questions. It is forbidden because scientists aren't allowed to entertain the possibility of any alternative to naturalism without risking their careers. But the bottom line is, naturalism is just an assumption. It's an ideology, a worldview, a doctrine of faith adopted by the scientific community. When we recognize this, we are free to put it aside and ask all the questions we like.

Evolution is fundamentally a bottom-up design approach. Simple things gradually become more complex. Smaller genes gradually produce larger ones. Things are pieced together through billions of years of trial and error. There is no plan or foresight. If something works, it's only because countless variations have failed, and an almost endless number of organisms have died to discover what works best.

The particular Forbidden Question I will focus on in this chapter is this: when we remove our evolutionary lenses, does life actually exhibit evidence of top-down design? Does the evidence we have actually fit this better than bottom-up design?

In a human trial, the same evidence is available to both the defense and the prosecution. The verdict depends on how that evidence is interpreted, and which interpretation better fits the facts. But if we only ever hear from one side, or only allow the evidence to be interpreted in one way, then it would be a crooked trial.

I have already spent many chapters discussing the bottom-up design approach by means of mutations and natural selection. Now it's time to look at the evidence through a different lens, one where life was actually designed and planned from the beginning. Does life make more sense from this viewpoint? Does the evidence support this idea?

I think there are ten major lines of evidence for a top-down design approach to life. First, consider the fact that life on Earth is critically dependent on language – specifically, the language used to translate coded sequences into proteins, called the “genetic code.” Even the simplest of lifeforms have ribosomes that are able to read sequences of code and turn them into proteins. A genetic code must have been in place before genes could begin to be stored and then translated into proteins.

Furthermore, science has shown that, out of a million different approaches, the one used by nature is optimal in many aspects.¹ How did nature manage to find such an optimal system? If it was trying out myriads of different genetic codes, how could proteins evolve and be produced in such an environment, since the meaning of a gene would change depending on the shifting language?

If you change one codon to mean a different amino acid, then you shift the meaning of all the genes in the genome using that codon. They would become different proteins and may even lose their functions. This suggests a top-down design approach, where the language is defined first, before anything can be written down in that language.

Curiously, the gospel writer John, while he didn't have the genetic code in mind, said essentially the same thing. If we take the “Word” as the language of DNA, and the information stored in a DNA molecule, which cells need to build proteins, life could be summed up in the same way that John does: “In the beginning was the Word,” and that “all things came to be through this one, and without this one, not one thing came to be which has come to be.” And finally, “the Word became flesh.”²

The literal Greek of this verse reads, “the Word became flesh and tabernacles in us.” I have already shown how the Hebrew Tabernacle depicts the eukaryotic cell. Our flesh is made of eukaryotic cells, which are miniature tabernacles.

The second line of evidence for top-down design is the way information is protected from mutations and damage. When copying the genome, error correcting processes reduce errors to a minimum, and I suspect they may be optimized based on time and space constraints. Without these processes, daughter cells would receive a genome riddled with errors.

Furthermore, thousands of nucleotides are damaged in the DNA molecule of cells every day. Without damage repair systems working hard each day, the cell's genome would quickly lose critical information.

These error correcting and damage repair processes need to be in place at or near the start of life on Earth, so that genetic information can be preserved. The existence of these systems is consistent with a top-down designer who wanted to

ensure organisms had the ability to preserve their genetic information, both for themselves and for future generations.

However, a bottom-up approach has the dilemma that these mechanisms would need to evolve in a highly unstable environment, where stored information would be mutated and degraded rapidly, before the systems needed to preserve it could come about. Furthermore, these systems limit mutations, yet evolution relies on mutations for better designs to come about.

The third line of evidence for top-down design is the existence of entire protein “libraries” available to each organism.

Earlier on we conducted a thought experiment where I showed that small proteins could potentially evolve on their own. But an important question we never actually asked is: why would they?

A hypothetical RNA World gets on just fine without proteins, because RNA does all the work. According to evolutionary theory, nature also gets along perfectly well without new proteins and functions ever coming along, because the new ones mostly evolve out of existing ones that are happily doing something already.

In other words, nature has no reason to bother evolving anything new, because it has no hopes, dreams or future ambitions. An organism’s primary goal is to survive and reproduce. If a new function or feature comes along, it is the result of incredible serendipity.

Engineers find solutions to problems. But according to evolutionary theorists, nature first finds a “solution,” and then it somehow finds a “problem” for the solution to solve. For example, it first evolves a new protein, and then somehow “recruits” it to perform a role in an organism that didn’t need it before.

By contrast, a top-down designer can decide exactly what is needed to build the organism, and then give it access to a library of proteins encoded in genes, so it can build itself based on the blueprints in its genome.

If the designer wanted to reproduce a function, feature or part that was in another organism, he could simply copy and paste the proteins and modules of code involved, either from the other organism or from master plans stored elsewhere, and then make any adjustments as necessary. If a new function was needed, he could invent the proteins and blueprints for it, either right there, or more likely he would plan for the function in advance.

This is also what computer programmers do. They often rely on “libraries” of functions that can be called up when needed, and they can copy and paste whole “modules” of code used in other programs. They don’t wait millions of years for code to evolve, and engineers don’t wait millions of years for parts to evolve either.

But if nature relies on evolution, it can’t plan for a nuclear pore complex in the future, and then hope that just the right proteins come along, in just the right quantities, and get posted to just the right places in the cell.

All lifeforms have access to their own protein libraries that often consist of thousands or tens of thousands of functioning proteins, each one built, in many cases, out of hundreds of amino acids.

Scientists can perform experiments where they mutate a gene or take it out of action entirely, and see what effect this has on the organism. They have discovered that many proteins perform critical roles, and in a few cases, even a single mutation can cause disease.

Some mutations don't seem to matter, but if you mutate a protein enough, it will usually lose its function, because the sequence of amino acids determines the folded shape of the protein. Mutate it too much, and it's likely to become a different shape, not suited to the job it was supposed to perform. In other words, many or even most proteins seem to be optimized for a particular job.

Every living organism on the planet contains its own library of proteins, and there are many overlaps across the spectrum of life. Evolutionary theorists argue that this is evidence of common descent – that all branches of life are descended from a universal common ancestor. However, it's also evidence of common design.

If you designed a dog, and then wanted to design a cat, would you start, to pardon the unintentional pun, from scratch? It would be far more sensible to simply copy and paste lots of the stuff that makes up a dog, such as genes and blueprints that make blood, bones, teeth and so on. To make a cat, you would then need to modify the shape and size, and make it a little more aloof.

Some proteins don't quite fit the branches of the supposed tree of life, so biologists argue that they got there by horizontal gene transfer. Bacteria can do it, so they assume higher life forms can do it too, even though they don't seem to have the equipment for it. But even if we assume that higher organisms can acquire whole genes perfectly intact from other organisms, how does the recipient know what to do with a gene that has just been transferred to it?

This is a similar problem to the one we faced when trying to stitch together two smaller proteins into one, except it is many orders of magnitude more difficult, because the newly inserted gene has to somehow find a functional role in the genome, and perhaps a new address label. However, an intelligent designer could transfer genes horizontally, vertically or any other way he wanted, and design the system so it could accommodate new genes.

Computer programmers re-use whole libraries of code for many different programs, and nature does the same thing. Proteins for essential life functions are re-used across the board, often with some tweaks for the specific organism. This is what we would expect from a top-down design approach. It would match what computer programmers and engineers do every day.

The fourth line of evidence for top-down design is the overall robustness of protein interactions. For example, in a large study of over 1,800 species ranging from bacteria to primates, and millions of protein interactions, researchers found that every

species had backup plans that allowed its protein machinery to find workarounds when problems arose.³

As usual, the researchers attributed this to evolution, but why would evolution bother to evolve backup systems? It has no foresight. But this is something a smart engineer would build, in anticipation of a potential fault or emergency. Across the spectrum of life, organisms come equipped with many backup systems, suggesting planning and forethought in their design.

The fifth line of evidence for top-down design is the cellular postal system. Earlier on I posed the riddle of how a protein gets an address label, in order to be transported to various places in the cell. And how does a new body part come about, without a zip code for the part?

A top-down design approach makes this easy. A city planner who was planning a new district would make sure it had a zip code, along with street names and house numbers, so the new residents could get their mail.

The sixth line of evidence is the constant re-use of design blueprints among organisms. Evolution is a tinkerer. Genomes must mutate, in order to have a chance of coming up with new designs and functions. Yet time and time again, biologists find similar designs and features in organisms of all shapes and sizes.

Most eukaryotic cells have an inner compartment, the nucleus, surrounded by a double membrane that contains nuclear pore complexes (or NPCs). There are some fairly minor differences across life, but they all share the same core shape.

When biologists see this, they use the term “conserved.” What they mean is, all organisms with this feature sprang from a common ancestor in the distant past, but the feature hasn’t changed much, even over assumed vast periods of time or across widely different creatures in that branch of the tree of life.

In the case of the NPC, because it plays such an important role in the survival of an organism, biologists argue that evolution can’t tinker with it to the same extent as it could perhaps do with other parts, and hence it stays roughly the same.

In one sense, this sounds perfectly reasonable. After all, if the nuclear pore complex fails to function, important material can’t get in or out of the nucleus, and the cell dies. Therefore, any mutations that stop the NPC from working will be ruthlessly weeded out by natural selection.

However, this doesn’t explain why the NPC has retained its core shape across the spectrum of life over a supposed billion or more years of evolution. Even if its shape is optimal, and evidence suggests that it is, why don’t we see nature at least testing out myriads of other designs? Why do they all have eight spokes? Why do we not see NPCs with six or nine spokes? Is there really only one way of designing an NPC? If so, how does nature know what it is?

There are also plenty of examples of features and functions that have supposedly evolved again and again independently in different branches of the hypothetical tree of life. Evolutionary theorists call this “convergent evolution.” I would

suggest that convergence and conserved features are actually evidence of top-down design.

For example, to design a frog, you first need access to the blueprints that make up all the parts of a frog, from small things such as nuclear pore complexes, to the proteins and blueprints required for building organs such as hearts, eyes and brains. If a designer has already created other organisms with these core functions, then creating a frog isn't much of a leap.

However, designing the ability of a frog to actually leap would be an interesting engineering challenge, and would probably require new proteins and functions, or at least re-purposed ones. A top-down designer is in a far better position to achieve this, knowing the desired outcome in advance, than an evolutionary bottom-up approach.

The fact is, across the spectrum of life, creatures use many of the same parts in their bodies. This is why evolutionary theorists argue for a universal tree of life, with each species evolving from a common ancestor. However, I would suggest it is also evidence of a designer who re-uses the core designs of particular features, but then endows certain types of creature with unique or distinctive features, such as the ability of a frog to leap, an owl to swivel its head, and a cat to stand precisely half in and half out of a door you've just opened for them.

Industrial manufacturers do the same. A car maker doesn't reinvent the wheel every time it wishes to design a new car. It uses the same wheel blueprint, even though it might embellish the design, or adapt it to suit a newly designed vehicle. The fact that all vehicles have roughly the same shape of wheel doesn't mean all cars evolved from a common ancestor out of an ancient Ford deep sea vent. Instead, they were designed based on common blueprints.

But according to evolutionary theorists, we are not allowed to apply this logic to biological life. Still, there's no good reason why we can't, if we put aside the assumption of naturalism. Many organisms share common features, including proteins, which have then been adapted to suit the particular type of creature. This could be seen as evidence of top-down design.

The seventh line of evidence for top-down design is that life already exhibits a top-down approach in its control of genes.

Think about the exquisite control that was needed to turn you from one tiny cell into a fully-grown human. The early cells needed to divide numerous times. They gradually needed to specialize to form different tissues and organs. Proteins needed to be switched on or off, or expressed in greater or lesser quantities, at just the right times. You needed to be kept alive during this entire process, even before you had a heart. Once your heart had been formed, blood needed to be pumped around your developing body, and energy needed to be circulated, despite the fact that you were constantly changing shape.

Some of this process is controlled by feedback loops at a local level, but the overall development of an organism is strictly controlled by gene regulatory networks in the genome. If this weren't the case, you would just be a big clump of the same kind

of cells – maybe a big ball of neurons, or a big eye; or maybe you'd have a random number of fingers, or arms that extended almost without end. If the development of an organism requires such careful and intricate top-level planning, why would this not be true of life itself?

Top-down control and regulation is necessary for many of life's processes. Recall the way the pond-dwelling *Oxytricha* breaks up its genome into nearly a quarter of a million pieces, and then rearranges them into 16,000 chromosomes. All of this requires elegant top-down control, but we are told to believe the process supposedly came about by the shuffling of nucleotides. Is this really plausible?

The eighth line of evidence for top-down design is the high level of efficiency of cellular processes. In the book of Revelation, God declares: "Look! I am making all things new."⁴ This happens quite literally all the time in the cell. Parts are disassembled, recycled, and replaced with new parts constantly.

Some biologists think this is inefficient, but I would argue it is supremely efficient. First of all, there is very limited space in a microscopic cell, so only making what it needs when it needs it makes sense.

Second, with physical machinery, wear and tear may cause the equipment to become less effective over time, or even to break down. However, if something stops working in a cell, there is a strong possibility the cell dies. Therefore, by constantly renewing the machinery, this eliminates the problem of wear and tear, and ensures its parts are constantly at or near peak performance, minimizing the chance of anything breaking down.

As another example of efficiency, biologists have shown that some proteins perform more than one role. For example, when the cell is undergoing division and the nuclear pore complex is disassembled, some of the proteins that made up the NPC go on to help in the process of cell division, when they might otherwise be floating around doing nothing. This is highly efficient.

Evolutionary theorists argue that this is an example of how one function could have evolved out of another function. But this implies one of the functions wasn't being performed before, which invites the question of how cell division took place without it.

However, an engineer would perhaps want to employ those proteins while they are hanging around waiting for cell division to take place. Why not draft them into use, precisely as nature does? This is evidence of smart design.

The ultimate example of efficiency is the human genome itself. It contains the control sequences and plans for every stage of human development, along with the blueprints for tens of thousands of proteins, and thousands of molecular machines needed to build a person. In other words, an entire human being consisting of trillions of cells is coded for in just 3 billion letters in a DNA molecule. Clearly the genome must use plenty of algorithms and be highly efficient.

This is stored in a molecule you can't see with your eyes. As a size comparison, it's the equivalent of taking a length of string that could stretch around the Earth ten times, and putting it inside a chicken egg. This is incredible efficiency.

The ninth line of evidence for top-down design is the magnitude of the engineering feats and inventions we find in nature. These are explained by evolutionary theorists through the use of simple stories, or meaningless phrases such as, "the eagle's telescopic eyesight evolved to help it catch prey" or "the frog's ability to leap evolved to help it survive." These aren't explanations. They're simply assertions. And pretty glib ones at that, because in the evolutionary paradigm, every feature that sticks around long enough does so because it conveys a survival or reproduction advantage, so that life is ultimately just about sex (or replication, if you're bacteria) and the survival of your offspring.

But nature is full of incredible inventions that demonstrate amazing variety and ingenuity. Anything we humans have invented, nature probably got there first. Reading and writing? Ribosomes and reverse transcriptase beat us to it. Electricity is an essential component of modern life, and yet the body used it before we did, because cells use proteins called ion channels to create a positive electrical charge, which can be turned into electrical pulses called action potentials.

The Internet is an incredible network of computers talking to one another, but neurons also form vast communication networks in the brain and nervous system. Humans thought they were smart when they first learned to send electrical signals down a wire, the basis for early forms of telecommunication; but a DNA damage repair system beat us to it, sending electrons down the DNA spiral to look for faults.

We use gears to drive at different speeds, but the planthopper got there first, literally using the same kind of gears we use in vehicles, to jump hundreds of times its body length.

It took knowledge, intelligence and ingenuity for us to come up with many of our inventions as humans, but according to evolutionary theorists, the shuffling of nucleotides was able to come up with such inventions in nature.

In reality, I would suggest this couldn't happen, because, to take just one example, the invention of gears requires an understanding of engineering principles that can't be discovered by changing letters in a DNA sequence. The two processes are at completely different levels of complexity.

However, a top-down designer with a solid grasp of engineering principles could give the planthopper its gears, and create proton pumps and electron transport chains so that subatomic particles can be shuffled around to create energy.

The tenth line of evidence for top-down design is the foresight displayed in nature. According to evolutionary theory, natural selection doesn't have foresight. It just selects from what is available at the time. Yet even in the evolutionary paradigm, nature continually comes up with new inventions that seem to anticipate future developments. This suggests intelligent planning rather than just luck.

The invention of a genetic code and a ribosome was necessary for proteins to be produced. At the same time, neither of these would be of any use without the existence of encoded genes in a genome.

Most of the chemical reactions required to sustain life would be far too slow without enzymes, which often make those reactions happen millions of times faster. But life can't afford to wait around for enzymes to evolve. The organism would be dead without them. Nature anticipated this need, by providing each organism with the proteins it needs to produce chemical reactions, along with the enzymes needed to rapidly accelerate those reactions. This would be the hallmark of a designer who knows in advance what is needed to achieve a desired end result.

In evolutionary theory, proteins can be accidentally duplicated, and then after the copy manages to find a new form, it can somehow get recruited to perform a useful new function in the cell, even though there is no recruitment agency to do this, and no system to give them new address labels when necessary. Yet nature continually shows foresight, by giving proteins functions and address labels.

The invention of mitochondria, the powerhouses of the cell, anticipated the existence of multi-cellular life which would require much more power.

The invention of chromosomes, and the special equipment needed to compress, decompress and read the DNA sequences, anticipated the much larger genomes that would be required by multi-celled organisms. In other words, nature supposedly invented the ability to store the vastly bigger genomes needed by cats and humans, before it could ever conceive of a cat.

The development of nuclear pore complexes and the nuclear envelope around a cell nucleus anticipated the need for greater control over the cell in eukaryotes.

Somehow, cells also became "pluripotent," able to become many different types of cell, which anticipated the development of plants and animals. For example, human red blood cells jettison their nucleus, and they utilize hemoglobin proteins to carry oxygen around the body. Single-celled organisms don't have a body as such, and some creatures such as insects don't need oxygen to be actively transported, because they are small enough to rely on it being passively circulated. But this also limits their size.

According to evolutionary theory, the lucky invention of red blood cells allowed creatures to grow bigger, which would then give them a survival advantage. In other words, nature solved a problem creatures didn't know they had – namely, being too small.

But red blood cells aren't the only things needed to transport oxygen around a body. An organism needs a cardiovascular system made up of a heart, blood vessels and capillaries, and a respiratory system involving lungs, airways and air sacs. The two systems also need to work together, to get oxygen from the respiratory system and into the blood. You need red blood cells to transport oxygen, but also a transportation network to be in place, for red blood cells to be of use. This requires foresight.

Neurons are another type of cell, with the ability to transmit electrical and chemical signals. As well as having a cell body containing a nucleus, most neurons also

have special equipment including an “axon” and “dendrites.” The axon looks like a tail with a sheath around it, and it transmits electrical impulses. Dendrites receive signals from other neurons across contact points called “synapses.”

Neurons work together in large numbers to create a communications network. They are, in effect, network devices. Therefore, the invention of the neuron anticipated that creatures would have brains and nervous systems, which suggests foresight.

Furthermore, to build a creature out of these different cell types, the first cells divide repeatedly, and then cells go on to specialize into specific types – such as skin, brain and blood cells. This means the blueprint for each cell type must be built into the organism’s very first cell, and the timing for the production of these specialist cells must also be written into its genetic blueprint.

In other words, the plan for the development of an organism is already fixed from the beginning, and there is no easy mechanism to invent new cell types such as neurons, let alone whole organs such as brains and hearts. Yet evolutionary theorists insist that the shuffling of nucleotides somehow managed to do it.

I would suggest a far better explanation is that neurons and blood cells, and all the machinery needed to fully utilize them, such as brains, nervous systems and hearts, were built by a designer who would know in advance where the creature’s brain or heart would be, and could put the plans for their construction into the organism’s very first cell.⁵

1 Freeland, Hurst, “The Genetic Code Is One in a Million”, *Journal of Molecular Evolution*, 1998. **2** John 1:1-3,14. **3** See the article “Species evolve ways to backup life’s machinery” by Tom Abate, posted at earth.stanford.edu on February 14, 2019. **4** Revelation 21:5. **5** A much more extensive discussion of the idea of foresight in nature can be found in the book *Foresight: How the Chemistry of Life Reveals Planning and Purpose* by Marcos Eberlin, published by Discovery Institute Press, 2019.

64. The Illusion Of Evolution

William Paley argued that if we came across a watch on a beach, we would assume it had not arisen by chance because of its complexity. Therefore it must have been designed. But then Charles Darwin came along, and argued that the complexity found in nature could be explained by the accumulation of small variations selected by nature for fitness over long periods of time. Those who developed his arguments asserted that life might look designed, but this was merely an illusion.

Unfortunately, neither William Paley nor Charles Darwin were alive to see the blockbuster movie sequel to the original story, in which the device on the beach turned out not to have been a watch after all, but some kind of advanced nanotechnology disguised as a watch. It contained huge quantities of coded information tightly packed into microscopic fractal spaces, as well as advanced circuitry that could replicate itself, manipulate subatomic particles, and build complex molecular machines that could be assembled and disassembled easily.

If such a device had been found on the Moon, it would be heralded as irrefutable proof of extraterrestrial intelligence; and yet most of the cells in almost every living organism on Earth are precisely such devices.

Outside of biology, such a device would be seen as obvious evidence of design, so why is design dismissed so easily in the case of the cell? The reason is, modern science is committed to the dogma of naturalism. Since this has become an almost unquestioned and unquestionable assumption in the field of biology, only theories based on naturalism are allowed, meaning intelligent design is excluded.

Since Darwin's day, scientists have gathered an incredible amount of knowledge about how the cell works, and it seems there is always more to discover. I would suggest that every person who believes, or has believed, that life arose by itself through natural processes, owes it to himself or herself to think deeply about the following important question:

Given that design was dismissed as an illusion by Darwin's adherents, could it be that what looks on the surface like evolution is really the illusion? In other words, instead of the illusion of design, what if we are looking at the illusion of evolution?

After all, when it comes to our assumptions and beliefs, which are things we tend to take for granted, it makes sense to conduct a reality check once in a while, to make sure they are grounded in truth, and not merely wishful thinking. This applies just as much for the believer as it does for the atheist and skeptic.

Now, before we can examine the idea that evolution might be the illusion, we need to recognize that the word "evolution" can mean different things to different people. To be clear, the form of evolution I am challenging in this letter is the ability of natural phenomena such as mutations and natural selection to produce all the variety of life as we know it – what some call "molecules to man" evolution.

This form of evolution assumes all life is related by common descent, and that each species is a branch on a universal tree of life. This is treated as an unquestioned

assumption starting from the school textbooks and continuing through scientific papers and the media.

Before biologists knew about what happened in the cell, many already believed that life had evolved. When they finally got to look inside the cell, they began to see a hazy outline of how life worked, including how proteins were encoded in the DNA molecule. But curiously, genes coding for proteins only make up a small fraction of the genome. They didn't know what the rest was doing there, so it was labeled "junk DNA" and assumed to be useless vestiges of evolution. This term persisted for several decades, fueled not only by popular science writers and magazines, but often by scientists themselves.

In hindsight, this label seems incredibly arrogant, but it shows what happens when assumptions are treated as facts. This is one of many examples where evolutionary theorists hindered science. After all, why research something that is mere junk?

Fortunately, not all scientists were put off by the junk DNA label, and more and more uses for the other DNA were found. We now know that the majority or even most human DNA is transcribed into RNA or has some other purpose, even though only a small amount is converted into proteins. Some of it is involved in other roles such as gene regulation, controlling development, or to serve as structural or catalytic components in conjunction with proteins. As our knowledge increases, so the amount of junk keeps shrinking. In other words, junk DNA, which for a long time was argued as being absolutely necessary for evolution to happen, turned out to be an illusion.

Before we were able to peer into the cell, many biologists believed that humans and apes had evolved from a common ancestor perhaps around six million years ago, because they shared certain similarities, including a somewhat similar bone structure, hands with thumbs that can grip onto things, and the ability to walk on two legs.

When scientists figured out how to compare DNA fragments, human and chimpanzee genomes appeared to be about 99% similar. When the chimp genome was sequenced more fully, researchers came up with a more precise difference of 1.23%, based on an alignment of 2.4 billion out of 3 billion base pairs in the human genome. This figure, about a 1% difference between humans and chimps, gave the strong impression that we are closely related.

However, this widely popularized figure only included base substitutions, where one nucleotide base is replaced with another. It didn't include insertions or deletions, or "indels" as they are called. These made up at least an additional 3% difference, bringing the similarity to around 95%, although the sample that had been compared still excluded hundreds of millions of base pairs. But it was idea of the 1% difference that somehow made it into the public consciousness, rather than the more accurate figures. No wonder one science writer dubbed it "The Myth of 1%." ¹

At the time, the DNA molecule could only be read in small chunks. These were assembled using the human genome as a template. However, later researchers acknowledged that this effectively humanized the ape genome, minimizing differences

between the species. When they assembled ape genomes without using the human one as a template, only an estimated 83% of their genome could be aligned with the human one, excluding chromosome Y. ²

It turns out, there are also dramatic differences in certain regions of the human and chimp genomes. Humans have 23 chromosome pairs, while chimpanzees have 24. However, the most striking difference is in the Y chromosome, found only in males, and which earlier sequencing analysis had excluded, perhaps conveniently, so it wouldn't disrupt the 1% myth.

According to the researcher who led the work into comparing the Y chromosomes of chimps and humans, they are "horrendously different from each other," like there had been "a dramatic renovation or reinvention of the Y chromosome in the chimpanzee and human lineages." ³

His research team found that the chimp Y chromosome has only two-thirds as many distinct genes or gene families as the human Y chromosome, and only 47% as many protein-coding elements. Furthermore, more than 30% of the chimp Y chromosome couldn't be aligned with a human counterpart, and the parts that could be lined up had been relocated. Given that the human Y chromosome consists of about 60 million base pairs, or about 2% of the genome, and earlier studies had excluded this, clearly the figure of 98% or 99% similarity can't be true.

There are many other significant differences. At the end of each chromosome are repeating DNA sequences called "telomeres" that protect the ends from deterioration, like the plastic or metal at the end of a shoelace. The telomeres of primates such as monkeys, chimps and orangutans are about 23,000 bases long, but human ones are only 10,000 bases long. ⁴

"Alu elements" are short sequences, about 300 nucleotides in length, that repeat themselves throughout the genomes of primates, which evolutionary classification includes humans. There are more than a million copies of Alu elements in the human genome, accounting for over 10% of it. They were originally assumed to be junk DNA, or selfish genes with the sole purpose of replicating themselves, like genetic parasites. But they are now known to have important functions. They help to regulate tissue-specific genes, and affect the way genes are turned on. There are at least 7,000 Alu elements unique to humans. One study identified about 15,000 mobile genetic elements that are specific to humans. ⁵

In other words, taking into account all the differences, and the fact that the human genome was originally used by researchers as a template for the chimp genome, it's highly unlikely that our genomes are even 95% similar. The high degree of similarity was another illusion, propped up by cherry-picking areas for comparison. Certainly the Y chromosome smashes this illusion to pieces.

But why does it matter whether we are 85%, 95% or 99% similar to chimps? According to evolutionary theorists, humans and apes descended from a common apelike ancestor around six million years ago. If we assume a 99% similarity, this is a difference of about 30 million base pairs.

In evolutionary theory, mutations can occur regularly, but a mutation is only significant over the long haul if it gets fixed in the wider population of a species. It takes time for a single mutation to be fixed, so it can be passed on to succeeding generations.

During most of the supposed six million or so years of human evolution, the population size of humans was fairly small. Assuming a new generation every 20 years, there have been about 300,000 generations from the supposed divergence of humans and chimps from a common ancestor, and 30 million mutations were fixed during this time, which means about 100 mutations needed to be fixed for each new generation born.

However, if the similarity between humans and chimps is closer to, say, 90%, this would take the number of mutations in each generation to around 1,000. This means evolution has to work ten times harder than at 99% similarity. In the end, this isn't a major problem for evolutionary theorists, because they can just tweak their figures to make it work in support of evolution.

I suppose they could argue for a higher mutation rate in the past, but this would throw doubt on the idea of mutations being regular and clock-like; and if they changed the length of time from which we supposedly diverged from a common ancestor, this would cause problems with their dates for existing fossils.

In any event, the reality seems to be that we are nowhere close to a 99% similarity, and some parts of the human and chimp genomes are drastically different, which is why researchers have talked about dramatic renovation and a rapid rate of change in those areas. This language reflects the built-in assumption that chimps and humans share a common ancestor. But maybe what researchers are seeing is an illusion created by their own assumption. Maybe humans and chimps share many similarities, but aren't actually related by common descent. Instead, perhaps they both have a common designer.

Many or even most of the proteins needed to make a human being would be similar to those needed to build a chimp, which would account for the similarity in the parts of the DNA that code for proteins. But a lot of major and minor tweaks would also be needed to make us distinct, which would also be consistent with what researchers have found.

Now, once scientists were able to sequence individual genes, they discovered an interesting pattern. The protein "cytochrome c" is an essential part of the electron transport chain, and is made up of about 100 amino acids. The gene is identical in humans and chimps. By comparing the cytochrome c gene in different organisms, scientists found there is greater similarity between species assumed to be more closely related in the evolutionary tree of life, and larger differences in species that are more distantly related.

For example, the gene is identical in pigs, cows and sheep, and there are only two differences between ducks and chickens. There are 11 differences between the human and dog versions of the gene, and 44 differences between the human and

yeast versions. This pattern would seem to be consistent with the idea of universal common descent, and that the bigger the evolutionary distance between organisms, the further apart the gene sequence gets.

However, another explanation is that the differences are related primarily to the needs or physiology of the creature. Humans and chimps aren't vastly different in shape and size, and neither are pigs, cows and sheep. However, humans tend to differ from yeast, so the needs of the two organisms are probably very different. Maybe the differences relate to the size, shape and makeup of the organism.

The fact that many of the amino acids in cytochrome c are the same across vastly different creatures suggests those amino acids serve an essential purpose. They can't change without breaking the gene.

Many biologists assume the ones that have changed are more neutral. In other words, those amino acids can change without significantly changing the function of the protein. In a sense, this would perhaps make them more like placeholders, which may be true in some cases, but others could have been put there deliberately.

Researchers create what are called "phylogenetic trees" based on similarities in the physical or genetic characteristics of species, and also of genes. They assume the tree represents an evolutionary history, in the same way a family tree diagram represents a family history. The assumed evolutionary lineage of a species or gene is called its "phylogeny." However, what these phylogenetic trees could be showing is mainly the physiological similarity or differences between creatures, rather than an evolutionary history.

For example, pigs, cows and sheep are all roughly the same size and have identical cytochrome c genes, even though each creature is presumed to have evolved separately. Ducks and chickens are also of similar size to each other, and they have just two differences in the gene. Humans and dogs are pretty different from a physical point of view, and the 11 differences in their cytochrome c gene could reflect their different physical makeup. Humans and yeast have 44 differences in the gene, maybe because they are very different organisms with vastly different needs. *Drosophila* fruit fly, wheat and yeast cytochrome c genes have several amino acids at the beginning that don't appear in the human or chicken version. Presumably these amino acids are useful for those particular creatures, but not for others.

Many genes have their own distinct pattern of differences across species. The protein "lysozyme" is a small antibacterial enzyme that forms part of our natural immune system, and is able to attack the cell walls of bacteria. It was discovered by Alexander Fleming while he had a cold. He added a drop of mucus to bacterial culture and discovered, to his surprise, that it killed the bacteria. The enzyme is found in places where nature doesn't want bacteria to grow, such as human milk, egg whites, mucus, tears and blood.

There are three distinct types of this gene, the c-type (chicken or conventional type), the g-type (goose type) and the i-type (invertebrate type). The lysozyme g version from goose eggs is larger than lysozyme c, and there isn't much sequence

similarity between them. In fact, the different forms aren't very similar in terms of amino acid sequences, but they do share similar overall structures, which is why biologists view them as three types of the same enzyme. This suggests the protein has been adapted to serve the needs of its different hosts.

For example, lysozyme found in the white of a hen's egg can reach a higher temperature than lysozyme in human milk, before it loses its antibacterial abilities. This means a mother hen can safely sit on her eggs and keep them warm, without having to worry about bacteria munching away at her offspring's only food source while they are still inside the egg. The gene sequence for this enzyme must be different between humans and hens, so the hen version can incorporate this feature.

For proteins, what matters most is the shape it folds into once it has been made by a ribosome. This usually determines its function. For example, the protein "myosin II" is responsible for producing muscle contraction in most animal cell types. It consists of two heavy chains about 2,000 amino acids in length, forming two "heads" and a "tail" domain. The tail folds into three segments. Despite turkeys and scallops supposedly being separated by 600 million years of evolution, their myosin II proteins are structurally identical.⁶

Phylogenetic trees of proteins are constructed in an attempt to trace their evolutionary origins across the tree of life. But if proteins didn't evolve that way, but instead were built into the first creature in a family, and were then somehow adapted to serve the needs of each creature, then phylogenetic trees are really just similarity trees, and don't necessarily reveal ancestry, except in closely related species.

In other words, gene comparisons and phylogenetic trees across widely different families may be giving the illusion of evolution. It could simply be that the bigger the difference in the physiology and needs of two creatures, the bigger the difference in the gene sequences.

Some genes such as cytochrome c are fairly similar across the so-called tree of life, while others such as lysozyme are very different. As evidence for evolution, the public are generally shown the ones that seem to differ in a regular clock-like manner, to imply a clock-like regularity of evolution from common ancestors.

But this is contradicted by the fossil record, in which large groups of creatures appear very quickly, as well as by genes that have completely different supposed rates of change, or that essentially stay the same, or that appear completely unexpectedly in whole branches of the evolutionary tree, and are therefore explained by magic wands such as "translocation" in the guise of horizontal gene transfer.

I think the evidence from genes as a whole suggests that genetic differences across the spectrum of life are related much more to function, physiology and the specific needs of the organism, rather than simply by how related organisms are on an assumed universal tree of life.

In other words, phylogenetic trees may be contributing to the illusion of evolution. They are drawn up based on similarities, and these are then assumed to be the result of evolution. But maybe they are just similarities, in the same way that a

Ford and a Chevy share many similarities. If we were to look at their design blueprints, we would find many almost identical features; but this doesn't mean they evolved from a common ancestor. They were both designed, and both manufacturers had similar intentions for their vehicles, which explains why many features overlap. But creating a phylogenetic tree involving a Ford and a Chevy would be misleading.

However, researchers looking at genetic sequences claimed they found clear evidence that proved we were directly related to chimps. Many creatures are able to make their own vitamin C and can produce it in large quantities. The manufacture of vitamin C in an organism involves several processes, the last of which requires an enzyme known as GLO or GULO. However, it seems the gene is broken in humans, chimps, guinea pigs and some other creatures. It has become a pseudogene. As a result, these creatures can't make their own vitamin C and need to get it from fruit and vegetables.

The deletion of a single nucleotide in the same position in this gene is shared by both chimps and humans, and this is claimed to be proof of common descent. Humans and chimps, it is assumed, inherited the same deletion from a common ancestor.

In the evolutionary paradigm, chimps and guinea pigs evolved along different paths, and their *GULO* pseudogenes are quite different. Despite this, a comparison of human and guinea pig sequences found dozens of matching substitutions, even though they had supposedly evolved along very different lines.⁷ In other words, if we assume "common mistakes" provide evidence of common ancestry, then based on this, we are much more related to guinea pigs than chimps.

What is the cause of such shared mistakes, even in species that are only distantly related according to the evolutionary paradigm, and therefore can't be the result of inheriting the mistakes from a common ancestor?

It seems mutations often occur in what are referred to by biologists as "mutation hotspots," areas in the genome that are much more prone to mutation.

For example, close to half of all insertions and deletions are concentrated in about 4% of the genome, most of which are caused by DNA polymerase, the machinery that copies the genome, pausing, backtracking and then repeating the sequence it had already copied. Furthermore, areas of the genome containing sequences of repetitive nucleotides are more prone to this type of mutation.

Single nucleotide variants are the most common in humans, where one nucleotide base has been changed to another base, and they comprise about 80% of the genetic differences between two people. On the other hand, in the gene coding regions of the genome, there are about seven times more of these type of mutations than short insertions and deletions.⁸

In a study of hundreds of *Arabidopsis thaliana* plants conducted in a lab, researchers found patches in the plant's genome with lower than normal mutation rates. These patches contained many essential genes such as those involved in cell growth and gene expression. Natural selection wasn't responsible for this, because of

the way the experiment was set up, so these areas of the genome were being protected from mutations in some other way, such as epigenetics. As one of the researchers concluded: "It turns out that mutation is very non-random and it's non-random in a way that benefits the plant. It's a totally new way of thinking about mutation." ⁹

Mutational hot spots could explain the dozens of apparent "common mistakes" between the *GULO* pseudogene in humans and guinea pigs, and is also a reasonable explanation for why primates and humans share the same mutation at one particular point. It could simply be a location in the genome that is more prone to mutation.

While the offending nucleotide has been deleted in both the chimp and human genomes, the same nucleotide varies in other animals. The letter at this position is a G in pigs and guinea pigs, an A in mice, rats and chickens, and a C in cows and dogs. In all of these creatures, the nucleotide is surrounded on either side by the letter G, suggesting they are much more stable positions than the one in the middle, and implying the mistake shared by chimps and humans is indeed a mutational hot spot within the *GULO* gene or pseudogene. ¹⁰

Incidentally, why is this gene broken in some creatures and not in others? Humans and chimps are able to obtain vitamin C easily enough from their diet, so when the gene broke it wasn't fatal. We could still survive without it. At the same time, while the *GULO* pseudogene was originally the last step for producing vitamin C, it may still have a secondary function, which would explain why it hasn't just mutated away but remains somewhat intact and recognizable. Alternatively, maybe the mutation happened fairly recently.

Skeptics and atheists ask, why would a creator put a pathway for making vitamin C in all these species, and then inactivate it? ¹¹ The question assumes the creator inactivated it, but that doesn't need to be the case at all. However, this shows why some kind of revelation or communication from the creator would be useful, otherwise we would be left to guess what was going on.

I have argued throughout this letter that such a communication exists, which explains quite clearly that humans fell away from God, and thus subjected themselves to breakdown, of which the *GULO* gene could be one example.

To give a human analogy: if a manufacturer offered a lifetime repair warranty for a product, but the customer rejected the warranty, they can't later expect the manufacturer to repair the product for them if it breaks down. Pseudogenes are consistent with this idea. They are evidence that we are devolving and losing genetic information.

There are also other reasons why pseudogenes exist, assuming they really aren't functional any more. Some sequences that have been called pseudogenes at one time have turned out not to be, or have other important functions.

Either way, pseudogenes would still exist in many creation models. For example, God could have created distinct "kinds" of creatures with the potential for variations, and those variations would eventually become all the species within a

family of creatures. As each species adapted to its environment, some genes might get turned off or broken, becoming pseudogenes. A good example of this would be the antifreeze gene discussed in an earlier chapter, which seems to have become a pseudogene in one species of codfish that no longer lives in freezing waters.

In other words, most creationists accept a limited form of common descent, where a species could be descended from a common ancestor in a family tree, but they usually reject the idea of universal common descent, where all species are connected in one tree of life.

Curiously, the vitamin C pathway isn't consistent across different forms of life. Yeast, plants and animals use different pathways to make it or a variation of it. Vitamin C is produced in the kidneys of some fish, amphibians and reptiles, but in the liver of mammals. In birds, it is a mixture.

This poses a challenge to the idea of a universal tree of life, but could be useful for determining whether there really are smaller phylogenetic trees of life based on genetically identifiable "kinds." At a minimum, it suggests a modularity to at least some of life's functions, where whole systems like vitamin C manufacture can be moved into different organs, even in the same type of creature!

Whatever the case, the idea that we must have a common ancestor with chimps could simply be another illusion of evolution.

Another part of evolutionary theory is the concept of convergence. When the same function or feature appears in creatures on different branches of the supposed tree of life, but not in their common ancestor, evolutionary theorists call this "convergent evolution," or "homoplasy" in more technical circles. It means nature invented the same thing more than once.

Echolocation is often cited as a good example of this. Some bats and dolphins are able to emit high-pitched sounds which they use to catch food, yet these creatures are only distantly related on the supposed tree of life. In the evolutionary paradigm, nature came up with echolocation at least twice.

Curiously, when researchers looked at the genomes of different creatures including bats and dolphins, they found that echolocating bats and the bottlenose dolphin, which also uses echolocation, had nearly 200 genes altered in a similar way, genes that seemed to be linked to hearing or vision, and that presumably contributed to the echolocation ability.¹²

The concept of convergence is used to explain features that keep cropping up and that don't fit neatly into a tree of common descent, but more and more examples are being found even at the genetic level.

In one study, researchers wanted to learn more about how the brains of birds develop. They compared the genomes of parrots with 30 other birds, and found that regions of the parrot genome regulating brain development are the same as humans. These elements supposedly evolved in both species at very different times, but with similar results.¹³

In another study, researchers found that short interspersed elements in humans and mice regulated the same genes the same way in both species, yet they are said to have evolved independently in the two lineages.¹⁴

How do evolutionary theorists explain this? They argue that creatures with a common feature were likely under similar selective pressures, and so natural selection gradually led them down the same path.

Since natural selection can only select from what already exists, I suppose it makes sense that a complex feature like echolocation would have to evolve from something already existing in a common ancestor of bats and dolphins; and that from a similar starting point, there may be only one way to build such a feature.

But evolutionary theory can't tell us in detail how echolocation evolved even once, let alone twice. If about 200 hearing and vision-related genes need to be altered for a creature to acquire this ability, how does nature arrive at this once, let alone twice? The theorist would answer, "cumulatively, in small steps," but this assumes there is a cumulative pathway available, with each step having a significant survival advantage. Theorists can perhaps describe these steps in broad storytelling strokes, but they rarely if ever test out all of the nucleotide changes that would be required along the path to echolocation; and even if such a path could be constructed on paper, this doesn't mean echolocation was built this way.

Incidentally, some species of bats don't have echolocation. Could they have lost the ability? Research suggests this may be the case. In early development, the inner ears of bats grow in a way that can facilitate the sonar ability, but this isn't sustained into adulthood in some species such as fruit bats, implying they may have lost the echolocation ability at some point. In other words, they could have devolved.¹⁵

Whatever the case, given that similar features and functions occur so frequently, could it be that "convergent evolution" is an illusion made up by evolutionary theorists, and that similar features exist in different creatures because they share a common designer? A car manufacturer doesn't need to reinvent the wheel every time it wishes to design a new vehicle. It can draw from existing blueprints and design principles, and re-use features from previous models. This is an intelligent process, and not done by gradually shuffling letters in the car manual.

What about the fossil record? The claim is often made that it supports the story of evolution. The record is usually broken up into periods or epochs within the evolutionary timetable. But if we remove our evolutionary glasses for a few moments and just look at the record without any assumptions, we simply see lots of dead creatures that fossilized within different layers of sedimentary material.

Fossilization is not the normal state of affairs for dead creatures, since a dead body usually decays quite quickly, although bones tend to take somewhat longer, and then scavengers and other organisms eat up the remains. Furthermore, the fossilization process is often assumed to take thousands or even millions of years, but experiments have shown that organic matter encased in sediment, and subjected to high pressure and temperature, can be fossilized in as little as a day.¹⁶ If only we could

conceive of a catastrophe that could cause animals to be covered in sediment so quickly!

One of the most interesting parts of the fossil record is the so-called Cambrian Period, in which a vast range of multi-cellular life seems to have appeared rapidly. This phenomena is often described as the “Cambrian Explosion.”

At the bottom are trilobites that moved over the sea bed, and are considered to have been one of the earliest creatures to have evolved. They appear suddenly in the fossil record around the world, with a complex body plan and multiple organs.¹⁷

Curiously enough, if we lose the naturalistic and evolutionary lenses and assume instead that a worldwide Flood happened, we would see exactly the same thing. Huge volumes of sediment would have been shifted around and deposited in layers, burying millions of animals and causing them to fossilize, with the poor trilobites at the bottom, because everything would have been dumped on top of them. Of course, this raises the question of dating and timescales, which I will discuss in a later chapter.

Another line of evidence used to support evolution are so-called transitional forms. Given that evolution is supposed to be a gradual process of change over time, we would expect to see the fossil record full of transitions, as nature tinkers constantly with forms. Yet it is surprisingly stable. True, there is plenty of variation, but we can usually recognize what family a dead species may have belonged to.

Nevertheless, a handful of creatures are held up as evidence of a major transition from one major form of life to another. *Archaeopteryx* is a well-known example, claimed to represent an evolutionary transition between dinosaurs and birds. Its feathers were identical to modern bird feathers, and it could probably fly for short bursts, like quails and pheasants.¹⁸

The fossil species *Tiktaalik* has also been assumed to be a transition from fish to land dwelling creatures. One writer called it “a fish with a wrist,”¹⁹ although a wrist has many more bones. However, it is similar to a modern fish that can move on land, so maybe it was just an ancient fossil of a related type of fish.

Perhaps the most famous of all so-called transitions is the *Neanderthal*, once portrayed as a primitive human, implying they were the “missing link” between humans and chimps. Later research showed that they were fairly similar to modern humans, who even interbred with them. However, to keep the human evolution story going, researchers keep digging up new bits and pieces of fossils, which they then give names to and declare to be our missing ancestors.

Now, I could spend many pages arguing about whether these creatures really are transitional forms on some kind of evolutionary scale, but instead I will make my point with a simple analogy.

Imagine that human society in the future has been wiped out by the artificial intelligence we created to solve all our problems and make our life easier. I suppose wiping us out did solve all our problems. Millions of years later, these AI entities have

entirely forgotten about their human creators, and believe that the forces of the Earth must have put their ancestors together, in some kind of evolutionary process.

As they examine the “fossil record,” they see evidence that reinforces their beliefs. They find creatures they label as belonging to the class they call *vehicles*. The AI scientists debate over the exact ordering, or phylogeny, in the evolution of the vehicles, but most agree that the *unicyclium* order came first, followed by *bicylium*. This was followed in rapid succession by the evolution of creatures in the orders of *carium*, *busium*, *truckium*, *coachium* and *motorbikium*. These all seemed to evolve relatively quickly, in a period they call the Wheelian Explosion.

Now, this analogy might be slightly amusing, or perhaps a little depressing, but it highlights the consequences of their flawed logic. Since their initial assumption that these things evolved was faulty, the entire process of identifying a tree of life would also be flawed.

They could come up with stories for how each group evolved. Obviously the *bicylium* came about as a result of tandem duplications of the *unicyclium* genes. Some *busium* and *truckium* parts seem similar, but with no clear common ancestor this was probably a case of horizontal gene transfer; although a faction of AI scientists argued that *truckium* evolved by the endosymbiosis or swallowing up of an ancient *motorcyclium* by a *busium*.

Of course, couching an idea in scientific terminology that sounds vaguely plausible doesn't make it true, because the entire reasoning is based on incorrect assumptions. This is what I am suggesting is also the case in reality.

If life was actually created in a top-down manner, with the initial creations capable of rapid speciation, and then large amounts of these variations were destroyed in a global catastrophe, the fossil record would be no different to what we see today. In this case, creatures such as *Archaeopteryx* and *Tiktaalik* wouldn't be transitional but simply variations, just as a bicycle isn't a transitional species between a unicycle and motorbike, but is simply another form of vehicle. Similarly, *Neanderthals* would just be an extinct branch of the human family, and not an evolutionary transition. In older textbooks they were made to look more primitive than they may have been, to support the illusion that we evolved from an apelike ancestor.

In Darwin's day, many creationists apparently believed each species was directly created by God; or at least, this is what Darwin argued against, with his idea that all species evolved from a universal common ancestor.

The famous finches studied by Charles Darwin on the Galapagos Islands are held up as icons of evolution for their beaks that vary in size. Three species of finch were known to occur together in the highlands of Floreana – the small, medium and large tree finch – each differing in body size and in the shape of the beak.

Later studies showed that the large tree finch had disappeared from the island. The evidence indicated it may have disappeared due to hybridization, where two species fuse into a single population. Similarly, on the island of Daphne Major, two

species of ground finch have been morphing into one, because of a change in the food supply. These things happened in the space of a few decades.²⁰

On the island of New Guinea in the Pacific Ocean, eleven species of *estrildid* finch proved to be even more interesting. The plumage of each species has its own distinctive patterns of black, brown, gray and white, along with differences in beak size. Yet when researchers studied their genomes, they were strikingly similar, suggesting all of the species arose quickly and recently, assuming the evolutionary timetable.²¹

The researchers identified about 20 genes that differed among the eleven finch species, including a handful which seemed to control coloration. Different versions of the genes, alleles, had been mixed and matched in the species, perhaps as a result of occasional interbreeding, providing wonderful variety. Millions of years of slow accumulating mutations weren't needed to produce these different species. It just needed a little sex between them.

The process of speciation is often assumed to be slow, happening by natural selection gradually fixing tiny mutations in a population over a long period of time. But research increasingly indicates this assumption may be wrong, and that species can arise quickly as a result of the reshuffling of genetic information, almost as if nature was designed to produce interesting and colorful variations quickly.

The finches we have just discussed are still finches. The genetic variation built into their gene pool allows for beak variations and a variety of colors and patterns, but I suspect they will always be finches. People are entitled to call this evolution, but it's really just variations on a theme, which is what many creation models predicted.

Genetic variation can also be seen in the peppered moth, often cited as an example of natural selection in action. During the Industrial Revolution, when soot from coal-burning factories blanketed the English countryside, light-colored moths began to stand out on trees. During this time, dark-colored peppered moths may have arisen, and they enjoyed better camouflage from predators. As a result, their population increased rapidly. Later, when pollution was reduced, the light-colored moth took over again.

Apparently, peppered moths weren't the only species affected by pollution. Dark forms increased in over 100 moth species during the Industrial Revolution, leading a group of researchers to wonder whether the moths were all relying on similar genetic mechanisms.

The researchers examined the genomes of the British peppered moth along with the "pale brindled beauty" and "scalloped hazel" moth species. The mutation for a dark trait seemed to occur in the same genetic region as a gene called *cortex* in all three species, but the origins of the trait in the other two species appeared to be much older than the one in the British peppered moth, which may have happened as recently as the 1800s, giving rise to dark-colored ones.²² According to the researchers, this implied there was a "master switch" for the dark trait in these moths.²³

Later research suggested that the ability to “go dark” is likely a feature of what are known as “micro RNAs.” These are short pieces of RNA about 20 base pairs long that act as genetic switches, playing a role in regulating gene activity and cell development.²⁴

The dark peppered moth is a good example of natural selection at work, but the evidence at the genetic level indicates it was likely switching on a trait already built into the species, but lying dormant – namely, the ability to “go dark.” The genes may have been designed in such a way that, if dark forms were needed for the species to survive, the trait could be switched on.

Once again, people are entitled to call this evolution, but it’s also evidence that traits have been designed to be flexible, allowing species to adapt to their environment rapidly. They certainly don’t need millions of years. The dark mode was switched on in the peppered moth within just a few decades. This would harmonize nicely with many creation models, where speciation and adaptation are predicted to happen very fast. It also suggests design ingenuity, where one or more switches related to a gene can effectively turn on the dark mode of a moth when needed.

Let’s examine one more evolutionary idea: the concept of “vestigial” organs. These are organs or features that have apparently lost all or most of their original function. They are often held up as evidence for large scale evolution.

The appendix is perhaps the most famous example, once considered a vestige of a redundant organ with digestive functions. However, the appendix turns out to be a safe house for useful bacteria that might otherwise get flushed out of the rest of the intestines, and may also play a part in the immune system.

Whales and dolphins have pelvic bones that are often assumed to be remnants from when their ancestors supposedly walked on land. But it turns out, the pelvic bones of these creatures help with reproduction. They’re actually doing something useful.²⁵

The coccyx, or tailbone, is supposedly the remnant of a lost tail. According to evolutionary theorists, it hasn’t disappeared because it serves as an attachment site for tendons, ligaments and muscles.

Now, if we remove our Darwinian lenses for a moment, and just look at the evidence for what it is, we see that the appendix, the coccyx and the whale’s pelvic bone all have useful functions, and the idea that they are vestiges of some lost function is just an assumption based on evolutionary thinking.

Incidentally, on occasion, human babies have been born with what appears to be a tail. One type was associated with birth defects, while another was assumed to be the remnant of an evolutionary ancestor. However, the evidence suggests that both are due to an incomplete fusion of the spinal column.²⁶

Wisdom teeth are often viewed as vestigial. It is assumed that our ancestors had larger jaws with more teeth, but modern humans have smaller jaws and therefore need less teeth. The fact that wisdom teeth still grow in many humans shows there is quite a lot of potential variability in the makeup of humans, but this isn’t really

evolution as such. It's just variation. However, if modern humans really are smaller, this suggests we might be devolving, which fits creation models.

Whatever the case, the concept of vestigial organs is used to prop up the idea that large scale evolutionary changes have occurred, when in reality, those organs perform a useful function, and everything else is yet another illusion, gifted to us out of the imagination of evolutionary theorists.

The point of this chapter hasn't been to go into detail about every issue related to evolution versus design. That would need a whole book, although I will tackle a few more important issues a little later.

Instead, I have selected a range of issues from junk DNA to vestigial organs, to show that when we remove the evolutionary lenses through which we have been conditioned to look at life, starting from the school textbooks and continuing right through to academia, science and the media, in many cases the idea that we evolved from fatty RNA protocells looks more like the illusion.

A stage magician relies on a number of psychological tricks to convince the audience of his illusion. He may misdirect them with a hand gesture, hide something important with sleight of hand, and rely on his authority to reinforce the illusion.

Could it be that those with a vested interest in the naturalistic dogma are using the same tricks to convince you that life came about all by itself? Evolutionary theorists say that life has the appearance of design, but this is simply an illusion. I'd suggest that evolution is the illusion.

I think the evidence indicates that life has the appearance of design because it is actually designed, by someone with a high degree of intelligence and ingenuity. But in the modern world in which we live, the stage magician's toolkit of authority, misdirection and sleight of hand has been employed by the magicians of naturalism, so the public only gets to see what those magicians want them to see.

1 See the article "Relative Differences: The Myth of 1%" by Jon Cohen, published in *Science*, June 29, 2007. **2** Kronenberg *et al*, "High-Resolution Comparative Analysis Of Great Ape Genomes", *Science*, 2018. **3** See the article "The fickle Y chromosome" by Lizzie Buchen, *Nature*, January 13, 2010. **4** Kakuo *et al*, "Human is a unique species among primates in terms of telomere length", *Biochemical and Biophysical Research Communications*, 1999. **5** Tang *et al*, "Mobile elements contribute to the uniqueness of human genome with 15,000 human-specific insertions and 14 Mbp sequence increase", *DNA Research*, 2018. **6** Jung *et al*, "Conservation of the regulated structure of folded myosin 2 in species separated by at least 600 million years of independent evolution", *PNAS*, 2008. **7** Inai *et al*, "The whole structure of the human nonfunctional L-gulonono-gamma-lactone oxidase gene--the gene responsible for scurvy--and the evolution of repetitive sequences thereon", *Journal Of Nutritional Science And Vitaminology*, 2003. **8** Nesta *et al*, "Hotspots of Human Mutation", *Trends in Genetics*, 2020. **9** Monroe *et al*, "Mutation bias reflects natural selection in *Arabidopsis thaliana*", *Nature*, 2022. For the quote, see the article "Genetic mutations may not be random" by Sophie Ormiston, published at [frontlinegenomics.com](https://www.frontlinegenomics.com) on January 14, 2022. **10** See Figure 3 in the article "An illusion of common descent" by Peer Terborg, published in *Journal Of Creation* and at [creation.com](https://www.creation.com) in 2010. **11** For example, Jerry Coyne asks this exact question on page 73 of his book *Why Evolution Is True*, Oxford University Press, 2009. **12** Parker *et al*, "Genome-wide signatures of convergent evolution in echolocating mammals", *Nature*, 2013. **13** Wirthlin *et al*, "Parrot Genomes and the Evolution of Heightened Longevity and Cognition", *Current Biology*, 2018. See also the

article “Parrots are clever because their brains evolved the same way as ours” by Chelsea Whyte, published in *New Scientist*, December 15, 2018. **14** Lucas *et al*, “Evidence for convergent evolution of SINE-directed Staufen-mediated mRNA decay”, *PNAS*, 2018. See also the article “Study finds convergent evolution of gene regulation in humans and mice” by Tim Stephens, published by UC Santa Cruz Newscenter at news.ucsc.edu on January 18, 2018. **15** Wang *et al*, “Prenatal development supports a single origin of laryngeal echolocation in bats”, *Nature Ecology & Evolution*, 2017. See also the article “Some bat species lost sophisticated sonar ability as they evolved” by Jamie Deasy on ucd.ie on January 9, 2017. **16** Saitta *et al*, “Sediment-encased maturation: a novel method for simulating diagenesis in organic fossil preservation”, *Palaeontology*, 2018. See also the article “Researchers Have Discovered How to Make Proper Fossils - In a Day” by Michelle Starr, published at sciencealert.com on July 27, 2018. **17** Paterson *et al*, “Trilobite Evolutionary Rates Constrain The Duration Of The Cambrian Explosion”, *PNAS*, 2019. For an interesting commentary on this article from an intelligent design perspective, see “New Paper Confirms the Trilobite Explosion” published at evolutionnews.org on March 15, 2019. **18** See the article “This Famous Dinosaur Could Fly—But Unlike Anything Alive Today” by Michael Greshko, published at nationalgeographic.com on March 13, 2018. **19** See *Your Inner Fish* by Neil Shubin, page 38. First edition, 2008. Published by Pantheon Books. **20** Peter R. Grant, B. Rosemary Grant, “Speciation undone”, *Nature*, 2014. Also “Hybridization increases population variation during adaptive radiation”, *PNAS*, 2019. **21** Katherine Faust Stryjewski, Michael D. Sorenson, “Mosaic genome evolution in a recent and rapid avian radiation”, *Nature Ecology & Evolution*, 2017. See also the article “Birds of a Feather: Finches from remote corners of New Guinea help solve an evolutionary puzzle” by Catherine Caruso, published in *The Brink* at bu.edu on February 12, 2018. **22** E. van't Hof *et al*, “The industrial melanism mutation in British peppered moths is a transposable element”, *Nature*, 2016. **23** E. van't Hof *et al*, “Genetic convergence of industrial melanism in three geometrid moths”, *Biology Letters*, 2019. See also the article “‘Industrial melanism’ linked to same gene in three moth species” published by the University of Liverpool at liverpool.ac.uk on October 16, 2019. **24** Richard H. ffrench-Constant, Alex Hayward, “Melanism: Cryptic control by non-coding RNAs”, *Current Biology*, 2024. **25** See the article “Whale reproduction: It’s all in the hips” by Robert Perkins, published by USC News on September 8, 2014. **26** See the article “Some Babies Are Born With 'Tails', But Not For The Reason You Might Think” by Carly Cassella, published at ScienceAlert.com on June 25, 2023.

65. The Symphony Of Life

I've tackled some fairly complex issues over several of the previous chapters, but behind each of those issues, there are really just two simple ideas competing with each other.

Life was designed. This is a fact. The real issue is: how was it designed? Was it done from the bottom up, primarily by natural selection and mutations over vast periods of time? Or was it built in a top-down manner, by an intelligent designer?

I have presented evidence that mutations and natural selection can't account for the ingenuity of design we see at all levels of life, and that intelligent design is a far better explanation. I have also given evidence to show that the designer was YHWH.

In this chapter I would like to address more general questions such as: does this mean evolution isn't true? If it isn't, why do so many scientists believe this is how life came about? And how do we know aliens didn't create us?

The debate between evolutionists and creationists often gets reduced to a simple black and white question: "Is evolution true or not?" However, the answer isn't quite as straightforward as a simple yes or no.

Most of the tools in the evolutionary toolkit are real to some extent. Natural selection is true in the sense that organisms better equipped for survival and reproduction are more likely to pass their genomes on to the next generation.

Mutations also happen, as a result of radiation, decay or copying errors. The question is whether mutations and natural selection together are really capable of building all of the upward, downward and parallel complexity we see today, from proton pumps and nuclear pore complexes, to frogs and princesses.

Evolutionary theory says that a continual sequence of mutations keep getting fixed in a population of organisms until it leads to some useful new function or sequence. This is mostly just an assumption. Theorists don't actually know how new functions begin to work. They just assume the right proteins evolve, and then they get drafted in to work together by some magical recruitment process.

They also assume most of the steps along the path to evolving a new protein or function somehow give the organism an advantage. In the case of a new protein that supposedly evolves from the duplication of an older one, dozens of useful cumulative steps may be needed, but these are rarely if ever tested out in the real world.

The situation is far worse for a new species such as humans. In our case, tens of millions of mutations needed to come about, to separate us from chimps, and many of those mutations need to be beneficial to become fixed in a population. This is a purely theoretical assumption, since there is no practical way to trace each small cumulative step in the supposed evolution of humans from an apelike ancestor. Indeed, the very notion that the differences are mutations is also just an assumption.

Horizontal gene transfer is true, in the sense that bacteria have the equipment to share DNA sequences. However, this term is often applied when genes move from one place to another even without a clear reason or mechanism. Words and concepts

become confused with mechanisms. In evolutionary stories, some things seem to translocate to just the right place as if by magic, which is more like storytelling than science. This is why I called translocation a serendipity wand.

There are also specific mechanisms that allow for genetic variety. If there weren't, we would all look almost exactly the same. But these mechanisms don't seem to allow frogs to become princes, no matter how hard they try.

This is why many creationists and some evolutionists like to make a distinction between "microevolution" and "macroevolution." The variations in Darwin's finches would be an example of microevolution. The different species are adapting to varying circumstances, but the genetic evidence indicates they are mostly shuffling genes between each other.

Something similar may be true of the dark British peppered moth, except instead of genes being shuffled, a genetic element may have switched on their ability to go dark. Whatever the case, these finches and moths remain finches and moths.

In many creation models, an original "kind" of animal may have been designed to later give rise to many species, perhaps through built-in genetic mechanisms similar to the ones used by the finches and moths. Darwin's finches are almost certainly related in a family tree by common descent, but they remain within their "kind." This would be microevolution.

Macroevolution, on the other hand, is a broader form of evolution, where entirely new creatures can evolve, in a universal tree of life. This is the form of evolution that is disputed by creationists.

However, evolution, as presented to the public, mixes up real processes with elaborate storytelling and elegant but flawed theory and inferences, so that the general public aren't able to distinguish between these things. It is a blend of science, stories and speculation.

Now, if the evidence for top-down design is as strong as I have claimed, and the evidence for bottom-up design so weak, why do so many scientists believe that mutations and natural selection are capable of producing all the life we see on Earth today?

I would suggest the primary reason is that modern science, and biology in particular, adheres to the principle of naturalism, which is that the natural world must be explained without resorting to supernatural causes.

This became an assumption, and then eventually an ideology or even a dogma, where anyone challenging it is accused of being against science or at least unscientific. When your career and income depends on accepting this dogma, and the peers who review your work buy into the assumption too, it's not surprising that scientists may be reluctant to express their doubts in these areas. Besides, if it appears that other scientists have more solid evidence for evolution than you, you may feel at ease treating naturalism not merely as an assumption but as a fact.

Furthermore, I think this is an example of the metaphorical serpent eating its own tail. Since biologists tend to treat evolution and naturalism as real rather than just

working assumptions, this often leads to atheism, because if everything appears to be explainable in natural terms, then there isn't any need for God. He becomes redundant. And once the scientist is an atheist, they will interpret the evidence through this lens, because people don't usually go out of their way to disprove their own worldview, but rather they seek to reinforce it.

I also suspect that quite a few scientists feel they don't have much choice but to accept naturalism. After all, the alternative is supernaturalism, the idea that a supernatural agency may have had a hand in creation. Many scientists see this as a problem, because saying "God did it!" doesn't really explain anything, which they see as the role of science. Furthermore, they claim this doesn't promote scientific inquiry, and therefore restricts science.

However, I don't think this is true. As an analogy, suppose I were to put a vehicle in front of you and I said, "The Ford Motor Company built this." Does my statement restrict science? Of course not. You could still take the vehicle apart to find out why each part is where it is, how each part works on its own and how they all work together. There is an immense amount of science you could do, unhindered by your knowledge that Ford manufactured the vehicle.

What you couldn't do is make up just-so stories, telling people that each moving part gradually evolved by the shuffling of letters in the user manual, or by the gobbling up of a Chevy, with parts being recruited by natural selection to form the engine. This would be an insult to the scientists and engineers who worked hard to design the vehicle. True, companies can take one another over, sell brands to each other, and re-use blueprints from other cars, but they do these things by design and planning, not by evolution.

Claiming that the shuffling of letters somehow built the vehicle would hinder you from doing real science. It would stop you from getting to the actual truth of how it was made, and the real purpose of each part. You would have to explain, say, the built-in music system, in terms of sex and survival. It would also prevent you from going to the manufacturers to learn more. Maybe they could teach you other useful things as well, or at least sell you a warranty.

As a more relevant example, take the discovery of ribosomes, the genetic code, and the information stored in DNA molecules. If scientists knew God designed these things, how would this hold back science? They could still find exactly the same things they have already discovered, because humans are intensely curious creatures. At the same time, they wouldn't be burdened with ideas like junk DNA, or jumping genes as genetic parasites, which for many decades held back science from discovering the real purpose of those aspects of the genome.

Origin of life research also has its use. Even if researchers were to accept that God was the source of life, their research is helping to highlight the immense difficulty in creating even a basic self-replicating protocell needed to get the evolutionary show started, and the sheer ingenuity required to create anything close to what we would

call “life.” I expect them to always be tantalizingly close to creating life from scratch, as long as their salaries continue to be paid and the research funds continue to flow.

I think naturalism is what really holds back science, because such a philosophy doesn’t inspire us to look for meaning beyond the basics of survival, selection and reproduction. If we looked at the world in the way naturalistic scientists do, we would have to say that Leonardo da Vinci painted the Mona Lisa mainly to get laid.

Now, maybe he did. This would perhaps explain the glint in her eyes. But maybe there are also other explanations. Maybe he liked the aesthetics of her face. Belief in an intelligent designer invites us to look for all kinds of purposes, which in turn encourages curiosity and inspires us to look deeper.

Either way, the “God did it!” objection is a red herring. Just because something may have been designed by God, this doesn’t prevent us from taking it apart and looking into it more deeply. This is what we do as humans anyway, and I think this is probably what God wants us to do, as long as we are respectful, and with the possible exception of the Ark of the Covenant. After all, what inventor doesn’t want to show off their inventions? And even the Ark, once hidden behind the curtain of the Most Holy in the Hebrew Tabernacle, has now been revealed to us, because it was designed to correspond to the DNA molecule hidden within the inner compartment of the eukaryotic cell, the tabernacle of our own bodies.

Besides, saying “evolution did it” isn’t all that different from saying “God did it,” except it is usually accompanied by elaborate storytelling and sweeping generalizations; and once an evolutionary story becomes widely accepted, it can hinder scientists from looking into other causes, including intelligent ones.

I think another problem is, biologists don’t actually know how to detect intelligent design. If a cosmic prankster had come along a thousand years ago and thrown in a particular feature into an organism that had otherwise supposedly evolved, how would biologists know the difference? If the feature was designed to be passed on to future generations, it would have to be built out of proteins or other genetic sequences. But without prior knowledge of what the prankster had done, biologists would simply invent a story to explain how the feature evolved.

Another big reason why evolution has been accepted so widely is because, I freely admit, it is an elegant idea. It is fairly simple to grasp, at least in the form presented to the public.

I suppose there is also elegance in the idea that all living things are related in a universal family tree of descent. This is why I can’t really fault Darwin for coming up with it. After all, we are all familiar with the idea of descent, because humans are related in family trees. Darwin simply extended the idea and asked: what if every living thing is related in an enormous family tree? This wasn’t an unreasonable question. In fact, it was a pretty good one.

The problem is, by the time we entered the era of genetics, biologists had adopted Darwin’s idea as the truth, and so they quickly became accustomed to looking at genetic sequences through purely Darwinian lenses.

However, as genetics has progressed, the universal tree of life has gradually been uprooted, and has become a complex web of genes supposedly transferring themselves all over the place, sometimes by known and verified mechanisms as in the case of bacteria, but quite often by serendipity wanders where genes appear, disappear or move as if by magic, under the cover of scientific words such as “translocation.” This is what happens when you increasingly try to fit a square peg into a round hole.

Tall stories also had to be invented to explain some things. For example, why is there circular DNA in the mitochondria, the cell powerhouses of eukaryotic cells? If you had a mouse-shaped organ in your body, and your child’s science teacher taught that it got there because one day a girl swallowed a mouse, and then her great, great grandchildren had mice organs that could make cheese in their bellies, you would probably be outraged that they were teaching such nonsense in school.

But this is basically what many biologists say happened with mitochondria. One bacterium was engulfed by or invaded a cell, and then the offspring of the bacterium fired off bits of their DNA that magically assembled into a cell battery within the host, with just the right address labels and control sequences to put all the parts together in the right order.

Few biologists dare to ask an obvious but forbidden question here: might circular DNA simply be a common design element used for both bacteria and certain organelles, in the same way that manufacturers sometimes use wheels in things other than cars? Is the idea of intelligent design here really inferior to saying, in effect, that a girl swallowed a mouse which turned into a mouse-shaped cheese factory inside her great great grandchildren?

No wonder some scientists have challenged the traditional view of evolution, and argued that cells must somehow engineer themselves. They see something like intelligence at work, but since they subscribe to the principle of naturalism, they are only willing to move the source of the engineering feats up to the level of the cell.

But if cells can be engineers, and they don’t even have a brain, why is it unscientific to suggest that something bigger than the cell can also be an engineer? We already know this is true, because humans are bigger than cells and can be engineers. But then, why should the buck stop at humans?

What I have shown so far in the second part of this letter is, life as we know it on Earth can’t arise from non-life without a medium in which to store information, a language in which to read and write information, meaningful blueprints that can be consistently converted into useful machinery by something like a ribosome, and a way of preserving those blueprints from the ravages of mutations and decay. These all present a challenge that only an intelligent designer could overcome.

Of course, a skeptic could say, “unguided life could obviously overcome these things, because we’re here now!” But this assumes life was unguided. An alternative explanation also exists, namely design. An intelligent designer could overcome the challenges I just listed, but we don’t know that unguided forces and chemicals can,

without a lot of help from scientists, which by definition makes it guided. Therefore, the existence of life itself is evidence of intelligent design.

Furthermore, life at the cellular level is the equivalent of complex nanotechnology. Each and every moment in your body, tiny protein chains are manipulating protons and electrons on your behalf to produce energy. These subatomic particles are thousands of times smaller than one full atom, which is many times smaller than one nucleotide that stores a unit of your genetic information.

Over three billion units of information making up your genome are stored in an incredibly compact manner in the nucleus of the cell, and arranged in such a way that the information can be accessed when needed.

Every moment of every day, microscopic machines are copying and pasting information in each of your cells and turning coded sequences into little machines or parts for bigger machines, some of them made up of hundreds of complex parts.

If we were to see all of these things in any other context, we would readily acknowledge this to be the product of extraordinary intelligence. And when we remove the evolutionary lens we have been conditioned to look through, we can see that life has all the hallmarks of intricate, incredible and ingenious design. It wasn't the product of nucleotides shuffling and machines stuttering and making errors every now and then.

I have chosen not to explore the many wonderful features of multi-celled organisms ranging from frogs to princesses, because if the complexity of life couldn't have evolved by itself at the atomic, molecular and cellular level, then neither could it do so at the level of bigger creatures. In other words, if nature can't put together an electron transport chain or a nuclear pore complex without outside design, neither can it put together a frog, no matter how long it is given.

But some might ask, in a slightly desperate "please God, anything but God!" tone of voice: what about aliens? After all, if life is the equivalent of nanotechnology, then maybe advanced aliens designed life.

If they did, how did the aliens come about? Were they created? If so, who created them? We could end up with an infinite regress of creator aliens. But if they say they evolved, how do they know this, given that many humans thought they evolved even though aliens apparently created us?

If aliens show up, making the claim to be our creators, hopefully skeptics would be just as skeptical and ask, "Where's your actual proof you evolved, but that you created us?" Maybe they would claim to be behind the Bible, the formation of Israel, the resurrection of Jesus and so on. This would mean they were claiming to be God.

Assuming YHWH exists and is actually God, and the aliens are impostors, I think sincere prayer to YHWH would reveal the truth about their claims. In fact, this is how you can establish the truth of the matter about anyone or anything claiming to represent YHWH. He says, "Call to me and I will answer you, and I will tell you great and hidden things that you do not know." ¹ You just need to know how to ask, and how to listen.

God has already explained how he intends to reveal himself to all humans, by means of the return of his Son. I suppose this is another reason why the Son needed to be human – so he wouldn't be alien to us. God gave the prophet Daniel a glimpse of what this return would be like, in a vision of the sign of the son of man in heaven:

"I was watching in the visions of the night, and look! one like a son of man was coming with the clouds of the heavens; and to the Ancient of Days he approached, and they brought him before him. And to him were given dominion, glory and kingdom; and all the peoples, nations and language groups will serve him. His dominion is an everlasting dominion that will not pass away, and his kingdom one that will not be destroyed." ²

Jesus Christ called himself the "son of man," and he further described the events that had already been seen by Daniel in vision: "Immediately after the tribulation of those days the sun will be darkened, and the moon will not give its light, and the stars will fall from heaven, and the powers of the heavens will be shaken. And then the sign of the son of man in heaven will appear, and then all the tribes of the earth will grieve, and they will see the son of man coming on the clouds of heaven with power and great glory." ³

Therefore, if there is to be any "alien" deception before this astonishing event, its purpose will be to obscure the nature of the "son of man" and "son of God," Jesus Christ, who has been appointed in advance by God for "dominion, glory and kingdom."

In any case, the idea that aliens created us would mean we were designed after all, but I would suggest that evoking aliens really just takes the problem to a different planet, galaxy or dimension. It is just a last, desperate attempt to avoid the idea that YHWH is, in fact, the Designer of life.

If we wanted to play word games, I suppose we could say that YHWH is alien, at least in the sense that he is extraterrestrial. He certainly didn't originate from Earth. The big difference is, YHWH created all things. Also, he is not really alien to us, because he designed us and therefore knows us deeply. He is "the First," and no gods or aliens were formed before him. He is the author of the genetic blueprints found within DNA molecules; and to confirm this, he put his signature in the story of Jacob. But he is not made of the same blueprints, any more than Mozart's body was made up of the notes his symphonies were written in. YHWH is the composer and conductor of the grand symphony of life.

1 Jeremiah 33:3. **2** Daniel 7:13,14. **3** Matthew 24:29,30.

66. In Six Days?

Now, what about the creation account in Genesis? Is it plausible? Can it be reconciled with science? Does it even need to be? Is it meant to be taken literally? Is it a reasonable story, compared to the idea that life arose by itself?

Some have suggested that there are two different creation accounts, one in Genesis 1 and the other in Genesis 2. But the first is simply a broad outline of creation, while the second is focused on the creation of humans in particular.

There are many differences of opinion over how to interpret the creation account. Throughout their early history, Jews probably took the six days literally. After all, one of the commandments given to Israel was to keep the Sabbath, the seventh day, sacred, and not to do any work on that day, because “for six days YHWH made the heavens and the earth, the sea and all that is in them, and he rested on the seventh day. So YHWH blessed the sabbath day, and made it holy.”¹

By working six days and resting on the seventh, God was setting a pattern for the Jews to follow, just as night and day sets the pattern for humans in their daily cycle of work and rest.

Moses wrote that, to God, a thousand years is like yesterday when it is past, and like a watch in the night.² When the creation account talks about days, could each day represent a thousand years? Some believers thought so, reinforced by the idea that God had said to Adam, “in the day you eat from it, you will certainly die,”³ talking about the fruit from the tree of the knowledge of good and bad. According to the story, Adam lived 930 years, just 70 years short of 1,000, indicating that maybe a day could mean a thousand years after all.

On this basis, some believers argued that the six days of creation followed by a day of rest perhaps indicated 6,000 years of creation followed by some kind of 1,000 year sabbath. This is also hinted at in the book of Revelation, where Christ is said to reign for a thousand years.⁴

The idea of a literal 1,000 year reign later fell out of favor when many Church writers, and then the Church itself, argued that it was symbolic. However, for a long time, many Christian teachers held the view that the Earth was 6,000 or at most 10,000 years old, and the Flood was usually accepted as having taken place literally, although some believed it to perhaps be a more localized flood, rather than one encompassing the whole world.

With the advent of science based on the Naturalistic Assumption, the Biblical worldview was challenged by three newly emerging scientific fields. The first major challenge came from the field of geology. James Hutton assumed the Earth was vastly old, and had been slowly transformed by natural changes. Charles Lyell argued that the present was the key to the past, and that changes to the Earth’s surface needed to be explained by causes known to be in operation at the present time.

The Flood was dealt with, not by disproving it, but by assuming it away, because it was a form of divine intervention, and Hutton and Lyell wanted to explain changes

to the Earth naturally. They assumed the Earth must be millions of years old, and that the fossil record, rather than being evidence of a global Flood, represented a record of the life and death of creatures over millions of years. Layers of rocks, sediment and fossils were assumed to represent long eras of the past, rather than material that had been sorted by vast quantities of water in a global catastrophe.

Charles Darwin was deeply influenced by this new geology and its naturalistic framework. He reasoned that if the Earth was vastly old, and that if geology had been shaped very slowly by small changes, then maybe life itself had changed in small increments over millions of years.

In other words, Darwin's idea of evolution by variation and natural selection followed on from the naturalistic assumptions made by the new geologists. Darwin extended those assumptions to the realm of life itself. His idea of evolution therefore posed the second great challenge to the Biblical account of creation.

Creationists of his day believed God had directly created each species, although the Genesis account only says he made creatures according to their "kinds" (Hebrew, *min*). Most creationists today think all the species we see probably descended from a relatively small number of "kinds." By contrast, in Darwin's hypothesis, all creatures evolved from a universal common ancestor, and are related in a universal "tree of life."

Later on came the modern field of cosmology. By this time, evolution and an ancient geological timescale had taken root and become widely accepted. Edwin Hubble showed that the universe seemed to be expanding at a fairly steady rate, known as Hubble's constant. This implied it must have started off much smaller, and had a beginning. While this idea is generally accepted today, it was resisted at first, because it sounded too much like the Genesis account, and many preferred to believe the universe had always been around in some kind of steady state.

But how do you get a universe in the first place? Physicists invented inflation theory to get the expansion of the universe going, using different laws of physics and a completely different definition of Hubble's constant that allowed the universe to grow exponentially in its initial moments.

The theory of inflation is still controversial, because it doesn't obey the laws of physics as we know them today. It is, in effect, a naturalistic version of a miracle, but couched in scientific terminology. It is naturalistic in the sense that physicists simply rewrite the laws of nature during this period. This is why inflation makes many scientists uneasy, but the idea persists because all of the other suggested ways for bringing a universe into existence are equally or more fantastical, usually invoking a theoretical multiverse.

Since we can see billions of light years across the universe, most cosmologists assume that the universe must therefore be billions of years old, in what I will call the "Distance/Age Assumption." The relevance of this will become clear after I have discussed the two main views of the Genesis creation account. Various other "clocks" have also been devised to try and measure the passage of time, which I will talk about a little later.

I have pointed all of this out, because how people interpret the Genesis account of creation depends on which assumptions they accept or reject. These assumptions form lenses through which they see the evidence. To a certain extent, it is also about naturalism versus supernaturalism, or the border between where God is allowed by humans to intervene, to cause something that wouldn't have happened by itself.

For example, most Christians are willing to accept that the resurrection of Jesus Christ was what we would call a miracle, in that it wouldn't have happened by itself. In other words, Christians allow for the idea that God can intervene to cause something that wouldn't have happened if nature had taken its normal course.

Now, let me briefly explain the two main views of the Genesis creation account among those who believe it to be inspired by God. The term "creationist" usually applies to someone who believes the account to be true in some sense.

"Old Earth Creationists" accept that the universe and Earth are billions of years old. Some accept or are neutral toward the evolutionary timetable for the appearance of different types of creatures, but dispute how they came about. Many "Intelligent Design" proponents also tend to fall into this category. Others reject the evolutionary timetable altogether. They accept the Earth as being old, but they view life itself as relatively recent. For some, humans are a particularly recent creation, thousands rather than millions of years old.

"Young Earth Creationists" reject the naturalistic assumptions made in the fields of geology, biology and cosmology, and the timetables produced on the basis of these assumptions. They view the creation of life on Earth as a recent event, about 6,000 years ago, or 10,000 years at most, with a worldwide Flood occurring around 2400BC or thereabouts. They believe the six days of creation involved miracles in the same sense that Jesus' resurrection, and his feeding of five thousand people from five loaves and two fishes, were miracles.

Now let me briefly explain how both Old and Young Earth Creationists interpret the creation account in Genesis.

I'll focus on the "Old Earth" viewpoint first. In this view, the six days of creation are usually seen as figurative, not meant to be taken as literal days. They are the equivalent of phases, eras or long periods of time.

The Genesis account says: "This is the history of the heavens and the earth when they were created, in the day when YHWH God made earth and heavens."⁵ Proponents of an Old Earth viewpoint argue that since the six days of creation are also collectively called a "day," the word doesn't have to refer to a literal 24 hour period.

They argue that when God created the heavens and the Earth in the beginning, this included the Sun, Moon and stars. Day 1 was the creation of light, perhaps in a symbolic sense. Day 2 involved a division of waters above and below the expanse. Some argue this involved the formation of a water canopy around the Earth, although it's difficult to see what would have held it up.

In the era of Day 3, the waters under the expanse were collected together into one place, called “seas,” while the dry land was called “earth” or “land.” In this same epoch, grass, plants and trees also came to be, laying the groundwork for animal life.

In the Day 4 era, God put the Sun, Moon and stars into the sky, to make a division between light and dark, and for day and night. Old Earth proponents argue that God didn’t actually create them here. They had already been created in the beginning, but now they came into clearer view from an Earth perspective.

On “Day 5” came sea creatures and flying creatures, and on “Day 6” came land animals and humans. Presumably creatures like dinosaurs would also have been created in these epochs. Some commentators note that the account says, “let the earth bring forth a living soul according to its kind.”⁶ They argue this indicates God may have used evolution to bring forth creatures. Even so, each creature would still be brought forth “according to its kind.”

At some point in the Day 6 epoch, humans came about, and God made them in his image.⁷ Some Old Earth proponents argue that it doesn’t really matter when humans were created, but rather what matters is, they were distinctive from other living creatures on the Earth. They reflected God’s qualities.

God rested on the seventh day. Some Christians argue this is still running, since there is no “evening and morning” at the end of it. Furthermore, the author of the book of Hebrews suggests there is still a day of rest for the people of God, which many view as a reference to the seventh day of creation.⁸

Now let me summarize the “Young Earth” viewpoint. They see the seven days as literal. During the first six days, God worked specific miracles to bring about life on Earth.

There was no source of light for the Earth at the start of Day 1, so this is what God created, perhaps as a result of the hovering or vibrating of God’s Spirit over the waters, causing it to heat up or produce light through sonoluminescence, in which bubbles and sound create light, or in some other way.

Together with the 24 hour cycle of the Earth’s rotation around its own axis, these would result in the very first evening and morning. In this sense, Day 1 was the beginning of time as measured by the rotation of the Earth and the light provided by God’s Spirit. It was Day 1 for the Earth.

For Young Earth proponents, this also defines the meaning of the word “day” when combined with a number. It is the sequence of a combined evening and morning. The Hebrew describes the first day as “day one,” while the others are described as “second day,” “third day” and so on.

The division of waters on Day 2 is the subject of debate. Some argue it is describing the creation of a water canopy, but a more common view is that it’s simply talking about the creation of an atmosphere out of the water. This is also called “heavens,” and it’s where birds are later described as flying.⁹ The Hebrew word for “heavens” (*shamayim*) is derived from a word meaning “sky” and the Hebrew for

“waters” (*mayim*). Some commentators have pointed out that the first part of the word may also be related to the word for “fire.”

The chemical composition of water, with its two parts hydrogen and one part oxygen, would be useful for making an atmosphere of oxygen. This might also be another effect of the vibrating of the Spirit over the waters on Day 1, perhaps causing oxygen to be released and clouds to form.

Incidentally, in Genesis chapter 2, which focuses on the creation of humans, it says that no rain had yet occurred. Some say that clouds only existed after the Flood. But from a Young Earth point of view, the atmosphere was new. It would perhaps take several days until the Earth’s water cycle fully kicked in. Rainbows could therefore still happen, they simply took on a more symbolic meaning after the Flood, just as crucifixions still happened before the cross became a symbol of Christ’s death.

God spoke to Job about the birth of the sea: “The sea was shut in by doors, when it rushed forth, from the womb it came forth. When I put as its clothing a cloud, and murky darkness its swaddling band, and I broke my statute over it, and I placed a bar and doors and I said, ‘to here you will come and no further, and here your proud mounds will be set.’”¹⁰ This mentions the formation of clouds, and suggests a breaking of the normal laws of physics when he says, “I broke my statute over it.” Unfortunately, most English translations don’t reflect the Hebrew very well here.

On Day 3, God caused the seas to gather and dry land to appear, and he also created seeds, plants and trees. Some seeds will germinate without light. They only need moisture and temperature. However, the account also suggests the Earth began to produce plants and trees as well, so they could have been created fully formed, but not yet sprouting. All that was missing would be sunlight, which would come the next day. Plants that relied on pollination by living creatures would only have to wait a few more days.

On Day 4, God created the Sun and Moon, and put them in the expanse of the heavens, to mark seasons, days and years. In other words, the original light provided by God’s Spirit for the first three days was replaced by more permanent light sources. The atmosphere and clouds created over the previous two days would shield the Earth from the intensity of the Sun. The Moon also controls the tides, and so would have been necessary to keep the sea from overstepping the boundary which had been set the previous day. I will talk about the stars in a moment.

On Day 5 came sea creatures and flying creatures, and on Day 6 came land animals and humans. From a Young Earth perspective, dinosaurs were part of these creations. Some interpret Behemoth and Leviathan in the book of Job as dinosaurs. Certainly, their descriptions sound majestic and fearsome.

Behemoth, for example, “bends its tail like a cedar” and is “the beginning of the ways of God.”¹¹ Of Leviathan, God says that a person is “hurled down even at the sight of it.” Also, “his sneezing shines light,” and “torches go from his mouth, darts of fire escape. Out of his nostrils go forth smoke, and shoot like a steaming cauldron. His soul sets fire to coal, and a flame goes from his mouth.”¹²

This sounds like some kind of a dragon! The dragon in the book of Revelation seems to be alluding to this same creature. God's description of Leviathan ends by saying: "There is nothing on the ground to rule it, the one made to be without fear. It sees all of the lofty. It is king over all of the sons of pride." ¹³

From a Young Earth perspective, these creatures were probably hunted to extinction, which would explain the widespread dragon legends across the world, from the Gilgamesh Epic to stories of kings and saints battling them. Whatever Behemoth and Leviathan were, God describes them as the mightiest of his earthly creations, and dinosaurs seem to have been the most awe-inspiring creatures to have ever lived on this planet – certainly more awesome and terrifying than a hippopotamus or a crocodile, as some have suggested they could be. Some have argued that perhaps they are also alluding to spirit creatures.

Whatever the case, if they were just mythical creatures, this would be like God telling Job to be in awe of the Snark and the Jabberwock, both inventions from the mind of English writer Lewis Carroll. "Here now is the Jabberwock, which I made just before Leviathan, to gyre and gimble in the wabe." I'm not sure this would have inspired awe in Job's mind, but rather confusion, as it did with Alice after reading the poem *Jabberwocky*.¹⁴ Behemoth and Leviathan had to be real, if readers of the book of Job, and Job himself, were to understand the point God was making.

From the Young Earth viewpoint, Day 7 was God's day of rest. It lasted one literal day, just as the Jewish sabbath lasts one literal day to mark God's rest day. He didn't need to signal evening and morning at the end of it, because the miracles to bring about life on Earth were completed. However, Jesus said: "My father has been working until now, and I am working."¹⁵ God only needed one day of rest before he got back to work. The "day" or "sabbath" of rest that Christians enter into, referred to in Hebrews chapter 4, is a metaphorical one, a rest from working only for themselves.¹⁶ It is not an ongoing extension of the seventh day.

I have aimed to treat both views fairly here, because while I may have a strong personal preference, I also appreciate that to go from atheism to acceptance that a Creator exists is already a major step, and so I don't wish to impose my view on you in this regard. However, I will set out my personal opinion more clearly in the next few chapters, along with my reasons for believing what I do.

Furthermore, the apostle Paul talked about one man who has faith to eat everything, but another man who can only eat vegetables. Paul wasn't talking about vegetarianism, but was giving an illustration about differing opinions and what people's faith can bear at the time.¹⁷

Sometimes a belief can be a stepping stone to a more nuanced one based on better understanding and deeper faith that comes with time, and so I don't want to put a stumbling block in the way of you coming to accept that YHWH exists, and really did create the heavens and the Earth, regardless of whether he did it in moments, millenniums, or millions of years.

However, many of the traditional views of the Genesis creation account were set in stone before the discovery, pointed out near the start of this letter, that the first chapter of Ezekiel effectively serves as another creation account, related to the formation of the early universe and its particles. Can this shed light on the Genesis account?

The answer is, yes it can. For example, in an early chapter I argued that the cherubs with four faces and wings in Ezekiel's vision symbolize helium-4 nuclei. These can be parted to create hydrogen nuclei. Alternatively, two helium-4 nuclei can be fused to make beryllium-8, and then in the "triple alpha process," well-known to physicists, this can be combined with a third helium-4 nucleus to make carbon-12, the basis of life on Earth. Add one more helium-4 and you get oxygen-16. Therefore, if the four living creatures seen by Ezekiel symbolize helium-4 nuclei, the vision contains the chemical pathways to create carbon, oxygen and water.

Of course, energy would also be needed. Ezekiel's vision says that the spirit of the living creatures was in their wheels, which could represent the energy shells for electrons. Therefore, when God's Spirit was hovering or vibrating over the waters, this could be a description of energy being used on the water to create light on Day 1 and then an atmosphere on Day 2.

What about the Sun? According to cosmologists, in the earlier universe, space was filled with gas and dust, some left over from supernova explosions. Most of this material was hydrogen and helium, and waves of energy pressed the gas and dust clouds together. The pressure and heat in this ball of mostly hydrogen and helium was enough to begin the process of hydrogen fusion that partly drives the Sun. According to them, this took tens of millions of years, happening all by itself.

Could the Sun have been created in a single day? God would need mostly hydrogen and helium atoms, which I have argued was readily available according to the vision in Ezekiel. God would just need to pull large numbers of them together and tightly compress them so that some would begin to fuse. In other words, it could be done if God had the energy and the will to do it.

Either way, from an Old Earth viewpoint, God could sit back for tens of millions of years and wait for a supernova explosion and gravity to kick in, or in the Young Earth paradigm, he could actively pull hydrogen and helium atoms together into a tight ball that would ignite the process of fusion. He wouldn't need to hang around for millions of years. The quicker version just requires work on God's part, which is what he was said to be doing during the six days.

What about the stars? Most Bible translations imply that God created the Sun, the Moon, and also the stars on Day 4. However, the Hebrew doesn't necessarily say this. Day 4 is focused on the creation of lights to make a distinction between day and night, and to give light on the Earth. Most English translations suggest that God created three things on this day: the greater light to rule the day, the smaller light to rule the night, and also the stars. However, the word "also" isn't in the Hebrew. It's an interpretation imposed by translators. The account more literally says: "God made the

two great lights, the great light to rule the day and the small light to rule the night and the stars.”¹⁸

In other words, according to the Hebrew, Day 4 may not actually be describing the creation of the stars at all, but could simply be saying the Moon would rule both the night and the stars. But even if not, stars could still be created in a similar way to the creation of the Sun, so this isn't a problem for Young Earth Creationists. It just requires a lot of energy, which presumably God has. For Old Earth proponents, Day 4 is only describing the luminaries becoming more visible from the Earth anyway, so none of them were directly created on this day.

Now, according to the account in Genesis chapter 2, God was forming the animals of the field and the flying creatures of the heavens, and was bringing them to Adam for him to name. He named all of the beasts, flying creatures, and animals of the field. Old Earth proponents might ask: how could Adam have done this in under 24 hours? Surely he would have needed much more time to study each animal before naming it.

Young Earth proponents would perhaps reply that Adam wasn't a naturalist. He didn't need to name everything, such as sea creatures, plants or bacteria. He also didn't have to name "species," since distinct species would only come later from the original "kinds" God had created.

For example, horses, zebras and donkeys are considered to be different species, but in the modern classification system they are in the same *Equidae* family, because they are thought to be closely related. Assuming this is true, Adam would only need to name an "equidae," and all species of horse, zebra and donkey could have come from this later on. There are less than 200 mammal families, so if the original "kinds" were at or close to the family level, Adam perhaps only had to name a few hundred mammals.

In other words, there were far fewer "kinds" than there are species today. As another example, the modern bird family *Fringillidae* contains over 200 species, including finches. Other finches are put into the *Thraupidae* family, which also has over 200 species in it. Both of these families could have come from one pair of birds, or perhaps a handful of different kinds.

Besides, Adam didn't need to be too imaginative. After God created the woman from one of Adam's ribs, Adam called her "woman," because "from man this one was taken."¹⁹ This hardly sounds like Adam had spent years deeply studying and pondering the nature of women. Instead, it sounds like an immediate observation. It was also a name for her "kind," rather than a personal name, just as he was "man."

Only after they had eaten from the tree of the knowledge of good and bad, did Adam give her a personal name, Eve, meaning "living one."²⁰ Was this many decades after her creation, or just a few days later? The account doesn't say, but based on the internal logic of the account, it would make more sense if this all happened very fast, within just a day or two of their creation. It would explain why the woman hadn't been

named yet, why the first human pair were so easily enticed, and why Eve listened to a talking serpent. They had literally no experience of life!

Most Christians believe that the talking serpent in the garden of Eden was really Satan, using the creature as a vehicle to catch the woman at a time when she didn't know much, and talking through it like a ventriloquist would talk through a puppet.

But this begs the question: who or what is Satan, and where did he come from? The word Satan means "adversary" or "accuser." While many people can become adversaries or accusers of others, the idea of a specific non-human adversary of God first appears in the book of Job, one of the oldest books in the Bible.

"There was a day," it says, "and the sons of God came to station themselves before YHWH, and Satan also came in their midst."²¹ The Hebrew says "the adversary," not just any old adversary. In a sense then, "the adversary" became something like a title, just as Jesus Christ in his pre-human form is known to Christians as "the Word," not just any word.

This makes Satan related to the "sons of God," which is sometimes used as a term for spirit creatures. Later in the same book, YHWH speaks to Job and asks: "Where were you when I founded the earth? Speak, if you have understanding. Who determined its measurements for you to know, or who stretched out the measuring tape over it? Into what were its pedestals sunk, or who laid its cornerstone, when the morning stars rejoiced together, and all the sons of God cried out in joy?"²²

In other words, these "sons of God" already existed at the time the Earth was founded, implying there may be some cosmic history beforehand, although the Bible doesn't specify how long.

There may also be a clue about the origin of Satan in the book of Ezekiel. God tells the prophet to take up a lament for the king of Tyre, but God also says this one is "sealing an outline"²³ or pattern, which could imply God is hiding something deeper in the details. Certainly the description of the king sounds more like someone else who wanted to be like God.²⁴ We are told, "in Eden, the garden of God, you came to be."²⁵ This would be true if Satan really was behind the serpent.

God says to this one: "You are the anointed cherub, the one covering, and I set you. In the holy mountain of God you came to be. In the midst of the stones of fire you walked. You were flawless in your ways from the day you were created until iniquity was found in you. By the increase of your trade they filled the midst of you with violence, and you sinned; and I will profane you from the mountain of God, and I will destroy you, covering cherub, out of the midst of the stones of fire. Your heart is haughty because of your beauty. You ruin your wisdom by your brightness. I will hurl you to the earth. I will set you before kings, for them to behold you. Because of your many depravities by the sin of your trading, you profaned your sanctuaries. And I will bring forth a fire from the midst of you which will devour you, and I will set you to ash on the earth in the sight of all those seeing you. All those knowing you out of the people will be appalled at you. You will become a terror, and you will be no more forever."²⁶

We have already seen from Ezekiel's first vision, where the four living creatures (later called cherubs) are first introduced, that the stones of fire likely represent particles. Indeed, where the Hebrew says that this anointed cherub walked in the midst of the stones, the *King James Version* here says he walked "up and down," just as in Ezekiel, reminding us that protons and neutrons are made of up and down quarks.

In other words, while this passage is nominally talking about the king of Tyre, it could also be a cryptic reference to a cherub who would become what we call Satan, the Adversary. He was the "covering cherub," although what this means is not entirely clear. He was flawless to begin with, but somehow became haughty, and for whatever reason he became God's chief adversary. He wasn't always this, just as a person isn't born a murderer, but becomes one once they commit murder.

Perhaps as confirmation that this is really talking about Satan, the book of Revelation also says that Satan was cast out of heaven to the Earth. "And the great dragon was thrown out, the ancient serpent, the one called Devil and Satan, the one deceiving the entire inhabited earth. He was thrown to the earth, and his angels were thrown out with him." ²⁷

The Greek word *diabolos* means "slanderer," which is where we get the word "devil" from, coming from a verb meaning "to hurl" as in hurling an accusation. Perhaps this is also why the king of Tyre is hurled to the Earth.

Whatever the case, both Old and Young Earth proponents recognize that spirit creatures must have existed at or prior to the founding of the Earth, because they were there to applaud it, and for the entity who would become known as Satan to develop his haughty heart. The Bible doesn't give any clear indication as to how long they were around for. That they are called "sons of God" implies they were created by God, but since they aren't part of earthly creation, they don't necessarily need to have been created within the "six days," but they may have been.

Now, I deliberately left a discussion of the Creation account until near the end of this letter, because I don't think it could be evaluated fairly until we had first examined what nature needed to achieve without a Creator, and also until we had fully looked at the assumptions we bring to the table when discussing the origin of life.

The Genesis account assumes the existence of a God who had the power to create the heavens and the Earth, and it claims he made specific interventions in the natural order he created, working with a purpose in mind – to bring about an abundance of life on Earth, including humans in his image. In short, it is a series of miracles with a goal and purpose.

The naturalistic creation story assumes that the universe inflated by itself out of almost nothing while defying the current laws of physics, although this could be still "natural" if we rewrite the laws of nature during that period.

Life came about all by itself from non-life, and then through the shuffling of nucleotides in molecules, it built for itself highly sophisticated reading and writing equipment, electron transport chains to manipulate subatomic particles, hundreds of

thousands of different proteins each built out of hundreds of amino acids, some of them organizing into incredible complexes, and cells organizing into organs of the body and forming into creatures such as frogs, flowers and cats; for no reason other than the immediate survival and reproduction of each wiggly thing that was lucky enough to evolve. Life is an endless cascade of naturalistic miracles, with no overall point to any of it, except to bring more wiggly things into existence and make them wiggle a bit longer. We are incredibly lucky to be here, but it doesn't actually matter because we won't be here again in just a moment.

In other words, and let's be honest here, both creation stories are, for all intents and purposes, miraculous. They are both absolutely incredible.

With the one creation story, the creators are luck and error, with individual creatures in a constant battle for survival until they inevitably become food for the worms. With the other creation story, YHWH is the Creator, who created the Earth and its inhabitants as an expression of his creativity and power, and out of a desire to share the gift of life with others, and who made humans in his image so they could enjoy life in abundance, this inevitable goal only suffering a temporary setback because of the human desire to remain separated from their Creator.

1 Exodus 20:11. **2** Psalm 90:4. **3** Genesis 2:17. **4** Revelation 20:1-6. **5** Genesis 2:4. **6** Genesis 1:24. **7** Genesis 1:26. **8** Hebrews 4:1-10. **9** Genesis 1:20. **10** Job 38:8-11. **11** Job 40:17,19. **12** Job 41:9,18-21. **13** Job 41:33,34. **14** See the poem "Jabberwocky" from *Through the Looking-Glass, and What Alice Found There*, by Lewis Carroll, 1871. "It seems very pretty," she said when she had finished it, "but it's rather hard to understand!" (You see she didn't like to confess, even to herself, that she couldn't make it out at all.)" **15** John 5:17. **16** Hebrews 4:10. **17** Romans 14:1-4. **18** Genesis 1:16. **19** Genesis 2:23. **20** Genesis 3:20. **21** Job 1:6. **22** Job 38:4-7. **23** Ezekiel 28:12. **24** Ezekiel 28:2. **25** Ezekiel 28:13. **26** Ezekiel 28:14-18. **27** Revelation 12:9.

67. Stretching Out The Heavens

I spent the previous chapter discussing the Creation account, and how it can be harmonized with both an Old Earth and a Young Earth viewpoint.

However, I think it's important to spend a few more chapters discussing the nature of time and how we measure it, because this has an important bearing on how we think of the past, the future, and the universe in which we inhabit; and it also reflects directly on the nature of God.

We usually measure time in relation to some kind of motion. For example, we define a "day" as one rotation of the Earth around its own axis, and a "year" as the time it takes for the Earth to make one orbit around the Sun.

Young Earth proponents argue that on Day 1, God was marking out the beginning of time on Earth, as measured by the planet's own rotation and the light from God's Spirit, combining to create the very first evening and morning.

However, scientists have also invented their own "clocks" which they consider to be measures of time on a much longer scale. Light itself is used as one of these clocks. Light travels at about three hundred million meters per second in a vacuum. A "light year" is defined as the distance light travels in a year.

The universe is billions of light years across, and seems to be expanding. Cosmologists equate distance with age, so it is assumed that the universe must also be billions of years old. This is the "Distance/Age Assumption" I mentioned in the previous chapter.

However, the theory of inflation, as taught in cosmology, suggests that in the beginning, the universe expanded from something very small, like a mustard seed, to millions of light years across, in almost no time at all. During this period of rapid inflation, distance wasn't a good measure of age.

Inflation theory is based on the principle of naturalism. In other words, according to cosmologists, God wasn't involved. But if a small universe can come into being and expand to millions or tens of millions of light years across all by itself in virtually no time at all, just think what God could have done, if He had been behind the inflation and expansion.

If God had continued the initial inflation a little longer, even just an infinitesimal moment longer, the universe would have inflated to the size it is today, and it would still be virtually zero years old, because during inflation, distance doesn't equate to age, at least not by the measure scientists use today.

The important thing to realize is, this was an expansion of space, which means that light and space itself would be stretched. To give you an illustration, let's say you took a large elastic band and cut it. You laid the piece of elastic on the ground in a straight line, and you put markings on it that divided it into ten equal segments. You then put Jack at one end of the elastic, and Jill at the other. In the measuring system we have just devised, Jack and Jill are 10 units apart, each unit being a segment of our piece of elastic.

Now, let's stretch the elastic significantly, so that Jack and Jill become much further apart, but are still standing at each end of the elastic. If we used the markings on our elastic to measure how far apart they were now, what would it say? It would still say they were 10 units apart, because the measuring line itself has been stretched.

This might sound strange, but this is exactly what happens as the universe inflates. Light may be the measuring tape of the universe, but the measuring tape itself is also stretched as the universe expands. If God had extended the period of inflation to stretch out a fully working universe, he could have done it very quickly in virtually no time at all, and the distance we see would have no actual bearing on its age.¹

This is how we could still see objects billions of light years away, even if they are new. Let's say we put ourselves at one end of our piece of elastic, and we placed galaxies at each one of the markings on it. If the piece of elastic stands for light, God could have stretched the elastic billions of light years out in virtually no time at all, and yet remarkably, we would still be able to see the galaxies on them, because the light itself had been stretched. The speed of the stretching would not be restricted by the speed of light, because light is part of what is being stretched out, the very thing we normally use as the speed limit of the universe.

If God really did create the universe this way, it may have been better to get most of the stretching done quickly, so it could be made ready to be inhabited. According to the prophet Isaiah, this is precisely what God did: "Do you not know? Do you not hear? Has it not been told to you from the beginning? Have you not understood the foundations of the earth? The One sitting over the circle of the earth, and its inhabitants are as grasshoppers. The One stretching out the heavens like a fine gauze, and he is spreading them out like a tent to dwell in."²

A person usually puts up a tent before dwelling in it, and they do it quickly, ideally before night comes or it starts to rain. And if we can create computer games that generate virtual worlds or even galaxies in a matter of seconds, why would it need to take God billions of years?

If we were to replace the elastic in our analogy with fine gauze, the analogy Isaiah uses, and put galaxies at the crossroads of each thread, we would still be able to see the galaxies as the gauze is being stretched out, and also once the main stretching has been completed, because light itself would also have been stretched. It is part of the fabric.

Through Isaiah, YHWH also says, perhaps with a hint of sarcasm to those who seem to know better than God: "Ask me about my sons, and instruct me about the work of my hands. I myself made the earth and created man on it. My own hands stretched out the heavens, and I instructed all their host."³

In other words, using a little more inflation than cosmologists normally permit, God could have stretched out the heavens almost instantly, to create a habitable universe. There wasn't any need to drag the process out over billions of years.

But this raises an interesting question. Let's suppose God really did create the universe ready for habitation almost instantly. In other words, it didn't take billions of years, but was stretched out to almost the size we see today by extending the period of inflation just a little longer. The question is, how old would it look?

This would depend on our criteria and assumptions for measuring age in the first place. Let me give you a comparison, to explain what I mean. According to all four gospels in the New Testament, Jesus fed a group of 5,000 men, and also women and children, from just five loaves and two fishes. Afterwards, the disciples collected twelve baskets of leftovers.

Now, if we apply naturalistic thinking here, then Jesus simply couldn't have done this. After all, to make enough bread to feed thousands of people would require large quantities of flour, yeast, water, oil or fat and perhaps some salt. It would also require plenty of ovens, or some kind of baking process that could heat the loaves to at least a few hundred degrees Celsius for thirty minutes or more. Since the apostles didn't carry around large quantities of baking products and portable ovens, at least as far as we know, Jesus couldn't have done what was claimed.

Of course, this line of reasoning is absurd, because if Jesus had done it the way loaves are normally made, he wouldn't be performing a miracle, he would be running an open-air restaurant. Perhaps it was called The Jesus Crust. Clearly then, we can't use naturalistic thinking when it comes to miracles.

But the more relevant question here is, how old would Jesus' loaves look? Presumably they would have contained all the necessary ingredients to make bread, and appear to have been baked at just the right temperature for the required length of time. They would probably even have a nice crust.

However, if a breadiologist, an expert at dating crusty bread, was able to take a small sample from the crust of one of Jesus' newly produced loaves, and he was able to examine it using the latest breadiometric dating techniques, I suspect he would have to conclude that the bread had been baked at over 200 degrees Celsius for at least thirty minutes, with an error margin of perhaps two or three minutes.

The scientific data would be in major conflict with the reality that Jesus produced the loaf almost instantly, a second or two before. The scientist, as a respected member of the Royal Society of Venerable Breadiologists, would have little choice but to report a "loaf age" of about half an hour; but his age would be out by a factor of up to 1,800, or three orders of magnitude.

As a result, skeptics and atheists would gleefully proclaim that the gospel story must be untrue, because breadiometric dating has proved that Jesus' crust was much older than Christians claim it to be. Either that, or Jesus must have been fooling scientists with an appearance of age.

Hopefully the logical flaws in their reasoning are clear. By definition, miracles don't follow the ordinary course of nature. This doesn't mean they are impossible or without explanation. They just require intervention in nature, in the same way that buildings don't make themselves, but require intervention in nature from humans.

Neither was Jesus trying to fool people with an appearance of age. It's just that a miraculously produced loaf of bread is presumably going to look like it has gone through the normal baking process, otherwise it wouldn't be a loaf of bread. It would be a blob of dough or something equally unappetizing.

The purpose of Jesus' miracle was to feed a hungry crowd, while also demonstrating his power and authority as the Son of God. But If Jesus had given them all lumps of dough, and told them to bake their own loaves, it would have been a little odd. If he'd given them all packs of flour, yeast, water, and then left them all to it, we would suspect a cosmic prank.

Crusts are normally the result of a baking process; but if Jesus' loaves had crusts, he wasn't fooling anybody. He was simply producing fully formed, appetizing loaves miraculously. It is the breadiologists who are in error, by thinking their dating technique could measure the age of the bread.

Now, I am using this "Jesus Crust" analogy, to make a very important and hopefully memorable point. Scientists often use "clocks" they think are appropriate based on their naturalistic thinking, but the clock may not be accurate at all if a miracle or some other factor was involved.

A universe that was created fully functional almost instantly would be similar to one of Jesus' loaves, in the sense that it would look fully baked. But if we assumed the distance we could see was equated to its age, then it would appear to be old.

Some people object to this, arguing that if this is the case, God is fooling us with an "appearance of age." But God isn't fooling anyone. Humans are simply fooling themselves with their Distance/Age Assumption. They assume that since we can see billions of light years across, the universe must therefore be billions of years old.

No wonder Isaiah said, "Do you not know? Do you not hear? Has it not been told to you from the beginning?" God has already told us what he did and how he did it. He isn't trying to fool anyone. He said he stretched out the heavens, and continues to stretch it. But he doesn't have to have done this at the same slow rate of expansion we see today.

Even according to cosmologists who don't credit the beginning of the universe to God, there was an initial period of inflation during which the universe expanded at an incredible rate. I am simply suggesting God continued that period a little longer than cosmologists would allow him to do so, until he had a universe close to the size of the universe we see today. In this case, the distance we see doesn't equate to age, and determining the age of the universe based on how far we can see would be a false assumption.

This begs the question: how could a coherent universe form so quickly, and how could the material be held together during the stretching? About 99.9% of the universe is in plasma form anyway, the fourth state of matter after solids, liquids and gases. Plasma is dominated by electrostatic and electromagnetic forces and fields, so electromagnetism may have held it together during an extended inflationary phase. Once the inflation was completed, gravity could perhaps take over.

One of the things that humans find difficult is to completely shift our way of thinking, without bringing prior assumptions along with us for the ride. We then find ourselves trying to fit a square peg into a round hole. Let's call this "Square Peg, Round Hole" thinking.

For example, someone might ask, what about the spiral arms of rotating galaxies? How could they possibly have time to form, if the universe is young? This is a good example of Square Peg, Round Hole thinking.

It is only an assumption that they have already been rotating for a long time, but we don't actually know this. This is simply a consequence of the Distance/Age Assumption. No human has been able to observe a galaxy make even one full rotation. A spiral shape could have been formed if the matter in a galaxy was unfolded at the same time as the stretching.

Actually, it is an ancient universe that has the real problem, because if the universe is billions of years old, spiral arms should have smeared out by now. Curiously, even very distant galaxies, assumed to be some of the youngest in the universe, appear to be very similar to older galaxies. Over the decades, scientists have come up with ideas to explain the preservation of spiral arms, including spiral density wave theory, and dark matter.

In this chapter, I haven't attempted to give a complete model of how the universe was formed. I have simply aimed to show that it could have been formed very quickly, as God stretched out the heavens.

Scientists assume the process has taken billions of years, because we can see billions of light years away. But inflation is not restricted to the speed of light, so God could have simply taken the process of inflation and extended it just a little longer, "stretching out the heavens like a fine gauze," to create a habitable universe very quickly; and since light itself is stretched in the process, this would still allow us to see distant objects, even if they are billions of light years away.

1 For more information on how light itself is stretched as the universe expands, see the article "Misconceptions About The Big Bang" by Charles H. Lineweaver and Tamara M. Davis, published in *Scientific American*, March 2005. **2** Isaiah 40:21,22. **3** Isaiah 45:12.

68. Is Deep Time An Illusion?

Let's now turn to "clocks" that humans have invented to measure the passing of time on Earth. One method of supposedly measuring time is called "radiometric dating" or "radioisotope dating." The basic concept is fairly simple to understand, and measures an assumed amount of radioactive decay.

We know that atoms are made up of protons, neutrons and electrons. A chemical element usually has the same number of protons and electrons, but the number of neutrons can vary somewhat. For example, a regular carbon atom has six protons, six neutrons and six electrons, and can be written as "carbon-12," which reflects the total number of protons and neutrons.

When the number of protons and neutrons are equal, the atom is stable. However, the number of neutrons can vary. For example, a carbon atom can hold six, seven or eight neutrons.

These slightly different atoms are called "isotopes" of that element, usually written as the symbol or name of the element, combined with the total number of protons and neutrons. For example, the carbon isotope with six protons and eight neutrons can be written as carbon-14.

Some isotopes, such as carbon-14, are unstable, because they have too many neutrons. They gradually emit particles, eventually transforming into stable elements in a process called "radioactive decay."

There are several types of decay. In "alpha decay," the nucleus of the isotope emits a helium-4 nucleus, traditionally called an "alpha particle," turning the original particle into a different one with two less protons and two less neutrons. (Incidentally, I proposed earlier that the living creatures in Ezekiel's vision represented helium-4 nuclei, plenty of which were present in the early universe.)

Another type of decay is "beta decay," where an electron, or its counterpart known as a "positron," is emitted from the nucleus, turning the atom into a different element but with the same total number of protons and neutrons.

Incidentally, the word "decay" is a little misleading, because atoms are really just transforming into different atoms. Ultimately, like many of us, atoms just want to settle down and become stable. Isotopes that decay are called "radioisotopes," and they eventually transform into stable atoms of a particular element.

The original isotope is called the "parent," and the one it decays into is called the "daughter." The rate of decay is measured by the "half-life," which is the time it takes for half of the parent atoms to transform into daughter atoms, assuming we started out with a sufficiently large collection of atoms.

For example, uranium-238 is radioactive and decays to lead-206, with a half-life of about 4.5 billion years. In other words, if you carelessly left a block of uranium-238 on your kitchen table for four and a half billion years, half of the block would have turned into lead-206 by the time you returned.

Certain radioactive isotopes are used to date rocks. In a rock, the amount of parent and daughter isotopes can be measured, and the ratio of parent to daughter is used as a guide to the rock's age.

For this ratio to reflect the true age of the rock, three assumptions must be made. The first is that the amount of parent and daughter atoms must be known at the beginning, when the rock was formed. The second assumption is that all of the daughter atoms measured today must have come about by *in situ* ("in place") radioactive decay of the parent atoms. In other words, it assumes a closed system, where the rock has been sitting there free from outside contamination for the entire length of its supposed age. The third assumption is that the rate of radioactive decay has been constant, and has always been the same as the rate we observe today; or there has been no disruption to the atoms throughout the rock's history, to cause them to emit particles in any process that might appear similar to radioactive decay.

If we knew only the amount of parent and daughter atoms, the first two assumptions wouldn't be possible to verify, without being able to travel back in time and observe the rock; especially as geologists tend to use radioisotopes with very long half-lives, ranging from tens of millions to over 100 billion years.

For example, let's use red and black balloons to represent atoms, because balloons are easier, prettier and more fun to imagine. Let's say that red balloons represent the parent isotope, and they have a half-life of 10,000 years. In other words, if we start with a reasonable number of red balloons, after 10,000 years, half of them will have turned into black balloons, which will represent the daughter isotope.

Now let's imagine a large cluster of balloons, some of which are red and black, while others are colors we're not really interested at the moment. Let's take a sample of balloons from the cluster. In our sample, we count 500 red and 500 black balloons. How old is the balloon cluster, based on this information?

The answer is, it depends on our assumptions. If we assume it started out with 1,000 red balloons and 0 black balloons, we would conclude that the balloon cluster has been through one half-life, and was therefore 10,000 years old. But the reality is, we don't know how many black balloons were there to begin with. It might have started out with 500 black balloons, and no radioactive decay has happened, meaning the cluster is still brand new.

In other words, with this method of measuring the number of parent and daughter isotopes, the only way to know how many of each were present when the rock formed is to go back in time; and the only way to know whether the rock has remained uncontaminated and unshaken is to observe it throughout its entire history. These things are impossible for us to do, especially if the rock is assumed to be very old, on the scale of millions or even billions of years.

Let's put down our pretty balloons for now, and turn to something more real. Let's say we were able to take a sample from a meteorite, and we found it had the same amount of uranium-238 as lead-206. What would this tell us?

Again, it would depend on our assumptions. Since uranium-238 decays into lead-206, we could assume it started with no lead-206, meaning that all of the lead-206 now present was from decay from uranium-238. This would mean half of the uranium-238 has decayed. It has gone through one half-life of around 4.5 billion years. Therefore, the meteorite would be about 4.5 billion years old.

But what if the meteorite was formed yesterday afternoon, with the same amount of uranium-238 and lead-206? In that case, we would be incorrect in our assumption that the lead-206 came from radioactive decay, and assigning an age of 4.5 billion years to the meteorite would be a grossly inaccurate figure, because it was actually formed yesterday afternoon, just after lunch!

By the way, it's important to note here, there is no physical way to look at a lead-206 atom and say whether it was around from the beginning, or whether it came about from radioactive decay, because one lead-206 atom looks the same as another lead-206 atom. There is no clear physical difference.

Let's take another example. The radioisotope potassium-40 decays into the stable isotope argon-40, and so the ratio between the two is used in the "potassium-argon" dating method. Argon is a gas, and so geologists assume that when rock such as basalt is formed from a volcanic eruption, any initial argon leaches out of the rock, so the amount of argon in it today must have come from the decay from potassium, with the exception of a small but known amount from the atmosphere. This is the supposed benefit of the potassium-argon dating method. Geologists don't worry about how much argon the rock started with. They assume it didn't start with any.

However, this assumption has proved to be false in rocks we already know the age of. (Incidentally, when geologists use a model or method, the age produced by that method is often called the "model age," which doesn't automatically mean the real age of the rock.)

For example, when rocks are dated from lava flows across the world, known to have occurred within the last few thousand years, potassium-argon dating often gives model ages ranging from hundreds of thousands to several million years old. This is presumably because the rocks inherited the excess argon from volcanic gases, over and above any that came from radioactive decay. When the lava cooled, it must have trapped in some of the argon from the volcano.

In summary, when using the potassium-argon dating method, geologists assume the initial argon all disappeared when the rock first cooled. But this assumption isn't true when we know the age of the rock already, so it is also likely to be false when we don't know the age of the rock. If a rock inherited argon from when it was formed, and this argon is assumed to be from radioactive decay, radiometric dating will give the rock a much older age than it really is.

Perhaps the best known radiometric dating method is "carbon dating," which measures the ratio of the radioisotope carbon-14, also called "radiocarbon," to its stable daughter nitrogen-14. Carbon-14 has a half-life of less than 6,000 years. As a result, it can only be used for ages well under 100,000 years, because after this there

shouldn't be enough carbon-14 left to measure. Certainly after a few million years there should be virtually no carbon-14 left at all in a sample of material, at least none from when the material was originally formed.

Now, to continue our discussion, I need to use specific language to distinguish between two very different views of geology and the age of the Earth. Most geologists subscribe to the principles of modern geology as initially set out by James Hutton and Charles Lyell. Although geologists no longer take their strict uniformitarian approach, most of them believe the Earth's geology was formed naturally over millions and billions of years. I will refer to these as "deep time" geologists.

However, an alternative viewpoint, held by those who believe in a Young Earth, is that the Flood shaped much of the geology of our present world. I should also point out, the term "deep time" isn't always used by geologists. But it's a term I will use from now on, as a reminder that this assumption of vast age determines how they see the world; and the term will also serve to distinguish between what we might call "orthodox" and "creationist" geology.

Carbon dating is used to date material that used to be in living plants and animals, such as wood and bones. But deep time geologists don't use it to date things they assume to be millions of years old, because the original carbon-14 atoms should have all decayed. Nevertheless, carbon-14 is indeed reported as being present in materials as diverse as marble, graphite, coal, gas and whale bones, all supposedly millions of years old.¹

Deep time scientists have many potential explanations for this. They argue it could be background from the machinery used to measure carbon-14, which means it isn't real carbon-14, it's just being reported as carbon-14 by the instruments used to measure these things.

Or perhaps it's real after all, but was introduced when the sample was transferred, stored or prepared; or perhaps it's *in situ* contamination, meaning the sample already contained carbon-14 before it arrived at the laboratory. The testing lab isn't particularly concerned about explaining outside sources, because this isn't their responsibility. However, it's called *in situ* contamination because it's assumed the carbon-14, which shouldn't exist, must have seeped into the sample when it was originally in the ground.

Whatever the cause, to eliminate this carbon-14 signal, laboratories tend to apply a high "standard background" to the samples they process, which could be the equivalent to a carbon age of as much as 40,000 years. This "background" amount is then subtracted from what they consider to be the "real" carbon-14 amount, based on their assumptions. If the result is zero or less, the lab calls it an "infinite age." This means it is assumed to have no carbon-14 even if it actually did, and therefore can't be dated.

This strongly biases the method away from being able to detect a young Earth. For example, let's suppose there was a worldwide Flood, and the intense pressure, water and heat from the crushing of vast amounts of organic matter produced the

coal seams we have today. They would still contain significant carbon-14, because they would only be thousands of years old, rather than millions of years as assumed by deep time geologists. This is indeed what is found in such coal samples, but it is usually dismissed as *in situ* contamination. This means there is indeed significant carbon-14 in the sample, and it isn't instrument background.

Some have argued that the so-called contamination was from the decay of other material such as uranium, but it's unlikely that any natural source is going to contaminate wood, bones, marble, oil and coal to roughly the same extent, or throughout the whole length of a coal seam in roughly equal measure. However, the persistence of so-called "background" carbon-14 in different sources would be evidence of a universal Flood and a young age of the material in question.

This phenomena was already reported in the scientific literature, but was dismissed by deep time geologists. However, around the year 2000, a group of geologists who believed in a Young Earth launched a project to research the age of the Earth, called "Radioisotopes and the Age of The Earth" or RATE for short. They used commercial labs to get dates for samples, as do deep time geologists.

As part of their research, they detected significant levels of carbon-14 in coal seams that were assumed by deep time geologists to have ages ranging from 40 to 320 million years. Ten samples from these coal beds contained carbon-14 equivalent to ages of around 50,000 years, indicating the beds were all formed fairly recently and at about the same time.

The RATE researchers also investigated the presence of carbon-14 in diamonds. Diamonds are the hardest known natural substance on Earth, highly resistant to corrosion and weathering, and not easy to contaminate. They are formed deep inside the Earth and are considered by most geologists to be ancient, maybe hundreds of millions or even a few billion years old, meaning they should be completely free of carbon-14. The researchers found that the diamonds they investigated contained levels of carbon-14 equivalent to an age of around 55,000 years.

Not long after the RATE researchers published their results, deep time scientists also conducted a similar experiment on nine natural diamonds conventionally dated to the Paleozoic age, making them supposedly well over a hundred million years old.²

Eight of the diamonds yielded radiocarbon ages ranging from 64,900 to 80,000 years. The ninth diamond was cut into six equal fragments, and each piece gave a radiocarbon age of around 70,000 years, suggesting that the carbon-14 was evenly distributed throughout the diamond.

In their paper, they mentioned that previous research by radiometric dating laboratories had yielded ages of about 70,000 years for graphite, 50,000 years for marble, and even 60,000 years for the wood blanks they used, that were supposed to contain no carbon-14 at all. For this reason, the deep time researchers who examined the diamonds also analyzed samples of graphite from Precambrian rock conventionally dated to around one billion years from the present. The samples gave ages of about 60,000 to 70,000 years.

These researchers believed in deep time. They assumed the diamonds were already of “great geologic age.” They considered it a “reasonable assumption” that the samples should contain no measurable carbon-14, and that the nature of diamonds “significantly reduce or eliminate exogenous contamination from more recent carbon sources.” In other words, they recognized that diamonds should be resistant to contamination.

Their conclusion, based on their own assumptions, was that the carbon-14 must have been “background.” They recognized the possibility of their instruments causing it, but they concluded that carbon-14 “from the actual sample is probably the dominant component of the ‘routine’ background.”

In other words, the bulk of what they were detecting was probably real carbon-14, but the researchers had to classify it as “background” because of the assumed “great geologic age” of the diamonds.

An alternative explanation, not contemplated by these deep time researchers, would be that the diamonds are actually young, which would also explain the presence of real carbon-14 as the “dominant component” of the so-called “background,” along with its presence in graphite, marble, bones, coal and oil.

Now, if the Young Earth viewpoint really is correct, an important question we could ask here is: why do the ages of the samples from coal, marble, graphite and diamonds come in at 50-80,000 years, when the Flood was supposed to be only 4-5,000 years ago, and the Earth is supposedly only 6-10,000 years old?

The point made by Young Earth advocates is that carbon dating assumes we know how much of the parent and daughter isotopes were present to begin with. If there was more carbon-14 in the atmosphere in the past, or more nitrogen-14 in the material than from radioactive decay, especially in samples older than the Flood, the age given by this dating method wouldn't accurately reflect a sample's true age. The modern industrial and nuclear age has significantly altered the amount of carbon-14 in samples, so what would a global Flood do? And what was the environment like before the Flood?

In other words, radiocarbon dating may work fairly well for dates after the Flood, once the environment had become more stable again, but since the environment may have been different before the Flood, and the Flood would have disrupted it in a dramatic way, a nice linear path from the present to the past, which is what radiometric dating requires, would be false.

However, if there really is a significant presence of actual carbon-14 in things ranging from marble and coal through to diamonds, the hardest natural substance, this would suggest it isn't local contamination; and more importantly, it would place an upper limit on the age of the things being sampled of around 100,000 years or so, since virtually all of the initial carbon-14 should have decayed.

Now, the main drawback with the methods I have discussed so far is, if we want to date something, we have to make assumptions about the amount of parent and daughter isotopes present when the material was formed.

However, one method that supposedly gets around this is called “isochron dating.” To explain this method, let’s return to our analogy of red and black balloons. If you recall, the red balloons represented the parent isotope, and they decayed into black balloons, the daughter isotope, with a half-life of 10,000 years.

We took a sample of balloons from an imaginary balloon cluster, and we found that our sample had 500 red and 500 black balloons. At the moment we have no way of knowing how old the balloon cluster is, without making assumptions about how many black balloons were there at the beginning.

But what if we could introduce a third balloon color? Let’s say brown balloons also existed in the balloon cluster, and they were related to the black balloons, except that the brown balloons don’t decay. They are a stable isotope of the black balloons.

The number of brown balloons doesn’t change over time. Since they’re stable, there should be the same number of them now as when the cluster was formed, assuming brown balloons aren’t added by contamination, or lost somehow.

With the isochron method, the brown balloons are used as a kind of reference point for the red and black balloons. Instead of looking at the number of balloons, ratios are used. The idea is, as red balloons gradually decay into black balloons, the ratio of red to brown balloons decreases, and the ratio of black to brown balloons increases. We don’t need to know the exact number of isotopes present at the beginning. All we care about is what proportions they existed in, relative to each other.

An important assumption of the isochron method is that, when the rock was formed, the daughter isotope, represented in our example by the black balloons, and its stable counterpart, the brown balloons, were mixed throughout the rock in equal ratios. We will see why this is important shortly.

Geologists think this is a reasonable assumption, because the isotopes are supposed to be chemically similar. For example, in the rubidium-strontium dating method, strontium-87 and strontium-86 are used as the black and brown balloons, and they are assumed to be similar. However, there are dozens of strontium isotopes, with half-lives ranging from about 29 years (strontium-90) to ones measured in days (strontium-89), hours (strontium-91) or even milliseconds. If isotopes are roughly the same, why do they have such dramatically different half-lives?

Furthermore, there are only four stable isotopes of strontium in nature: strontium-84 (although this might actually decay), strontium-86, strontium-87 and strontium-88. They occur in very different proportions: about 0.6%, 10%, 7% and 82.6% respectively. Only strontium-87 is a daughter isotope in a radioactive decay process (the term is “radiogenic”), in this instance from rubidium-87.

If deep time geological assumptions are true, that these isotopes are similar and so would be mixed in similar proportions to begin with, the same would surely be true overall. We should see roughly the same proportions of strontium-86, strontium-87 and strontium-88 in the Earth today, although we would expect a higher proportion of strontium-87 because it is radiogenic.

The fact that we don't, and actually see more strontium-86 than strontium-87, and vastly more strontium-88, suggests the initial assumption, that the stable daughter and its counterpart would be distributed in the same ratio, is false, or at least questionable.

However, for the sake of argument, let's run with the assumption for now, so we can understand how the isochron dating method works. We'll continue to use balloons because they're easier to visualize, but keep in mind they just represent different types of atoms.

Let's assume we have a large cluster of balloons containing red, brown and black balloons. We know that red balloons decay into black balloons, and the half-life for red balloons is 10,000 years. We know that brown balloons are a stable isotope of the black balloons. We'll start out with a brand new balloon cluster.

Now, let's take three different samples from the cluster. In our first sample, we have 800 red balloons, 100 black balloons and 200 brown balloons. In the second sample, we have 600 red balloons, 150 black balloons and 300 brown balloons. In the third sample, we have 500 red balloons, 200 black balloons and 400 brown balloons. Notice that the ratio between black and brown balloons is the same for each sample. This is a necessary starting condition for isochron dating to work. In this example, I decided the ratio would be 0.5, which means that to begin with, there are half as many black balloons as brown balloons in each sample.

Now let's leave our samples for one half-life, which means finding something better to do for 10,000 years. When we come back, we find that in the first sample there are now 400 red balloons, 500 black balloons and 200 brown balloons. This is because half of the initial 800 red balloons have now decayed into black balloons. In the second sample there are now 300 red balloons, 450 black balloons and 300 brown balloons. In the third sample there are now 250 red balloons, 450 black balloons and 400 brown balloons. The number of brown balloons in each sample remains the same as before, because they represent stable atoms that don't decay.

Let's suppose we managed to find something else to do for another 10,000 years, allowing our samples to go through one more half-life. When we came back, we would find that in the first sample there are now 200 red balloons, 700 black balloons and 200 brown balloons. The number of red balloons has halved again, and 200 more of them have become black balloons. In the second sample there are now 150 red balloons, 600 black balloons and 300 brown balloons. In the third sample there are now 125 red balloons, 575 black balloons and 400 brown balloons.

In real life, geologists are only able to directly obtain the last set of data from a rock, which is represented in our analogy by the balloon cluster. They wouldn't have the first two sets of data. However, something quite clever can be done with this last data set.

First of all, if we were to create an X, Y graph, and plot the ratios of parent (red balloons) to the stable isotope of the daughter (brown balloons) on the X axis, and the ratios of daughter (black balloons) to its stable isotope (brown balloons) on the Y axis,

we would have 3 points on the graph. (For reference, I have put the coordinates in a footnote.)³

We could then draw a straight line through these points. Through the magic of math, and as a result of our assumption that the initial ratio between brown and black balloons were the same to begin with, the line would cut through the Y axis (called the “intercept” of Y) at 0.5, which is precisely the initial ratio of brown and black balloons we chose when we created the balloon cluster 20,000 years ago. And since the number of brown balloons in a sample are assumed to never change, we can now deduce how many black balloons were there to begin with.

The line itself is called an “isochron.” Intriguingly, the slope of the line can also tell us how many half-lives the samples have been through, and we can then put this number into a formula, to tell us the age of the balloon cluster. In our example, we can calculate that the balloon cluster is 20,000 years old. (I have put the math and formula in a footnote.)⁴

This is how isochron dating works in theory. As I have demonstrated here, the math itself works perfectly well, if radioactive decay really is being measured. However, real-life dating using this method relies on several critical assumptions that may simply be untrue.

The first and most important assumption, one that is usually just taken for granted, is that the rock is already very old, and therefore lots of radioactive decay has taken place. This is necessary, at least for the radioisotopes geologists tend to use when dating rocks they consider to be old.

The second assumption is that the daughter isotopes, the ones being used for isochron dating (the black and brown balloons in our example), were mixed throughout the rock in the same ratio to begin with. This assumption is critical, so that if the data points can be made to fit on a straight line, the intercept on the Y axis accurately tells us this starting ratio, and then the slope can tell us the rock’s age.

The other assumptions are that the rock hasn’t been contaminated or significantly disturbed since it was formed, and that the rate of radioactive decay has remained the same throughout the time of the rock’s existence, or that the atoms haven’t been excited in some other way, to give off particles.

These are the main assumptions of the isochron model. However, as I will show, the method geologists use to date rocks also involves a huge amount of bias and selection, heavily skewed toward producing and reinforcing the deep geological ages that the researchers already expect.

For example, in a 1956 paper entitled “Age of meteorites and the earth,” the ratios of lead isotopes were measured in five meteorites, and using the isochron method, a model age of 4.55 billion years was produced.⁵

Since the ratios of oceanic sedimentary lead on Earth also matched up with the isochron, it was assumed that 4.55 billion years was also “the time since the earth attained its present mass.”

The paper also shared the ages of meteorites by other researchers who had used potassium-argon dating, producing model ages ranging from 2 billion to 4.8 billion years. To account for the differences, assumptions were made about argon being lost, or less effective processing methods.

These reasons may perhaps be valid, but as we will see, this is the general pattern when it comes to deep time dating: data that falls into line with the researcher's expectations is considered valid, while data that contradicts their assumptions is usually explained away or just ignored.

In the end, 4.55 billion years became the age of the Earth, and therefore the reference point for all other ages. Logically, every other geological event on Earth or in the solar system now had to fit around this age. Indeed, the 1956 paper even provided researchers with two equations, to help them know whether their samples could be aligned with the new "age of the Earth" model.

I think this partly helps to explain why many meteorites line up with this date. It's a form of self-selection. The ones that do, do, by definition, and those meteorites get added to the list "confirming" the 4.55 billion year age. The meteorites that don't, don't make it to the list.

However, what about the model age itself? Could there be an alternative explanation? I think so. Keep in mind, isochron dating only cares about ratios. It also needs several data points, so a line can be plotted on a graph. The data could simply reflect isotope ratios that are close to the same values as when the rock was formed.

As I said earlier, uranium-238 decays to lead-206, with a half-life of about 4.5 billion years. In other words, if we start out with 1,000 uranium-238 atoms and nothing else, after 4.5 billion years we would have 500 uranium-238 atoms and 500 lead-206 atoms. But if the rock had started out with this ratio, and we just assumed the lead-206 had come from radioactive decay, the age of the rock would seem to be 4.5 billion years older than the real age.

If the Earth, Moon and these meteorites were all formed at about the same time in the recent past, and no significant radioactive decay of elements such as uranium-238 has taken place, surprisingly, isochrons could still consistently report billions of years. To explain why, we need to look a little deeper at how isochron dating works.

Let's look at another popular radiometric dating method: the rubidium-strontium clock. Rubidium-87 is radioactive, and has 37 protons and 50 neutrons, for a total of 87 "nucleons" which make up its nucleus. It decays to strontium-87, which has 38 protons and 49 neutrons, with a half-life of about 49 billion years. It decays by beta decay, which means one neutron in a rubidium-87 atom becomes a proton, turning the atom into strontium-87, while also ejecting an electron.

The daughter isotope strontium-87 is stable, and strontium-86 is also a stable isotope of strontium, so these and the parent rubidium-87 are used in rubidium-strontium dating.

Using this clock means we are already assuming an old age for whatever we're trying to date. Since rubidium-87 has such a long half-life, the method would be unable to detect if the rock was young. Hardly any of the rubidium-87 atoms would have decayed if the rock was only thousands of years old.

On the other hand, obtaining a model age of tens of millions of years is practically built into the formula for calculating age, when using the rubidium-87 half-life. For example, even if the slope of the isochron is tiny ($a=0.001$), it would still produce a model age of about 70 million years.⁶

The key to getting an "age" from an isochron, whether accurate or not, is to get some kind of upward slope from the line. If the data points can be roughly plotted on a line, making them "linear," you can get an age calculation.

For example, let's plot three points on an X,Y graph, at (0.1, 0.7142), (0.2, 0.7228) and (0.4, 0.7317). In many rocks, the abundance ratio of strontium-87 to strontium-86 hovers around 0.71 or a little higher, so I chose slightly higher figures than this for the Y axis. If we were to make a line on a graph which represented a rubidium-strontium isochron, these three points would give a model age of 3.9 billion years, although the data is actually meaningless!

Even if we added 2 to each of the first numbers, so we had points at (2.1, 0.7142), (2.2, 0.7228) and (2.4, 0.7317), the isochron would still report exactly the same age.⁷ In other words, the isochron method is able to give you a deep "age," as long as the points line up reasonably well, and produce an upward slope.

Geologists assume that if the data points fit on an upward sloping line, then it indicates radioactive decay over tens or even hundreds of millions of years. However, if the rock is young, just thousands of years old, as long as the rock samples have some variation in their ratios, an upward sloping line could perhaps still be plotted, which if interpreted as an isochron, could report an age of tens of millions of years, even if virtually no radioactive decay has taken place.

Before I show you a real-life example of this, let's look at how deep time geologists tend to date rocks. First of all they assume the rocks have been formed by natural forces over millions or perhaps billions of years. Of course, these forces could be different – volcanic eruptions, lava flows and so on. But a global Flood isn't part of their thinking, which if we recall, was assumed away by the founders of modern geology.

Therefore geologists use the structures of rocks, rock formations and sedimentary layers to deduce relative ages, which are inevitably on a scale of tens to hundreds of millions of years, because of their assumptions; and they also use dates set by previous researchers as reference points.

As a result, when they take an interest in poking and prodding a particular rock to date it, they already have a rough estimate of its age, based on their assumptions about its geological surroundings, including the assumed ages for the rocks above or below it, and the strata it is found in. In other words, the rock they're interested in already has an "expected age" even before geologists touch it.

Now let's say they have in mind a rock they assume to be about 200 million years old, based on their deep time assumptions about how the rock layers were formed in the first place. But they want to get a more "precise" date.

Next they have to decide on a dating "clock" they wish to use. Since they already believe the rock is tens of millions of years old, they will inevitably pick one that can detect this age. They won't use carbon dating, because if they believe the rock is 200 million years old, it should be completely free of carbon-14, except from sources like contamination; and besides, geologists don't usually carbon-date rocks with mixed origins, such as sedimentary rock.

Instead, they will pick a method with a long half-life. Let's say they decide on the rubidium-strontium method to date the rock. As I have already pointed out, due to the incredibly long half-life of rubidium-87, if the researchers are able to collect samples that form even a tiny upward slope on a graph, they should be able to get an age at least somewhat within their expectations. Remember, they only need the line to slope by 0.001 to get 70 million years.

Next they select an appropriate rock or set of rocks that look undisturbed, and perhaps minerals that are going to have a useful rubidium to strontium ratio. They also select minerals that look undisturbed, and reject the ones that seem to have been disturbed or weathered, even though the rock itself was apparently undisturbed. These choices bias the selection towards samples that are going to behave well when it comes to crunching the data. If a schoolteacher removes all the naughty children in her class, she can say she has a well-behaved class.

Several samples from the rock or minerals are taken. They are processed in a laboratory, and the rubidium-87 to strontium-86 ratios along with the strontium-87 to strontium-86 ratios in each sample are found.

Now comes another series of decisions for the geologists. When the ratios are plotted on an X, Y graph, the data points might form a fairly straight line. If so, as long as the line has an upward slope, it can be treated as an isochron and produce a "model age." But now the researchers have to decide whether this fits their "expected age" or not.

If the data doesn't fit onto a neat line, they have a "miss." They can reject the data as a whole, and there are plenty of excuses for doing so. Maybe other material got mixed in, or the samples were disturbed somehow. If none of their samples produce anywhere close to their expected age, they are likely to think the data is wrong and simply not publish it, unless it can be used to create some kind of controversy or intrigue, which isn't easy when it comes to rocks.

In other words, there is an inherent natural bias towards publishing research that has some element of "success" to it, because there is less value in research that appears to be all "wrong" or a "failure." Unfortunately, we can never know how much research doesn't get published because it didn't produce any "hits" at all.

However, if they have collected enough samples, then at least some of the data might plot nicely enough on an isochron, and the resulting age or ages might be close

enough to their expectations to count as at least a partial “hit,” and make the research worth publishing. Before it gets published, the data can also be grouped in a way that produces a well-behaved isochron matching expectations, while data points that don't line up can be explained away, and left off the isochron.

If the isochron produces an age of, let's say 100 million years, when the strata the rock is found in is supposed to be 200 million years old according to their assumptions, then from the geologist's point of view, the isochron must be wrong. They can reject the data for plenty of reasons, such as materials being mixed together, producing what they call a “mixing line.”

In other words, over time, the whole field becomes a series of assumptions and biases built on previous assumptions and biases, all conveniently excluding even the merest possibility that the rocks could be as young as those pesky creationists say they are. This is an example of The Crooked Trial, taken to ideological and industrial levels.

Incidentally, I don't mean to imply geologists are being deliberately dishonest. I think, for the most part, they are honest; but they are definitely not impartial. Every system, tool and model they use assumes deep time, which is a built-in expectation; and they are also often selective in which data to include or exclude in their isochrons, or which data to accept or reject, depending on how it fits or doesn't fit their expectations.

Now, if this all sounds far-fetched, let's look at a real example. Let's examine the data from a study of samples taken from the Tarim Basin in Northwest China. I have picked this study because it contains a lot of data points, and I think the researchers are also honest about their selection process. Plus, the research report has a catchy title.⁸

Previous researchers had dated three areas in the Tarim Basin using the potassium-argon system, producing model ages of 125 Ma (where “Ma” means millions of years from the present), 389 Ma and 234 Ma. Later researchers wanted to date the same areas using rubidium-strontium dating, so they took five samples, each containing five subsamples. (For easy reference, I have included the data from each sample in the footnotes.)

Incidentally, I should point out that the dates represented the apparent timing of “hydrocarbon charge” rather than the exact time of the sample formation, but this is directly related to the formation of the material being studied.

The first sample, labeled “YM 35-1,” didn't produce a straight line, because one of the five subsamples was too high. When it was removed, the remaining four subsamples produced an isochron giving an age of around 100 million years. This was rejected by the researchers as being far too young, and very different from the potassium-argon age. It was a “miss.” The explanation was perhaps “hydrothermal alteration” causing “extensive subsample-scale redistribution of Rb-Sr atoms,” where Rb is the chemical shorthand for rubidium and Sr for strontium.⁹

The second sample, "H6," gave an age of 148 Ma, with a 68 million year uncertainty. Since this was close enough to the 125 Ma reported by potassium-argon dating, it was considered a "hit," even with such a high level of uncertainty.¹⁰

The third sample, "KQ1," gave an age of 351 Ma with a 97 Ma uncertainty. One subsample deviated slightly from the main trend. Without it, the line would yield a lower age of 332 Ma with a 32 Ma uncertainty. This was considered a "hit" when compared with the potassium-argon date of 389 Ma.¹¹

The fourth sample, "Q1," produced a straight line, which came in at around 480 million years. However, this was older than the apparent age of the early Silurian host strata. The researchers interpreted this as a mixing line. They also speculated that it may have been due to "isotopic heterogeneity, which results in an apparent age that is older than the formation age of its host." In other words, perhaps the stable isotopes weren't mixed in equal ratios beforehand. In any case, the data was rejected. It was a "miss."¹²

The fifth sample, "TZ 67," gave an age of around 235 Ma, and matched up very well with the potassium-argon age of 234 Ma. Obviously this was considered a "hit."¹³ In other words, taking the study as a whole, data that lined up with their expectations was accepted, while data that didn't was rejected.

However, I think the data also supports an alternative hypothesis, which is that the samples are close to their initial element ratios, meaning very little radioactive decay of rubidium-87 has actually taken place. In this hypothesis, the differences between the subsamples are mainly due to sorting of the elements, chemicals and minerals, along with some random variation.

Let's look more carefully at the data. What's curious is, comparing subsamples within a sample, the isotope ratios are quite similar, but they differ substantially between samples. For example, in the sample labeled "YM 35-1," the five subsamples had very similar rubidium-87 to strontium-86 ratios that fell within a narrow window between 13.35 and 13.86, while these ratios in the "H6" sample fell within the small window between 7.169 and 7.342, and in "KQ1" the window was 4.449 to 4.971.

These differences between samples aren't due to radioactive decay. If we start out with 1,000 rubidium-87 atoms, and then wait half a billion years, we would still have about 993 rubidium-87 atoms by the end, because half a billion years is only about 1% of its half-life.¹⁴

In other words, the ratio of rubidium-87 to strontium-86 atoms wouldn't change all that much, even after a supposed half a billion years of radioactive decay. Therefore, even if we assume all this radioactivity took place, the ratios measured today would still be very close to the ones the samples and subsamples started out with.

Therefore, in the main, the differences between samples can't be due to radioactive decay. They must be due to some kind of element, chemical or mineral sorting. This would explain why the "YM 35-1" sample has a rubidium-87 to strontium-

86 ratio averaging around 13.54, while the "H6" sample averages around 7.24 and the "KQ1" sample averages at about 4.68.

While the strontium-87 to strontium-86 ratios could potentially differ much more after half a billion years of radioactivity, they are also clustered around very narrow windows, which may also be similar to the ratios they started out with.

Even if we assumed the isochron method produces accurate ages, the starting ratios for each sample are different. For example, based on the data from the research paper, the "YM 35-1" sample, with the third data point removed, began with a strontium-87 to strontium-86 ratio of about 0.742, while the "Q1" sample started out at around 0.699.

To switch back to our balloon analogy for a moment, to make things a little easier to follow, we know with a high degree of certainty that the samples all started out with different red to black balloon ratios, and different black to brown balloon ratios; and yet the isochron model insists that in all the subsamples in any one sample, the black and brown balloons were initially mixed throughout the material in perfect proportions, even though this perfect proportionality doesn't show up anywhere else, except in the world of assumptions.

This assumption is what allows geologists to draw a straight line and call it an isochron, which in turn produces a model age of millions of years.

Alternatively, what may be happening is, the samples may be young. They just didn't start out with daughter isotopes in perfect ratios, and the variations we see in the samples are primarily due to the geological sorting of elements, chemicals and minerals, along with small natural variations; and the ratios haven't changed much at all. No radioactive decay has taken place, or at least only a negligible amount, at least for radioisotopes with very long half-lives.

This would also explain why geologists keep getting isochrons that don't fit their expectations, and so have to be explained away. They are continually trying to fit square pegs into round holes, except because of the nature of the system, they will get "hits" if they are careful about how much sampling to do, or about how to interpret the data.

The "YM 35-1" sample from the Tarim Basin report doesn't fit on an isochron, but it does if you delete one data point. Then it gives a model age of about 100 million years, which can't be the real age, because it's far too young, compared with the potassium-argon model age. The "Q1" sample yields a model age of around 480 million years, which is far too old, older than the strata it is in. But the dating method can't be at fault, in the mind of geologists. It must be the sample's fault.

Only the "TZ 67" sample lined up with the potassium-argon model age. The "KQ1" sample agrees with the potassium-argon date, give or take 97 million years; and agrees with it even less if you remove one data point. The "H6" sample also agrees, or it might be up to 68 million years out, because of the uncertainty.

This begs the question: why do researchers not take many more samples from the same area, to remove the uncertainty? After all, 10 or 20 data points on a line

would be far more impressive than 4 or 5. I suppose a good excuse is budget; but I suspect another reason is that, in many cases, it would break the nice straight line needed for an isochron, or it would yield a very different date, especially if the "age" is just an illusion produced by using isotopes with multi-billion year half-lives, and isn't really the sample's real age. It's also easier to get the isochron you want with just 4 or 5 data points, because you can always say that any one or two of the points that don't fit your expectations are anomalies.

Whatever the case, let me briefly outline a model of creation that assumes the Earth, Sun, Moon and solar system were created by God and are 6-10,000 years old. I am not trying to provide a comprehensive model here. This is simply an outline.

To evaluate this, we would first need to remove the assumption of deep time, and any ideas and methods that rely on this assumption, so we aren't fitting square pegs into round holes. This would mean most isochron dating methods are invalid, at least the ones geologists tend to use to date rocks.

There would be two primary events impacting Earth geology. The first would be the creation of the Earth, Moon and Sun, presumably out of some "primordial" matter existing prior to their formation, although I use the term "primordial" not to imply any vast age.

The primordial matter may have contained ratios of isotopes and elements similar to the ones we see today. This would explain why the Moon and many meteorites have roughly the same model age in isochron dating. They were formed at around the same time out of the same primordial matter, and are still young, so not much has changed for many of the isotope ratios.

This would explain the coincidence of the supposed age of the Earth to the half-life of uranium-238, which is around 4.5 billion years. This is because it isn't a coincidence. Assuming the primordial matter contained roughly the same proportions of uranium and lead isotopes we see today, very little natural radioactive decay of uranium has really taken place, and the lead could have been around from the start. If there was an initial 50/50 ratio of uranium-238 to lead-206, this could be interpreted as 4.5 billion years of radioactive decay, when it isn't.

Variations in these ratios could be due to the loss of some of those elements, particularly for meteorites flying in space, passing close to the Sun, entering the Earth's atmosphere, and then hitting the Earth. If sample data from these meteorites could be plotted on an upward sloping line, the line could be interpreted as an isochron giving a model age of billions of years, because the sample would still have most or some of its primordial lead left in it.

God may have also caused a process that would appear to be radioactive decay, in the act of making the Earth ready for habitation. For example, to generate heat and produce an atmosphere, God could have used his energy to cause atoms in certain elements such as uranium to vibrate and give off a limited burst of radioactive decay very quickly. While this would obviously violate the ordinary laws of physics, this is precisely what God says he did when clothing the sea with clouds. In the book of Job,

the original Hebrew says, "I broke my statute over it." ¹⁵ In other words, I think God is telling us that, in order to produce an atmosphere of clouds, he violated the laws of physics he had already put in place.

This could have started on Day 1, and could have burned off enough water to create an atmosphere on Day 2 and allow dry land to appear early on Day 3, but the process was halted before the creation of life on Earth, so that no living thing would be harmed. It would also be a way of producing heat, prior to the creation of the Sun on Day 4. Some of this atomic excitation could appear to be radioactive decay spanning millions or billions of years.

The second event that would impact on geology and isotope ratios would be the Flood, which would have changed the entire face of the Earth. The floodwaters would cause immense quantities of rocks and sediment to be churned for many months, and then deposited in enormous sedimentary layers, which would be sorted perhaps according to mass or chemical composition. In other words, it would involve a huge amount of element, chemical and mineral sorting, perhaps with heavier elements sinking lower.

Indeed, even deep time scientists acknowledge this sorting process in the formation of the Earth, which is how they explain why the core of the Earth contains large amounts of heavy metals such as iron. They say it sank down to the core, although curiously, not lead. A global Flood would have a somewhat similar sorting effect, although restricted to nearer the surface of the Earth.

Creationists debate which geological layers were formed in the Flood, and which ones existed prior to it, and I don't intend to follow that debate here; but since fossils exist in the Cambrian strata, presumably everything in and above this layer would have been laid down shortly after the Flood. This would also explain why the strata from the Permian down to the Cambrian are considered, even by deep time geologists, to have originated in water or be transitional between water and land. In a Young Earth model, this was probably due to the inclusion of floodwaters in the sediment.

In any case, much of the world's geology would have been reshaped by the Flood. Chemicals, elements and minerals would also be sorted to a certain extent, and this would obviously have an impact on the ratios of elements and perhaps their isotopes, which is all that isochrons are really measuring. They are ultimately just detecting different isotope ratios based on different rock layers and compositions, and these have been interpreted as representing age, because the isochrons that geologists use assume millions of years of radioactive decay has taken place.

These deep age assumptions were also baked in from the start of modern geology. James Hutton, sometimes referred to as the "Founder of Modern Geology," said that the past history of the Earth must be explained by what can be seen to be happening now, and that no powers were to be employed that weren't natural to the globe. A global Flood wasn't natural, and so was simply assumed away.

In his own words, Charles Lyell said he wanted to “free the science from Moses.”¹⁶ Of course, this could only happen if the Earth was millions of years old or more, and not thousands as implied by Moses. In other words, modern geology was invented to get away from the Creation and Flood accounts, and ultimately, I would suggest, from God himself. If I may speak bluntly, I think this has been the real agenda ever since, because there can be no molecules-to-man evolution if the Earth is merely thousands of years old, and therefore no atheism.

Radiometric dating, and particularly the isochron method, relies on the assumption that vast amounts of radioactive decay has taken place. These dating methods, and the assumptions they help to support, are then used to “prove” the Earth is old. But this produces circular reasoning.

Furthermore, they assume the daughter isotopes were initially distributed throughout the rock in perfectly equal ratios, and that the rock has been sitting undisturbed in a near pristine condition for vast ages of time.

But if there really was a global Flood, it would have disrupted the landscape of the whole Earth, so rocks wouldn’t have had the luxury of sitting around quietly for a billion years. And given that rubidium reacts violently with water, and strontium burns spontaneously in air, what would a Flood do for rubidium-strontium dating?

Now, one objection that could be raised here is that geologists can use different methods to date the same rock. This is true, but I think the same biases exist here that I mentioned before. If new researchers get a model age that is somewhat similar to a previously published model age, they will see their results as a “hit” and publish it. But if the date is significantly different, they are likely to view the results as a “miss” and not publish it, and we won’t ever see the “failed” research; or they may publish it but reject the data that doesn’t line up with their expectations; and so the whole field becomes a house of cards, with assumptions built on top of assumptions.

We saw this in the Tarim Basin data I examined earlier. The potassium-argon and rubidium-strontium dates agreed in one instance, while having only some agreement in two instances, but with large amounts of uncertainty which could have been resolved by taking a lot more subsamples to begin with; and they differed dramatically in two other instances.

Let me sum up the issues with using isochrons to date rocks. Isochrons can give the illusion of vast age, which can easily be nudged in the right direction by geologists. The method already has millions of years built into it, simply by using radioisotopes with long half-lives.

Some kind of linear upward slope isn’t difficult to achieve, as long as the daughter isotope ratios are fairly close but have some variation, which would probably be the case even if no radioactivity had taken place at all, and the rock was young. It would be the result of chemical, element or mineral sorting, and some random variation, rather than radioactive decay.

Geologists then have plenty of tools to align the data with their expectations, including but not limited to: not taking enough samples to eliminate uncertainty and

therefore leaving room for the data to “agree” by ignoring a data point or two, ignoring or explaining away data that doesn’t make an isochron, explaining away data points that don’t line up nicely, and dismissing isochrons that don’t match up with the assumed ages of the rocks or strata around it.

In other words, just as neo-Darwinian evolution is a critical but flawed assumption in biology, deep time geology is a house of cards, built on one critical assumption that is necessary to “free the science from Moses” - namely, that things are millions or billions of years old. Because if rocks aren’t millions of years old after all, then neither is there time for evolution, and the naturalistic worldview sinks like iron in water.

Now, there are many other methods scientists have developed to measure age based on their deep time thinking. I won’t go into them all, because this chapter would then become a book within a book that is supposed to be a letter.

However, let’s quickly look at one more. Tree rings are sometimes used as a dating method, because under normal growth conditions, trees add one ring to their trunk every year. Some trees have several thousand rings, which is then assumed to be their age. Furthermore, nearby dead wood is used to extend the ring count many thousands of years further back in time, by aligning tree rings.

There are several assumptions used in this dating method. The first is that one tree ring represents one year. However, it is well-established that trees can grow multiple rings per year, known as “multiplicity,” in certain conditions.¹⁷

For example, Bristlecone Pine trees growing in the White Mountains of Eastern California are thought to be some of the oldest living trees on Earth, supposedly around 5,000 years old. The ones with thousands of rings are living in harsh conditions, where soil and water are somewhat scarce. In conditions of better moisture, the Bristlecone Pines only had hundreds of rings.¹⁸

It seems that trees in harsher conditions can grow multiple rings a year when they need to preserve resources such as water. Trees lose a significant amount of water vapor through the bark, so the extra rings may preserve water.

This also helps to explain the “strip growth” habit of trees with more than a few thousand rings. As trees grow older and larger, their surface area gets bigger, which means an increase in water loss. When strip growth takes over, it leaves only one long living strip of bark running up the side of the trunk, allowing resources to be conserved, and adding layers of growth in a different direction, causing the trunk to become more slab-shaped than cylindrical.

What this all means is, the assumption that one ring equals one year may not be true in older trees, particularly in arid conditions. The supposedly oldest Bristlecone Pines with thousands of rings may have simply grown rings at a much faster rate because they are in harsher conditions, where water was much more scarce. In other words, they are not really thousands of years old.

Another assumption in this dating method is that dead wood in the surrounding area has survived intact for thousands of years, to extend the chronology

given by the tree rings. The dead wood in the supposedly oldest trees has disintegrated, while wood lying on the ground is supposed to have survived for thousands of years, which is highly implausible.

Furthermore, the White Mountains are eroding at a rate of at least one foot every thousand years, so if this dating method were accurate, it would mean the mountains have eroded several feet while the wood on the ground remained intact, which is very unlikely.¹⁹ More likely, the wood on the ground simply isn't as old as supposed.

Now, the one thing I hope to have made clear in this chapter, is that our assumptions play a critical role in how we interpret evidence. I have spent some time on the issue of dating, because how we measure time makes a big difference to what we believe, as well as on the nature and character of God.

It is not my intention to impose my viewpoint of the world on you. But since we are nearing the end of his "letter," I feel obligated to give you a summary of my opinion, because this is what I think is the truth, and truth is highly valued by God, who says he will become known as the "God of truth."²⁰

I believe the Bible is the inspired word of YHWH, in the sense that its human authors were influenced by God to write what they did. That inspiration may have taken different forms. Some prophets were told to write certain words directly, such as Moses with the Law covenant, or Isaiah at times when he was told to make a pronouncement from YHWH. Other things may have come more from the writer's own heart and mind, but God still inspired the preservation of those words for the benefit of future generations.

Since no human was around to witness the founding of the heavens and the Earth, I believe God revealed those things to Moses, his first prophet, who then wrote the creation account in Genesis.

The creation of an entire universe might sound like it should take a vast amount of time, but scientists already have a concept, which they call inflation, allowing for the creation of a small but expanding universe in virtually no time at all, without any divine help. God simply needed to extend this inflationary period a moment longer, and he could have created a full-size universe "in the beginning."

If we use light to measure age, the universe would appear to be billions of years old, since we can see billions of light years away. But light itself would be stretched in the extended inflationary period, and so it isn't a suitable measure of age. God isn't fooling anybody with a misleading "appearance of age." He simply created a fully functional universe almost instantly. Scientists are simply misinterpreting what they see, and are therefore fooling themselves.

God set the first measure of time for Earth and its eventual inhabitants by defining "day one." There may have been a small window of time prior to Day 1, during which he created spirit life forms that didn't inhabit the Earth, occasionally referred to in the Bible as "sons of God," because they were already present at the founding of the

Earth. That window may have been a few thousand years, long enough to enable at least one particular cherub to rebel, but the Bible doesn't say.

God then worked to make the Earth habitable within just six days. He could have taken billions of years, but I don't think this was necessary. The creation of the Sun is a good example of why. God could have waited millions of years for a supernova to form the raw materials to make the Sun, or he could have pulled all the necessary helium-4 together almost instantly. Is it really too incredible to believe that God Almighty can manipulate matter this way? Humans can manipulate matter on a small scale, and we only play at being God sometimes.

I think God wanted us to know they were actual days, commencing with "day one" and marked by actual evenings and mornings. Those days were filled with a series of miraculous events, work by God, performed in a logical order. This is also why he had Israel work six days and rest on the seventh, because "for six days YHWH made the heavens and the earth, the sea and all that is in them, and he rested on the seventh day."²¹

I believe God later brought about a worldwide Flood, because life and the Earth had been ruined. I think humans were already on the brink of destroying themselves, and so the Flood was not an act of malice, but was done to preserve earthly creation. All land creatures alive today are the offspring of those on the Ark.

There is plenty of evidence for the Flood, and belief in it was widespread among the people and tribes of the Earth in the past, but humans have a tendency to forget their past, and true accounts become myths and legends over time.

The apostle Peter also predicted that the Flood would pass into legend, and become the basis for ridicule: "In the last days scoffers will come, proceeding according to their own desires and saying, 'Where is the promise of his presence? For from the time when our forefathers fell asleep, all things have continued from the beginning of creation.' For they are willingly ignorant of this, that the heavens and the earth of old were, out of water and through water, brought together by the word of God, through which that world perished by being deluged with water."²²

This is precisely the "willingly ignorant" path that science took in later days. The modern field of geology was founded by James Hutton in the late 1700's, who insisted that the past must be interpreted by things happening today, thus eliminating the Flood with the stroke of the philosophical pen, and by Charles Lyell in the early 1800's, whose desire was to "free the science from Moses."

The evidence for the Flood hadn't disappeared. It was still there, and remains there to this day, literally and figuratively buried in the geological columns and rocks. It was simply reinterpreted to be the operation of processes that took millions of years. Inspired by this, Charles Darwin applied this thinking to the world of living things, and came up with his idea of evolution by variation and natural selection.

In other words, I think that science took a major misstep from the days of Hutton, Lyell and Darwin. Science no longer became a quest for truth regardless of

where it leads, but it became a quest to explain all things as being accomplished by nature alone.

It is certainly not wrong to try and figure out causes in a scientific manner, and not just say "God did it!" Isaac Newton believed in God, yet this didn't stop him from discovering and writing extensively on gravity. But it can be hard to believe in God when the scientific world repeatedly insists that life is billions of years old, that it all evolved from primordial sludge, and that everything can be explained without God.

However, I have included this chapter to show that, in many ways, geologists have created an elaborate illusion for themselves, as a result of rejecting Creation and the Flood, which is exactly what the apostle Peter predicted. Once we shatter the illusion, and the spurious "clocks" that give the appearance of vast age, it is easier to accept that God did indeed create the heavens and the Earth.

1 For a list of research papers, see Table 1 in the article "Carbon-14 Content Of Fossil Carbon" by Paul Giem, published in *Origins*, 2001. The article is also an interesting discussion of carbon-14 in relation to both Old Earth and Young Earth viewpoints. **2** Taylor, Southon, "Use of natural diamonds to monitor ¹⁴C AMS instrument backgrounds", *Nuclear Instruments and Methods in Physics Research B*, 2007. **3** The three points on an X, Y scatter graph would be at (1, 3.5), (0.5, 2) and (0.3125, 1.4375). The X axis should be the red/brown balloon ratio, and the Y axis should be the black/brown balloon ratio. **4** The slope can usually be calculated in a spreadsheet or scientific calculator by using "linear regression." Each point on the X,Y graph falls on a straight line satisfying the linear equation $y=ax+b$ where a is the slope and b is the intercept through the Y axis. In our example the slope is 3. For calculating ages, a "decay constant" is used, often denoted by the Greek symbol λ , which is calculated as $\ln(2)/h$ where h is the half-life in years. (\ln is the natural logarithm.) In our example, $h=10,000$ and so λ is $6.931471806 \times 10^{-5}$. The age can then be calculated using the formula $(1/\lambda) \cdot \ln(a+1)$ where a is the slope of the line. In our example this would become $(1/6.931471806 \times 10^{-5}) \cdot \ln(3+1) = 14,426.95041 \cdot 1.386294361 = 20,000$. **5** Claire Patterson, "Age of meteorites and the earth," *Geochimica et Cosmochimica Acta*, 1956. **6** Let's take the value of λ as 1.4×10^{-11} . With a slope of $a=0.001$, this produces a model age of $(1/\lambda) \cdot \ln(a+1) = (1/1.4 \times 10^{-11}) \cdot \ln(0.001+1) = 71.42857134 \times 10^9 \cdot 0.0009995 = 71,392,857$ years. **7** Taking λ as 1.4×10^{-11} , for the first set of data, the slope a of the isochron would be 0.056357142857143 and the intercept b on the Y axis would be at 0.70975. For the second set, the slope would be the same but the intercept would be at 0.597035714285714. **8** Li *et al*, "Direct Rubidium-Strontium Dating of Hydrocarbon Charge Using Small Authigenic Illitic Clay Aliquots from the Silurian Bituminous Sandstone in the Tarim Basin, NW China", *Nature: Scientific Reports*, 2019. **9** The YM 35-1 sample data can be plotted on an X,Y graph at: (13.35, 0.760815), (13.86, 0.761497), (13.45, 0.762334), (13.49, 0.760862), (13.54, 0.761158). A straight line can't be drawn. However, if the third data point is removed, we get a line with slope 0.001370929700023 and intercept at 0.742497172315091, which would give a model age of about 98 million years, with $\lambda = 1.396 \times 10^{-11}$ as used in their paper. **10** The H6 sample data can be plotted on the following points: (7.342, 0.728876), (7.28, 0.728789), (7.169, 0.728541), (7.222, 0.72874), (7.205, 0.728636). These produce a line with slope 0.001836334002547 and intercept at 0.715414731019148, giving a model age of about 131 million years. **11** The KQ1 sample data can be plotted on the following points: (4.971, 0.735775), (4.709, 0.73466), (4.449, 0.733376), (4.473, 0.733485), (4.8, 0.735392). These produce a line with slope 0.004855825080354 and intercept at 0.711810396293909, giving a model age of about 347 million years. **12** The Q1 sample data can be plotted on the following points: (11.4, 0.774273), (10.71, 0.769862), (12.15, 0.779446), (11.42, 0.774809), (11.45, 0.775439). These produce a line with slope 0.00667388741186 and intercept at 0.698509962432088, giving a model age of about 476 million years. **13** The TZ67 samples can be plotted on the following points: (4.462, 0.72473), (3.559, 0.721805), (4.629,

0.725351), (4.507, 0.72492), (4.176, 0.723921). These produce a line with slope 0.003278604349936 and intercept at 0.710156906680564, giving a model age of about 234 million years. **14** The formula $1/2^n$ defines the proportion of radioactive atoms remaining after n half-lives. Since we only want 1% of a half-life, we get $1/2^{0.01} = 0.9930925448$. Therefore, 1,000 radioactive atoms would leave about 993 of the same atoms after 1% of its half-life has passed. **15** Job 38:10. **16** *Life, Letters And Journals Of Sir Charles Lyell*, edited by Katharine M Lyell, 1881. Volume 1, p268. **17** Glock *et al*, "Classification and multiplicity of growth layers in the branches of trees, at the extreme lower forest border", *Smithsonian Miscellaneous Collection*, 1960. **18** LaMarche, "Environment in Relation to Age of Bristlecone Pines", *Ecology*, 1969. **19** LaMarche, "Rates of slope degradation as determined from botanical evidence" *White Mountains, California, Geological Survey Professional Paper 352-I*, 1968. **20** Isaiah 65:16. **21** Exodus 20:11. **22** 2 Peter 3:3-6.

69. Dating With DNA

In this chapter I'd like to spend a little more time discussing attempts at dating using DNA. The mutation rate of the genome is used in evolutionary theory as a "molecular clock," a way to estimate when two species are said to have diverged from a common ancestor.

For example, if theorists want to work out roughly when humans and chimps supposedly split off from an apelike ancestor, they divide the number of DNA differences between the two species by the rate of mutations assumed to have occurred each year.

However, this method relies on several critical assumptions. The first is that the two species being compared really do share a common ancestry. In the case of humans and chimps, it is assumed that both are related by descent from some kind of apelike ancestor.

The second assumption is that we have an accurate count of the number of DNA differences between the two species being compared. In reality, researchers try to harmonize both genomes as much as possible before counting differences. Furthermore, to make the early claims of a roughly 1% difference between humans and chimps, insertions and deletions were ignored, along with dramatic differences in the Y chromosome.

Third, the molecular clock is usually calibrated to the fossil record, which is assumed to provide an independent method of dating. However, if the fossil record doesn't reflect a gradual evolutionary change, but simply shows the sorting of materials and organic matter in a worldwide catastrophe such as the Flood, it wouldn't be a reliable way to calibrate the molecular clock.

Fourth, the mutation rate is assumed to be broadly accurate. For a long time, scientists had used single nucleotide substitutions to calculate a rate of about one mutation in every billion base pairs for humans, implying humans became distinct about six million years ago. However, later research suggested the mutation rate was half of this, which would push the evolution of humans back at least another six million years, if we are truly related to chimps by common descent; but this would create a problem when it comes to aligning the molecular clock with the fossil record.¹

The fifth assumption is that the mutation rate is regular and predictable – that is, clock-like. However, evidence indicates that it isn't. Instead, many mutations are the result of dynamic and highly regulated stress responses, with multiple simultaneous mutations occurring within local clusters in the genome. For this reason, the authors of a review paper on mutations wrote: "Assumptions about the constant, gradual, clock-like, and environmentally blind nature of mutation are ready for retirement."²

Whatever the case, the so-called "molecular clock" in the genome can't be used to prove human origins without circular reasoning. In the case of humans and chimps, it assumes the two species are related by a common ancestor, and that a slow accumulation of mutations over millions of years is responsible for the differences.

But if humans and chimps were designed to be distinct from the start, then the differences between their genomes wouldn't be the result of mutations, so using them as a kind of "clock" would produce very inaccurate dating.

However, there is another feature of eukaryotic cells that has the potential to be used as a kind of clock. As I have discussed elsewhere, most organisms have DNA in their mitochondria (known as mtDNA for short). In humans, this is just 16,569 base pairs in length. It contains genes that seem to be essential for mitochondria to function, and so the genes are preserved by natural selection. However, other parts of the mtDNA sequence don't code for genes, and so they are potentially freer to mutate without harming the organism.

Comparing these freer parts across the animal kingdom has allowed researchers to notice something interesting. What they found is that each species has its own specific sequence, which is identical or very similar in other members of the same species; a kind of distinctive "barcode" as it were, in their mtDNA.

Based on this, the researchers concluded that most of the current living species on Earth must have arisen recently, and haven't had time to develop a lot of diversity in their mtDNA. This means there was a genetic bottleneck in the recent past.³

For these deep time researchers, the 'recent' past meant within the last one to several hundred thousand years. Rather than use the mutation rate of mtDNA, the study relied on the molecular clock to make an estimation of when the bottleneck occurred – but this would make the dating unreliable, if any of the assumptions of the molecular clock are false.

The researchers weren't proposing any catastrophic events to account for the bottleneck. However, we would expect to see a genetic bottleneck if there was a global Flood as described in the Bible. Large numbers of species would have died out, and the ones we have with us today would be the offspring of the animals on the Ark.

Now, if we were to look at mutation rates of mtDNA today, we could potentially use this to say how much mtDNA diversity should exist in a population after a specific number of years have elapsed.

For example, let's start with a single female founder of a population and her children (since mtDNA is usually passed down from the mother to her offspring), and assume one mutation happens in mtDNA per generation. In early generations the number of mutations would be small, but as more generations come and go, more and more mutations would accumulate, and people's mtDNA sequences would differ more widely.

If we could take DNA samples from enough people in a particular generation, we could calculate the average number of differences between the samples, and make an estimate of when the population began. Conversely, starting with a female population of one, we could make predictions about how different each DNA sample should be, if the population had been around for a specific number of years.

Using this method, and based on current mtDNA mutation rates, creationists have shown that the variation in human mtDNA is not consistent with the

evolutionary paradigm, but lines up well with a founding population dating back about 6,000 years ago.⁴ Of course, this method also assumes that mutations are somewhat regular and consistent throughout the generations.

Whatever the case, if humans are a fairly recent creation, thousands rather than millions of years old, this would explain an apparent anomaly in the Bible. According to the creation account in the book of Genesis, Adam and Eve, the first human pair, were told to be fruitful and become many. But if they were the only humans around to begin with, their offspring would have needed to marry close relatives. Yet this was forbidden in the Law covenant given to Israel through Moses.

There is a simple genetic explanation for why marrying close relatives was outlawed at that time, as well as being a bad idea today. Close relatives could have similar or the same mutations in their genetic information. If both parents have a gene with a damaging mutation, they are much more likely to pass it on to their offspring, potentially leading to a baby with genetic defects. On the other hand, if the parents aren't closely related, even if one parent carries a defective gene, there is a much better chance that the other parent will have a functional version of the gene, so their offspring can still inherit a working gene.

If God really did create Adam and Eve, as the Genesis account says, there would have been few if any mutations in the DNA of their immediate offspring, so marrying close relatives wouldn't have been a problem. God only outlawed it much later, once mutations had accumulated enough to cause issues with this. The fact that the Law covenant forbade marrying a close relative reflects a good understanding of genetics.

Incidentally, if humans didn't evolve from an apelike ancestor after all, but were created directly by YHWH, how old would Adam look at his creation? Presumably he would be a full-grown man. To our eyes, he would look at least a few decades old, yet he would have a chronological age of zero. Was God trying to fool possible observers with an appearance of age? Not at all. He simply created a functional man and woman from the start, which meant Adam's biological age didn't match up with his chronological age, his actual age. This same point could apply to anything God chooses to create, whether a loaf of bread, or an entire universe meant for habitation. Why would God need to make a loaf in the same way we need to make it?

While we're on the subject, another interesting question we could ask is: why did God create Eve from a rib? This was a question that perplexed the Jewish philosopher Philo; or to be more precise, he didn't take these details too literally, but saw them as figurative. Writing in the first century AD, he asked, "how can any one believe that a woman was made of a rib of a man, or, in short, that any human being was made out of another?" And "why, when there were so many parts of a man, did not God make the woman out of some other part rather than out of one of his ribs?"⁵

He went on to give the kind of elaborate answer that theological people do when they wish to interpret a scriptural passage figuratively rather than literally. However, Philo didn't know that there was a simple scientific answer to his question. Unlike other body parts, human ribs can grow back!⁶ It's also worth noting that bone

marrow contains stem cells, which have the potential to become different types of cells found in a body.⁷

While I think God created Eve from one of Adam's ribs so the first two humans weren't independent creations, but were of the same kind, figuratively as well as literally "one flesh," perhaps he was also using this as an object lesson to those who view the account as a parable or myth. God just happened to pick the part of Adam that could grow back naturally, and that contains stem cells, details that science has only recently discovered.

According to the Genesis account, Adam and Eve could have potentially lived forever, but they chose to become like God, knowing both good and bad. They and their offspring became separated from the source of life. Humans became subject to breakdown and death, which happens in part because of the accumulation of mutations in our cells over time.

Furthermore, as I discussed in the first part of this letter, God made a statement prior to the Flood that sounded very much like a limit to the human lifespan: "My Spirit will not reside with the human forever while he is flesh, and his days will become 120 years."⁸ I think this was done to restrain the human ability to entrench evil. The Bible records a dramatic drop in lifespans after the Flood, which would make sense if the changed environment caused damaging mutations to accumulate at a higher rate.

In any event, human lifespans have varied throughout history, depending on factors such as medical knowledge, the environment and the availability of food. However, even in more modern times, with our much better understanding of what kills us and what keeps us alive, looking at a list of the verified oldest people strongly suggests there is indeed an upper limit to the human lifespan.

At the time of writing, most of the one hundred oldest men, whose ages have been verified, died between 111 and 115 years of age, with one living to 116. For the one hundred oldest verified women, most of them died between 114 and 117 years of age, with one living to 118, and two living to 119. Jeanne Louise Calment, who died at 122 years of age, is the only person in history who has been verified to have reached the age of 120. This exception seems to highlight the rule, stated by God several thousand years ago, that without God, "his days will become 120 years."

Fortunately, God has provided a way for each of us to reconnect with the source of life.

¹ P Moorjani, Z Gao Z, M Przeworski, "Human Germline Mutation and the Erratic Evolutionary Clock", *PLOS Biology*, 2016. ² Devon M. Fitzgerald, Susan M. Rosenberg; "What is mutation? A chapter in the series: How microbes 'jeopardize' the modern synthesis", *PLOS Genetics*, 2019. ³ Stoeckle, Thaler, "Why should mitochondria define species?", *Human Evolution*, 2018. See also the article "Far from special: Humanity's tiny DNA differences are 'average' in animal kingdom" published by Rockefeller University at phys.org on May 21, 2018. ⁴ See the article "A Young-Earth Creation Human Mitochondrial DNA 'Clock': Whole Mitochondrial Genome Mutation Rate Confirms D-Loop Results" by Dr. Nathaniel T. Jeanson, published on September 23, 2015 in *Answers Research Journal*. ⁵ Philo Judaeus, *Allegorical Interpretation II*, Section VII. ⁶ See the article "Humans And Mice Can Regenerate Missing Rib" posted by Cristy Lytal at

futurity.org on September 15, 2014. **7** See the letter titled "Adam's rib and the origin of stem cells" in *American Journal of Hematology*, first published 11 February 2011. **8** Genesis 6:3.

70. The Next Steps

When I began this work, it was meant to be much shorter, which is why it is called a "letter." But I wanted to cover a broad spectrum of evidence for God, and also highlight the false assumptions that lead people away from God, which meant this letter became a book.

The apostle Peter wrote that Christians should be "always ready to make a defense to everyone asking you to give an account about the hope that is in you, with mildness and respect." ¹

This book is my account of the hope that is within me, although I admit I have also used a little sarcasm and humor as well, which Peter didn't say much about. I believe I have presented a strong case for the existence of God, and more specifically for YHWH as the One who created the heavens and the Earth and all life in and upon it, the One who led Israel out of Egypt and established them as his people, and who gave his Son for us, so we could know him better, get closer to him, and have life in abundance.

Charles Darwin, at the end of the first edition of his book *On The Origin Of The Species*, said that "from famine and death, the most exalted object which we are capable of conceiving, namely, the production of the higher animals, directly follows," and that "there is a grandeur in this view of life," where "from so simple a beginning endless forms most beautiful and most wonderful have been, and are being, evolved."²

This might make life grand in its overall scope, but it also makes each individual irrelevant. One organism's life means virtually nothing, their death merely serving to fuel natural selection. We are here by an accident of nature. Our purpose is to survive and reproduce. There is no real purpose beyond this. If there is a grandeur in this view, it is also somber and sobering, like the procession of a funeral.

Personally, I think the existence of YHWH is much more exciting. It means life on Earth was created for a purpose, and with humans in mind. They were given stewardship of it and its creatures, but humans were also allowed to go their own way for a time.

God has already revealed the answers to the four key questions we asked early on in this letter: Why are we here? What is the purpose of life? Why is there suffering? What does the future hold?

We are here because God willed it, and because he desired to be a Creator, just as humans desire to be parents. This springs from a desire to share life with others. The purpose of life for the first humans was to become a fruitful family and manage the Earth wisely, but God also knew they would desire to seek out their own path, and so he allowed them to go their own way.

Suffering was not part of God's purpose, but became a temporary consequence of the human desire to become independent of their Creator, their source of life. As a result, it did indeed become a world governed by the survival of the fittest, and so

Darwin was right in that sense. But I think God anticipated this, and so he gave creatures their own equipment and strategies to survive during this period. I suspect these things were built into their genomes, ready to be switched on as needed, just as the peppered moth can switch on its dark mode when needed.

We would also suffer consequences from a more volatile environment, which would no longer be kept in check by God, because of the human desire to become like gods, independent of their Creator.

But now that humans know good and bad for themselves, God has purposed to remove the bad, and put things right again: "I saw a new heaven and a new earth, for the former heaven and the former earth passed away." ³

And again: "Look! The tabernacle of God is with humans, and he will dwell with them, and they will be his people, and God himself will be with them. And God will wipe away every tear from their eyes, and there will be no more death; neither will there be mourning nor outcry nor sorrow anymore, for the former things have passed away." ⁴ And God himself says: "Look! I am making all things new." And "write, for these words are faithful and true." ⁵

I think YHWH's existence is exciting, but I also recognize that many people may initially find this unpleasant or even disturbing. I think a big reason for this is, they see God as "The Big Bossy Dad In The Sky."

As humans, we spend our early years discovering the wonders of the world, and our own powers and abilities. Many of us then spend our teenage years trying to escape the authority of our parents so we can exercise our own power, desires and abilities, and we finally become free after much effort. I can therefore appreciate why the discovery that there is yet another Parent we are subject to may not be appealing. However, I would suggest that many humans respond this way because they don't fully understand God's purpose.

My belief, which I have implied throughout this letter, is that God is ultimately engaging humans, both collectively and as individuals, in a process of growth and maturity. He does indeed deal with us in the same way human parents deal with us, but normal, healthy parents treat their offspring differently depending on their offspring's stage of development.

When you were born, you were utterly dependent on your parents. They would speak to you like a baby, because you couldn't even speak a language, let alone comprehend deep things. As you became a child, you were reliant on your parents and were expected to obey them. As a teenager, these things were still true, but you began to discover your own abilities and desired independence. As an adult, you hopefully enjoyed a more mature relationship with your parents; but if not, then I think it's fair to say that a deeper, more mature and less childlike relationship is the way it was meant to be, even if some aren't fortunate enough to experience this.

I think God's way of dealing with humanity in general also reflects three main stages of human development: childhood, student, and adulthood.

Children are given commands. They are told what to do, and expected to do as they are told. They are given rewards for obedience and punishments for disobedience. I think this “childhood” stage of human development also reflects how God dealt with humanity in their early stages.

We see this in the story of Adam and Eve. Physically they were adults, but they were like children in terms of understanding, wisdom, maturity and self-control. They were given one simple command: Don’t eat from a particular tree, or you’ll die. But like children, they just couldn’t keep their hand out of the cookie jar. Telling them they couldn’t have it just made it more desirable. All it took was a few words planting doubt and skepticism about God’s intentions, and they were easily enticed. This is the same story we see today, except the tools used to create doubt and skepticism have become more sophisticated.

We also see a reflection of the childhood stage of human development in the founding of ancient Israel. God gave them laws, including the Ten Commandments, where they were told not to murder, steal, commit adultery or testify falsely against their fellow humans, things that mature adults should find pretty obvious. But this was a people who, after they were brought out of Egypt with miracles and wonders, built a carved image of a bull and declared it to be their god, because Moses was busy on the mountain. They were adults, but still like children in their maturity and wisdom, so God dealt with them like children.

We also see this to a certain extent in the book of Job (usually found just before the book of Psalms), one of the oldest books in the Bible. Job was a wealthy man from the Orient who, according to the account, was blameless before God. For this reason, Satan wanted to put him to the test. He claimed that Job was only blameless because God was protecting and blessing him. Take those things away, and Job would probably end up cursing God.

To answer the accusation, God permitted Satan to test Job. Soon after, a raid by the Sabeans killed some of Job’s servants and stole his flocks. Fire fell from the heavens and blazed among the sheep and servants, consuming more of them. The person reporting this to Job assumed it was fire from God. The Chaldeans raided the camels and killed yet more servants. Finally, a great wind struck the house and killed Job’s sons and daughters. These things must have been devastating and perplexing for Job, but despite this, he didn’t sin or ascribe any wrongdoing to God.

Satan then extended his accusation. He said that a man would give everything for his own life, and that if God would touch Job’s flesh and bone, he would curse God, presumably to save his own skin. God allowed Satan to afflict Job with painful sores all over his body, although he wasn’t permitted to take Job’s life. Despite this, Job didn’t sin with his lips.

Later on, three of Job’s acquaintances arrived to comfort him. They sat with him for seven days, saying nothing because they saw his pain was great. Finally, they started talking, and much of the book of Job is a record of the debate between Job and his so-called comforters.

The bottom line is, Job's companions accused him, either directly or by implication, of being bad. Job must have done bad things, or maybe he was so righteous that he had become arrogant, which was also bad. Why else was he experiencing these trials from God? Job couldn't understand it either. If he had done something wrong, he pleaded to know what it was. He insisted he was a man of integrity.

As readers of the book of Job, we are given the privileged position of seeing what was really going on. We get a vantage point that Job and his friends didn't have. Job was right to say he hadn't done anything wrong to bring on his calamities. Near the start of the book, God's description of Job to Satan was that "there is no one like him in the earth, a man flawless and upright, fearing God and withdrawing from bad."⁶ Therefore his friends were wrong to ascribe Job's suffering to any badness on his part.

In many ways, the logic of Job's friends was impeccable, but only from their limited vantage point. As a result, they were actually reasoning like children, because they couldn't see what was really going on from a higher perspective.

Job also fell into the trap of faulty reasoning. During the debate, he reasoned that God must have found fault with him; but by not revealing what his fault was, God was denying him justice. Job was aware that God punished the wicked, but since Job insisted he was blameless, he concluded that God must inflict both the wicked and the good, so there wasn't really any advantage in being good.

Elihu, a fourth friend of Job who had been silent because he was younger than the others, added to the debate near the end by pointing out how Job was basically accusing God of being unjust. Elihu concluded his argument by saying that they couldn't really draw up their case, because they were in the dark about the reasons for Job's calamities.

Immediately after this, God himself intervened in the debate, by speaking to Job out of a windstorm. To emphasize the fact that Job might not have the full story, God questioned Job on various topics, including: the founding of the world, the path and abode of light, what binds the constellations, the laws of the heavens, and the design of several creatures and their strength and wisdom (or lack of it). After this relatively short summary of God's most awe-inspiring creations, Job had to admit that he spoke rashly of things he didn't understand, and he said that he repented in dust and ashes.

After this, God restored Job's fortunes and gave him double what he had before, including a big family and an abundance of livestock. Nevertheless, a skeptic might see God's actions in this account as troubling. God might not have been the direct source of Job's calamity, but by allowing it, we could say he indirectly caused it. Why did God allow Satan to do this?

This is where the "student" level of human development comes in. The book of Job doesn't directly answer this question for us, and similarly, the Bible doesn't directly answer every question we might have. Instead, we are invited, like students, to think more deeply about the issues raised. This is how students learn best. They are given

lessons, but the answers aren't usually handed to them on a plate. They are encouraged to think and formulate an answer for themselves.

Sometimes a more accurate answer means seeing a bigger picture than is available from a single lesson. Sometimes it means recognizing that life isn't always about things that are black and white, but that often shades of gray are involved.

In the case of Job, I think there are several reasons why God allowed this to happen. First of all, it was an opportunity to pull back the curtain a little, to give humans a glimpse of what was really going on, above and beyond their ordinary everyday lives. It drew attention to the existence of Satan (which means "adversary" or "one who opposes"), which humans would have been unaware of without this divinely revealed information.

Second, by allowing Satan to test Job, God was exposing Satan as the adversary not only of God but also of humans. After all, it wasn't God who wanted to bring calamity on Job, but Satan. This may be another reason why humans experience suffering.

Third, Satan's challenge was admittedly a valid one, which is why God allowed it to be answered. Maybe Job was only blameless because God was, in effect, protecting him. What would he be like if this protection was withdrawn? Maybe Job only blessed God during the good times. What would he be like during bad times? Would he curse God?

The bottom line is, while he did well to begin with, as his suffering went on, Job ended up saying things about God that weren't true, which is perhaps why God literally stormed into the debate at the end, to defend himself against Job's accusation that justice from the heavens was being denied, and that the heavens must be wrong in this instance.

God provided justice by giving to Job double what he had lost. And although some of his family members died, death can be reversed by means of a resurrection. In other words, any loss on Job's part was only temporary. In this, Job shared in the same suffering and loss that all humans experience for the present.

A fourth reason for allowing Job's suffering, or at least a side benefit from it, is that it would have allowed Job, who was a wealthy and privileged person, to feel more empathy toward people who were suffering, having experienced it himself. And although we don't know whether Job was ever told of the circumstances behind his suffering, his encounter with God allowed him to grow in appreciation, understanding and wisdom.

Fifth, the book of Job highlights how human reasoning can go astray without insight. In this sense, Job's temporary suffering was humanity's gain. We get to see how, if we start with faulty assumptions or if we're missing a bigger picture, we can draw false conclusions. We can see the flaws in the reasoning of Job and his friends based on their limited understanding, which helps us to move from the child to the student stage of development.

Finally, Job's story foreshadowed that of Jesus Christ, who also suffered in a similar way. Just like Job, Jesus was a righteous man who seemed to have been plagued and struck by God. Just like Job, it could be said of Jesus that there was "no one like him in the earth, a man flawless and upright, fearing God and withdrawing from bad." Jesus was also tested by Satan, just like Job was, although Jesus was aware of the test, while Job was not.

The story of Jesus set the stage for humanity to enter its "adulthood" phase, in terms of maturity and wisdom. Jesus showed us how to have an adult relationship with God. He invited us to see God not just as a cosmic Lawmaker, but as a loving and caring Father.

Adults aren't motivated only by rewards and punishments, but also by higher principles and values, and Jesus taught that the highest principle was love. He even laid down his life on our behalf, to put that principle into action.

Now, someone might object to this idea of adulthood, and say: didn't Jesus teach his followers to become like children? This is true, but every statement we make has a frame of reference, and the same is true of what Jesus said. The apostle Paul explained this best, when he wrote: "Brothers, do not become children in your disposition, but be young children to what is bad, yet become mature in your disposition."⁷

Curiously, the word here translated "disposition" is only used once in the New Testament, and is often translated as "understanding." Whatever the word means, the apostle didn't take Jesus' words to be a blanket statement. Paul applied it in reference to badness, while encouraging his readers to become like adults in terms of their attitude or perception. This is a useful way in which we can evaluate statements made in the Bible, or indeed anywhere else – by asking, what is the frame of reference here?

In any case, the development from childhood to student to adulthood is, in my opinion, the real story of the Bible. It is the story of the growth to maturity of the human race.

God allowed humans to go their own way for a while, to experience good and bad for themselves, and thus to go from childhood to student, and then to adulthood. At the same time, God has made his presence felt in the world, first through the nation of Israel, to demonstrate his power and authority, and then through Jesus Christ and his apostles, to demonstrate his love and desire for reconciliation with all people.

Remarkably, God has ensured that both Israel and Christians would continue to exist somewhat independently down through the centuries, to provide not just one but two witnesses testifying about God, in their own distinctive ways.

Now, while God has encouraged humanity as a whole to grow to maturity, I believe he is also keenly interested in the growth of each individual person. But I am referring here to a different type of growth than physical growth. In a sense, it involves growing in wisdom and understanding, and in truly knowing God.

I think four things have to happen for this growth to take place. The first is an awareness that God is real. Hopefully, this book has helped you become aware that God exists after all. It has also raised your awareness of the many assumptions humans bring to the table when they reason about God.

The second thing is a recognition of God's true nature. When I say this, I don't mean what God is made of, or how old he is, or how many persons make up God. I have already given my opinion on these matters, and I will leave any further discussion of them for theologians to split hairs over. I mean the fact that he is actually interested in us and has our welfare in mind. This is God's true nature.

For example, even when God seems to have acted harshly in the past, it was for the long-term benefit of humans. After all, who of us today wants to live in a city that tolerates gang rape, as Sodom did, or with neighbors who sacrifice their children to Molech? The reason we don't live in such a world is because God dealt harshly with those people in the past.

This recognition of God's true nature also helps us to see that he has given us more than we may have realized. He has given us life itself, along with a breathtakingly beautiful planet, and the senses and sensations in which to enjoy it.

Contrary to popular opinion, God is not opposed to pleasure. Instead, this is how we were designed – from the simple pleasures derived from a smile and laughter, or from eating a delicious meal, to the ecstasy of an orgasm. These are gifts from God to the human race. He simply asks us to enjoy these things in a balanced way, without harming ourselves or others in the process. Too often our pursuit of pleasure can become an obsession which first consumes and then ruins us, or causes physical, psychological or emotional harm to others; and this is what concerns God.

He also inspired humans to write letters and books that were later collected together into what we now call the Bible, which can help us acquire knowledge and wisdom. As we learn to put aside our skepticism, we come to see that the human authors of those books and letters weren't liars, deceivers or fools, but were simply telling the truth. This includes the gospel writers. They weren't involved in an elaborate conspiracy to fool you into believing a false story. They weren't deluded, deceived or exaggerating. They were simply telling the truth. They witnessed Jesus' resurrection, and reported it honestly.

I think the third thing necessary for growth, and which I hope to have given you by means of this book, is that of appreciation. God has gone beyond what was necessary, and provided humans with even more proof of his existence, by outlining particle and quantum physics, DNA and ribosomes, and the structure of the eukaryotic cell, thousands of years before humans would discover the physical reality of these things. God encoded them within ancient scripture and in the life of his servants of old, and then patiently waited thousands of years to reveal these things to us. I believe this demonstrates, in a striking way, the real wisdom and patience of God.

Incidentally, I only started to discover these things in the Bible a month or two after I made the decision to write this Letter To The Atheists in early 2018. I had no

idea they were there before. This is how I am convinced God has also gone out of his way to give atheists the extraordinary evidence they demand, because after allowing me to find them, he revealed them first, not to Jews or Christians, but to atheists! To me, this shows he cares even for those who deny his existence. Or, perhaps I should say hopefully, for those who formerly denied his existence. Once we put away our skeptical attitude towards God, we can then begin to take a leap of faith and trust, and begin to grow into true adulthood.

I think the fourth thing necessary for growth is the concept of reconciliation – that is, making up with God. Humans alienated themselves from him for a time, but God’s will, desire and passion is to reconcile all things back to himself, to bring them back into his family as it were.

Indeed, this was one of the primary purposes of sending Jesus Christ. The apostle Paul describes God as “the one reconciling us to himself through Christ, and giving us the ministry of reconciliation – namely that God was, in Christ, reconciling the world to himself, not reckoning their sins to them; and he put the word of reconciliation in us.”⁸

In other words, the ministry of Christ and his disciples was really a ministry about reconciliation with God. Christ is the means by which we make up with God, and begin to have a real relationship with him. God takes the initiative, by blotting out our sins through Christ and giving us a clean slate, a fresh start. This is why he is not only “Son of God” but also “son of man.”

Once we have an awareness that God is real, and we recognize God’s true nature, that he is actually on our side, and when we gain an appreciation of what God has already given us and done for us, I think this leads naturally to a desire for reconciliation with God, just as he desires to reconcile with us.

But how can we reconcile ourselves to God? I think there are a few steps, and in my opinion, none of them are burdensome, if we acknowledge that we are all still works in progress from God’s point of view.

The first step is to get to know God better, which you have already done to a certain extent. In fact, simply by reading this book, I think you now have more knowledge about God than a lot of the people on Earth. However, this book isn’t a substitute for the Bible, the primary source of knowledge about God.

Although reading the Bible from beginning to end at some point is a good idea, it may help to start with the gospels, because God reveals his nature through Christ. As Jesus said: “The one who has seen me has seen the Father.”⁹

Some things may be difficult to understand at first, without a better understanding of the context, the frame of reference, the intent, and the bigger picture; so let me throw you in at the deep end as it were, so everything else will be much easier by comparison. Let’s look at two of Jesus’ most difficult statements. If we know how to tackle these, any other issues become much easier to resolve.

Just as the fledgling nation of Israel was fed manna in the wilderness after coming out of Egypt, Jesus compared himself to bread that came down from heaven.

He then said to his audience: “Most truly I say to you, unless you eat the flesh of the Son of man, and you drink his blood, you have no life in yourselves.” ¹⁰

His disciples were shocked at hearing this, and many of them departed from him. Those who were stumbled stayed as children in their level of understanding. They were reasoning in black and white, and their only frame of reference for evaluating Jesus’ words was the Law given through Moses.

They knew drinking blood was against God’s law, and yet here was Jesus advocating drinking his blood, so Jesus couldn’t possibly be from God. After all, what man of God would tell them to drink blood?

Like Job’s friends who reasoned that Job must have been wicked or arrogant, their logic was impeccable. They were also like modern-day skeptics who point out statements in the Bible that seem to contradict other statements, and declare that those contradictions mean the Bible can’t be from God.

Jesus could have explained what he meant, but he chose not to at the time. I think Jesus said things like this to filter out those who weren’t prepared to find out what he was really saying.

Nevertheless, the apostles stayed with him, although none of them acted on Jesus’ words there and then. As far as we know, none of them started gnawing at Jesus’ arm. At the time, they probably didn’t understand what he meant, but they had enough faith in him to believe they would learn more if they stuck around.

Their understanding came later on, the night before Jesus’ execution, when they were eating the Passover meal together, and Jesus revealed to them that the unleavened bread they were eating and the wine they were drinking were his body and blood. This is how they were to eat his flesh and drink his blood – through the bread and wine. Fortunately for them, they didn’t have to munch on Jesus’ arm.

This is why we need to think about the intent of the speaker, the context and frame of reference for the words we read, as well as aim to understand the bigger picture, which comes as we gradually acquire more knowledge, understanding and wisdom.

Let’s look at one more example. Jesus said to the crowd: “If anyone comes to me and does not hate his father and mother and wife and children and brothers and sisters, yes, and even his own soul, he cannot be my disciple.” ¹¹

Now, I don’t know of any Christian who takes this literally. Perhaps they should, but I think this is another example of where Jesus is saying something to provoke the crowds into thinking more deeply about his words, and into using wisdom and discernment rather than simplistic black and white thinking.

For a start, I doubt Jesus was contradicting one of the Ten Commandments, which said to honor your father and mother. And what is the point of marriage if you are to hate your spouse? And how can a mother hate her own child?

This is where we need wisdom and discernment. An understanding of the bigger picture can also help. This is, after all, the same man who said that we should love our neighbors as ourselves, even though they may be strangers!

Elsewhere, in reference to the effect his teaching would have, Jesus said: "A man's enemies will be those of his own household. The one loving father or mother more than me is not worthy of me, and the one loving son or daughter more than me is not worthy of me." ¹²

I think this statement helps to clarify his other one, as well as to think about the bigger picture. Jesus' new disciples were living in a culture where family was everything, and the offspring were expected to obey the customs and traditions of their forefathers. In many ways, tradition had become even more important than God's law, or rather, it had become one and the same in the minds of many of the people in Jesus' day.

Jesus' disciples were about to break free of those traditions, which would result in severe opposition, disassociation from family members, expulsion from the synagogue, the very center of the community, and perhaps even death. In a sense, they were going to find themselves expelled from society itself.

In the face of such intense social pressure, the question every disciple of Jesus had to ask themselves is: who would they love more – their family, or Jesus? In other words, we need to consider not just the immediate context of the words, but also the social context.

Another incident sheds light on Jesus' real intent. When someone told him that his mother and brothers were outside looking to speak to him, he said: "Who is my mother, and who are my brothers?" And stretching out his hand over his disciples, he said: "Look! My mother and my brothers. For whoever does the will of my Father who is in the heavens, he is my brother and sister and mother." ¹³

In other words, when Jesus told his disciples to "hate" their own family members and even their own souls, I think he was speaking both in a relative sense, and also in a way that emphasized physical connections as being far less important than spiritual ones. Jesus didn't hate his own mother, he loved her. But during his ministry he treated her more like a disciple than a mother.

I also suspect Jesus used the word "hate" to help his disciples break free from the intense social pressure they would face, just as an alcoholic might need to "hate" alcohol in order to break free from their addiction, while people who are not addicted can take a more balanced approach to alcohol. In a sense, the people of Jesus' day were addicted to their traditions.

Furthermore, if a person truly hated their own soul, they could become suicidal, which I don't think was Jesus' intent at all. By telling them they needed to hate even their own souls, I think he meant in the sense of not seeing their own life as important in relation to the far more important mission they had been given, in the age they were living in. If they loved their own souls, they wouldn't be willing to die for Jesus, which was probably the fate of some of his early disciples.

This is why he often spoke in parables. His real disciples needed to stick around to discern a deeper meaning. Therefore, when he said to "hate" your father, mother, children, partner and even your own soul, I personally conclude that his intent was to

make it clear that, in the Jewish system in which they lived, what should be important to his disciples wasn't physical ties, but spiritual ones, and completing the mission given to them, which would take them across the country and later the world. In addition, they were about to be severed from a very strong tradition, which would be emotionally difficult. Jesus was, in essence, toughening them up for it in advance.

However, I can only conclude this by thinking deeply about Jesus' words, and because I am already familiar with the Bible. Of course, I could be wrong. Jesus really might have been telling us to hate our mothers! But as far as I know, none of the early Christians took him literally in this matter, because they knew the character of Jesus, and so they discerned that his purpose and intent here was more subtle.

Incidentally, I think Jesus' way of speaking also provides evidence that he was real. Who would make up a character that would say such things? His speech wasn't acceptable to the Jewish leaders of his day, and many Christians don't take some of these statements literally anyway, so who would even make these things up?

Fortunately, most of what Jesus said is much easier to understand. I have picked two of his most difficult statements, to give you an indication of how I tackle them, which means understanding intent, frame of reference, motive, context and the bigger picture. Whenever there is something you don't understand, considering these things is usually helpful.

As you start to read the Bible with wisdom and discernment, I think the next step to reconciling with God is to learn to communicate with him. After all, he is called "the one hearing prayer."¹⁴

If you have never prayed before, this may feel a little awkward or difficult. The disciples asked Jesus to teach them how to pray, and he gave them what is now often referred to as "the Lord's prayer." It can be found in chapter six of the gospel of Matthew. Some people recite it like a mantra, but I think it was intended to be more of a model or outline. After all, Jesus also said not to say the same things in prayer over and over again.¹⁵

If we view it as a basic model for how we can pray, we see that first of all we acknowledge God for who he is: our Father in heaven. Then we pray for his will first, which can include his name being made holy and his kingdom to come. Then we focus on our needs, and also ask for forgiveness of our sins. We can also ask to be kept from temptation and delivered from the wicked one. Many Christians say their prayer in or through Jesus Christ, and most tend to end it with "Amen" which means "so be it."

Now, forgiveness is an important part of the process of growth. It is the third step in reconciling with God. We need to forgive others in order to receive forgiveness for ourselves, and it is also part of the process of our own repair.

I admit, forgiving people who have hurt us can be hard. The normal and arguably even natural human response to people who hurt or wrong us is to want revenge. At the very minimum, we want justice.

Certainly, there is nothing wrong with seeking justice, especially when a crime is involved. In fact, part of the role of governments and authorities is to administer

justice, and to inflict punishment for crimes. As the apostle Paul said: "It is God's servant to you for the good. But if you are doing what is bad, be in fear, for it is not for nothing that it bears the sword; for it is a servant of God, an avenger of wrath to the one practicing what is bad." ¹⁶

In other words, if you have been hurt or abused in a way that constitutes a criminal act, the appropriate response is to report it to the relevant authorities, because ensuring justice and punishing badness is the role given to them by God.

However, when we suffer injustice or hurt from others, this can also lead to anger and resentment that can eat away at us, damaging our mind, body and heart. We could become consumed by a desire for vengeance. I think the apostle Paul also does an excellent job of summing up the concept of forgiveness and peacefulness that we are all encouraged to cultivate:

"Do not render to anyone evil for evil. Provide good things in the sight of all men. If possible, as far as it depends on you, be peaceable with all men. Do not avenge yourselves, beloved, but leave room for the wrath; for it is written: 'Vengeance is mine. I will repay,' says the Lord. Therefore, 'if your enemy is hungry, feed him. If he is thirsty, give him a drink. For by doing this you will heap coals of fire on his head.' Do not be conquered by the bad, but conquer the bad with the good." ¹⁷

This is why Jesus encourages us to forgive, to turn the other cheek, and even to pray for our enemies. These are difficult things to do, but they break the cycle of revenge and retaliation. They can sear the other person's conscience. They inspire us to take a kinder, gentler and more merciful approach to others. They allow room for the other person to come to regret their actions, or if not, perhaps to experience the wrath of God, through the authorities or by some other means.

I also think of forgiveness as "letting go" – that is, letting go of anger, resentment and the desire to retaliate. This can be hard, because sometimes we like to identify with our wounds, and they can even define us. But only when we let go of those wounds, and their power over us, can we begin to truly heal.

However, even if we can forgive others, often the hardest person to forgive is ourselves. But forgiveness needs to also extend to ourselves. If we have done bad things, we may find it hard to believe that God can forgive us; but God's ways are higher than our ways. God forgives in a large way. He is vastly more forgiving than humans are.

At the same time, forgiveness doesn't necessarily shield us from the consequences of our actions. For example, King David committed adultery with Bathsheba who was married to Uriah, a soldier in Israel's army. In time, she became pregnant. David sent for Uriah and asked how the war was going, and invited Uriah to go back home, hoping that Uriah would sleep with his own wife so that David's actions would be concealed. However, Uriah slept outside the king's house, because he didn't want to return home while there was a war on.

Therefore David got him drunk, but Uriah still wouldn't return home. Finally, the king ordered the army commander to put Uriah on the front lines of the battle, and to

retreat behind him, so he would be struck down and die. After Uriah died, King David took Bathsheba as his wife.

What David had done was bad in God's eyes, so God sent the prophet Nathan to make it clear to the king what he had done. Not only had he stolen Uriah's wife, in effect he had committed murder, by plotting to ensure Uriah would be killed. Under the Law covenant, the king was liable to death.

David admitted, "I have sinned against YHWH." Nathan replied: "YHWH has therefore let your sin pass. You will not die; except that you have certainly given the enemies of YHWH a cause for contempt in this matter. Therefore your son born to you will certainly die." ¹⁸

The king was forgiven, but he still had to pay a heavy price, because he had caused an innocent man to be killed. If God had simply let David off without consequences, God's enemies would have said, where is justice for Uriah?

Of course, skeptics could still say, what about David's son? What did he do wrong? The answer is: nothing. However, his death was a stark reminder to the king that actions still have consequences. God is willing to forgive in a large way, but sometimes a person needs to pay a penalty or experience the consequences of their actions, just as a criminal can be forgiven by God but may still need to go to prison or make amends, to satisfy human justice and also to pay a meaningful price for what they have done.

Incidentally, in the case of the son of David, the boy can be resurrected by God, so he was not lost forever; and I think God also used the incident as an analogy for Jesus, the true Son of David, who was also innocent and yet died for our sins. He paid the ultimate price of his life, so our sins could be blotted out.

Another step toward reconciling with God is what Christians have traditionally called "confession" and "repentance," which involves admitting to what we have done and seeking to change; although in reality I think these are also processes, rather than just a single event or moment in time.

When we didn't know God, we didn't know we were sinners. Indeed, atheists and many skeptics reject the notion of sin altogether, because it requires a divine benchmark for defining wrongdoing, but human laws and notions of good and bad constantly change over time and in different cultures.

As we come to know God, we come to realize that we fall short of God's standards in many ways, which is basically what sin is. In this sense, we are all sinners. We all fall short of the glory of God. Therefore, we are all works in progress. Nevertheless, we are encouraged to move closer to God's benchmark. The big question is: How can we do this, as the flawed human beings we are?

I think there are three critical insights we need, before we can truly make any lasting changes. The first insight can be found in what Jesus said to the Pharisees, who asked him why his disciples weren't following the traditions of their forefathers, such as washing hands when about to eat a meal.

Jesus said that whatever enters a person's body doesn't defile a person, "but the things going out of the mouth come out of the heart, and those things defile the person. For out of the heart come wicked reasoning, murders, adulteries, sexual immorality, thefts, false witnesses, blasphemies. These are the things defiling the person. But to eat a meal with unwashed hands does not defile the person." ¹⁹

The Pharisees were so busy following religious rules involving washing, they forgot to wash their hearts, the real source of their sins. The heart represents our desires, passions and what we love. It is, metaphorically, the source of our emotions. The problem is, as flawed human beings, we fall in love with things that corrupt us. We are also inclined to badness, which is our real problem.

This is why commands are an inferior substitute for the laws written in a person's heart. The ancient nation of Israel had divine laws against most of the things Jesus listed above, but this didn't stop them doing such things. God's law was in their mind and on their lips, but it wasn't in their heart.

One of the purposes of Christ was to show Israel how to put the law into their heart. When we learn to love God and love our fellow human beings, our heart naturally becomes less inclined to badness. The first insight, then, is to realize that our sins and inclinations tend to stem from the desires of our heart, which by itself is often inclined to doing bad, until we begin to change our heart as it were.

The second insight is to realize that Jesus' teachings aren't just a set of dry religious commands, with rewards for obedience and punishments for disobedience. Instead, he was teaching us the way to truly live. For example, take the Sermon on the Mount, which can be found in chapters six to eight of the gospel of Matthew. If I had to sum up the key principles Jesus taught in it, it would go something like this:

Be merciful, peaceable, pure in heart. Be trustworthy. Don't return evil for evil. Love even your enemies. Don't do things for show, or be hypocritical. Pray with sincerity and from the heart, not with repetitive words and phrases. Forgive others, so that God forgives you. Don't be materialistic. At the end of the day, it's all just stuff. Instead, store up treasures in heaven. Don't be anxious about your needs. When you seek God's kingdom first and his righteousness, the things you need will be added to you. Stop judging. Deal with your own shortcomings first, and then you can better address the faults of others. Treat others as you want to be treated yourself.

This isn't merely a religious blueprint or a set of commands for Christians. Jesus was teaching everybody how to live a healthy life now. It was, in effect, a blueprint for life. He ended his sermon by comparing those who heard and did these things to a wise man who built his house upon the rock. The rain, wind and flood came upon that house but it didn't fall because it had been founded on the rock. Those who heard but didn't do them were likened to a foolish man who built his house on the sand. The rain, wind and flood came upon that house and it fell, and its collapse was great.

When we go against the way God intended for us to live, we often experience ruin. We hurt ourselves and others. When we realize that Jesus' teachings aren't simply religious commands but are the way to a happy and fulfilling life, this can

provide us with the motivation for change. Jesus shows us how to build our house on the rock, rather than on the sand.

For example, for those looking for the ideal partner, Jesus teaches us to work on first becoming the ideal partner – loving, forgiving, honest, kind, self-aware, treating others how we want to be treated. For those looking for happiness, Jesus teaches that happiness doesn't come from owning more stuff, but from trusting God, and being at peace with God, with ourselves, and with others as far as possible.

The third insight that helps to facilitate change is to realize that most sins are better thought of as injuries we inflict on ourselves or others, causing unjust hurt and damage.

For example, "you must not commit adultery" is one of the Ten Commandments. Now, we could say it's a sin simply because God says so, and leave it there. But God wants us to truly understand why he considers it bad. For example, through the prophet Malachi, he explained it was a source of emotional pain, a betrayal of one's partner, and a source of domestic violence.²⁰ In other words, adultery was wrong not just because God said so, but because of the unjust hurt and damage it caused.

The desire to please God can be a powerful motivation for change, but since most sins are damaging to ourselves or others, the real motivation for change often comes when we desire to stop causing unjust hurt and damage.

Sometimes change can't happen until we resolve deeper personal issues. This requires us to be honest with ourselves, and to recognize we have those issues in the first place. To give you an analogy, a man might ask God: "Lord, send me the ideal woman!" But the man is emotionally guarded, hot-tempered, and blames others for his shortcomings, which means it's always other people's fault that he's the way he is.

I suppose God could send him a woman who can deal with his emotional distance, someone who is willing to put up with his outbursts and who doesn't mind being blamed for his failings. But even then, it's likely the man won't see her as ideal, or she will eventually leave him, and then he blames God for clearly sending him the wrong woman. In reality, the man was simply not ready to receive what he wanted. Metaphorically, he needed to "cleanse first the inside of the cup and of the dish, so that the outside of it may also become clean."²¹

This helps to explain why people don't always get what they want from God the moment they ask for it. They may need to go through a process of growth or emotional healing before they can receive it; or the growth process itself may be the answer to their prayers. It may not seem to be as miraculous, but cleansing the inside is necessary before the outside can be cleansed, and the process may be much more valuable to the person than an instant miracle.

Of course, people prefer instant healing or instant justice, but God's way is often more instructional, putting people on the path of deeper inner changes to resolve the root of their problems. This is precisely what he has done with the human

race for thousands of years. He has allowed them to work through their issues with him in a process of growth.

This doesn't mean we can't get assistance when we need it. For example, when we pray, we can ask for the Holy Spirit to help us and reveal our shortcomings to us. Jesus describes the Holy Spirit as "the spirit of the truth" as well as a helper and comforter.²²

We may also need to get outside help for some of our issues, from those who are qualified to deal with them, and particularly from those who understand them at a spiritual level. In a sense, God has appointed every human being to be a minister to others, at least in some capacity. This is why the apostle Peter wrote to his fellow Christians: "Above all, have sincere love among yourselves, for love covers a multitude of sins. Be hospitable to one another without murmuring. To the extent each one has received a gift, administer it as good stewards of the variously expressed grace of God." ²³

I am not necessarily talking about official ministering positions here. In a sense, every husband is a minister to his wife, and every wife is a minister to her husband. Friends minister to one another, and some people have been trained to minister on certain subjects and matters. These can also be seen as gifts from God, and ways in which he helps people to change.

I suppose this leads naturally to the question of whether you should join something or not. I didn't write this book to promote any church, denomination or organization. My aim has simply been to provide evidence that YHWH exists, and that Jesus Christ is God's Son, as he and his disciples claimed.

I am not trying to get you to join anything. But neither do I wish to hinder you from doing so if you desire. When you accept Christ as Lord in your heart, you come to belong to something called the "body of Christ." ²⁴ Jesus also said, "where two or three are gathered together in my name, there I am in their midst." ²⁵ In other words, the "church" of Christ is the body of believers, not a building. However, it is often through his people, the "body of Christ," that God administers help.

If you do join a church or organization, you will be expected to accept their distinctive views, doctrines and interpretations of scripture, and follow their rules. I will not give my opinion on any specific group. However, I will give my general opinion.

I think there are merits in many Christian organizations. Some have ancient and venerable traditions, and are focused on helping the poor and needy, which is part of what it means to be a Christian.

Some are younger, fresher and are determined that they have the exclusive truth, which is the source of their zeal, and are highly focused on evangelizing. This is good, because Jesus encourages us to invite others to him.

Some are focused on singing and expressing themselves through the Holy Spirit. Others are focused on deep knowledge and understanding. This is important, especially in these times of skepticism.

All I can say in this regard is: does not God love variety? Look at the endless variety we see in nature, in species and even in the colors and shades within species. Do not all humans differ? Do not cultures and dress codes differ? And there are different body parts, but they are all one body. If all Christians were focused on singing and dancing, who would ever have time to sit down and write a “letter” to atheists, with all the complex and occasionally tedious detail it would involve?

I believe there is only one true way to a close relationship with God, and that is through Jesus Christ; but God has given us the freedom to express this in various ways, which has resulted in the variety of churches and organizations we see today, just as God has created almost endless varieties and species.

Besides, life is a continual journey. A train passes through many stations along the way. As we grow in understanding, wisdom and maturity, we may outgrow one form of expression, just as a child outgrows its clothes many times on the journey to maturity.

I suppose my point here is, you are free to join or not to join an organization or church, because when you believe, you already come to belong to “the body of Christ.” Just keep in mind that the New Testament was written with fellowship of believers in mind, and it is through other believers that Christians can minister to one another.

However, an important step in reconciling ourselves to God is baptism. This was part of the Great Commission that Jesus gave to his disciples: “Go, therefore, and make disciples of all the nations, baptizing them in the name of the Father and of the Son and of the Holy Spirit.”²⁶ Baptism is an outward symbol of repentance for forgiveness of sins. It is “an appeal to God for a good conscience, through the resurrection of Jesus Christ.”²⁷

In the end, we are all encouraged to grow to maturity. For example, Jesus gave a parable of a man who went out to sow.²⁸ Some seeds fell alongside the road, and the birds ate them up. Some fell on the rocks where there wasn’t much soil. The seeds sprang up but then withered because they had no root. Others fell among the thorns, and the thorns choked them. Others fell on fine soil, and they began to produce fruit.

At first glance, this seems to be about how people respond to Jesus’ message. For some, it falls on deaf ears. Some hear the word and accept it with joy, but they have no root in themselves, so are stumbled in a time of tribulation or persecution. Some are metaphorically choked by anxieties and the deceptive power of riches. The one sown on the fine soil is the one hearing the word and getting the sense of it, and bearing fruit.

However, the parable also has a deeper function, in that it serves as a continual reminder. It is possible for Christians to experience any of these scenarios throughout their life. For example, they may produce fruit, and then later become distracted by anxieties. Jesus’ parable serves as a gentle reminder throughout their life. If they find themselves distracted, this parable may come to mind, and can have the effect of putting them back on the right track.

Jesus talks about having a root in oneself.²⁹ Roots give a plant its nourishment and allow it to truly grow. The things I have talked about in this chapter, and really the whole of this letter, are provided to help you develop a root in yourself, so that you can grow to maturity.

One more thing is also asked of us, and that is to share our knowledge with others. This is because God makes the following invitation to all:

“Hey, all you thirsty ones. Come to the waters! He who has no money, come, buy and eat! Come and buy wine and milk, without money and without cost. Why are you spending money for what is not bread, and your labor for what brings no satisfaction? Listen intently to me, and eat what is good, and your soul will find great delight in fatness. Incline your ear, and come to me. Listen, and your soul will live, and I will make with you an everlasting covenant.”³⁰

And again: “Let the one hearing say ‘Come!’ And let the one thirsting come. And let the one who wishes take the water of life for free.”³¹ This is so that, as the prophet Isaiah foretold, “the earth will be full of the knowledge of YHWH, as the waters cover the sea.”³²

This is what we would expect, from the only living and true God. I have even made this easy for you. If this book has been of use to you, then you are welcome to share the PDF version with others for free. “You received freely, give freely.”³³

1 1 Peter 3:15. **2** Charles Darwin, *On The Origin Of The Species*, First Edition, 1859, p490. **3** Revelation 21:1. **4** Revelation 21:3,4. **5** Revelation 21:5. **6** Job 1:8. **7** 1 Corinthians 14:20. **8** 2 Corinthians 5:18,19. **9** John 14:9. **10** John 6:53. **11** Luke 14:26. **12** Matthew 10:36,37. **13** Matthew 12:46-50. **14** Psalm 65:2. **15** Matthew 6:7. **16** Romans 13:4. **17** Romans 12:17-21. **18** 2 Samuel 12:13,14. **19** Matthew 15:18-20. **20** Malachi 2:13-16. **21** Matthew 23:26. **22** John 16:7,13. **23** 1 Peter 4:8-10. **24** Ephesians 4:12. **25** Matthew 18:20. **26** Matthew 28:19. **27** 1 Peter 3:21. **28** Matthew 13:1-9,18-23. **29** Matthew 13:21. **30** Isaiah 55:1-3. **31** Revelation 22:17. **32** Isaiah 11:9. **33** Matthew 10:8.

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