Introduction to the Mathematics of Evolution

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Chapter 1

Why the Theory of Evolution Exists

> *"In the preface to the proceedings of the [Wistar] symposium, Dr. Kaplan commented about the importance of mathematics in such matters as theorizing about origins [of life]. He said that to construct a history of thought without profound study of the mathematical ideas of successive efforts is comparable to omitting the part of Ophelia from Shakespeare's play, Hamlet"*
> Darwin's Enigma, Luther D. Sunderland, Revised Edition, Chapter 6

Introduction

Many times students hear that the theory of evolution is a "proven fact of science."

The reality is that the theory of evolution is ***NOT*** a proven fact of science.

For example, the theory of evolution requires that life be created from simple chemicals. It requires the conversion of “life from non-life.”

Such a conversion has never been demonstrated and such a conversion has never been proven to be possible. For example, the complex chemical binding of many amino acids, necessary to create proteins, has never been demonstrated to be possible outside of cells.

Even the simplest life on earth, which does not require a host, is far too complex to form by a series of accidents. Therefore the theory of evolution requires that the first “life” was a form of life which does not exist on this earth any more. Thus, according to the theory of evolution, the “first living cell,” meaning the first living cell on this planet, is a species which no longer exists on this earth.

The theory of evolution also requires massive amounts of new genetic information form by totally random mutations of DNA. For example, the “first living cell” would have had a very simple and very short DNA strand. However, human DNA would be much, much longer and far, far more complex. In other words, human DNA has millions of times more complex genetic information than the “first living cell” would have had according to the theory of evolution.

New genetic information, including at least one new gene, has *never been observed* in nature, nor has new genetic information, created by random mutations of DNA, ever been accomplished in a science lab.

When discussing the probability of the theory of evolution, things get really absurd for the theory of evolution. The Wistar symposium, mentioned in the quote at the top of this chapter, which *shredded the theory of evolution by mathematical analysis*, should have dispensed with the theory of evolution over 40 years ago (several world-famous evolutionists were at that symposium), but of course that did not happen.

No fully functional computer program on earth has been improved upon by randomly changing and adding “bits” of information. Likewise, no fully functional DNA strand has been improved upon by randomly changing and adding nucleotides.

The truth is that any honest geneticist will tell you that the DNA of almost all plants and animals is deteriorating (this is called “genetic entropy”). “Point mutations,” meaning a mutation of a single nucleotide, are overwhelmingly negative. But even when point mutations yield a positive result, it is generally an environmental coincidence caused by a *loss* of genetic information.

Even though scientists have tried billions of times to create new genetic information in DNA by random mutations, they have never created any new genetic information by mutating existing DNA.

Thus, why would the scientific establishment claim that the theory of evolution is a proven fact of science; when in fact every shred of actual scientific evidence is overwhelmingly against the theory of evolution?

It is important for the reader to understand *why* the scientific establishment makes such a brash, but absurd, claim that the theory of evolution is a proven fact of science and why they stand behind a theory which is known to be scientifically false. That is what this chapter is about.

Before getting into the heart of the issue, it is necessary to distinguish between a "scientist" and "science."

A "scientist" is a person who has studied the field of science. Many scientists believe in God and do not believe in evolution. On the other hand, many scientists believe in the theory of evolution and do not believe in God.

While an "evolutionist" is not necessarily an "atheist," the fact is that by looking at all the concepts claimed in the theory of evolution (e.g. that humans are descended from other primates), the only logical conclusion of someone who strongly believes in the theory of evolution would be that there is no God.

Science

Now let us talk about the term "science." The term "science" means the "scientific establishment." Organizations like the National Academy of Sciences, and magazines such as National Geographic and Scientific American, make up the "scientific establishment."

Thus, the term "scientist" cannot be generalized, because many scientists are creation scientists and many scientists are evolutionists.

However, the term "science" can be generalized because the term “science” always involves organizations which have a *total and absolute support* for the theory of evolution. All member organizations of the "scientific establishment" are strong supporters of the theory of evolution.

Thus, let us examine in this chapter why the theory of evolution still exists and why it is still supported by “science.”

UCTV

During a series of television shows on evolution, UCTV (i.e. University of California Television) allowed both evolutionists and creation scientists to speak. UCTV is to be *very strongly applauded* for allowing creation scientists (i.e. creationists) to represent their own views in the mass media. This is very rare since normally only evolutionists are allowed to speak on television.

Because UCTV allowed actual creation scientists to speak, a great deal of concepts *which are hidden from the public* were revealed. For example, during this series, a well-known professor of law, who is also a creation scientist, Phillip E. Johnson (author of several books, including Darwin on Trial), stated:

> *"Science is committed to philosophical naturalism and therefore science must assume that no Creator, and no purposeful intelligence, is behind our existence ... All that science can address is the question of: 'granted that we are here as a result of purposeless material mechanisms, what's the most plausible purposeless material mechanism that we can imagine?'"*
> Phillip E. Johnson, author, attorney; quoted on UCTV

Read that quote three or four times very carefully, because it is a superb summary of modern "science."

Here we see a clear reference to the term "science" as representing the "scientific establishment," because many individual scientists are creation scientists. Thus, Mr. Johnson is referring to the scientific establishment.

His comments are the kind of comments a person would *never hear* from the scientific establishment.

"Naturalism" (Mr. Johnson actually refers to "philosophical naturalism") is essentially a way of describing how events happen by "natural" means.

Mr. Johnson uses the phrase "science is *committed* to philosophical naturalism." "Philosophical naturalism" is technically not the same thing as atheism, what it technically means is "*by natural events, meaning without supernatural events, meaning without God*." In other words, science is committed to explaining nature, including the

Universe, without any consideration of supernatural events, which can only mean science does not consider the existence of God.

To put it another way, what he is saying is that the scientific establishment (i.e. "science") does not allow itself to consider that there might be a God who is a factor in the creation of anything. They are "committed" to "natural" explanations, meaning *no supernatural explanations, which would imply no mention of God,* are allowed.

The significance of this is that the scientific establishment attempts to describe the existence of human DNA, and the DNA of all other species, by purely "naturalistic" mechanisms (or as he called them: "purposeless material mechanism"). This means, by definition, "without God."

Since all of the major events of the theory of evolution happened before modern society, saying "without God" means "by total accident." In other words, their goal is to explain the Universe, human DNA, the DNA of millions of other species, etc., all by totally accidental (i.e. natural) means.

Most people assume that science has carefully considered whether human DNA was designed and built by God or whether it was not designed at all. According to Mr. Johnson "science" is *only considering natural events* (i.e. random events) and does not consider any supernatural events provided by God.

As professor Johnson said: "All that science can address is the question of: 'granted that we are here as a result of purposeless material mechanisms, what's the most plausible purposeless material mechanism that we can imagine?'"

Because science excludes the possibility of God having an effect on creation, and thus they do not allow themselves to consider the possibility of God, the theory of evolution is their "best guess" (i.e. "most plausible purposeless material mechanism") as to how human DNA, and the DNA of millions of other species, came to be.

The important point is that the general public *assumes that the scientific establishment is in search of absolute truth and thus has carefully considered every possible explanation* for the existence of human beings (i.e. human DNA), including the possibility that God created human DNA. *But the scientific establishment has only considered one possibility*; the possibility of "naturalism," meaning "purposeless material mechanisms." The possibility of God is ignored.

Thus, the public's assumption that the scientific establishment is looking for absolute truth, is dead wrong. The scientific establishment leaves a huge hole in its research by not considering the existence of God.

The superb movie: *Expelled - No Intelligence Allowed* addresses this very issue.

Thus, when the science establishment claims that the theory of evolution is a "proven fact of science," what they are really saying is this: "ignoring the possibility of a God, the theory of evolution is our 'best guess' as to how human DNA came to exist."

To further understand this, let us look at an official publication of the National Academy of Sciences.

The Definition of "Science"

Most students do not fully grasp the relationship between "science" and God. The relationship is easy to explain: God is not welcome in science textbooks or in science classrooms. There is no room for God in science even if He exists. This is curious, because God does exist and He is many billions of times smarter than any scientist.

It is as if the scientific establishment doesn't want any competition from God by forcing science students to worship high ranking scientists.

Let us consider the definition of "science" as given in a small booklet published by the National Academy of Sciences.

> *"In science, explanations are limited to those based on observations and experiments that can be substantiated by other scientists. Explanations that cannot be based on empirical evidence are not part of science."*
> Science and Creationism[1], Page 1

It sounds like a good definition, and in fact it is consistent with many other definitions of "science" which have been around for many decades.

But *the main thing this definition is designed to do is exclude God* from "science." Let us analyze the above definition.

First, note the term "limited" above. What that implies is that anything which is not overtly in the definition is excluded from consideration as being "science."

For example, if God creates something (like the Universe or human DNA), according to the above definition, it is not defined as "science" because it cannot be "substantiated by other scientists," nor can it be "observed" by scientists, nor can it be replicated with "experiments" in a lab by scientists. Nor are God's actions "empirical" (i.e. based on practical experience).

Thus there are five different ways that God is excluded from "science," by the above definition:
1) By "limiting" the definition of science exclusively to what is in the definition,
2) Because God's actions cannot be substantiated by other scientists,
3) Because God's actions cannot be observed by other scientists,
4) Because God's actions cannot be replicated by experiment by other scientists,
5) Because God's actions are not part of the practical experience of other scientists (i.e. empirical evidence).

Thus, the term science is "limited" to what scientists can do in a lab. The term "science" therefore means: "the absence of God."

However, this is a two-edged sword. Scientists cannot create a Universe in their lab, thus the Big Bang theory, meaning a theory that the Universe came to be by an accidental Big Bang, is not science, *using their own definition* of "science."

Scientists cannot create huge "black holes" in their labs. Thus, since they cannot replicate the Big Bang in their labs; a theory which includes an accidental Big Bang is not part of "science" either, by definition.

Thus, *no theory of how the Universe came to be is technically "science" by the above definition because it is impossible to replicate the Big Bang in a science lab, whether it was accidental or carefully planned or there was some other mechanism*.

However, as might be suspected, there is a double-standard in science.

The scientific establishment *rejects* the claim that God created the Universe *via a highly controlled Big Bang*, because it cannot be substantiated by scientists. However, the scientific establishment *accepts* the claim that random accidents created the Universe even though such random accidents cannot be replicated or substantiated by scientists.

In other words, the scientific establishment, using *absolutely zero scientific evidence*, considers a "Big Bang" created by a series of accidents to be "science," but a Big Bang initiated by God is considered "unscientific" and such a belief is not part of "science" and is not allowed in science classrooms.

Did you understand what was just said? If God created a controlled Big Bang, it is *not* "science." But if scientists have a ludicrous theory about how the Big Bang happened by a series of impossible accidents, even though they cannot replicate how this could have happened in their labs, or prove it could have happened; this theory *is part of science*.

Astronomers, to get published in official scientific publications, must explain the existence of the Universe without mentioning God. In other words, astronomers who believe God created the Universe are *not allowed to voice the reasons for their views* in "scientific publications" (i.e. literally translated via the above definition: "publications without God") because *God is not a scientist*.

Thus, the above definition of "science" is only designed to do one thing - *exclude God from science*. *Other than being used to exclude God, the definition is largely ignored*.

About Evolution

Like an accidental Big Bang, the theory of evolution has not been replicated in any lab and it has not been observed in nature (without *assuming* the theory of evolution is true), but it also is considered "science."

The bottom line is that the term "science" is *carefully designed* to exclude God from being considered as the Creator of anything. This is one way they get God kicked out of "science classrooms" (i.e. literally translated: "classrooms without God").

It is interesting that in court trials, the evolutionist side of the trial try very hard to get creation scientists to admit that "intelligent design" is an admission of God. But on the other hand, they refuse to admit that claiming that humans are descended from other primates is not an admission of atheism. This is another double-standard.

Biologists are equally required to explain the existence of human DNA, etc. as the result of a long series of accidents - if they want to get published. No mention of God is allowed in official science publications because God is not a scientist, nor would such a paper be considered "scientific," meaning the paper would be considered "unscientific."

Because science does not allow itself to consider that God created anything (i.e. they do not allow the consideration of "supernatural" events), therefore they must find some reason to claim that "nature" created everything (i.e. this is the definition of "naturalism"). They are required by their own rules to try and explain how the incredible complexity of DNA came to exist by a long series of accidents. They have set the rules, and science will not diverge from their chosen path.

Thus, the only reason the theory of evolution exists at all is because of the two step process which science has defined for itself:
1) Science has a complete and absolute commitment to "naturalism," meaning a supernatural God is not allowed to be considered as a causal factor for anything.
2) Given that God is not allowed to be considered, what is the "best guess" explanation that science has for the existence of human DNA? This is the question posed by Mr. Johnson above.

This is the key: science has ***not*** carefully considered whether God exists or whether God created anything. This was not in their plan. Their plan all along was, as professor Johnson stated: "granted that we are here as a result of purposeless material mechanisms [i.e. naturalism], what's the most plausible purposeless material mechanism [i.e. purely naturalistic explanation] that we can imagine?"

Their answer, which ***excludes God by definition***, is the theory of evolution.

That is why the theory of evolution exists and that is what the theory of evolution is all about.

Many individual scientists have considered the possibility that God exists, or may exist, and have looked at the evidence. Many of them have concluded that the evidence overwhelmingly favors the theory or belief that God is a far better explanation for the existence of the Universe and the existence of human DNA, than the Big Bang theory and the theory of evolution, respectively.

But such views cannot be published in "scientific" publications.

Has science proven that the theory of evolution is a scientific fact? No, all they have demonstrated is that if you ignore the possibility that God exists, the theory of evolution is their "most plausible" explanation for human DNA.

It is also interesting that the above definition of "science" does not mention any type of quest for absolute truth. A quest for absolute truth would force a person to consider the existence of God. Such a quest would be repulsive to the scientific establishment.

So why does the theory of evolution even exist? It exists because the leaders of the scientific establishment don't want any competition from God. They know they (i.e. the scientific establishment) did not create the Universe or human DNA, so the next best

thing for them to do, to look smart in the eyes of the general public, and to pretend to be the smartest people in the Universe; is to tell the general public that the theory of evolution is a proven fact of science (thus eliminating any higher intelligence than their own).

By telling the general public the theory of evolution is a proven fact of science they are essentially saying: "we have proven there is no God or that God did not create anything meaningful, thus we scientists are the highest form of intelligence in the Universe."

Copernicus and Galileo would roll over in their graves.

In the days of these two great scientists, the powers that ruled the world wanted the earth to be the "center of the Universe." If the earth was the center of the Universe, then the smartest and most powerful people in the Universe were the smartest and most powerful people on this planet (since we were the center of the Universe.)

Nothing has changed. Today, even though astronomers know that our earth is not the center of the Universe, by "science" claiming that all phenomenon in the Universe which they did not do, was done by a long series of small accidents; means that the scientists on our planet are the brightest scientists and smartest beings in the Universe.

The things that scientists can do are called "science"; the things that scientists cannot do are called "accidents"; and the evidence of the creation scientists is called "unscientific."

In other words, *our "scientists" are the center of the Universe* in terms of knowledge and intelligence.

Hogwash!!!

The real goal of "science" is to put our scientists at the top of the food chain of intelligence. It is nonsense, absolute nonsense.

Not only does God exist (and He is billions of times smarter than any of us), but there are no doubt billions of scientists *throughout the Universe* who can design DNA as easily as we can use Lego® blocks to design plastic buildings.

Sorry, but we are not the center of the Universe.

Knowing that the scientific establishment claims that the theory of evolution is a scientifically proven fact; and knowing that this claim is nothing but gibberish to claim that the theory of evolution is their "best guess;" what would happen if someone were to consider God or consider that the "best guess" of the scientific establishment is scientific nonsense? That is what this book is all about.

Footnote:

1) Science and Creationism - A View From the National Academy of Sciences, Second Edition, Washington, DC 1999

Introduction to the Mathematics of Evolution

Chapter 2

The Empty Box of Evolution

"And when you trust your television
What you get is what you got
Cause when they own the information, oh
They can bend it all they want."
Lyrics of "Waiting on the World to Change," by John Mayer

The Empty Box

The original theory of evolution supported the theory of "gradualism," which meant that new species would arise gradually; meaning new species would appear for the first time on the earth evenly spaced over time.

The original theory also meant that a high percentage of fossils would be "transitional" species, meaning species which were "between" two other species. Because evolution was supposed to have happened slowly, in small steps, large numbers of transitional species were a requirement for the theory.

However, the fossil record, both before and after Darwin's death, did not support either of these theories.

This is how Charles Darwin explained why the data in his day did not support his theory:

> *"The geological record [is] extremely imperfect and [this] will to a large extent explain why we do not find intermediate varieties, connecting together all the extinct and existing forms of life by the finest graduated steps. He who rejects these views on the nature of the geological record, will rightly reject my whole theory."*
> Origin of Species

Darwin thought that future discoveries would vindicate his theory. He was wrong.

What paleontologists did find both before and after Darwin's death was that species did not appear in the fossil record spread out evenly over time, but rather new species appeared in "clumps."

Technically this is called "punctuated," meaning in a short amount of time many new species appeared; then for long periods of time very few new species appeared on the earth for the first time.

Nor did paleontologists find the transitional species Darwin predicted. Valid transitional species are rare; and even when they are found, they are frequently controversial and seem to be more of a figment of someone's vivid imagination than an obvious transitional species.

What happened several decades ago was that the theory of evolution was dying because a growing number of scientists were starting to question its validity due to the fossil record (see: Darwin's Enigma - chapter 1).

It should be clearly understood by the reader that many key parts of Darwinism have been completely disproven over and over. Many of the key concepts of Darwin's original theories are now considered false, even by the scientific establishment.

If we compare the theory of evolution of Darwin to a box, we can initially put four things in this box: first, gradualism; second, a large number of transitional species; third, natural selection or survival of the fittest; and fourth, common ancestry or common descent.

Paleontologists removed two of these things from the theory of evolution box: gradualism and transitional species.

The third and fourth items, natural selection and common ancestry; do not belong in the theory of evolution box because they do not delineate between the theory of evolution and creationism. In other words they are "non-differentiating," as will be discussed in a future chapter.

Thus, *the original theory of evolution box is empty*. There is nothing in it that is valid from a scientific standpoint; as far as Darwin's original theories are concerned.

False Theories

In most cases, when integral pieces of a theory are proven to be false, the theory as a whole is rejected by science. Even when all pieces of a theory are absolutely true, theories are frequently rejected by science because "science" is not always interested in truth for a variety of reasons (generally pride and vested interests).

Thus, when four of the key pieces of Darwin's theory of evolution were shown to be false (or non-differentiating), any sane person would predict that science would totally and absolutely reject Darwin's theory and look for its replacement.

Instead of automatically rejecting the theory of evolution of Darwin, the scientific establishment found itself in a dilemma. On the one hand the original theory of evolution had big and key chunks of it disproven, especially by the fossil record. On the other hand, the scientific establishment wanted to maintain its cherished "naturalism."

What do you think they did?

The primary goal of orthodox science is not truth, but the goal is to avoid, at all costs, any mention of God. Darwin's "naturalistic" explanation of how species came to be *had to be protected and preserved*, no matter what the scientific evidence was.

To abandon Darwin would have been to abandon the best "naturalistic" explanation science had for how human DNA, and the DNA of millions of other plants and animals, came to exist without God.

To abandon Darwinism would have been an admission that God designed and created the earth and all life on earth. *Such an admission is totally repugnant and unacceptable to the scientific establishment*. It is totally unacceptable for science to allow a discussion of God, much less to admit that He lives and that science was wrong!!

Thus, instead of the obvious answer that science would flatly reject the theory of evolution; science had no option except to try and "fix" the theory of evolution in order to maintain its highly coveted "naturalism." And that is exactly what happened.

For example, when new species were consistently found to appear on earth in "punctuated" clumps, two well known evolutionists, Dr. Niles Eldredge (of the American Museum) and the late Dr. Stephen Jay Gould (of Harvard), coined the term "punctuated equilibrium" in 1972 to explain the fact that gradualism did not fit the data.

Thus, rather than admitting the theory of evolution was false, they modified the theory of evolution to fit the data.

Yet another double-standard is pushed on the public.

In other words, the way science "fixed" the theory of evolution was to ignore its flaws and replace false theories with recent discoveries.

In other words, *they modified the theory to fit the data*. That is how they "fixed" the theory of evolution.

To revive the theory of evolution, and to put something in its empty box, they converted the term "gradualism" into the term "punctuated equilibria" or "punctuated equilibrium."

DNA

An even more dramatic example of how the theory of evolution has been modified to fit the data; is the discovery of DNA. At no time prior to the discovery of DNA did the theory of evolution predict that DNA would be discovered. At no time prior to the discovery of DNA was any part of the *mechanism of DNA* predicted by the theory of evolution.

Yet, when DNA was discovered, the theory of evolution suddenly became the proprietor (i.e. owner) of the creation of DNA and it was claimed that the theory of evolution explained how human DNA was formed by a long series of complete accidents.

This is amazing considering that the theory of evolution did not even predict the discovery of DNA or any of its many mechanisms. Yet evolution took possession of explaining how DNA came to be.

Essentially, the term "evolution" was replaced with the term "neo-Darwinism." Thus, DNA gradually became part of the "new" (or "neo") theory of evolution's empty box.

As the incomprehensible complexity of DNA is slowly unraveled, the theory of evolution always gets the credit for creating the complexity.

The reality is that as discovery after discovery is made, the scientific evidence gets further and further away from Darwin's original theory. Yet, no matter how far the evidence moves away from Darwin's original theory, *his original theory is simply modified to fit the new data*.

This is not science, it is a scam.

New discoveries are simply put in the theory of evolution empty box, as if Darwin had predicted them.

The "theory of evolution" today is nothing more than a list of recent scientific discoveries. Any time there is a discovery in science, the theory of evolution gets the credit.

The Theory of Evolution is Unfalsifiable

A scientific theory is "falsifiable" if it can be shown to be false. For example, if someone claimed the moon was made of Swiss cheese; such a theory would have been proven false when America started landing probes on the moon.

A theory is "unfalsifiable" if it cannot be shown to be false.

For example, the Big Bang, meaning the theory that the Universe was created by an accidental explosion, is unfalsifiable because it is impossible to prove or disprove a theory that the Universe was created by an accidental explosion many billions of years ago.

The theory of evolution is also unfalsifiable, meaning it cannot be proven to be false. As with the Big Bang, *the reason evolution cannot be proven false has nothing to do with either truth or the scientific evidence*. *The reason the theory of evolution cannot be proven false is because when a discovery is made that disproves the theory of evolution; the theory of evolution is simply modified to incorporate the new discovery.*

Any discovery which disproves a portion of the theory of evolution is simply put into the empty box of the theory of evolution *or it is blacklisted*.

In other words, *the only reason the theory of evolution is unfalsifiable is that it is a moving target*. The theory of evolution is "moved," meaning changed, every time there is a new discovery. Sometimes it is moved so the arrow hits the target and sometimes it

is moved so the arrow will miss the target so the discovery can be buried and blacklisted.

This behavior is unprecedented in the history of science. Instead of science looking for absolute truth, science keeps changing a false theory to fit any new data.

What is happening is that whenever some new discovery is made in biology or paleontology, the discovery is simply put into the evolution box.

It is incredible, but even DNA was put into the box and the claim was made that random mutations of DNA, coupled with natural selection, allowed evolution to create human DNA (this is neo-Darwinism in a nutshell).

The concept that human DNA "evolved" from the DNA of much simpler animals; was put into the evolution box, even though there was absolutely no scientific evidence that any new DNA has ever been created, or has "evolved," by random means.

The concept of "natural selection" was always in the box, but even it was modified to fit the discovery of DNA. Some claimed that "natural selection" worked at the nucleotide level; others claimed that "natural selection" worked at the gene level; but most claimed it worked at the species level after random mutations had done their job.

The result of this scientific nonsense is that *all new discoveries in science are converted into "evidence" for evolution or they are ignored and blacklisted*.

If the theory of evolution were equated to a painting, the painting made by Darwin would look nothing like the painting today. Science constantly modifies the theory of evolution to fit new data. Thus, science now claims that the data fits the theory of evolution.

But this is not science, it is a magic trick.

Science has not proven the theory of evolution is true; what science has done is define the theory of evolution to equal all scientific discoveries.

The "theory of evolution" is not a theory, it is a definition.

Introduction to the Mathematics of Evolution

Chapter 3

The Five Pillars of Evolution

> *"But after [the theory of evolution] has been changed a hundred times and it is still falsified, at some point someone ought to throw in the towel."*
> Luther D. Suderland, Darwin's Enigma, Revised Edition, p. 39

The Five Pillars of the Theory of Evolution

There are five main pillars holding up the claim of orthodox science that the theory of evolution is a "proven scientific fact." *None of them have anything to do with science or truth*. This is because there is no truth in the theory of evolution, thus they cannot use truth as a pillar to hold up the theory of evolution.

First, evolution is considered a "fact" because God is excluded from any discussion of science. Science has eliminated their competition by using clever definitions of the term "science." And they have used the courts to keep creation science and intelligent design out of the classrooms.

The scientific establishment has many very wealthy "friends" who think nothing of dropping millions of dollars into a court trial to make sure creation science is not taught in the classrooms.

But the scientific establishment does not just ignore creation science, it attacks creation science:

> *"The arguments of creationists are not driven by evidence that can be observed in the natural world. [A belief in] special creation or supernatural intervention [by God] is not subjectable to meaningful [scientific] tests, which require predicting plausible results and then checking these results through observation and experimentation. Indeed, claims of 'special creation' reverse the scientific process. The explanation is seen as unalterable, and evidence is sought only to support a particular conclusion by whatever means possible."*
> *Science and Creationism, page 8*

Knowing that there is not one shred of scientific evidence for the theory of evolution, try to count how many double-standards there are in the above quote.

Second, evolution is a "fact" because the theory of evolution keeps changing to fit the data. The theory of evolution is a "moving target" which adapts to every new scientific discovery. The theory of evolution is evolving.

Third, is the control of information received by the general public. Evolution is a "fact" because science controls what information the general public hears. The general public is carefully deceived into believing the theory of evolution has scientific evidence behind it.

Fourth, the theory of evolution is a "fact" because pro-evolution articles (i.e. no mention of God) are the only articles allowed to be published in "scientific" journals. Discoveries and evidence which challenge or disprove the theory of evolution are blacklisted and/or ridiculed. Science closely monitors their journals and (usually) only admits into publication scientific discoveries which support the theory, assume the theory is true or do not seriously challenge the overall claims of the theory of evolution. But never is a favorable mention of God allowed.

Fifth, it is critical that the research and claims of the creationists (i.e. creation scientists) are totally and absolutely suppressed. The public must never hear from a real creation scientist. The public must never hear their evidence and reasoning. In this way the scientific establishment can portray to the general public that creation scientists are a bunch of goons. That is why the UCTV series was so rare because real creation scientists were allowed to speak on television!!

These are the five pillars which "hold up" the theory of evolution. *Note that "truth" or a "quest for truth" are not one of the pillars!!*

The Pattern

Did you notice a pattern? All five of these items have to do with the manipulation of information, and have absolutely nothing to do with scientific evidence or truth.

Item number one above, excluding God, means they use their power in the media and schools to prevent any student from hearing the evidence that God created anything.

Item number two above, the moving target, refers to modifying the information given to the general public every time there is a new discovery in paleontology, biology, genetics, etc.

Item number three above, is the brainwashing of the general public with weak, misleading, fraudulent and simply absurd "evidence" that the theory of evolution is somehow scientific.

Item number four is the control of "scientific journals." Only "scientific" (i.e. no mention of God is allowed) information is allowed in "scientific" journals.

Item number five above is the complete and absolute blacklisting of the evidence of creation scientists.

The scientific establishment is like the Big Bully in the 4th grade class taking the candy away from the first and second graders every day. The scientific establishment, the Big Bully in the media and in education, keeps taking new discoveries and giving the new discoveries to their pet naturalistic theory (i.e. the theory of evolution).

The theory of evolution is looking at the rear-view mirror as it drives down the highway. When it sees something in the rear-view mirror that it likes, it then bullies its way into taking ownership of the new discovery and people think evolution was looking out the front window.

But this is not good science, this is bad science.

Either the original theory was true or it was false. It is now known that the original theory of evolution was false. But the theory keeps being revived by being constantly modified and by putting all new discoveries into its bottomless empty box.

The fact that orthodox science is "naturalistic" not only drives their philosophy; but it also drives their scientific ethics, or the lack thereof. Naturalism is driving their insatiable drive to keep the theory of evolution alive, no matter what the scientific evidence and no matter what lack of integrity which is needed to keep it alive.

The fact is that there is not one shred of scientific evidence, either by a study of nature or by lab experiments, that human DNA, or the DNA of any other animal or plant, could have been the result of accidental mutations of DNA. What scientific evidence there is is directly opposed to the theory of evolution.

Their "evidence" is based on vivid imaginations, and an insatiable desire for "naturalism," not by any quest for science truth.

These five pillars are why the theory of evolution is unfalsifiable. They control the information the general public and most students hear.

Here is an example of how the theory of evolution is a moving target. For years the scientific establishment preached that only 2.5% of human DNA was necessary for life. They used this as an excuse to claim that God did not exist, because certainly God would not have created DNA which was 97.5% worthless.

However, as scientists found out more and more about DNA, suddenly science changed their song and dance and suddenly quit mentioning this argument. The reason is that science now knows that over 50% of DNA is necessary for life, and many scientists suspect the real number is close to 100%.

Another "evidence" for the theory of evolution which resulted from thinking only 2.5% of human DNA was useful, was that "old DNA" from "ancestor species" (i.e. species, either living or extinct, from which humans evolved according to the theory of evolution) had not been purged from the DNA of humans. Thus, some or most of the 97.5% of worthless DNA was considered to be left over "junk DNA" from evolution (i.e. from ancestor species). This was a major "evidence" for the theory of evolution.

Not any more. Now that scientists cannot prove that a single part of human DNA is worthless, suddenly they quit talking about left over genes from the ancestor species of humans.

Yet, the virtually perfect human DNA, and the massive complexity of human DNA, somehow is twisted into a "proof" for the theory of evolution. The theory of evolution is nothing but a chameleon.

When geneticists make the final determination as to what percentage of human DNA is necessary for life, and it will be close to 100%, this conclusion will be put into the box of evolution without a single shred of scientific evidence to support it and without a single comment about their "old" theories!!

An unfalsifiable theory should not be part of "science," it should be part of religion. "Science" should only deal with falsifiable theories which do not constantly change. Again, we see an exception for Darwinism because it is the best "naturalistic" theory they have. And science will always have a "naturalistic" explanation for everything.

The Obvious Question

Let us assume, for a moment, that God *did* create the Universe and all living things? If that were the case, *should this fact be omitted from science classes*?

In other words, should "science" be a quest for truth or should it be a quest for naturalism?

Ponder that ethics question for a couple of minutes before reading on.

According to the NAS booklet, the answer is that any mention of God should be omitted - no matter what. Anything that mentions God is not science and should not be taught in science classes, *even if God did create the Universe and everything in it*.

Thus, "science" is not looking for absolute truth; science is looking for theories to explain things as long as the theories exclude any mention of God.

Science has a huge hole in it - the lack of interest in truth.

Most people think that "science" is a quest for "absolute truth." Not according to the NAS definition of "science." Nowhere in their definitions is there any mention of absolute truth (which would of necessity, should they be truthful about their quest for absolute truth, include a consideration of God).

The NAS clearly states that "science" is limited to what "scientists" are capable of doing in their labs.

Here is another quote from this booklet:

> *"Scientists have considered the hypotheses proposed by creation science and have rejected them because of lack of evidence."*
> Science and Creationism, Page ix

This quote is a blatant lie. It is a claim by the NAS that science has carefully considered the possibility that God created the Universe and human DNA, etc. They have not. That is forbidden.

The possibility that God created the Universe and human DNA is millions of times more logical than the theory that the Universe and human DNA resulted from a series of mindless, purposeless, directionless random mutations of DNA.

Thus, what is the "lack of evidence" they talk about in the above quote? Well, since they haven't considered the possibility that God exists, then it must mean a "lack of evidence" that God created anything.

According to their logic, if you *assume* God does not exist; then you have "evidence" that He did not create anything. In other words, if you assume God does not exist; then there is a "lack of evidence" that God created anything.

Certainly evolutionists and creation scientists have the same physical evidence from fossils, rocks, DNA, etc. Thus, the "lack of evidence" is not physical, it is philosophical. The philosophy of science is that God does not exist or that He was not part of any type of creation. Thus, the "lack of evidence" really means the "lack of evidence" (from their perspective) that God lives or that God has done anything meaningful.

What "evidence" does the evolution establishment have that God does not exist and God did not create anything? *How can you prove that God didn't do something?* How can you scientifically prove that God does not exist? Yet they claim to have done that.

Let us continue the above quote:

> *"Furthermore, the claims of creation science do not refer to natural causes and cannot be subject to meaningful tests, so they do not qualify as scientific hypotheses."*
> Science and Creationism, Page ix

This quote really gives away their clever definitions. They state: "the claims of creation science do not refer to *natural causes* ..."

This can be translated: "the claims of creation science *are not naturalistic* ..."

In other words, to talk about God is not acceptable because only "naturalism" (i.e. "natural causes") is acceptable in a discussion of "science." To qualify as a "scientific hypotheses," only naturalism is accepted.

The message to creation scientists is clear: If creation scientists want to be accepted by the scientific establishment, they must quit talking about God and must start talking

about "natural causes" of everything. God is not acceptable to the establishment. This quote makes this very clear to the creation scientists.

In other words, a belief in God does "not qualify as scientific hypotheses."

They are excluding creation scientists as "scientists" because they are not "naturalists," meaning they exclude creation scientists as "scientists" because they believe in God. The reason? What God did cannot be "subject to meaningful tests" and thus are not "scientific hypotheses."

But is that really the reason? Does the real concern of the scientific establishment have anything to do with "scientific hypothesis?" No, their real concern is the preservation of "naturalism." Everything else is window dressing.

Creation scientists represent the "enemy," meaning those who are trying to expose the flaws in their assumption that all of nature was the result of a long series of fortuitous accidents.

The term "science" must exclude any reference to God, even at the sacrifice of truth.

The Art and Science of Brainwashing

Very few people truly understand the goal of brainwashing. Most people believe that brainwashing is designed to repeat the same thing over and over again and suppress any opposing viewpoint.

While this is true, it is the *objective* of brainwashing which needs to be understood.

Read this next quote several times until you understand every word of it.

> *"No one understood better than Stalin that the true object of propaganda is neither to convince nor even to persuade, but to produce a uniform pattern of public utterance in which the first trace of unorthodox thought immediately reveals itself as a jarring dissonance."*
> Alan Bullock, Hitler and Stalin: Parallel Lives

This "uniform pattern of public utterance" is exactly what the scientific establishment has achieved. Any time the word "creation science" is uttered in a scientific classroom, students are brainwashed *into an immediate dissonant response* which is manifest as an immediate episode of laughter.

> *"During times of universal deceit, telling the truth becomes a revolutionary act."*
> George Orwell

The average person has absolutely zero clue how powerful the media is and how effective their carefully crafted brainwashing tactics have become.

For example, suppose the media told a lie (in other words, suppose they were on the air). They can lie to millions of people in an instant. They can brainwash scores of millions of people within a few days. They have produced a mind-numbing "uniform pattern of public utterance in which the first trace of unorthodox thought immediately reveals itself as a jarring dissonance" over virtually every citizen in the United States on a large number of issues.

So let's suppose someone told the truth. The media would not mention it. The media would blacklist it.

So what is the person going to do, start a website? Who is going to read that website? There are many billions of web pages on the Internet. How many "hits" do you think this new website of yours would get? I will tell you - none. It will take years for Google to put it in the top 100 sites for any common search string, and that assumes you have hundreds of web pages to attract "hits."

The sooner a person understands these facts, the sooner they will be able to see the real reason the theory of evolution survives. It has nothing to do with truth, or even the quest for truth; it has to do with the control of the media, the control of the universities, the control of the scientific journals, and so on.

The war about evolution is not about science, it is a war about information, meaning getting "press."

Introduction to the Mathematics of Evolution

Chapter 4

The Debate - Part 1

Overview

The scientific establishment; meaning the entities which control what is considered "science," including scientific journals, the television stations, the magazines, almost all universities, etc. etc.; all claim that the theory of evolution is a "proven fact of science."

Aside from the fact that the theory of evolution is scientific nonsense, one of the key things that the scientific establishment wishes to do is *suppress* the research and claims of the creationists.

If the claims of the creation scientists were known to the general public, and were placed on an equal basis with the claims of the scientific establishment, the general public would consider the claim that the theory of evolution is a "proven fact of science" to be laughable.

The data and theories of creation scientists are far, far superior to the data and theories of the theory of evolution. But few people know that fact.

If the truth be known, every major argument of the theory of evolution is based on false information, assumptions and pure deception.

There is no scientific evidence that a "first living cell" came to exist by a random series of accidents. There is no scientific evidence that *any* segment of DNA on the planet earth came to exist by random mutations of nucleotides of DNA.

Creation scientists literally dissect the claims of the scientific establishment and rip them to shreds.

This chapter and the next chapter will present a non-mathematical discussion of the theory of evolution versus a hypothetical creation scientist; by telling a story. The story is about a discussion between yourself, the reader (an evolutionist); and a young man named "Herman," the creation scientist.

This chapter and the next chapter will represent one specific way of representing the debate between "evolution" (i.e. the evolution establishment) and creation science or creationism and will explain why it is so important to the scientific establishment to suppress the discoveries of creation scientists.

This chapter and the next chapter are essentially a "big picture" of what is going on in "science" today. Many details of what is wrong with the theory of evolution will be given in later chapters.

The Debate

To visualize the debate between the two different camps (evolution versus creation science), suppose there is a football field and all the contestants in the evolution debate are on the field. There is a fence that crosses the football field on the 50 yard line (which divides the field into two equal parts).

You (a high school student in this case) are standing at one end of the fence, on the sideline, at the 50 yard line, looking across the fence. On your right side (i.e. the right side of this fence from your perspective) are all of the people chosen by the scientific establishment to represent the theory of evolution in the debate.

On your left side (i.e. the left side of the fence from your perspective) is a rag-tag group of under-funded creation scientists; who you did not even knew existed; and who are always broke and thus are not dressed in fancy clothes; among whom is a young man named Herman.

Many times in school you have heard that the creation scientists are “renegades” or "religious fanatics" who are simply not smart enough to understand true science. You have been told many times to ignore them. After looking at what they are wearing, you tend to agree with what you have heard.

Yet, today you have the choice of listening to the "establishment" (i.e. the evolutionists on your right side) or the "renegades" (i.e. the creation scientists on your left side) or both. This is the first time in your life you have seen a real creation scientist (i.e. someone who knows the issues in the scientific debate), so what do you do?

How will you proceed to find the truth (as best as you are capable of honestly determining as an "open-minded" person): Is evolutionism or creation science correct based on the scientific evidence currently available? Let us suppose you have no other options. You cannot leave the field until you make up your mind.

Your Quest Begins

Suppose you decide to start your decision-making journey by first talking with the establishment evolutionists; because everything you have heard in school is that evolution has been scientifically proven to be true. So you head to the right side of the fence and start talking to an evolutionist.

Suppose this person tells you all the reasons why evolution occurred by a series of accidents. He talks about microevolution, macroevolution, why transitional species cannot be found in many cases, punctuated equilibrium; the other evidences from fossils the paleontologists have found, and so on.

After this conversation, you are impressed and you start to walk away, but the evolutionist stops you and calls you back. Then this same evolutionist starts telling you all of the things that are wrong with the creationists. He tells you one theory after another of the creationists and why each theory cannot be true and why all creationists are a bunch of uneducated goons who don't know how to talk, but can only babble.

You marvel that he has mocked the creation scientists so much, and you wonder why he has done this; but since he has portrayed himself as a brilliant scientist, you think that he must be right.

After this conversation, you thank him and you now feel that you understand both the evolutionist's theories and the creationist's theories about how mankind came to be. You decide it is not necessary to go to the left side of the fence and talk to a creationist because you already think you understand their views and why their views are wrong.

At this point the only thing you know about creation science is what an evolutionist has told you.

The Four Concepts of a Truth Table

If you decided not to visit the left side of the fence, you would be making a huge, ***but common***, mistake: you have heard both sides of the issue, but from only one person on one side of the fence. You have really only heard how the people on one side of the fence feel about both sides of the issue. But you haven't heard the arguments of the creationists, ***from the mouth of a real creation scientist***, nor have you heard why the creation scientists think that the evolutionists are wrong.

There are actually four categories involved in the two sides of the fence. These are the four things in the "truth table" that you need to hear to make an informed decision:

The Truth Table

The four parts of the truth table can be broken down into two groups, the evolutionist perspective and the creation scientist perspective:

From The Right Side of the Fence (the evolutionists)

1) The pro-evolutionist arguments (from the evolutionist side of the fence),
2) The anti-creationist arguments (from the evolutionist side of the fence),

[The above two items are the two things you have already heard.]

From the Left Side of the Fence (the creation scientists)

3) The pro-creationist arguments (from the creation science side of the fence),
4) The anti-evolutionist arguments (from the creation science side of the fence).

[At this point, you *don't know anything* about these last two items because you haven't talked to a real creation scientist.]

In other words, from the right side of the fence you have heard the pro-evolutionist arguments (item #1) and *also from the right side of the fence* you have heard all of the anti-creationist arguments (item #2).

But these things only represent two of the four categories. It is at this point that most people stop looking for the truth because they have been told all their lives it is not necessary to listen to the renegades because the establishment has all the answers.

It is at this point that science (i.e. the scientific establishment) wants people to stop looking and thinking!!

The most common error people make is to think they are experts in a subject when they have only heard from the people on one side of the fence. *They haven't heard a word from the mouth of a renegade, yet they think they are experts in what the renegade creation scientists believe!!*

After talking to the evolutionist, you may think that you are an expert in both evolution and creationism. *You are not an expert in either subject!!*

***THIS IS THE KEY**!!* If the evolutionists will exaggerate the validity of the theory of evolution, they will also exaggerate the faults of creation science. Ponder that again and again!!

If they will deceive you (via their ignorance or intentionally) about the validity of evolution; they will also deceive you about the flaws in creation science. That is why everything you have heard to this point, about both sides of the fence, *may be wrong*.

That is why you cannot, at this point, be an expert in either belief; and certainly you are not an expert in creation science!!

It is exactly this type of control of information which forms one of the five basic tactics of modern science to manipulate and control information. Evolutionists cannot tolerate that a student might actually listen to a real creation scientist. If it forbidden. It is taboo. It is unacceptable according to the Supreme Court. All information about creation science must come from an *approved evolutionist* under highly controlled conditions.

At this point in your search for truth, however, even though you have only heard half of the four items listed above, you probably wonder why anyone could be a creationist. You might think this because you haven't heard yet about creationism from a creation scientist.

(This is another key point!) You have been taught in school all your life that an "open-minded" person is someone who absorbs the propaganda of why the establishment is always right, and defends the storyline propaganda of why the renegades (the people on the left side of the fence) are always wrong. You are taught never to talk to a renegade or your mind might become contaminated.

So in reality "you" (the hypothetical person at the end of the fence) probably have absolutely no desire to talk to anyone on the left side of the fence. You have heard everything you think you need to hear. You feel you are an expert on both sides of the issues. Thus, you are a member of the establishment and a certified "defender of the faith" of the evolutionists.

End of story - time to go home.

Your Trip to the Left Side of the Fence

Oh well, just for the heck of it, out of morbid curiosity, and to test your debate skills, you decide to walk over to the left side of the fence and talk to a creation scientist. You randomly pick a person and you decide to try and convince him to become an evolutionist, now that you feel you are an expert in the errors of what the creationists believe.

You carefully walk up to (gulp, drum roll): Herman the Horrible Hermit Heretic. Be careful, you say to yourself, close your ears and don't listen, this person is an idiot. Oh well, because you have been taught in Sunday School to be courteous to your enemies, you shake hands with him and start to listen.

(Note to the reader: Do not be intimidated by the terminology Herman uses below, some of these terms will be discussed later in the book.)

After shaking hands with Herman and exchanging pleasantries, you are immediately amazed at something: Herman can talk! You had always been taught that creationists had the IQ of a rodent and wore beanie caps with rotors.

Herman starts by talking about life on earth. He states that life on earth began with a single cell, according to the theory of evolution. This "first living cell" on the planet (which would be the first living thing and it would only have been a single cell); had to have an RNA or DNA component and it had to have a cell membrane, among many other things.

He states that the "first living cell" would have needed at least 300 specialized proteins in order for it to survive and divide. He estimates that the 300 genes which created these 300 proteins would have needed an average length of 1,000 nucleotides.

By the way, Herman tells you; in human DNA the average gene can create 10 different proteins and is much, much longer and vastly more complex than the genes of any imaginary "first living cell". Some human genes can create 50 different proteins he says.

Getting back to the "first living cell," Herman says that each of these genes would have needed an additional 2,000 nucleotides to: manufacture the proteins from the genes, fold the polypeptides, incorporate the proteins into the cell, etc.

Herman defines for you what a "gene complex" is. He says it is a gene plus all of the other nucleotides necessary for the gene to be manufactured, folded, incorporated into the cell, etc.

Thus, Herman estimates the minimum size of the DNA or RNA of the "first living cell" would be 3,000 nucleotides (for the average gene complex) times 300 genes, or about 900,000 nucleotides long.

Herman then asks this question: "Has science ever created a 900,000 nucleotide RNA or DNA chain by purely random means?"

The answer, he says, is an emphatic 'no'. Furthermore, he says, there are many reasons, especially from chemistry, that such a chain of amino acids (note: proteins are made from amino acids) could ever have formed by accident.

Herman states that amino acids form proteins, but that amino acids cannot bind to each other in a stable fashion. He states that to create proteins, amino acids must have a chemical bonding, controlled by a chemical agent, and that the *natural attraction between amino acids could never create a protein*. Herman states that science has many theories as to how such chemical bonding could have happened in nature, but that all of these theories are not possible.

Herman also says that all single-celled entities today, which are able to sustain life *without a host (as the "first living cell" must have done)*, are very, very complex and even the evolution establishment admits that a prokaryotic cell or eukaryotic cell could not have been made by accident in a prebiotic (i.e. pre-life) pool of water. Thus, says Herman, the "first living cell" of evolution is now extinct. "How convenient," Herman says sarcastically, "that the evidence of a "first living cell" is gone."

He also asks whether science will ever create life from non-life, meaning a living cell created by a series of random events which replicate the prebiotic (i.e. pre-life) world. Herman states with great fervor that they never will create life from non-life by random means, but he says he doesn't have time to explain why it is mathematically impossible.

However, Herman does provide a partial explanation of the mathematical problems of this happening when he states that it would have been impossible for a randomly created nucleotide chain that long to have had a "permutation of nucleotides" which could have created the necessary exactness to create life. You think you have a vague idea of what he is talking about, but you are not quite sure what a "permutation" is.

You then ponder on your own that the "first living cell" only had a 900,000 nucleotide chain, but that human DNA has 3,000,000,000 pairs of nucleotides. You realize the creation of human DNA by random processes would have been far more impossible than the creation of the "first living cell" both because of the length of the DNA and the much smaller tolerances for error because of the vastly added complexity.

Introduction to the Mathematics of Evolution

Chapter 5

The Debate - Part 2

"Why may not the Bible and especially the New Testament be read and taught as a divine revelation in school? Where else can the purest principles of morality be learned so clearly or so perfectly as from the New Testament?"
U.S. Supreme Court, 1844,
Vidal v. Girard's Executors,
Justice Story delivered the Supreme Court's unanimous opinion

Microevolution and Macroevolution

Herman then states that Darwin's "evidence" for evolution (i.e. the finches) is actually based on data from *micro*evolution, which is variation within a single species.

Herman tells you that one person has red hair and another person has brown hair and another has black hair because of microevolution. The three people not different species because they have exactly the same DNA structure, but there is variety within the nucleotides of their DNA.

Thus, Herman says, even the data of Darwin had nothing to do with true evolution (i.e. true evolution is equated with "*macro*evolution, not *micro*evolution").

He also states that microevolution is quite powerful, and gives as an example, Darwin's famous finches. Each of them was the same species, Herman says, but microevolution gave them very different shapes and abilities.

"Macroevolution," Herman says, is totally different because macroevolution means the two plants or animals have a different structure of DNA. For example, a horse and a mouse have a different structure of DNA. They have a different set of genes, for example.

True evolution, if it existed, would require macroevolution. It requires "new genetic material," which would include at least one new gene complex, and probably many new gene complexes.

Herman states that in order for science to be honest, every time they use the term "evolution" they should be referring to an example where there are new genes, as part of the new genetic information and new genetic material.

Yet, says Herman, every example of "evolution" science uses has nothing to do with any new genetic material; it is only the result of microevolution or their vivid imaginations.

For example, Herman mentions the peppered moth. The various colors of peppered moths is no different than the different colors of human hair, it is an example of microevolution. Yet textbooks claim it is an example of macroevolution. This is false, Herman says.

Another example Herman gives is viruses which are claimed to "adapt" a resistance to medications, such as for AIDS. Herman says this is absolute and total nonsense.

Herman states that some microbes have very, very high rates of point mutations (i.e. a "point mutation" is a mutation of a single nucleotide) and they multiply in huge numbers. By pure coincidence, by combining their huge populations with very, very high mutation rates, they purely and coincidentally have a point mutation or two which provides a resistance to drugs.

Herman states that textbooks make it sound like viruses have intelligence and are constantly trying different experiments to develop an immunity to a medication. Science textbooks make it sound like the viruses hold a convention to discuss how they can change their DNA to "adapt" to drugs. Herman says this is pure fantasy.

Herman states that there is no new genetic material (i.e. additional sequences of nucleotides and new genes) developed in these microbes at the time they develop a resistance to a drug.

He then states that *everything which is claimed to be caused by evolution must have new genetic material, meaning the DNA must have new sequences of nucleotides and new genes added to the DNA of the species in order to create a new species*.

Herman warns you that every time you hear the term "evolution" you need to ask yourself: "have they proven that there is new genetic material, including new genes, and that the new genetic material was created by random mutations of DNA -- or are they just using clever definitions and their vivid imaginations?"

The fact is, Herman says, *scientists have never, never seen useful new genetic material form by random mutations of nucleotides*. All they have observed is very, very rare partially beneficial *point mutations*. Herman then says with a flare: point mutations do *not* represent new genetic sequences of nucleotides, including new genes!! *There must be new genes formed by random mutations*, Herman adds, with voice raised, *to truly constitute evolution*!!

A point mutation, Herman says, involves one or two or three nucleotides, but a gene complex involves at least 3,000 new nucleotides!!

Herman takes a minute to calm down. Herman then states that all of the "evidence" for macroevolution (i.e. true evolution, meaning the creation of new genetic information) comes from the study of microevolution (variety within a single species); but that microevolution and macroevolution are as different as a rock and a jet airplane. Both a rock and a jet airplane can fly, but he tells you that throwing a rock into the air

(microevolution), does not qualify a person to design, build and fly a jet airplane (macroevolution).

You then learn about the improbability of irreducible complex protein systems forming large numbers of complex inter-related proteins in the same random mutation event in macroevolution. He gives the bacterial flagellum as an example. Its parts are so complex they could not have "evolved" by gradual random mutations. Until all the proteins were in place, the flagellum would have been a burden to the bacteria.

Herman states that attempts by orthodox science to dispute the claims that "irreducible complex" mechanisms are evidence of creation; are ridiculous, but because the scientific establishment controls the media, people don't know how absurd their attempts to refute this evidence really are.

You then hear about the "morphing of the embryo," which is the time period between the fertilization of the egg and the time the baby is born.

A new creature starts out as a single cell, a fertilized cell, which is undifferentiated (meaning it has no specific function in the body), but when the "baby" is born it has hundreds of different kinds of differentiated cells, mixed with massive amounts of natural chemicals (which came through or from the mother).

To accomplish hundreds of different kinds of cells; when cells divide, they must divide into one or two different kinds of cells which are not the same as the original cell, or some mechanism must go back and "fix" some of the cells. The timing of these many strange cell divisions has to be with pinpoint accuracy.

You learn that the instructions for this pinpoint accuracy must be built into the DNA, thus making random mutations even less likely to be advantageous (i.e. requiring more precise chains of nucleotides, meaning the percentage of "correct" permutations of nucleotides is much smaller than might be expected if only genes are considered).

Herman states that every different kind of cell in the body must create different kinds of protein structures within the cell. He states that these different kinds of cells have exactly the same DNA, but each type of cell must pick different subsets of genes to create the protein structures for that specific type of cell.

Herman asks: how could a single undifferentiated cell turn into hundreds of different kinds of cells, each of which knows which subset of genes to pick to meet the needs of that kind of cell?

Then Herman talks about the circulatory system, the nervous system, the lymph system (including the lymph nodes), the electrical system (including the brain), and the immune system of the body. He tells you the DNA must contain unbelievably complex morphing algorithms to properly put all of these systems in place as the embryo is being formed.

He describes this as trying to put the electrical system, plumbing system, water systems, windows, pipes, desks, rest rooms, etc. into a tall building as the steel beams are being put into place and are being riveted. In other words, as the steel workers are riveting I-Beams for the 50th floor (of a 100 story building), hundreds of other people are standing on that I-Beam waiting to put the desks, water fountains, plumbing, pencils, etc. in place.

Herman also talks about the human heart. The heart starts beating in about week 5 after conception. If the heart started beating before the circulatory system was enclosed the embryo would bleed to death. Herman then asks you how the cells are given oxygen prior to the heart starting to beat? You don't know. Herman says a very specific chemical reaction keeps the new cells alive until the heart can beat.

Herman then says that as animals got more complex (assuming the theory of evolution), so did the morphing of the embryo algorithms on the DNA. The more complex the animal the more complex the algorithm and the less likely it could have happened by accident.

When Herman started taking about the morphing "timing" issues, the incomprehensibly complex computer programs which needed to be built into the DNA to control the morphing of the embryo, etc. you started thinking that Herman might not be retarded after all, like you had always been taught.

Herman interrupts your thinking by explaining that modern science wants you to think that the morphing of the embryo algorithms built into DNA are simple, and only involve a handful of nucleotides. Herman explains this is like claiming that the computer programs which put astronauts into space were written by monkeys.

Herman then starts talking about the evolution of species which had both a male and female. He starts talking about how the same random mutations must occur in the germ cells (i.e. the cells involved in reproduction, meaning the sperm and eggs) in both the male and female in order to have viable offspring.

Herman likens this to two different people (who do not know each other) receiving an email with a 10,000 volume encyclopedia. Each of the two people is instructed to independently make 20,000 random word changes to their soft copy of the encyclopedia. These 20,000 word changes can be to any of the pages in any of the 10,000 volumes.

Herman states that the probability that the DNA of both a male and female germ cell having the same random mutations (and thus being able to have offspring with new genetic material) is equal to the probability that the two different people coincidentally make the same 20,000 random word changes to the 10,000 ***volume*** encyclopedia. Herman actually started laughing at such an absurd possibility.

Yet, Herman says, such an improbable event would have had to have happened ***millions of times*** in order for the theory of evolution to be true!!

Herman then started talking about a few things for which you had no clue what he was talking about. All you could make out was that it involved the male and female issue, coupled with multi-generational changes to DNA to form a new set of inter-related genes.

Then Herman starts to talk about the evolutionists (this is the anti-evolution part, heard from a creationist viewpoint, the fourth item in the truth table).

He tells you that the first argument the evolutionists use (when confronted with the severe problems caused by probability and statistics, such as the issues related to

permutations of nucleotides) is to respond by saying that "we exist, thus our existence is proof of evolution and the statistical issues related to evolution can be ignored."

In fact, Herman tells you that every time an evolutionist looks at a fossil bone, this bone is claimed to be a "proof" of evolution.

Herman then uses a common analogy (common to him, but you had never heard it before) and likens their logic to the theory that all of Shakespeare's plays were written by six monkeys locked in the basement of a building. It is someone's theory that Shakespeare did not write his works, but that the works attributed to Shakespeare were actually written by these six monkeys randomly pointing to letters on a chart on the wall.

He states: is it logical that because Shakespeare's plays "exist," that their existence is proof that six monkeys actually wrote Shakespeare's plays?

If the answer is 'no', then why do evolutionists claim that the mathematical problems with their theory are irrelevant because humans exist?

You then hear how "punctuated equilibrium" (e.g. the Cambrian Explosion) is really many super irreducible complex protein systems forming at the same time, and you hear how absurd it is for science to challenge irreducibly complex protein systems, but at the same time to believe in punctuated equilibrium. Herman tells you this is like choking on a single sunflower seed, then swallowing a large watermelon in one gulp.

You hear why the phylogenetic tree was designed by scientists who were assuming that evolution was true; then it was used by other scientists to "prove" evolution. In other words, they assumed evolution was true in order design the tree; then the tree was used to "prove" evolution was true. Herman spends an hour talking about the logic tricks used by the evolutionists.

You also learn about the massive assumptions evolutionists make with regards to carbon dating of bones and how these assumptions allow them to come up with the "right answer" when they need it.

The theory of evolution, he tells you, in order to be true, requires massive amounts of time (hundreds of millions of years). Herman tells you the public must be convinced that life has been on this earth that long in order to justify the theory of evolution. In order to appear that life on this earth has been around for hundreds of millions of years, they use dating techniques *which are known to be defective*.

Herman tells you the defect is because moisture leeches radioactive atoms from samples (and thus throws off the accuracy of radiometric dating). This extremely relevant fact is intentionally ignored by labs in order to obtain the huge time periods needed for the theory of evolution.

Herman tells you the age of the earth is not a big issue (i.e. few people really care about the age of the earth, but some do), but it is the dating of bones and fossils which are the key issue.

Herman tells you that fossils are the "best" evidence for the theory of evolution, but in fact the fossil record absolutely disproves the theory of evolution.

Herman tells you that bones of humans have radiometric dating techniques used on them which are known to be false, in order to date the bones to be older than the Biblical account of Adam and Eve. Herman tells you this is pure fraud and that these fossils are no where near as old as labs claim.

Regarding fossils, Herman says, obvious transitional species simply don't exist in the fossil record. Second, and more importantly, is that many ***hundreds of millions*** of random mutations to DNA would have been needed to create evolution, but this would mean that new species would appear on the earth in an increasing, but ***gradual*** count.

In other words, Herman says; if Darwin had known about random mutations of DNA, and if Darwin would have had a computer to simulate evolution, he would have concluded that the fossil record would display "a slowly increasing gradualism." The gradualism would have been an "increasing gradualism," not a flat gradualism, but it would have been gradualism nonetheless.

The fact is, Herman says, when you have huge numbers of random events, which would be required for evolution to be true; the main data is very predictable.

However, the "increasing gradualism" predicted by any computer model of evolution, using random mutations of DNA as the driving factor, is not what is observed in the fossil record.

In other words, Herman states: "punctuated equilibrium" is not at all compatible with random mutations of DNA and he states that there is no way to explain the Cambrian Explosion by using random mutations of DNA.

Herman states that the permutation of nucleotides issue is the very issue which makes the theory of evolution totally ludicrous because as DNA got longer and more complex (as species got more and more complex); the issues related to permutations of nucleotides would have become more and more impossible to explain.

Herman tells you that mutations on DNA are always at random locations on the DNA, but that evolution assumes that all mutations are precisely in the locations where they are needed.

Herman then states there is overwhelming scientific evidence that the DNA of all plants and animals is slowly deteriorating (i.e. genetic entropy). He states that geneticists have ***never observed*** new genetic material form by mutations.

In fact, geneticists see nothing but genetic entropy, and no new genetic material. Thus, what scientists actually observe (entropy of DNA) is not in harmony with what the theory of evolution claims (constantly growing and improving DNA sequences by random mutations)

In other words, says Herman, every factual amount of information from the study of genetics is ***exactly the opposite*** of the claims of evolution!!

Thus, Herman says, the overwhelming mathematical and observed data all point to the fact that evolution could never have happened on any planet, or on any Galaxy.

Furthermore, there is zero evidence from labs that evolution is even possible under controlled conditions, much less in truly random conditions.

When all is said and done, Herman says, there is not one shred of evidence for the theory of evolution.

Ten hours pass and you realize the sun went down and it is now dark - and Herman is still talking. You also realize that for four of the ten hours you had no clue what Herman was talking about.

You also realize that this is not what you expected. You expected some wild and crazy theories. But in fact you realize that creation scientists are not stupid and they really do have some very strong arguments.

But most importantly you realize that what you had been taught by the evolutionists, about what the creation scientists believe, was totally wrong. You realize you had been deceived into thinking the creationists did not have any strong arguments.

You finally thank Herman for his time, and go back to the end of the fence a very confused person.

Afterthoughts

As incredible as this sounds; it is very, very difficult to get people to grasp the concept of hearing both sides of an issue from both sides of the fence. All your life you have been taught that it is not necessary. Society always has all of the right answers, for both sides of the fence, and anyone who does not agree with society is a crackpot, quack, moron, rebel, incorrigible, mentally unstable, or whatever.

Of course, many individual scientists and many individual educators are strong believers in God and do not believe in the theory of evolution. There are many known flaws with the theory of evolution, but above all, there is simply zero evidence for the theory of evolution. It is a theory, and a very poor theory at that. It is based on poor chemistry and very poor mathematics and a massive amount of falsehoods.

Yet, in the public arena, the scientific establishment has such total control of information; that anyone who defends God is an outcast and a renegade and is ridiculed. Nobody wants to be a renegade; it is very lonely. People would much rather be a conformist:

> *"When they give a person a Bachelors degree, they take away their mouth, when they give them a Masters degree, they take away their brains, and when they give them a PhD, they give them back their mouth."*
> Helen Kehr Billings, PhD (1901-1995) (an aunt of the author)

Not all renegades are right, but many of them are.

> *"The reasonable man adapts himself to the world. The unreasonable one persists in trying to adapt the world to himself. Therefore all progress depends on the unreasonable man."*
> George Bernard Shaw

While the media and many schools have portrayed the creation scientists as the "unreasonable man," the reality is that it is the evolutionists who are using their vivid imaginations to invent things that science and mathematics simply cannot even remotely support.

The reality is, and don't forget this fact, *creation science has a complete and absolute monopoly on good science and good mathematics*; but the evolution establishment (i.e. "science") has a complete and absolute monopoly on the control and manipulation of information. That is what the evolution debate is all about.

The debate is between overwhelming scientific truth (i.e. creation science) versus the overwhelming control and manipulation of information (i.e. the theory of evolution).

Note To Reader

The community of creation scientists is large in size but is virtually unknown to the general public. The large number of creation scientists, as a whole, can totally shred the absurd theory of evolution.

However, even though the community is large they do not always agree among themselves.

For example, how long did it take to create the earth and all life on earth?

Some creation scientists think it took six 24-hour calendar days to create the earth and everything on it.

Others claim it took six thousand years (via versus in the New Testament which define the term "day" to mean a thousand years).

Others claim it took six creative periods, of indefinite and not necessarily equal time periods. In other words, some creation scientists define the term "day" to mean "period" and have no problem with believing it took *God* millions or billions of years to create all of the life on this earth.

The reader may dismiss some of these theories because of the age of the earth and the age of fossils as determined by radiometric dating and other methods.

Few creation scientists refute that the earth (as a large rock) is billions of years old; but some do refute it and they have good evidence for their claims because they believe in the power of God.

The point is that the reader should not assume that just because a person is a "creation scientist"; that they necessarily agree with all other creation scientists or that they agree with your beliefs.

The creation science community is a close knit community in condemning the perceived corruption in mainstream science; but they are not close knit with regards to all issues relative to the actual creation.

Many of the creation science books are written to support the specific creation science beliefs of a specific group of creationists or religionists. Thus, just because a book is a creation science book, does not mean its focus is on the same brand of creation science the reader believes.

The scientific establishment has a "field day" (i.e. a good time) criticizing "Young Earth Creationists" (Y.E.C.) because their claims do not fit the data of geologists and others.

While God is certainly capable of creating this planet in six calendar days or six thousand years, the claims of the Y.E.C. are an easy target (which is called a "straw man") for evolutionists, even though the creation scientists may be correct.

The reader should also note that there are many people who believe in a combination of evolution and creation science. For example, some people believe God created the "first living cell" and then left the rest of creation to evolution.

Those who believe in a hybrid of evolution and creation science most likely do so because they have been taught over and over again that the theory of evolution is scientifically valid.

However, as this book will show in graphic detail, every aspect of the theory of evolution is scientific nonsense.

Introduction to the Mathematics of Evolution

Chapter 6

Non-Mathematical Concepts

"If the brain were simple enough to understand, we would be too simple to understand it."
Quoted in: Listening to Prozac by Peter D. Kramer

Story #1: The Space Shuttle

Let us suppose you had been in charge of building the first American space shuttle. You would have had hundreds of PhDs, and other experts, working for you, directly or indirectly.

Let us consider some of the things involved in building the first space shuttle.

First, you (or someone who works for you) would have to have an understanding of the mathematics of planetary motion and space flight. You would have to be able to calculate where the space shuttle is going to go. Of course, there had been space flights before the shuttle, but the mathematics still has to take place because each flight is unique.

Second, there is the technology of metals and ceramics. The space shuttle has to go into space and has to come back. Thus, the metal must be protected from the extreme heat of re-entry. Plus the space shuttle has to be as light as possible, but strong enough to survive each trip (the shuttles are designed to be reusable).

Third, is the technology of chemistry. Very dangerous chemical reactions occur during a space flight, and these dangerous toxic chemicals must be safely removed from the shuttle after landing.

Fourth, are the computers, both on the ground and in the spacecraft. An enormous amount of effort needs to go into the software (i.e. the computer programs) and the hardware (the computers).

Fifth, are the communications equipment. You don't go down to Radio Shack® to buy the types of radios they used to communicate between the ground and the space shuttle.

Sixth, is the actual construction of the space shuttle. The space shuttle wasn't built in someone's garage by a group of car mechanics. It is an enormous structure which requires a huge building for its construction and many people to construct it.

Seventh, are all of the issues related to launching the space shuttle, such as the chemicals in the rockets. These are the people to whom the common term "rocket scientist" refer (e.g. the popular phrase: "What do you think I am, a rocket scientist?").

Eighth, is the aerodynamics of the space shuttle. In order to be reusable, it must land safely. It must come all the way from space and land on a landing strip that must seem, to the astronauts, the size of a postage stamp.

Ninth, is the training of the astronauts and the many people who work with them.

And the list goes on and on. Building a space shuttle, launching it, and landing it, is a huge task involving thousands of people who are technical experts at what they do.

The First Grade Class

Suppose you had been in charge of coordinating all of these highly trained astronomers, mathematicians, chemists, numerous kinds of engineers, etc. etc.

Now suppose, as the head of the space shuttle team, you are invited by a first grade class (i.e. 6 year old students), at a local grade school, to come and meet with the class. There are 25 first graders in the class. You agree to come and talk about the space shuttle.

You walk into the class, with all kinds of pretty pictures. However, the class does not want to see any pretty pictures; they want to actually build a space shuttle as a class project!!

What they want you to do is give them enough technical information so they can build their own full-size space shuttle. You find out they will give you half an hour to tell them how to make a space shuttle. Then, after your lecture, they are prepared to take over and they are confident they will be able to build, launch and land a full-size space shuttle by themselves.

You, of course, would be both humored and horrified. You know that this class cannot build a space shuttle any more than 25 alley cats can build and fly a Boeing 747.

You know that perhaps when these children grow up, and if they were joined by thousands of others, perhaps they could ***help*** build a space shuttle, but you also know that a class of 25 first graders is not going to be able to build a space shuttle from scratch, after a thirty minute lecture or even ten thousand hours of lectures.

How This Relates to the Theory of Evolution

When human DNA was first discovered and analyzed, it was thought that it was not very complex, just like the above school class did not understand the complexity of building a space shuttle.

Some of the first estimates as to what percentage of human DNA was necessary for life were 2.5%.

Scientists claimed that the other 97.5% of human DNA contained a lot of leftover DNA from our ancestor species, which was no longer necessary for humans. This was a major "evidence" for the theory of evolution for many years.

However, as time passed a lot of things changed. The incredible complexity of DNA started to be unraveled. It is now known that at least 50% of DNA is necessary for life, and there are strong suspicions that almost all of our DNA will eventually be shown to be necessary for life.

Over time, the concept that our DNA contained a lot of leftover DNA from our ancestor species (such as genes which had been used for our ancestor species, which are not needed by humans), was no longer mentioned and the concept was buried because it looked like all of our DNA would eventually be understood to be important.

So what happened to all of the genes which were needed by our ancestor species, but which are no longer needed by humans? There is no mechanism to remove these obsolete genes, thus they would forever be stuck on our DNA.

I call this phenomenon: "genetic leftovers." Scientists cannot find these leftover genes and other genetic material on our human DNA. This is strong evidence that the theory of evolution is false. Nucleotides which would be on human DNA, if evolution were true, are not there.

DNA has 3 billion pairs of nucleotides. In one hundred years, scientists will look back at 2009 and state that scientists didn't have a clue how DNA functioned in 2009.

Yet, there is already a dictionary specific to genetics called: A Dictionary of Genetics, by King, Stansfield and Mulligan. This is a standard size book, with small print, which has 484 *pages* of definitions and more than a hundred pages in its Appendix. Did you note that there were not 484 definitions, there were 484 *pages* of definitions? That is how complex the study of genetics is. Yet scientists still don't have a clue about many key things with regards to DNA.

Discoveries in genetics happen so fast that any dictionary (even online dictionaries) will be slightly obsolete within weeks after they are published and will be totally obsolete within a few years.

DNA is composed of pairs of molecules called nucleotides. There are four different kinds of nucleotides, which have the initials: A, C, G and T. There are 6 billion nucleotides in one human DNA, but they are paired together. Thus, there are 3 billion pairs of nucleotides in each human DNA strand. They are pairs because an 'A' is always paired with a 'T" and a 'C' is always paired with a 'G'.

Each and every one of the 100 trillion cells in our bodies has the same DNA strand (each person's unique DNA strand) of 3 billion pairs of nucleotides (there are a few exceptions to this rule). Different kinds of cells will pick different subsets of these 3 billion pairs of nucleotides in order to create the proteins needed for that type of cell.

This means there are about: 600,000,000,000,000,000,000,000 nucleotides in the average person's body!! When the person was conceived there was one DNA strand and 6 billion nucleotides.

So what is a DNA sequence or DNA strand used for? DNA is essentially nothing but information. The DNA contains sequences which are called "genes." Genes are templates for making proteins (though it is a lot more complex than that, as will be discussed in a future chapter).

The DNA is also a template for making the molecules needed to convert the genes into proteins and to control what happens to the proteins after they are made.

The DNA also includes what might be termed "computer programs." These programs are a complex system of timers and feedback mechanisms needed to control the morphing of the embryo, the clotting of blood when you get a cut, how your eye reacts to light, and many, many things which happen inside the cells or outside the cells (e.g. in the blood stream).

The computer program which controls the morphing of the embryo is more sophisticated than any computer program ever written by a human being. It is more complex than any person *can even comprehend*!! That is why scientists cannot find all the pieces of the computer program on the DNA. They don't know what they are looking for because they have only a small clue how the program works.

DNA is a lot of highly, highly complex information. Never forget that. While the amount of information in DNA may be compared to a huge set of volumes of an encyclopedia; when taking into account the complexity of information in human DNA, DNA has more complex information in it than any library.

Where is science in their understanding of DNA?

First, let us consider the brain:

> *"They (the speaker's son and another medical student) learned of a brain bathed in fluid which continually receives signals from 130 million light receptors in the eyes, 24,000 hearing receptors in the ears, 10,000 taste buds, and hundreds of thousands of receptors in the skin, with specialized commission to recognize touch, vibration, cold, heat and pain."*
> Douglas L. Callister, 2005

How in the world could a single cell, at the time of conception, end up being transformed into a brain (see the quote at the top of this chapter) and many other organs and biological structures?

When the egg of a mother is fertilized, the new baby starts as a single cell, meaning the fertilized egg. When the new baby is born it has a brain capable of the above mentioned feats. The information needed to create the brain, which by itself has hundreds of different kinds of cells, is totally and completely built into the DNA in the mother's egg. Yet not one brain cell of the future baby exists at the time of conception. The fertilized egg is called "undifferentiated," meaning it has no specific function.

Do you think scientists could design DNA to replicate making a brain as just mentioned? It would be easier for the first grade class above to build and fly a space shuttle.

As another example, suppose a paleontologist dug up a complete skeleton of a rare type of dinosaur which went extinct millions of years ago (using the time frame of the evolution establishment). This fossil would have zero DNA left in it.

Could scientists design the DNA of this creature, and put the DNA in several egg shells, along with other things inside the egg shells; such that several dinosaurs would hatch and the species would live again and be able to generate new generations of dinosaurs? The answer is: absolutely not!!

Until scientists can do that, they really don't know much about DNA.

Scientists can build a space shuttle fairly easily, but they are nowhere near able to design and build DNA; put it inside of several egg shells and revive an extinct species, both male and female, which are able to reproduce.

And that is the point. Designing DNA as complex as human DNA is a technology which is far, far beyond the current capabilities of human scientists.

Furthermore, scientists would *NEVER* be able to figure out how DNA works without being able to study what God has already done.

Here is a test for science. Isolate 100 very smart students who are in first grade. Isolate them from all other students for 20 years. Do not tell them about DNA or anything related to DNA. Do you think they could figure out what DNA was, or do you think they could design the DNA necessary to create a human brain or recreate an extinct dinosaur? Not in ten thousand years. *Scientists have to see DNA in order to have a clue what it does*. Science has to steal ideas from DNA in order to understand anything about DNA.

Since scientists have no clue how the morphing of the embryo algorithm works in DNA, scientists would have no clue how to design a morphing of the embryo algorithm. They have to steal the plans from existing DNA. But they can't even do that yet.

Everything scientists know about DNA they learned by studying existing DNA, and they still don't understand human DNA very well, after over 50 years of studying it. Without stealing thousands of ideas from existing DNA, scientists would have an impossible task designing the DNA of an extinct species.

Current scientists are not even in the "first grade" when it comes to being able to design new DNA for new species (or new DNA for extinct species). Yet, as always, they claim to be ready for the challenge like the first grade class mentioned above.

Science claims that the complex motor in bacteria with flagellum are not signs of intelligent design. Then why don't they have someone who has never seen the DNA of any type of bacteria; build a new DNA strand which can create the complex motor (including all the incredible specifications of the motor and the actual construction of the motor and the repair of any damage to the motor) in the bacterial flagellum??

A better challenge would be for them to design the bacterial flagellum DNA by using random mutations of DNA. Computers are fast enough to generate trillions of random mutations of DNA (in a computer). But I guarantee you they cannot do that either.

Modern evolutionists are not even to the point of being first graders, when it comes to creating DNA for a new species which is not a slight modification of an existing species. Yet they proclaim they are in graduate school in understanding DNA.

Yet, even though they are not in first grade yet, they claim to know enough to proclaim that evolution created human DNA by a long series of accidents over a long, long period of time.

Can something which is incomprehensibly sophisticated be created by accident?

Evolutionists claim that there is nothing which is so complex as to justify believing in "intelligent design." Yet, their understanding of DNA is still less that that of a "first grader."

There is something functionally wrong with their claims. They don't know what they are talking about.

If very intelligent human beings are no where near being able to design the DNA of an extinct species (even after already spending over 50 years looking at DNA designed by God), it is absolute nonsense to believe that human DNA was created by a long series of accidents.

Story #2: Air Force Pilot Manuals

One retired Air Force pilot was asked: If all the textbooks and frequently used reference manuals he studied during pilot school were stacked on top of each other, how high would the stack be? His reply was: "About 12 feet."

There is more information, and more complex information, in the DNA of a mouse than in those 12 feet of books!!

The pilot training books and reference manuals were written by experts in their field, much of it by long-time pilots themselves; but also by many engineers and others. The amount of expertise in these manuals is staggering.

Do you think that future pilots would want someone to start randomly changing the words in their textbooks and reference books; and randomly changing the numbers, drawings and diagrams in their books?

Yet, the theory of evolution is based on taking a perfectly good DNA strand, and randomly mutating it to end up with a superior species which has new ***and superior*** genetic information!!

Phase 1

Let us consider the 12 foot high stack of textbooks and frequently used reference books used to train pilots in the Air Force.

Suppose there are ten sets or copies of original textbooks (and reference books) used by Air Force pilots in their training. Suppose ten different people are each given one 12 foot tall stack of textbooks and they are told to make 10,000 different random changes to the pages in their stack.

These changes include changes to words (e.g. randomly changing the word "north" to "east" or "south"), numbers (e.g. randomly changing 35 degrees to 47 degrees or 12 degrees), graphs (i.e. changing the slope or shape of a graph), etc.

After these ten different people make 10,000 random changes to their copy of the original stack of books, there are ten different mutated copies of the 12 foot high set of books.

Now suppose ten different groups of 100 student pilots are trained to fly using these 10 different stacks of mutated books (each group of 100 student pilots exclusively uses a different set of modified stacks of books), not knowing that they are looking at modified versions of their original textbooks and reference books.

The stacks of books used by the groups of student pilots are called: Group 1, Group 2, Group 3, etc.

These ten stacks of mutated textbooks and reference books represent the random mutations of DNA in the theory of evolution.

But now we need to simulate "natural selection." This is how we will "select" which set of mutated books are "superior": We will "select" the set of mutated books which kills the least number of pilots over the course of the first two years after they finish pilot school.

To be more specific, two years after these ten groups of student pilots complete their training (exclusively using their set of mutated books); we will note how many of the pilots are still alive in each group.

Suppose, in this hypothetical example, two years later, in two of the groups, 35 of the pilots are still alive. Suppose these are Group 3 and Group 7. The rest of the groups have less than 35 of their original 100 pilots still alive.

Using this statistic (i.e. survival of the pilots) we will "select" the two stacks of books which were used by these two groups (Group 3 and Group 7) and throw the other stacks away (i.e. survival of the fittest).

Phase 2

We will now make 5 copies of the Group 3 stack of books and 5 copies of the Group 7 stack of books. All 10 groups of books have already had 10,000 random changes made to them from the first round of random mutations.

We will then have ten new people make 10,000 ***additional*** random changes to each of the 10 stacks of already mutated stacks of books (5 from Group 3 and 5 from Group 7).

These 10 stacks of books now have a total of 20,000 cumulative random changes made to them. Beneficial mutations, which just happened to improve the information in the books, are extremely, extremely rare, but let us assume such events do happen. But the vast number of mutations made to these books create either: harmless, false or dangerous information.

Now we will again take ten new groups of 100 student pilots, who will use these 10 new stacks of mutated books in their training (each group of 100 student pilots uses a different set of modified stacks), not knowing that there were any changes made to their books.

The stacks of books and groups of student pilots are called: Group 3-1, Group 3-2, Group 3-3, Group 3-4, Group 3-5, and Group 7-1, Group 7-2, Group 7-3, Group 7-4, and Group 7-5.

After 2 years we note that only one of the groups has any of the new pilots left. This is Group 3-5 (of the new group of pilots) and it has 3 pilots still alive.

Using the "natural selection" and "survival of the fittest" criteria above, for selecting which stack of books will be used for the next sets of pilots and which will be thrown away; we will "select" the stack of books which were used by Group 3-5.

We will now make 10 copies of the Group 3-5 stack of books. These stacks of books already have 20,000 random changes made to them.

We will now have ten new people make 10,000 additional random changes to the words, numbers and graphs in these books. Likewise, ten new groups of 100 student pilots will use these new mutated textbooks and reference books.

The ten stacks of books have 30,000 randomly modified words, numbers and graphs.

The stacks of books and groups of pilots are called: Group 3-5-1, Group 3-5-2, Group 3-5-3, etc.

We note that within 2 months of graduation, none of the pilots are alive in any of the ten groups.

Now we have a problem. All of the groups had the same number of surviving pilots (none). How will we decide which of the stacks of books to "select" for the next group of pilots?

Comments

In this process we "selected" the sets of mutated books which killed the least number of pilots for use for the next new set of pilot trainees.

Here is the question: Is this a good way to train pilots for the Air Force?

The answer is obviously: no.

When you start with a virtually perfect set of manuals, mutations almost always do harm to the information, and thus to the pilots. Yes, there will be extremely rare instances where a mutation actually improves the information in a book, but these will be very rare and will be overwhelmed by the negative changes.

Overall, the changes to the books and reference manuals made them increasingly dangerous to the students.

In actual genetic research, it is common knowledge that virtually all point mutations, and other types of mutations, are neutral or harmful. Yes, there are rare beneficial, or partly beneficial, point mutations, but these are extremely rare and usually involve a loss of genetic information.

When you start with something that works, and you randomly modify it, it will get worse, not better.

In fact, the rate of good mutations tells geneticists a lot about how perfect the DNA is. In all animals and plants, beneficial mutations are extremely, extremely rare. Thus, the DNA of all animals on earth is virtually perfect, meaning there are very, very few imperfect nucleotides which can be fixed by random point mutations.

Considering that all DNA on earth is virtually perfect (because almost all mutations are neutral or negative), and considering that genetic entropy (i.e. the deterioration of DNA), combined with this fact, is a proof that all species on this earth are very new species (to this earth), meaning only a few thousand years old.

To better understand this concept, consider the theory of evolution. If evolution were true we would have inherited all the genetic entropy of our ancestor species. Over a period of hundreds of millions of years genetic damage caused by mutations would have been passed on from one species to the next, and within the same species, from one generation to the next. If evolution were true, our DNA would be incredibly damaged. But that is not the case. Rather, our nearly perfect DNA is one of the strongest proofs of the Biblical account of creation.

In other words, if the theory of evolution were true, we would have inherited all the genetic mutations of our ancestor species - going back 660 million years and our most

distant *homo sapiens sapiens* ancestors would have lived 100,000 years ago. Were these facts, and considering genetic entropy; virtually every human on earth would have been born with many, many millions of genetic defects from our ancestor species and several significant genetic defects from our *homo sapiens sapiens* first parents. But that is not what geneticists have observed.

Thus, the perfection of our DNA and the DNA of all other plants and animals is absolute proof that the theory of evolution is false. But pursuing DNA as a proof of evolution (using the perfection of our DNA as the evidence) requires computer simulations (mainly to teach and prove concepts) which will actually be discussed later in this book.

The "First Living Cell"

Now let us consider the "first living cell." Suppose a "first living cell" was created by evolution and that its DNA was perfect (it would not have been perfect, but we will assume it was perfect). Do you really think that tampering with it's DNA will create new and improved DNA and new and improved species?

That is the point to this discussion. As Bert Lance stated: "If it ain't broke, don't fix it."

But yet that is the whole basis of the theory of evolution. You start with something that is perfect (i.e. the "first living cell"), or nearly perfect, then you start to randomly make changes to it and end up with something better than the original. Does that make any sense? That is absolutely *not* what is being observed by geneticists.

There have been millions of species on this earth. Each had perfect DNA or nearly perfect DNA. Yet the claim is that each of these species was created by randomly mutating the DNA of a prior species with perfect or nearly perfect DNA. This is nonsense.

This is as absurd as trying to convince the Air Force to improve their textbooks and reference books by randomly mutating them by people who couldn't build a paper airplane.

Suppose a book existed with over 250 pages of computer simulations, statistics, etc. on the subject of evolution. What would you learn from this book? The main thing you would realize is that "if it ain't broke, randomly mutating it will do more harm than good!!"

This is exactly what is observed in nature (i.e. genetic entropy).

Yet the theory of evolution operates on exactly the opposite premise!!

Randomness never makes something better (unless it is totally wrong to begin with, which is impossible among living things or the species could not exist).

Thus, if it is alive, it cannot be improved upon by random mutations.

Look at it this way, if a DNA is 99.999% perfect, it is almost certain that all mutations will be negative or neutral because they will be affecting "right" nucleotides (i.e. 99.999% of the nucleotides are correct, thus changing them will not improve them).

The entire premise of the theory of evolution is that random mutations do more good than harm. That would only be true if our DNA was extremely defective. But if our DNA was that defective we couldn't survive.

The prime directive of the theory of evolution is not only mathematical nonsense; but it totally violates what geneticists have observed numerous times. They have never seen an instance where random mutations created new genetic information which was useful. All they have seen is a very, very rare beneficial point mutation and lots and lots of detrimental or neutral point mutations.

But a point mutation is a change in existing genetic material; it does not represent new (i.e. additional) genetic information; which would include one or more new gene complexes.

Story #3: Changing Computer Programs

Let us take the Air Force example one step further. Now we will not only change the textbooks and reference books these pilots study, but we will also randomly mutate the computer programs in the jets they fly.

When you start to randomly change computer programs, by choosing random "bits" of information in the program, and replacing these "bits" with randomly generated '0's and '1's, how long do you think the computer program in a jet will continue to function and the plane will continue to fly?

Even highly trained computer programmers have a difficult time getting complex computer programs to work. Once they work, randomly changing them is not going to be a good thing. It would be like mutating a DNA strand which is 100% perfect.

Even though the DNA of any living thing is far more complex, and far more perfect, than any computer program on earth, it still would be suicide to randomly change "bits" in a computer program that controlled jet airplanes.

How many of the first group of pilots would still be alive after 2 *days* of flying (not 2 years as above), if the computer programs in their jets were tampered with?

Depending on how many changes are made, and in what sections of the programs they are made, the chances are that none of the pilots would still be alive after two days of flying.

There are many sections of DNA where even the slightest mutation can cause severe damage to the animal or human under consideration. This is particularly true in the morphing of the embryo algorithms, but it applies to other areas as well.

Even animals which lay eggs are subject to the morphing of the embryo algorithms. There is a lot of morphing going on inside the egg, whether it be a duck egg or an insect egg.

DNA contains incredibly complex computer programs, especially for the morphing of the embryo of animals which have live births or lay eggs. If you start randomly changing these computer programs, built into the DNA, the number of "live births" will quickly drop to zero.

Another issue with regards to the morphing of the embryo is that if there is a flaw in the DNA morphing algorithms (in either the male or female germ cells), there will not be a new species because there will be no live births. The morphing algorithms are a zero defect computer program, just like the computer program which controls a jet airplane. You only get one shot at getting it right or the plane crashes (or the baby of the new species does not survive, thus the new species will not survive).

This is significant for the theory of evolution. Evolution is based on random mutations of DNA. If a pair of animals have their DNA randomly modified so that a new species can exist; but there is a slight defect in the morphing of the embryo algorithm; even a slight defect in the morphing of the embryo will likely prevent the new species from ever existing. *There are no second chances*.

Yet the morphing of the embryo algorithm is the most complex algorithm in DNA and it is the most easily damaged by the slightest defect!

Story #4 - Writing Computer Programs

Have you ever tried to get a computer programming job at a large corporation? You had better have credentials because that is what they look at.

Suppose you believe in evolution. Suppose you know absolutely nothing about writing computer programs, but you have bought a computer program which randomly generates (or changes) long strings of '0's and '1's (by the way, "evolution" knows nothing about designing DNA; the fact is that all mutations to DNA are totally random).

Suppose you go to the Human Resources department of a large corporation and say this: "I have never written a computer program in my life, but I did purchase a random number generator over the Internet and I want the job of a computer programmer. I will take an existing computer program which works, but you want to improve, then I will randomly make changes to the 'bits" in the program and create 1,000,000 new computer programs, each of which is a randomly mutated copy of the original program. I will then "select" the "best" of these 1,000,000 new computer programs, and then mutate this program 1,000,000 times, and so on. Eventually, you say, I will end up with computer programs which are far superior to what your computer departments are capable of writing."

Do you think you would get the job? I will save you the time and embarrassment. You won't get the job.

Computers now have the speed to generate billions of randomly generated computer programs. They also have the ability to evaluate these billions of randomly generated computer programs for certain kinds of effectiveness.

Yet, with all this computing power, no corporation in their right mind would try to write a computer program by using "evolution," meaning by randomly generating '0's and '1's or by randomly changing the '0's and '1's in an existing computer program which works perfectly well.

Even using the step by step process of evolution (whereby each new species is only slightly better than the previous species) will not help you write new computer programs.

Why won't this process work to write new computer programs?

The reason is permutations (which will be discussed many times in this book). There are estimated to be 10^{80} atoms in the known Universe. This doesn't look like a big number, but it really is a huge number. It is the number:
100,000,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,000,000,000,000,000

You could write a unique computer program, one unique program for each atom in the Universe, *using less than 300 'bits' of '0's and '1's*.

In other words, you can uniquely order 300 '0' and '1' bits more times than there are atoms in the known Universe.

Most computer programs that large corporations write are millions of bits long. Do you realize how many trillions of centuries it would take to *randomly* write a simple computer program (randomly generating '0's and '1's) which was one million bits long; a program that actually did something useful?

Actually, it would never happen during the time that 10 million consecutive Universes were created and died - because random numbers don't generate the same kinds of patterns that intelligently designed programs generate.

The point is that you don't take something that works perfectly well, and then improve on it by randomly mutating and changing it. Yet, that is the very mechanism by which the theory of evolution works.

Do you really think that science has "proven" that the theory of evolution is a "proven" fact of science? Are you beginning to see why the theory of evolution is scientific nonsense? It gets worse for the theory of evolution as this book progresses.

Introduction to the Mathematics of Evolution

Chapter 7

Natural Selection and Common Descent

"We are in the process of creating what deserves to be called the idiot culture. Not an idiot sub-culture, which every society has bubbling beneath the surface and which can provide harmless fun; but the culture itself. For the first time, the weird and the stupid and the coarse are becoming our cultural norm, even our cultural ideal."
Carl Bernstein, U.S. journalist. Guardian (London, June 3, 1992)

Natural Selection

"Natural selection," also called "Survival of the Fittest," is one of the two foundations of the theory of evolution. The other foundation is the way species change, which originally was based on morphology (i.e. a study of the physical features of an animal), but is now based on random mutations of DNA.

Natural selection claims that a "fit species" will survive better than "less fit species."

What exactly does a "fit species" mean? Science generally defines a "fit species" as a species which is better able to reproduce or for some other reason has more offspring.

However, the "average man on the street" defines "fit species" as a species which is able to eat or kill its competitor species or in some other way is able to survive better than its competitor species.

Either way, if a new species is able to survive, because of natural selection, this new species is able to get a foothold in the animal kingdom. This in essence elevates the overall standard of membership in the animal kingdom. Once the overall standard of survival increases, the next new species has an opportunity to be even better.

This increasing "standard of survival" is claimed to escalate until eventually natural selection, coupled with random mutations of DNA, led to human beings.

To better understand why natural selection is part of the theory of evolution, let us consider an example from the automobile industry.

This example will show how natural selection fits with random mutations of DNA.

The Contest

Suppose there are ten car manufacturing companies, called Company One to Company Ten. All ten of them have totally inept employees. The "car companies" represent different species. The "inept employees" represent random mutations of DNA.

Let us compare natural selection to a contest between 10 cars (one car made by each company) and their ability to climb a long and steep hill.

The goal of the contest is for one of the cars to climb to the top of this very high hill (the top of the hill represents the creation of human DNA by evolution).

All ten car companies have totally inept employees. The employees are lazy, they never work, they are not trained at all, they totally resist any training, they don't obey orders, they don't understand a single part of the car - and don't want to know, they rarely come to work, and when they do come to work they are either sleeping or eating or watching TV, and so on.

For many thousands of years none of the companies can create a car which has an engine that starts; much less can climb to the top of a hill.

Finally, after many thousands of years, and by pure accident, one of the car companies, Company One, is able to start their engine and climb 1% up the hill.

Suppose, by natural selection (natural selection in this case is the ability of the car companies to financially survive) the other 9 car companies go out of business because everyone buys their car from Company One.

Now suppose that ten new car companies come on the scene. They are called Company Eleven thru Company Twenty. Almost all of the employees of these car companies came from Company One, which is by now a very big company with a lot of inept employees.

Now there are employees in eleven car companies which are totally inept.

There is a new race up the hill. Suppose Company Thirteen, by pure accident, is able to get 2% up the hill. At this point the other ten car companies (including Company One) soon go bankrupt.

Now the only car company is Company Thirteen and most of its employees came from Company One. But Company Thirteen has employees, regardless of where they came from, which are just as inept as the old Company One.

Company Thirteen grows and grows even though its cars can only get 2% up the hill.

Now ten more new car companies come on the scene, named Company Twenty-One thru Company Thirty. Almost all of their employees came from Company Thirteen.

There is a new race. In this race Company Twenty-Five gets 3% up the hill. The other ten car companies soon go out of business.

This process continues until there are a hundred races and one of the cars from Company One Thousand-Seven gets to the top of the hill. It took many, many thousands of years for this race to be won.

The Assumption

The above example explains how natural selection aids in evolution. Only the "best" car company financially survives.

In essence, when a superior species shows up on the earth, natural selection is the mechanism which guarantees the survival of this new species.

By new species leap-frogging over one another, the overall mixture of species improves over a period of many million of years.

Because over time natural selection preserves better and better species, you get a better and better mixture of species on the earth and eventually you end up with human beings.

So what is wrong with natural selection?

First of all, consider that in the above example, natural selection is irrelevant until the car companies build their cars. In other words, *natural selection works during the hill climb, not during the manufacture of the cars*.

Natural selection did not make the employees of the car companies any less inept.

In the world of biology, new genetic material can only be made by random mutations. The sequence needed by evolution is this:
1) Random mutations make new genes and new species (this is where the car companies build their cars using inept employees),
2) Natural selection preserves the new species if it survives better than other species (this is the hill climb).

But what if #1 above never happens? What if random mutations are never effective at creating new genes and new species?

The theory of evolution assumes item #1 creates a fantastic amount of new genetic material. The assumption which allows natural selection to work is that DNA gets better and better and better by purely random mutations.

But note that natural selection has absolutely nothing to do with making random mutations any more favorable. Natural selection does not protect any "correct" section of DNA from becoming the victim of a mutation.

Natural selection has nothing to do with new genetic material being formed or the introduction of new species. Natural selection is only useful after ***multiple*** new species already exist. Then it can work.

Natural selection only works after random mutations have created new species. After the new species is walking around the earth, trying to survive, then and only then does natural selection become a factor. But natural selection has nothing to do with the creation of new species.

The reality is that random mutations never create new genes or any other part of DNA. Much of this book will discuss this very issue.

Thus, if random mutations never create any "improved genes" (i.e. a gene which leads to the creation of a superior protein) then natural selection is never a factor in evolution.

Let us go back to our car example.

Let us suppose that over the time period of 660 million years, not a single car company is able to get their engine to start (which is the most likely scenario because engines are complex). Natural selection is never able to operate and crown a victor after the first hill climb.

Natural selection only works when the cars are on the side of the hill. Natural selection doesn't work until the engine, the battery, the starter and the transmission all work - and there is gasoline. If any of these things fail, natural selection has nothing to do.

Suppose ten car companies started the contest, and 660 million years later, these same ten car companies are still making cars unable to have their engines start, or their transmissions work, or their starters turn over, etc.

Thus, for 660 million years, natural selection would have had nothing to do.

When talking about evolution, natural selection is totally useless unless random mutations are able to create new and improved species. But as this book will show, random mutations are never able to create a new gene, much less a new species.

The bottom line is that natural selection is totally irrelevant in the support of the theory of evolution unless the DNA mutations problems of evolution can first be dealt with.

In other words, until it can be shown by evolutionists that mutations of DNA could have created new genes; many, many, many millions of times; the entire issue of natural selection is moot (i.e. irrelevant).

Some people ask the question: "Doesn't the vast number of species which have existed on this earth prove that DNA has been mutating and new genetic material has been formed by random mutations?"

Actually, this question is a paradox. The vast number of species which have existed on this earth is a proof that random mutations were not involved. It is doubtful random mutations could have created a single, very simple single cell, much less the complex DNA of humans.

What about God? Some might ask: "Why would God create so many species which have so many common morphological features?"

First of all, species have to move in one of four main ways: walk on two legs, walk on four legs, fly or swim. Of course there are other ways, but these are the main ways that most advanced animals move.

When you design millions of animal species, but only have four modes of transportation, there is going to be a lot of morphological similarities.

For example, think about automobiles. Automobiles have four wheels. There have been many hundreds of different automobile designs by many different manufacturers. But note that there are a lot of physical similarities between cars made by different manufacturers.

The point is a person cannot use natural selection as an evidence for the theory of evolution until they can prove that random mutations of DNA could have produced all the species which have existed on this earth, in the time period since the Cambrian Explosion.

In other words, random mutations of DNA would have had to create millions of different species, each with a unique DNA (by definition) in order to even be able to talk about the importance of natural selection.

But also note that in each car race above, nine car companies were eliminated by "natural selection." Suppose all nine of these car companies had made some progress, but just not enough progress to win the race.

Even though all nine companies, in each race, made advances, they are eliminated.

What this means is that "natural selection" ***reduces*** intelligence (i.e. it reduces the gene pool) because it eliminates species which are not quite good enough to survive, but may have had some new and important features.

With natural selection reducing the gene pool, even more of a burden is placed on random mutations to create massive numbers of new genes.

The point is that natural selection is likely to hinder evolution, not help it, because all it does is reduce the gene pool.

Natural Selection is Non-Differentiating

Another problem with natural selection is that there is nothing in natural selection which is differentiating. In other words, natural selection is a concept which applies equally well to the concept of Creation.

For example, if God had created all the species on earth, natural selection would still be in force. This is because species which are more powerful, faster, smarter, etc. will have

a better chance of surviving. But in this case, natural selection did not start operating until God created the species.

Thus, when science looks at situations where one species is wiped out by another species; or they look at a species which has survived when other species didn't survive; this is not an evidence for the theory of evolution because *natural selection would work no matter how the species got on the earth* or how the species became extinct.

Natural selection, or survival of the fittest, simply does not differentiate between the theory of evolution versus the theory of creation. Natural selection simply means that superior species survive.

Natural selection is ignorant in the sense that *it has no idea how the animals came to be*, it only operates on the animals which exist at any given time. Natural selection doesn't know, and doesn't care, how the animals came to be; it simply waits for animals to exist.

Thus, whether the animals came to be by random mutations of DNA, or whether the animals came to be by creation, natural selection would work exactly the same.

Thus, natural selection cannot be used as "evidence" for the theory of evolution because it is non-differentiating.

Common Descent

One of the most often used "proofs" of the theory of evolution is that of "common descent," meaning that the similarities in physical features; and thus similarities in DNA; between different species; is a proof of the theory of evolution.

It is nineteenth century morphology technology but it is clearly the most commonly used "evidence" for the theory of evolution.

For example, in a recent pamphlet issued by the National Academy of Sciences, is this quote:

> *"... species that appear to be more distantly related from their positions in the fossil record are found to have correspondingly greater differences in their DNA than species that appear more closely related in the fossil record."*
> "Science, Evolution and Creationism,"
> by the National Academy of Sciences

This theory is called "common ancestry" or "common descent."

To understand some key concepts; suppose you studied every automobile model made in the world, which is still being sold as new (i.e. they are not "used cars").

Furthermore, suppose you visited the factories which make all of these cars, and you watched how they were made.

Then, suppose you additionally studied every automobile model which is no longer sold as new, including many antique cars.

Suppose you also studied all of the historical reports you could find which discussed the manufacturing plants and processes used to create cars which are no longer being manufactured.

Would you see similar features in the new automobiles and old automobiles and the way they are and were manufactured? Of course you would.

Would you see progression and changes in features over time in such things as: engine designs, steering wheel designs (including new functions, such as a built-in cell phone controls, volume controls for the radio, speed controls, etc.), tire compositions, the shape of glass, fender designs, air conditioning, etc. etc. Of course you would.

Would you conclude that the new automobiles had a "common ancestor?" Most likely you would, and most likely you would be right.

Modern automobiles are "descended" from very old antiques. Modern automobiles have "evolved," to use the term loosely.

The problem is that every automobile which has ever existed on this earth was ***designed by intelligent beings***. In this case, the intelligent beings are human beings.

The point is that when we see the "evolution" in automobiles, in fact it was ***not evolution by random design***; it was ***evolution by intelligent design***. People got smarter and smarter as they were designing automobiles.

Thus, ***even when you see similarities and progression in features; intelligent design can be the cause***. In fact, when you see so many similarities between manufacturing and the end product, you would conclude that ***intelligent design had to have been involved***.

Side Note

This is ***not*** to imply, however, that God was learning things as He created the species on this earth. He knew everything long before this earth was created. The "order" that science claims the species on this earth appeared is largely based on the ***assumption*** of the theory of evolution. The real order that species appeared on this earth for the first time is largely unknown.

But in any case, consider that some of the animals in the Cambrian Explosion had very advanced eyes and other very advanced physical features.

Human beings progress in their knowledge (they do not progress in terms of their intelligence), but God does not progress in His Knowledge or Intelligence.

Are Commonalities in DNA Differential?

So how does the DNA of different species differentiate between the theory of evolution and creation science?

Just like "natural selection" is non-differentiating, because it has nothing to do with the origin of the species; finding similarities in the DNA of different species is also non-differentiating, but for an entirely different reason.

That reason will now be explained.

How can the scientific establishment claim that they know that DNA was not designed (i.e. intelligently designed)? What is their evidence?

Their evidence is that DNA sequences are *predictable and consistent* between species (i.e. between the physical features of species).

Well, if DNA was designed by God, then the design of the DNA would probably be *predictable and consistent* between species!! Duh.

In fact, if the design of DNA is predictable and consistent, this is *overwhelming proof* that DNA was intelligently designed.

But fortunately for the scientific establishment, Darwin, who knew nothing about DNA, but knew a lot about morphology (i.e. the shapes of animals and their bones) came up with the concept of common ancestry, which is now called "common descent."

Even though Darwin was thinking about morphology, it just so happens that intelligently designed DNA can also be used to claim common descent. This is one of those things which "fell into the lap" of the scientific establishment.

By using the intelligent design of DNA, but claiming the design was caused by evolution (similar shapes will be generated by similarities in DNA), the scientific establishment can pull the common descent feather out of their cap and claim that DNA (*which is intelligently designed* because it is predictable and consistent) is proof of evolution (i.e. a proof of common descent).

But when the evolution establishment claims that predictable and consistent DNA design is a "proof" of common descent; they do not stop there; they continue to talk about how *predictable and consistent* DNA is a *proof of evolution*, meaning it is a proof that *intelligent design is false*.

This is nonsense. They claim that the very thing (intelligent design); which provides their evidence for common descent; is false (i.e. they claim that intelligent design in false).

The evolution establishment should be grateful and thankful to God for providing intelligently designed DNA (or else humans would not exist). But does the evolution

establishment thank God? No, they ignore Him and they use the works of God to pretend that God does not exist (i.e. to prove evolution) using clever logic!!

Let us summarize this:
1) Because of intelligent design by God, there is *predictability and consistency* of DNA design,
2) Because there is predictability and consistency of DNA design, the evolution establishment claims this is proof of common descent, then
3) The evolution establishment claims that the proof of common descent is *a disproof of intelligent design*.

Thus, the *result* of intelligent design is turned into a *disproof* of intelligent design by using clever logic.

If science would simply say that predictability and consistency of DNA is non-differentiating between creation science and evolution, all would be well. But they do not do that. They do not even admit that with the issue of natural selection. They act like natural selection would not be true if God existed; and they claim predictable and consistent DNA design would not exist if God existed. *These claims are absolutely inexcusable.*

The evolution establishment seems to forget that if DNA was designed by God, *the DNA so designed would also be predictable and consistent*.

Apparently the NAS believes that if DNA *was intelligently designed*, it would *not* be laid out carefully, predictably and consistently. Ponder that carefully. But such is the tilted logic of the scientific establishment.

A creation scientist would look at exactly the same data and conclude that the predictability and consistence of DNA is *proof of "intelligent design*."

But "intelligent design" would imply God exists. So the data of creation scientists (*which is the same data as the evolution establishment*) is rejected as being "unscientific." Of course, by definition, everything that points to God is "unscientific" because God is excluded from "science."

Thus, predictable and consistent DNA segments is "unscientific" if it leads to evidence for creation science.

But, predictable and consistent DNA segments is "scientific" if it leads to the theory of evolution.

Thus the data that supports the theory of evolution is "scientific;" but the same exact data (which also supports intelligent design) is "unscientific."

In addition to theses things, it should be noted that there are huge, huge, amounts of data in the DNA of millions of different species. Carefully selected data which supports your theory can *easily be found* (and data which doesn't fit your theory can *easily be ignored*).

DNA templates are used by the body to create proteins. Proteins are used to create the functions of cells. Cells are what are used to create the functions of the animal. Thus, if two animals have the same functions they would have the same kinds of cells, and thus the same kinds of protein structures in the cells and thus similarities in DNA. *This would be true with intelligent design or evolution.*

It is ludicrous to use DNA to prove DNA wasn't designed by God!

Ponder this carefully: What features of DNA would a scientist use to prove that DNA was not intelligently designed?

Can we humans design DNA yet? No, we can't; so how can we claim we can "prove" DNA was not designed by God?

Suppose scientists get to the point that they can design DNA for extinct species. If they ever get to this point, it would *only be because* they studied and copied ideas from the DNA of existing species. In fact, they would have copied many segments of DNA of existing species.

When and if scientists can design the DNA for extinct reptiles, will they then say that the DNA which *they carefully designed*, over many decades, and was copied and pasted from existing DNA, is a proof that DNA was not intelligently designed? Yes, they will.

If they want to get published in a scientific journal, they will have to figure out some way to claim that the DNA *they intelligently designed* is a proof that human DNA was not created by *God's intelligent design!!* Does this make any sense?

If scientists did design the DNA of an extinct species, would the DNA be predictable and consistent? Of course it would, because they designed it by stealing ideas and DNA from living species.

In short, the consistency of DNA design can be used to prove intelligent design or the consistency of DNA can be used to prove common descent.

But the consistency of DNA design *cannot* be used to *disprove* intelligent design any more than it can be used to *disprove* common descent.

This debate is a "draw." *It is a non-differentiating phenomenon*. And that is the point. No matter what similarities and patterns exist in the DNA of various species, any "proof" there is evidence of common descent is also proof that the DNA was intelligently designed by God. And vice versa.

The "winner" in the debate will not be the team with the best evidence; it will be the team which has the most power in the media. That is why a person never hears that this issue is a non-differentiating issue.

But like natural selection, this is also an issue which comes into focus *after* DNA exists. Before DNA exists there is nothing to talk about and nothing to compare DNA to.

The bottom line is that both natural selection and common descent are non-differentiating.

What this means is that *everything in evolution* depends on the ability of random mutations of DNA to create new and improved DNA.

Introduction to the Mathematics of Evolution

Chapter 8

Radiometric Dating

> *"Arizona State University anthropologist Geoffrey Clark echoed this view in 1997 when he wrote that 'we select among alternative sets of research conclusions in accordance with our biases and preconceptions -- a process that is, at once, both political and subjective.' Clark suggested 'that paleoanthropology has the form but not the substance of a science."*
> Icons of Evolution - Science or Myth? Jonathan Wells, page 223

Introduction

Dating of bones, fossils, rocks and other items is a very controversial issue. To understand just how controversial it is, the same fossil might be dated by the evolutionists to be *hundreds of millions of years old*; yet the same fossil might be dated by creation scientists as being *no more than 6 thousand years old*.

Radiometric dating is the process by which bones or fossils are "dated," meaning an estimated date is chosen as to when the animal lived and died on the earth.

In the case of fossils; which are essentially bones that have fossilized, meaning turned to stone; fossils are generally dated on the basis of factors other than radiometric dating; such as a particular date may be chosen for a fossil because *the date is consistent with aspects of the theory of evolution*.

In other words, in dating fossils it is quite common that *an assumption that the theory of evolution is true is used as a factor in dating fossils.* This is a self-serving way of dating fossils, but it is a common tactic because scientists are so confident that the theory of evolution is true.

For example, by using morphology and an assumption of the theory of evolution, it may be assumed that "Fossil A" evolved before "Species B" "evolved." Thus, if "Fossil A" is believed to be 4,000,000 years old, "Fossil B" may be dated to be 3,700,000 years old solely on the basis of the date of "Fossil A" and a belief in evolution (i.e. it is dated based on where "Fossil B" fits on the phylogenetic tree relative to "Fossil A").

While the reader may assume that it takes millions of years to turn a biological specimen to stone, actually it has been demonstrated to have happened in *less than 100 years* (not 100 million years, just 100 years). This is not theory; it is based on actual samples.

Because of fossilization, and other reasons (e.g. when an unstable parent atom becomes a stable daughter atom, the dating of the specimen can no longer be done accurately), dating of old fossils is generally impossible to do directly. Thus, many assumptions must be made to date fossils. These assumptions are generally made to be harmonious with the theory of evolution.

These assumptions leave the door wide open for huge debates as to when a particular species lived on this earth.

Radiometric Dating

Radiometric dating is generally done on bones or tissue which has not fossilized, and is supposedly the most scientific and most accurate dating technique.

However, even radiometric dating is a subject of controversy. The truth is that flaws in radiometric dating are intentionally ignored in order for the specimen to yield dates which are very old.

It is not that the technique itself is inaccurate or that the theory behind the technique is flawed; it is the intentional way that key factors are ignored that is the key complaint. In other words, factors which can have a huge affect on the dating of a sample are totally ignored in order to get the results scientists want; so the date is harmonious with the theory of evolution!!

Why would science want to intentionally misrepresent when an animal lived on this earth? The reason is that the theory of evolution needs many, many, many millions of years to justify the time necessary to "prove" the theory of evolution could have happened.

But even more important than that, it is critical for the scientific establishment to date human skeletons to be older than Adam and Eve, the first humans mentioned in the Bible.

Thus, evolutionists tend to favor techniques which lead to huge numbers of years since the specimen died. The important issue, however, is that scientists use techniques which are *scientifically known* to be massively flawed.

The Radiometric Dating of Bones and Tissue

All living tissue has radioactive isotopes in it. For example, carbon-14 is a carbon molecule with 14 electrons.

It is well known how much carbon-14 is in the tissue of an animal (including a human being) while they are alive, meaning at the time of death.

After an animal dies (including humans) the amount of carbon-14 naturally "decays" over time, meaning the radioactive atoms decay into non-radioactive atoms over time. In other words, the amount of decay is a function of time.

Thus, if scientists can determine the level of radioactive carbon-14 in the bone of a dead animal (including humans); they can determine when that animal died by looking at their decay charts.

There are actually many different types of radioactive atoms which can be used to perform radiometric dating and many different techniques and theories.

But there are severe problems with radiometric dating. I will not discuss all of the potential problems with radiometric dating; I will simply provide a few examples.

Leeching of Radiometric Material

To understand the problem, suppose there are two animals that died on the same day. The first animal, at the time of death, was immediately moved to an air conditioned building located in the desert and it was placed in a dark room. The humidity in this desert was very, very low. Furthermore, because the specimen was indoors, no moisture from the rare rainfall ever touched the specimen. Furthermore, the specimen was kept cool and in a dark room.

On the other hand, the second specimen was buried next to a river in a shallow grave. The bones were exposed to the moisture in the soil due to the river. The bones were exposed to the high humidity of the general area. The bones were exposed to the extreme moisture of the flooding of the river; during which time the specimen was literally soaking underwater. And the specimen was exposed to the water from rainfall since it was in a shallow grave. Water flowing down from nearby hills would have increased the amount of water the bones were exposed to due to the rain.

Will radioactive dating, after two hundred years, give the same date for both specimens? Absolutely not!! The second specimen may date to be *ten times older, or more,* than the first animal.

Why is this so?

The reason is that moisture, from any source, will "leech" or draw out radioactive material from the bones of the sample. If one specimen is exposed to very high levels of moisture, a great deal of radioactive material will leech out of the specimen and the radiometric dating will date the species far, far too old.

This radioactive material which has leeched over time will be interpreted by scientists as radioactive decay. But it is not radioactive decay, it is leeching of radioactive atoms by moisture.

The problem is that radiometric labs don't make any type of adjustment in their dating of bones for known or potential moisture or heat which might have affected the sample.

For example, if the first specimen dated to be 200 years old, the second specimen might have dated to 2,000 years or more. Yet the two animals died on the same day!!

It is not that the radioactive isotopes were miscounted; it is because the lab totally failed to take into account the environment the sample was decaying in.

Caves

All of the common types of caves are formed by water. The water may have come from above (e.g. rainfall or a creek) or it may have come from below (i.e. a hot springs), but all of the common types of caves were cut-out by water.

Caves are very, very humid because there is almost always an existing source of water in the cave, such as a creek or dripping water, to name but two sources.

Thus, skeletons found in caves are, by definition, highly exposed to moisture.

Do scientists take the massive amount of moisture found in caves into account when they date a skeleton found in a cave? The answer is 'no'.

Even though the moisture in a cave can be more accurately estimated than the moisture a skeleton found buried next to a river is exposed to; scientists still do not take this into account.

Is this because scientists are simply incompetent or is it because scientists intentionally want us to believe that all skeletons are very, very old?

Since caves are places where "cave men" have dwelled, it is critical to calculate very high dates for "cave men," meaning it is important to make their bones seem very, very old. The goal is to get the date prior to 6,000 B.C., when most Christians believe Adam and Eve lived. When they can do that, by intentionally ignoring key factors, it appears the Bible is not accurate.

In addition, most cave drawing were drawn using organic material, such as blood. Would the humidity in caves affect the dating of cave drawings? Absolutely!! Yet the dating of cave drawings never takes into account the high humidity in caves.

Kennewick Man

"Kennewick Man" (or Richland Man) is a skeleton which was found in central-southern Washington state in 1996.

The skull of Kennewick Man was found in a pond or lake which had been formed by the McNary Dam in Kennewick on the Columbia River. The dam had been completed in 1954.

The dam was built for irrigation purposes, meaning the annual rainfall in that area is lower than normal (about 6 to 8 inches of annual rainfall).

While his skull had been found in a pond, the rest of his bones had been scattered and were found near the Columbia River.

Because the dam was finished in 1954, the vast majority of the time Kennewick Man was in the ground there was no dam in that area of the Columbia River.

No matter when Kennewick Man died, his bones were exposed to the flooding of the Columbia River, plus the bones were exposed to rain, humidity, moisture in the soil (i.e. water which came from the river through the soil), and so on.

The dirt near a river is always very moist because the water seeps through the dirt near the river. Thus, his bones would have been subject to constant moist dirt.

Furthermore, if there had been any hills around where the bones were found, the run-off from the rain which landed on the hills would have passed right over Kennewick Man's bones.

Furthermore, because his skull was found separated from his body, his body had probably not been buried deep beneath the soil, meaning his body was probably originally put in a shallow grave, near the river. Had it not been put in a grave, animals would probably have eaten the flesh and bones many years earlier.

Thus, the bones of Kennewick Man were constantly subject to moisture and constantly the radioactive isotopes of his bones were being leeched or pushed out of the bones by the moisture.

Under ideal conditions, the lowering of the percentage of radioactive material in a sample is only caused by decay over time. But in the case of this man, the lowering of radioactive material was exacerbated (i.e. intensified) by the additional actions of water leeching radioactive materials from the bones.

Thus, when scientists determined the percentage of radioactive material in his bones, if they did not take into account an estimate of how much *extra* radioactive material was leeched out of the bones by a river flooding, by rainwater, by moist soil next to a river, etc., their dates would be very, very wrong.

In reality, *the scientists did not take any of these things into account*. All they did was measure the percentage of radioactive isotopes!!

When the Kennewick Man skeleton was radiometric dated, his skeleton was dated to be 9,000 years old. This is scientific nonsense because zero moisture the bones would have been exposed to was taken into account in the date.

Rather than providing a single date; scientists should have chosen a range of dates for this skeleton, where both endpoints of the range took into account an estimate of moisture and heat. However, scientists totally ignored these items and simply gave a single date as if the skeleton, on the day he died, had been wrapped in plastic, frozen and protected from all kinds of moisture, heat and light.

To ignore the moisture, heat and other items; is incompetence at best. But there was no incompetence; there was intentionally sloppy science which reflected an inexcusable lack of integrity. The dates they provided for this skeleton were wrong by a wide margin.

This skeleton was probably of a man who died less then 500 years ago. It is highly unlikely this man died more than a thousand years ago, considering he died and was buried next to a large river.

So here is the key question, why would scientists intentionally ignore a large number of factors related to the dating of his bones?

By giving his bones a date of 9,000 years old, they are claiming to prove that Adam and Eve were not placed on this earth about 6,000 years ago, which would be the date a Bible scholar would pick for the creation of Adam and Eve.

In other words, their pretended incompetence was really a ***highly calculated attack*** on the divinity of the Bible!!

Scientists wanted Kennewick man to be dated 3,000 years prior to Adam and Eve, even if it took blatant negligence to come up with that date!!

Not only is the theory of evolution based on a long series of bogus science and absurd assumptions, the theory of evolution is supported by a total lack of integrity. Any scientist should know that moisture leeches radiometric isotopes from bones, thus to intentionally ignore highly significant leeching can only be called a calculated lack of integrity.

Other Pre-Historic Humans

The bones of any true human being (*homo sapiens sapiens*), which truly date back before the flood of Noah, may have been submerged in massive amounts of water for more than a year due to the flood in the time of Noah. The bones of these individuals (if any have been found) are also not adjusted for massive leeching of radioactive materials in the bones.

Most of the bones which scientists have found of "near humans" are not true *homo sapiens sapiens*. The origin of these near-humans is unknown. But you can rest assured that the truth about when true *homo sapiens sapiens* have died is consistent with the Biblical account, if the flood of Noah and other known factors which affect radiometric dating are taken into account.

But these factors are not taken into account, thus the dating of true ***homo sapiens sapiens*** is not in any way accurate!!

Here is my point. The theory of evolution is ***not*** about truth and the theory of evolution is definitely ***not*** about science. Science today is all about justifying the theory of evolution, even if it takes outright deception. Deception, in this case, is intentionally ignoring known scientific facts. If the date of bones is calculated to be before Adam and Eve, science accepts the date because it is "what they want to hear" to justify philosophical naturalism.

Additional Situations

In nature, animals need water. In certain locations, such as water holes (i.e. small ponds or other sources of water); animals tend to congregate.

When you have a wide variety of animals at a specific water hole, there is likely to be fighting, either because these species always fight when they are in the same location or they may fight to get water, such as during a drought.

In either case, water holes are common locations to look for, and find, animal skeletons. These skeletons have exactly the same potential problems for dating errors that the Kennewick man had.

In addition, some climates have a lot more rain than other climates. This is never taken into account when dating skeletons.

In addition to these things, little is known about how much of the earth was covered with water during the flood of Noah. We do know that parts of the earth were covered with water for more than a year.

However, some parts of the earth may have been covered by water for less than a year or for no time at all (Noah didn't travel all over the world to know how much of the world was covered with water). Other parts of the earth could have been covered by water for much, much more than a year.

For example, suppose Africa was covered with water for 50 years after the flood of Noah. This would mean that all skeletons of all animals (including near-human skeletons), which died prior to the flood, would be submerged for 50 years, yielding dates *far too high* (i.e. far too long ago) when dated by radiometric means. Many of these near-humans could also have been directly exposed to the rain and heat for many years.

What is interesting about the flood is that the writers of the Bible did not know that radiometric dating techniques would be intentionally flawed in the twenty-first century. Thus, *the writers of the Bible cannot be accused of fabricating the flood of Noah in order to justify God placing Adam and Eve on this earth about 6,000 years ago*. There was no scientific reason to fabricate the flood of Noah when the Bible was originally written because they didn't know about radiometric dating (though certainly God knew).

A great deal is made by scientists that the ark of Noah could not have held animals unique to Australia, for example. The Biblical account of Noah was written by Noah or from records written by Noah. Noah did not know how much of the earth was covered with water and he probably never visited Australia.

Furthermore, even if many animals had become extinct in Australia (for example), there is no reason to think that God could not have put them back in Australia after the flood, assuming they were there before the flood.

This, of course, is just one example. It must be remembered that the Bible was not written as a science textbook, it was written to teach about God and his prophets. Many, many details about the flood and other events in the Bible are left out because science was not the purpose of the Bible.

Another Problem - Radiation (including Heat)

Suppose a skeleton is found in the middle of a large desert. Is this skeleton exempt from errors in radiometric dating?

The answer is that it is ***not*** exempt from gross errors.

Scientists may not know when the climate changed and an area of earth which was highly exposed to water (e.g. the area was covered by an ocean) suddenly or slowly became exposed to dry heat and became a desert.

But that is not all, radiation, including heat, can speed up the appearance of decay of radioactive material. This can be caused by evaporation (technically: volatilization), the migrating of atoms, exciting the atoms by heat, etc.

For example, consider the Kaupelehu Flow, Hualalai Volcano; which occurred in 1800-1801. Twelve different samples were taken of the lava. The dates for these samples ranged from 140 ***million*** years ago to 2.96 ***billion*** years ago. While the ocean water may have affected the dating of these samples; many things could affect the dating of any sample! For example, volcanic rock is known to be hot both during and after the explosion.

Thus, a volcano which is known to have occurred a little over 200 years ago, dated to as much as 3 ***billion*** years ago using state-of-the-art dating techniques.

Five different samples were taken from Mt. St. Helens, in Washington state; which erupted in 1986. The samples dated from ***half a million*** years ago to almost 3 ***million*** years ago. No ocean water was involved in Mt. St. Helens, only heat was involved.

What does this tell us about fossils of near-humans who were killed by a volcano, or whose skeleton had volcano lava run over it after the death of the individual? It tells us the dating of fossils is a very inexact science. That is exactly the way the scientific establishment likes it because their current methods give them the dates they want.

What Should Be Done

First, scientists should do many experiments to try to understand just how significant a skeleton soaked in water (due to flooding of a river, flooding of a pond by rain, etc.) and other scenarios, affects the dating of organic matter.

For example, they should take two bones, either from the same animal or from two animals which died on the same day, and expose the two bones to vastly different conditions over several years time. Then they should date the bones.

Using information from their research, they should then give ***realistic ranges of possible dates*** as to when a person or animal died, since current weather conditions are not necessarily the same weather conditions which existed a thousand years ago.

For example, in the case of Kennewick man, instead of saying that this man died 9,000 years ago, ***which is totally ludicrous***, scientists should have taken into account highly probable flooding rates, the known moisture of soil next to the river, estimated rainfall levels, nearby hills, etc. etc. Then they should have given a ***range of dates*** as to when he died.

The true ranges of dates, if integrity had been used to date Kennewick man, would ***not*** have been from 500 years to 9,000 years, for example, because it is known that this river would have flooded and that the soil was moist (because the body was next to a river) and that a 9,000 year date would be ludicrous.

The true range would have been something like: from 500 to 2,000 years old. Actually, the bones could have been of a man who died 200 years ago. That is how much water this skeleton may have been exposed to.

The example of Kennewick man is a good example of the passion of scientists to justify evolution. There is simply no excuse to simply take a bone they know nothing about and measure the level of radioactive material in the sample. It is inexcusable!!!

However, even though it is inexcusable, there is a reason for their incompetence. The reason is that the "scientific establishment" (the people who control the media, schools, etc.) wants to get the dates of fossils as old as possible to justify the theory of evolution and belittle those who believe in the Bible.

When Did Adam and Eve or George and Mary Live?

The Biblical dates of Adam and Eve are about 6,000 years ago. The theory of evolution dates George and Mary to be 100,000 years ago, at least.

According to the Bible, the length of time from Adam and Eve to the B-2 bomber was 6,000 years.

According to the theory of evolution, the length of time from George and Mary was 100,000 years?

So which is more logical when thinking about technology?

First of all, scientists can only trace significant technology (e.g. the use of the wheel for transportation and the building of roads) back perhaps 4,000 years (ignoring bogus dating techniques).

This means that in the time span of 4,000 years, humans went from knowing very little about technology to building a B-2 bomber and putting men in space.

With this in mind, if George and Mary had existed 100,000 years ago, it is safe to say that humans should have built the B-2 bomber 90,000 years ago (being generous, as always, to the theory of evolution).

Why in the world did it take 100,000 years to build the B-2 bomber? Why, for the first 96,000 years, did humans not progress at all in science and then suddenly, in 4,000 years time, they perfected the wheel for transportation and built the B-2 bomber?

As always, the theory of evolution ignores reality. If George and Mary had our DNA, the B-2 bomber would have been build 90,000 years ago.

Summary

In summary, the dating of bones and fossils is a very imperfect science, riddled with intentional errors. It is one of the most subjective aspects of the evolution debate. A person can read into the evidence any way they wish.

From an unbiased, scientific viewpoint; the creation scientists have a far stronger case for their dating techniques than do the evolutionists because they take environmental factors into affect.

As far as the evolution debate is concerned, this aspect of the debate is so complex and so affected by pre-conceived notions (such as the fact that many dinosaur fossils are dated according to their location on the phylogenetic tree), that for all practical purposes, dating techniques cannot be used as a proof for evolution or as a proof for creation science.

Considering that modern dating methods are corrupted by known flaws in radiometric dating; by techniques which are known to be based on an assumption that the theory of evolution is a fact; and by other flawed techniques, it is clear that the dating of bones, fossils, etc. is a non-differentiating issue (i.e. the issue cannot differentiate between the theory of evolution and creation science).

While the reader may think that more information is needed to determine who "wins" this issue; the fact is that all the information in the world isn't going to end this aspect of the evolution debate. Some people are blind to the truth because they don't love truth.

The good news is that there are other issues of the evolution debate in which the data is very convincing because real scientific data is available from living species. One of these sources of excellent information is that of "genetic entropy," meaning the deterioration of the DNA of all animals. Much will be said about verifiable data throughout this book.

Introduction to the Mathematics of Evolution

Chapter 9

DNA and RNA

Introduction

The rest of this book will get increasingly involved with DNA. This chapter will introduce the reader to the molecule called: DNA.

Subsequent chapters will get more and more involved with DNA, so it is important to have a sold basis for understanding DNA.

It would also be wise to look at outside resources which discuss DNA. It is far beyond the scope of this book to discuss many issues related to DNA. This book will focus on very specific issues. A broader understanding of DNA would be very helpful to the reader as this book progresses.

DNA (Deoxyribonucleic Acid)

DNA is a very large, very complex molecule made up of several different kinds of small molecules.

"Nucleotides" are a type of molecule found in DNA. There are only 4 different kinds "nucleotides." Nucleotides are the key to what DNA is able to do. The sequence (i.e. order) of nucleotides is what provides the "information" that is needed for the cells to function.

To understand DNA, consider a large encyclopedia of 100 volumes. Even though a large set of encyclopedia volumes is a huge set of books, and would be very, very heavy to lift, the encyclopedia only consists of 26 letters of the English alphabet. A person could say that an encyclopedia consists of only 26 different letters; however, all of the letters are repeated many, many times in an encyclopedia.

Yes, an encyclopedia will also have numbers (e.g. 0,1,2,3,...,9), special characters (e.g. space, %, $, @, &, etc.), but still an encyclopedia, no matter how many volumes, still has only 26 letters of the alphabet, plus a few other characters.

For example, consider that a word in the English language, such as the word: "tergiversation" (which is the act of being deliberately ambiguous) is nothing but a permutation (i.e. a unique way of ordering the letters) of the 26 possible letters of the English alphabet which happens to have 14 consecutive letters in it.

An encyclopedia has a lot of words and thus a lot of individual letters, if we ignored the words and only looked at the letters. In fact, when we look at DNA we may look at the letters (i.e. the nucleotides) and forget to look at DNA as "words" or "segments" which have meaning as a group of letters.

DNA only has 4 letters in its alphabet but the "words" in DNA are far more complex than the words in an Encyclopedia. Human DNA consists of a chain of 3 billion nucleotides or 3 billion "letters"!! Thus, DNA is really nothing but a long string of 4 nucleotides. Actually the nucleotides are paired together, thus there are technically 3 billion "pairs" of nucleotides in human DNA, meaning 6 billion individual nucleotides.

More About DNA

Visually, DNA can be imagined to be like a very long ladder. A ladder has two sides (i.e. two long side-rails). These two sides are joined together by the steps, which, in a real ladder; people step on to climb the ladder. When a person is climbing a ladder, their hands usually grab onto the two side-rails of the ladder, and their feet step on the rungs.

When comparing a ladder to DNA, the side-rails of the ladder can be compared to a long sequence of alternating types of molecules. A sugar molecule and a phosphate molecule alternate many times to create each side-rail of the ladder.

In other words, many "sugar-phosphate" molecule pairs make up each side-rail of the DNA ladder to create two "sugar-phosphate backbones," one on each side of the DNA molecule.

For example, human DNA has 3,000,000,000 alternating pairs of the sugar-phosphate backbone in one long row. This is just one side-rail of the ladder. The other side-rail also has 3 billion alternating pairs of the sugar-phosphate backbone.

The two side-rails of DNA are designed such that the sugar molecules are across from each other. Each of the sugar molecules (dioxyribose) attaches to a "nucleotide" molecule on the "step." Each sugar molecule (on each side-rail) has a nucleotide attached to it. Because each of the side-rails attach to a nucleotide, the "steps" of the ladder are a pair of nucleotides because each of the two nucleotides attach to an opposite side-rail.

Thus, when there is a rung on the DNA ladder, there are four consecutive molecules. A sugar molecule on each side-rail and a nucleotide attached to each side-rail. The two nucleotides are bound together by hydrogen bonds.

On each side-rail, and between each sugar molecule (which is where the rungs are), is a phosphate molecule holding the sugar molecules together on the side-rails.

DNA can be drawn like this (the hydrogen bond is not a physical object, but a type of attraction between two molecules):
(S=sugar, P=phosphate, N=nulceotide, H=hydrogen bond)

```
P        P
S-N-H-N-S
P        P
S-N-H-N-S
P        P
S-N-H-N-S
P        P
S-N-H-N-S
P        P
S-N-H-N-S
P        P
...
```

The two alternating P and S molecules are the two side-rails of the DNA ladder. The S-N-H-N-S combination constitute a rung.

There are four different kinds of nucleotides (which are also referred to as "bases"):
'A' is for Adenine
'T' is for Thymine
'C' is for Cytosine
'G' is for Guanine

Substituting one of these nucleotide bases for each 'N' in the above chart, we might see this sequence:

```
P        P
S-A-H-T-S
P        P
S-T-H-A-S
P        P
S-C-H-G-S
P        P
S-G-H-C-S
P        P
S-C-H-G-S
P        P
...
```

Note in the above graph that if an 'A' attaches to one sugar molecule, on one side-rail of the DNA, a 'T' is supposed to attach to the opposite sugar molecule, on the other side-rail of the ladder. These two molecules are bound together by hydrogen bonds.

Likewise, if a 'T' attaches to one sugar molecule, on one side of the DNA, an 'A' attaches to the opposite sugar molecule, on the other side of the ladder.

In other words, an 'A' and a 'T' should always be joined together on the same rung.

Likewise, a 'C' and a 'G' should always be joined together to form a single rung of the ladder.

Adenine actually forms two hydrogen bonds with thymine. Guanine forms three hydrogen bonds with cytosine. These hydrogen bonds, along with the two nucleotides, are referred to as "base-pairing."

Now we can take the above chart and improve on it ('2H' means two hydrogen bonds and '3H' means three hydrogen bonds):

```
P         P
S-A-2H-T-S
P         P
S-T-2H-A-S
P         P
S-C-3H-G-S
P         P
S-G-3H-C-S
P         P
S-C-3H-G-S
P         P
...
```

Because if we see an 'A' on one side of the rung, we know that there is a 'T' on the other side of the rung, generally scientists only talk about one side of the "ladder," and thus when the reader sees an 'A' in a chart, they are supposed to mentally supply the 'T' on the other side. Or if the reader sees a 'T" they are supposed to understand that an 'A' is on the other side. Ditto for 'G' and 'C'.

Thus, the entire chart above would normally be designated as simply:
ATCGC

"Unzipping DNA"

In the process of protein synthesis, which will be discussed in the next chapter, DNA is "unzipped." What does that mean? What it means is that all of the hydrogen bonds are broken and the DNA, instead of being one ladder with two sides, becomes two ladders with one side. For example, the above diagram would look like this:

```
P               P
S-A           T-S
P               P
S-T           A-S
P               P
S-C           G-S
P               P
S-G           C-S
P               P
S-C           G-S
P               P
...
```

Once "zipped apart," the two half-sides of DNA can be built by new nucleotides either to make two complete DNA strands (which is how one DNA molecule is converted into two DNA molecules) or a side can be used to make RNA, which will be discussed later.

More Terminology

As mentioned above, when describing the sequence of nucleotides in a DNA strand, scientists generally only talk about the nucleotides which are connected to one side-rail of the ladder.

Thus, when you see something like this (the space is simply to make it easier to view):
ATCGCATCTG GGAAGCTACC
these "letters" represents the consecutive nucleotides *on one side of the ladder*. The reader is expected to fill in the other side, if needed.

The above DNA section can be represented without showing the hydrogen bonds, and it can be shown like this (a '-' represents a phosphate molecule and a '=' represents a sugar molecule on the side of the ladder):

```
-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
 A T C G C A T C T G G G A A G C T A C C
 T A G C G T A G A C C C T T C G A T G G
-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
```

A DNA molecule is a double-helix (a 'helix' means a spiral shape), meaning it is looks like a very, very long ladder that has been twisted like a spiral staircase.

When "counting" how many nucleotides there are in a DNA strand, generally only one side is counted, as mentioned above. Thus, when it is said that human DNA has about 3,000,000,000 nucleotides, they are really talking about 3,000,000,000 nucleotide *pairs*, meaning they are really talking about 6,000,000,000 nucleotides in a single human DNA.

The human body has about 100 trillion cells. Each cell has a complete DNA strand inside its cell nucleus. Exceptions to this rule are eggs, sperm and red blood cells. Thus, your body contains about 100 trillion DNA molecules, each of which has 6,000,000,000 nucleotides (counting the nucleotides on both sides of the DNA).

> *"If the chromosomes in one of your cells were uncoiled and placed end to end, the DNA would be about 6 feet long. If all the DNA in your body were connected in this way, it would stretch approximately 67 billion miles! That's nearly 150,000 round trips to the Moon."*
> The New Genetics Chapter 1

But the most amazing thing about human DNA is not its shape or size, but what it does.

The sophistication of what human DNA accomplishes is literally beyond the ability of the human mind to comprehend.

As if that weren't enough, every cell in our body also has multiple mitochondria. Mitochondria have their own DNA, though the DNA in mitochondria is very short compared to the very, very long main DNA of the cell.

But mitochondria are not the only organelle in the human cell that has its own short DNA.

This discussion of DNA is very primitive. It is like describing the space shuttle as a "big grey tube with wings." People get PhDs and Nobel Prizes for discovering things about DNA.

RNA

An RNA molecule has only a single side-rail. RNA is much like one of the unzipped DNA molecules above. Each sugar on this one side-rail has a nucleotide attached to it. The sugar in the side-rail of RNA is a different combination of sugars than that found in DNA.

In RNA, the four nucleotides are:
'A' is for Adenine
'U' is for Uracil (replaces Thymine)
'C' is for Cytosine
'G' is for Guanine

Thus, an RNA strand might include this segment:

```
-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-
 A A U G C A U C U G G G A A G C U A C C
```

RNA can also be looped.

RNA has many functions, and thus there are many different kinds of RNA.

DNA Replication

Due to the way that DNA is designed, it is easy (from a visual perspective) to understand how DNA is replicated (i.e. how one DNA strand is converted into two DNA strands).

Now instead of looking at DNA as a ladder, let us think of it as a very long zipper.

In DNA replication, the DNA is "unzipped," as shown above, and the DNA is broken into two half-DNA strands, which look like RNA, but have a different set of nucleotides.

Each half-strand consists of one side-rail and the nucleotide that is associated with the sugar molecule on that side-rail.

A process essentially takes *each* of the two half-DNA strands, and builds a new, complete DNA strand by combining new nucleotides with each half; by matching an A with a T, a T with an A, etc.

So if we follow a single rung, after unzipping the DNA, suppose there is an A on one rung. Attached to the A will be a T (which will be on the new rung).

The other side of the unzipped DNA will have a T on that rung. Thus, an A will added to the new rung.

This results in a single DNA molecule becoming two identical copies of the original DNA strand.

Using the above unzipped DNA section, this is what it would look like:

```
P     P       P     P
S-A-T-S       S-A-T-S
P     P       P     P
S-T-A-S       S-T-A-S
P     P       P     P
S-C-G-S       S-C-G-S
P     P       P     P
S-G-C-S       S-G-C-S
P     P       P     P
S-C-G-S       S-C-G-S
P     P       P     P
...
```

Note that the two DNA sequences are identical.

If the reader has any problems understanding this chapter they are encouraged to look at a biology book to get more of a graphical understanding of what is going on.

Introduction to the Mathematics of Evolution

Chapter 10

Protein Synthesis

Introduction

In the next chapter we will begin our detailed discussion of how DNA fits into the issue of evolution. But first, it is necessary for the reader to understand what a "protein" really is and how proteins are made in the body.

Think, for a minute, about a wooden rocking chair. If you look at the individual parts which make up the chair you will see the 4 legs, the seat, the structure the person leans back against, the wooden rods to strengthen the back of the chair, the curved wood which allows the chair to rock, and so on.

If you took the rocking chair apart, piece by piece, you would see several different kinds of wooden patterns which are put together to make the chair.

There are hundreds of different kinds of cells in the human body. Each type of *cell* in the human body has many structures in them which can be compared to a rocking chair. Each of these cell structures are made up of smaller structures, much like a wooden rocking chair is made up of smaller wooden rods and other pieces.

In a cell, the individual parts of the chair can be compared to proteins. The entire structure of the chair might be called a "protein structure." The pattern to make the different designed parts of the chair (i.e. protein structure) come from sections of DNA called "genes."

For example, let us consider the "ports" in the cell membrane through which food and other things pass into the inside of the cell. Essentially a "port" is a hole in the side of the cell membrane. However, it is a "hole" which is made of proteins which are bound together to form a structure.

The "port" is a protein structure which is made up of proteins with different shapes. The DNA includes the templates which are used as patterns for making the different shaped proteins used in each port.

Just like a person would look at a blueprint before starting to build the individual pieces which make up a wooden rocking chair, the body turns to the DNA to find the blueprint (i.e. template, pattern or cookie-cutter) to make the pieces (i.e. proteins) which make up the structures inside of cells (or on the surface of the cell or outside the cell).

Protein synthesis, or protein biosynthesis, is the process by which the genetic information in DNA (deoxyribonucleic acid) is converted into proteins. All of this occurs inside the cells. The term "proteins" in this context includes proteins, enzymes and some other complex molecules which are made from polypeptides, which will be discussed below.

A gene is a pattern, or cookie-cutter, or blueprint, which is used by the cell, during protein synthesis, to make the individual proteins needed by the cell. The DNA is the starting point for making proteins.

DNA is like the blueprint of a building, however, DNA also includes the blueprint for the construction of the building, including the supervisors (supervisor proteins), the laborers (laborer proteins), the messengers (messenger proteins), etc., all of which are functions accomplished by proteins inside the cell.

The DNA does not become the proteins, rather it is used like a "copy machine," it simply allows other molecules to "copy" its patterns over and over again.

Bacterial Flagellum

As one example, in certain kinds of bacteria there is a protein structure called a flagellum. The flagellum is like a long tail which sticks outside of the bacteria cell, by which certain bacteria swim around. It is a large protein structure. The "motor" which turns the tail is inside the cell. Both the motor and the tail are made of proteins.

However, this large protein structure is made up of smaller protein structures. Taken together, this large structure has been compared to an outboard motor engine for a speedboat.

Here are some of the smaller protein structures which make up the flagellum, which is itself a large protein structure:
Hook (similar to universal joint)
Filament (similar to propeller), meaning the long tail
Rod (similar to drive shaft)
S ring and M ring (similar to rotor)
Bushing, L ring and P ring
Stator, studs and C ring
Inner (plasma) membrane
Outer membrane
Peptidoglycan layer
Periplasmic space
and so on.
(see: Darwin's Black Box, by Dr. Michael J. Behe, page 71)

The point is that each of these smaller protein structures are made up of individual proteins, which came from patterns on the DNA.

Building this large protein flagellum requires supervisors; just like building a skyscraper would require supervisors. The supervisors who oversee the construction of the flagellum *are proteins*.

The workers which actually put the proteins in place, as they are built, *are also proteins*. The accountants who tell the DNA which proteins to make next are also proteins. The messengers who provide information to the DNA for repairing damages to the structure are also proteins.

The entire process by which the flagellum is made is done by proteins, even the communication processes are accomplished by proteins.

The process by which these patterns on DNA are used to form proteins is the subject of this chapter on protein synthesis.

The terms used in this chapter will be used freely in subsequent chapters, so it is important to understand the process of protein synthesis, especially the last step.

While the process of protein synthesis may seem complicated, in reality this chapter is a highly simplified overview. An entire book could be written on all the complexities and exceptions which occur in different organisms with regards to protein synthesis.

This chapter will describe what goes on in a eukaryotic cell and especially in bacteria.

Step One - Phase One of Transcription

Transcription is the actual act of using the DNA as a template to create a new protein.

DNA resides in the nucleus of the cell. DNA consists of about 3 billion "nucleotides," or to be more accurate: 3 billion *pairs* of nucleotides.

Step one is to convert a section of DNA into RNA, which is a molecule similar to DNA. RNA itself will later be used in the process as a template in the process of choosing the sequence of specific amino acids which will actually make up the protein. It is the amino acids which become part of the protein, not the original DNA or even the RNA copy of the original DNA.

Thus, transcription takes a *stationary* blueprint (the DNA) and copies it onto a *traveling* blueprint (the RNA) which will travel to a different part of the cell (outside of the nucleus) where the protein is actually built.

In other words, the DNA will stay in the nucleus, so it can be used over and over again, but the copy of DNA, the RNA, will travel outside of the nucleus and will become the actual pattern which will be used to make the protein.

Transcription, the conversion of DNA into messenger RNA, or mRNA, is actually in two phases.

In phase one of transcription, a molecular machine (called: RNA polymerase) unzips a section of DNA. However it should be noted that RNA polymerase does not act alone. Each type of cell provides different "helper proteins" to help the RNA polymerase do its job for that type of cell.

Starting at one end of a gene, called the "promoter sequence" or "promoter region," and continuing until it reaches the "terminator" sequence, it starts building a type of RNA called "pre-mRNA" (i.e. pre-messenger RNA) or "Nuclear RNA" because it is inside the nucleus of the cell.

In other words, the RNA polymerase "unzips" a section of DNA so that the double helix is now two single-sided helix strands (it unzips only a single section of DNA). The unzipped section is not the entire DNA, only the section of DNA needed for this particular job.

This process picks one of the two sides (a specific side) of the DNA and uses it as a template to make complementary single-sided RNA, namely pre-mRNA.

On a DNA strand, an "A" always has a "T" next to it on the DNA (unless there has been a mutation). However, when converting a side of DNA into pre-mRNA, an "A" is actually paired with a "U" (uracil), as the following chart shows:

An "A" on the DNA becomes a "U" on the pre-mRNA (uracil).
A "T" on the DNA becomes an "A" on the pre-mRNA.
A "C" on the DNA becomes a "G" on the pre-mRNA.
A "G" on the DNA becomes a "C" on the pre-mRNA.

These combinations are called "complimentary" because if you know one of the nucleotides, you automatically know its "complement" (i.e. what is on the other strand).

Thus, DNA has nucleotides: A, C, G, T and RNA has nucleotides: A, C, G, U.

RNA polymerase has been described as a "battery-powered spider" as it crawls along the DNA unzipping a section of the DNA.

The gene portion of DNA, which is what is unzipped, contains alternating sequences of exons and introns. Exons and introns are segments of nucleotides, but like all segments of nucleotides, they have names to identify their functions.

Exons are the section of the gene which will actually "code" for proteins, meaning the exons actually become the finished blueprint for making the protein.

Introns do not code for proteins, thus they do not become part of the proteins, but are thought to be instructions to determine which exons are needed for the specific protein being requested.

For example, the average gene in human DNA can be used to create 10 different proteins. Some genes can create 50 different proteins. It is thought that introns contain the instructions on how to put together these different proteins from the same gene.

In any case, in this step of transcription; both the introns and exons are kept and are put on the pre-mRNA. The pre-mRNA is an exact copy (actually it is a complement) of one side of a section of DNA, except that a U replaces a T. More will be said about exons and introns in the next step.

Step Two - The Second Phase of Transcription

In the second phase of transcription (also called "RNA splicing"), the pre-mRNA is itself copied, and its copy is called mRNA. mRNA is the actual blueprint to make the protein.

In copying pre-mRNA into mRNA the introns are left out of the copying, meaning they are "spliced" out of the RNA and are not part of the mRNA.

Thus, pre-mRNA contains both exons and introns, but mRNA only contains exons.

However, it is also in this phase that "RNA splicing" *removes some of the exons*. In Step One all of the exons are copied to the pre-mRNA. However, in this phase, not only are all of the introns spliced out, but also some of the exons are intentionally spliced out.

Why are some of the exons left out? The reason is that the DNA is being used to create one protein at a time, even though it is capable of creating ten different proteins (in this example). In other words, there are enough exons to create ten unique and different proteins, but it only creates one protein at a time, thus not all of the exons are used in the creation of a single protein (the protein at this point is still an mRNA).

That is why, in the process of creating a single protein, many of the exons are left out during the second phase of transcription.

It is in this RNA splicing that *different patterns of exons are combined together* to ultimately be the pattern to create the exact protein which was requested!!

If you think this is simple, consider that some human genes can create 50 different proteins. The exons on the DNA must stay in the same sequence (i.e. order) on the mRNA, but different exons are left out for each type of protein. Try to figure out how to do that in your spare time!!

The intron, as it is spliced out, no doubt provides the intelligence to determine if the exon, which is next to it, is also spliced out or if it stays to become part of the mRNA. This is called "alternative splicing" because different sets of exons lead to different proteins.

Thus, pre-mRNA and mRNA not only differ in the fact that there are no introns on mRNA, but they also differ in that there is only a subset of exons on the mRNA, so that a specific protein can be manufactured later in the process.

Step Three - Moving the mRNA out of the Nucleus

In eukaryotic cells (OK, in most eukaryotic cells) the DNA is protected inside of a membrane called the "nuclear envelope." The nuclear envelope has two layers. The envelope has many ports which are called "nuclear pores."

mRNA is made inside of the nuclear envelope, but processing of the mRNA occurs outside of the nuclear envelope. Thus, the mRNA must travel through one of the nuclear pores. Each nuclear pore is itself built of many proteins.

Ribosomes (to be discussed next), which are also proteins, are also created inside the nuclear envelope in a subnuclear body called the nucleolus. Ribosomes also must pass through a nuclear pore.

So how does a large molecule pass through a nuclear pore? The answer is a "carrier protein." The carrier protein must be able to latch onto the mRNA and guide it through the nuclear pore. This is how one website describes the carrier protein:

> *"Each carrier protein is designed to recognize only one substance or one group of very similar substances. The molecule or ion to be transported (the substrate) must first bind at a binding site at the carrier molecule, with a certain binding affinity. Following binding, and while the binding site is facing, say, outwards, the carrier will capture or occlude (take in and retain) the substrate within its molecular structure and cause an internal translocation, so that it now faces the other side of the membrane. The substrate is finally released at that site, according to its binding affinity there. All steps are reversible."*
> Wikipedia - Carrier Protein

Actually, various molecules are constantly passing through the nuclear envelope in both directions.

Step Four - Translation

Once the mRNA is outside of the nucleus it then heads for a section of the cell which includes the ribosome. The ribosome area of a cell is one of the most fascinating areas of a cell. It is also one of the most complex areas of the cell.

The ribosome looks like a large ball of yard. In other words, it looks like a sphere that is made of yarn. This is how one website describes the ribosome.

> *Ribosomes are among the biggest and most intricate structures in the cell. The ribosomes of bacteria contain not only huge amounts of RNA, but also more than 50 different proteins. Human ribosomes have even more RNA and between 70 and 80 different proteins!*
> *. . .*

For many years, researchers believed that even though RNAs formed a part of the ribosome, the protein portion of the ribosome did all of the work. Noller thought, instead, that maybe RNA, not proteins, performed the ribosome's job. His idea was not popular at first, because at that time it was thought that RNA could not perform such complex functions.

Some time later, however, the consensus changed. Sidney Altman of Yale University in New Haven, Connecticut, and Thomas Cech, who was then at the University of Colorado in Boulder, each discovered that RNA can perform work as complex as that done by protein enzymes. Their "RNA-as-an-enzyme" discovery turned the research world on its head and earned Cech and Altman the 1989 Nobel Prize in chemistry.

The New Genetics, Chapter One

It should be noted that the discovery of Cech and Altman also helped the evolutionist cause by helping evolutionists explain that complex enzymes did not need to exist to perform some of the tasks needed for the "first living cell." It you want to win a Nobel Prize, discover something which helps the evolutionists.

Rachel Green, however, later discovered that the RNA nucleotides were not needed for assembling a protein. Instead, she found, the RNA helps the growing protein slip off the ribosome once it's finished.

By the way, ribosomal RNA is called rRNA. There are many different kinds (i.e. functions) of RNA.

Well, now that the history lesson is complete, let us look at what really happens in the ribosome area.

First, the mRNA, which came through the nuclear port, and at this point is as straight as an arrow, is attached to the ribosome. Once attached, the ribosome can do its work.

There are four terms which need to be understood at this point:
First, the mRNA (which contains instructions/patterns taken from the DNA)
Second, amino acids (proteins start as a string of amino acids)
Third, polypeptides (polypeptides are the resulting string of amino acids)
Fourth, proteins (proteins are polypeptides which have been folded into the shape of the protein).

Study that list for a few moments.

Ribosome looks at mRNA three consecutive nucleotides at a time. How many different ways can three consecutive nucleotides be ordered? The answer is 4^3 or 64. The '4' is the number of different nucleotides and the '3' is the number of nucleotides which are looked at at the same time by ribosome.

Three consecutive nucleotides are called a "codon" or triplets or tri-nucleotide sequences.

Now we have a problem. There are only 20 different kinds of amino acids. We have 64 different codons, but only 20 amino acids. Try to figure out how 64 codons can make 20 different amino acids.

Not to worry, the ribosome can make the conversion. The "dictionary" which controls which codon is matched with which amino acid is called the "genetic code" (though the genetic code is not universal between species).

However, three of the 64 codons do not translate into an amino acid. The codons: UAA, UGA, and UAG serve as "stop-translation" signals, which terminate the making of the polypeptide. AUG can be a start codon or can be made into the amino acid methionine.

Within the cell are free-floating amino acids. A type of RNA called transfer RNA (i.e. tRNA) captures these amino acids and takes them to the ribosome. Actually there is a different type of tRNA for each type of amino acid and each tRNA can correspond to one or more codons.

The ribosome analyzes each codon and then selects the correct tRNA, meaning the correct amino acid is chosen to add to the growing polypeptide. It does this until it reaches a "stop-translation" codon, which tells the ribosome to "stop" the building of the polypeptide and release it.

The rRNA then helps the polypeptide be removed from the ribosome and you then have a free polypeptide.

All of this happens amazingly fast!!

This step of protein synthesis is far more complex than anyone truly understands. But given enough time, scientists will figure it out in even more detail. Much is already known about tRNA, but I will not discuss the details here.

Step Five - The Folding of the Polypeptide

OK, at this point we have a polypeptide which has been removed from the ribosome. We can think of it as being "straight as an arrow" at this point, just like the mRNA was.

But proteins are not straight; they have a very specific shape. Actually, it is the shape of the protein which determines its ability to be integrated into a protein structure. Actually, it is more complicated than that.

Not only is the folding of the amino acids (i.e. polypeptide) important for the protein structure, but also at certain locations on the shape certain amino acids must be located so the different proteins will bind together or repel each other, etc.

In other words, in order for a protein structure to be strong, it must not only have proteins which have the right shape; so they can fit together like a puzzle; but the proteins (i.e. the amino acids) must "stick together" or repel each other, at just the right points. This is accomplished because some amino acids (remember a protein is nothing but a chain of amino acids) bind to other amino acids.

Also, some amino acids repel each other, which is also important in some cases. Some amino acids repel water and other amino acids are attracted to water. And so on. The

point is that it is not only the shape of the protein which is important, but also the order and types of the amino acids on the protein which is important.

So how do polypeptides get folded into the proper shape of a protein?

Polypeptides are folded, and in many cases chemically altered, in order to become proteins. A full discussion of this topic is far beyond the scope of this book. Instead a couple of key paragraphs from a book will have to suffice:

> *The explanation for the cell's remarkable efficiency in promoting protein folding probably lies in chaperones, a family of proteins found in all organisms from bacteria to humans. Chaperones are located in every cellular compartment, bind a wide range of proteins, and may be part of a general protein-folding mechanism. There are two general families of chaperones: molecular chaperones, which bind and stabilize unfolded or partially folded proteins, thereby preventing these proteins from being degraded; and chaperonins, which directly facilitate their folding. Chaperones have ATPase activity, and their ability to bind and stabilize their target proteins is specific and dependent on ATP hydrolysis. Binding of chaperones to partially folded proteins suggests that the folding process could be regulated at intermediate steps.*
> Molecular Cell Biology, by Lodish, Berk, et. al.

Here is a section of another paragraph:

> *Proper folding of a small proportion of proteins (e.g., the cytoskeletal proteins actin and tubulin) requires additional assistance, which is provided by chaperonins. Eukaryotic chaperonins, called TCiP, are large, barrel-shaped, multimeric complexes composed of eight Hsp60 units.*
> Molecular Cell Biology, by Lodish, Berk, et. al.

Suffice it to say: polypeptides are folded, and in some cases chemically altered, as they are converted into proteins.

Note the vast number of critical chemicals that are in your body, such as the amino acids. These come from foods. Now you know why your mother told you to eat healthy foods.

Step Six - Placing the Protein In the Cell

At this point we have the protein (so in a sense "protein synthesis" is complete), but the protein is not in its proper place in the cell yet.

A protein can basically be placed into one of three places:
1) Inside the cell, such as part of a protein structure,
2) Built into the cell membrane, such as a "port," where each port is composed of many proteins, and is itself a protein structure,
3) Placed outside the cell membrane, such as to "bind" to something or as part of a protein structure which extrudes outside the cell (such as the flagellum).

At this point the new protein has to be placed into the proper place. In many cases the new protein needs to be integrated into a complex biological structure, such as a flagellum, which is in the process of being built *or repaired*.

Guess what? More proteins come into play at this point to guide the new protein into the proper place.

However, at this point we need to pause and reflect.

In Step One above, the RNA polymerase was activated to start the process of converting a gene into a protein. What initiated or ordered the RNA polymerase to create a protein? The RNA polymerase is a puppet, doing only what it is told; so what is the puppeteer which is telling the RNA polymerase what gene to use?

For example, suppose a bacteria cell has just divided and it needs to create a flagellum so it can glide through fluids. Which proteins in the flagellum would logically be created first; the proteins in the base of the flagellum or the proteins in the tip of the tail of the flagellum?

Obviously, the proteins in the base of the flagellum would be created first.

We can compare this to the construction of a tall, one-hundred story building. What if the purchasing agent/accountant for the construction company ordered 20,000 desks to be delivered to the construction site before the foundation for the building was even dug? Would the construction workers be happy about having to navigate through 20,000 desks sitting on the ground as they went to and from the building site? Probably not.

First, you build the foundation, then you build the steel frame, then you pour the concrete for the floors, etc. etc.

Likewise, when a new cell (created by cell division) needs to start construction on a flagellum, it needs the proteins for the base before it needs the proteins for the tail.

The point is that the order of the creation of the proteins is very important. Something has to control which genes the RNA polymerase uses first, to create the proteins.

In the book: The Edge of Evolution, also by Dr. Michael Behe, he describes the creation of the celium and flagellum in certain kinds of bacteria. He describes the various kinds of "control elements," "checkpoint proteins," "boss proteins," "subboss proteins," "helper proteins," the proteins which actually become part of the structure, the switching on of genes, etc. etc. All of these functions are done by different proteins.

It is actually this phase of protein synthesis which controls the first phase of protein synthesis, meaning the order in which the proteins are requested to be manufactured.

It is impossible for this book to duplicate what Dr. Behe has done in explaining the complex processes involved in building protein structures in a cell. The reader is strongly advised to obtain a copy of Dr. Behe's "Edge" book and study chapter 5 in detail. This chapter in this book is only an introduction to the process.

Perhaps in 20 or 30 years a complete, detailed schematic of what happens when the cell has to create a complex protein structure, such as a flagellum, will be written. But for now, scientists are just beginning to see the light at the end of the tunnel.

Comments

Do you see a pattern here? Proteins are everywhere in the cell, doing all of the vast number of different complex jobs in the cell. Not only that, it is proteins which become part of the protein structures.

The DNA must contain all of the patterns for all of the proteins in the cell, which include the many different functions and structures which are needed by the cell.

An "irreducibly complex" system is a "complex" system which cannot function until all of its parts are completely in place. Dr. Michael Behe coined the phrase and wrote the book: Darwin's Black Box, which was written about this subject.

Evolutionists do not like Dr. Behe's books because they do not like the concept of "irreducibly complex" systems because these systems imply a "design," which implies a "designer," which is what they really don't like.

But the fact is that protein synthesis (and I have just scratched the surface and given a broad overview) is an irreducibly complex system.

For example, without RNA polymerase there would be no protein synthesis and no proteins. Without ribosome proteins and rRNA there would be no protein synthesis and no proteins. Without a folding mechanism there would be no complex life on earth. And so on.

Science, which fanatically tries to segregate the theory of evolution from a "designer," would say that the protein synthesis of the "first living cell" was simple and that as animals got more and more complex the protein synthesis mechanisms slowly got more and more complex.

What evidence is there for this theory? None. It is pure pie in the sky. There is no "simple" cell on the planet earth. All of these imaginary "simple cells" only exist in the minds of evolutionists. Likewise, a "simple" protein synthesis is also pie in the sky.

Shall we talk about other things that go on inside the cell, such as the mitochondria, ATP molecules, glucose, pyruvate, the Citric Acid cycle, the Electron Transport Chain (ETC), and so on? All of these things are necessary to provide energy in the cell and involve the mitochondria, which, by the way, have their own DNA (though it is very small DNA).

Science has not even proven that a "first living cell" could have formed. Nor has science explained what imaginary protein synthesis existed in the imaginary "first living cell."

The same protein synthesis which exists in human beings also exists in single-celled bacteria. There is *no "increasingly complex" protein synthesis in any living thing on the planet earth!!* All of it is incredibly complex. The concept of an "increasingly complex protein synthesis" is a pure scientific fairy tale.

While it is true that protein synthesis in prokaryotic cells is a little less complex than in eukaryotic cells; even the protein synthesis in prokaryotic cells is far too complex to have happened by accident. It too, is highly, highly irreducibly complex.

It seems that all of the "evolution" of protein synthesis occurred in a long, long sequence of species *which are all now extinct*. How convenient. The "evidence" is dead and gone.

Actually, the evidence is not gone. The evidence never existed.

Is the theory of evolution a "proven" fact of science? Considering that there is no "simple cell" on the planet earth, and even evolutionists admit that random events could not create a prokaryotic cell in a prebiotic pool, it would be safe to say that the theory of evolution has no factual basis. It is a "theory," and a very unscientific theory at that.

Introduction to the Mathematics of Evolution

Chapter 11

The Pre-Liver

On the Complexity of Organs

To get a better perspective of the complexity of DNA, and the problems the theory of evolution faces because of the complexity of DNA, let us consider a hypothetical situation.

Suppose that several close relatives of a certain scientist died due to a disease called cirrhosis of the liver. It is a disease common among heavy drinkers of alcoholic beverages. Drinking large amounts of alcohol can destroy the liver because the liver is overburdened with processing and filtering out the toxins from the alcohol. The toxins are mainly mycotoxins, which are the waste products of microbes, such as yeast. Alcohol is largely made of mycotoxins.

Suppose this scientist discovers exactly which toxins cause cirrhosis of the liver. Further suppose this scientist decides to design a new organ for the body that is specifically designed to safely filter out these toxins before they get to the liver.

The new organ will be called the "pre-liver."

The Next Generation

The first problem is that the scientist can't help his living relatives. He can only help the "next generation" of relatives who have not yet been conceived.

You might wonder why he can't help his existing relatives.

The reason is that a new organ of the body requires massive changes to the circulatory system, nervous system, brain signals, lymph system, etc. *You cannot make these changes to a living person.* The bodies of living people have already had their body manufactured by their DNA; thus changing their DNA will not help them. The design of their body was controlled during the morphing of *their* embryo.

The generation of the scientist was born without a pre-liver, because the morphing of their embryo did not create it.

The sequence to create a pre-liver for the *next* generation is this:

First, the instructions for creating the new organ (i.e. the pre-liver) must be made to the DNA of living people, a male and a female. Actually the changes must be made to their germ cells, which combine to create a fertilized egg.

Second, this couple must mate so that their modified DNA exists in a newly fertilized egg.

Third, during the morphing of the embryo, all of the new instructions in DNA are followed and the new organ can be made, the new circulatory system can be made, the new nervous system can be made, the new programming in the brain can be made, etc.

Fourth, when the new baby is born, after the morphing of the embryo, the new baby will have the new pre-liver and all of the other changes necessary for the new pre-liver to function.

Thus, when the scientist designs the DNA to build this new pre-liver, the DNA changes he makes *must be made to the egg of a living woman and the sperm of a living man* so that the fertilized egg they create will contain the proper DNA to create the pre-liver, and many other new things, during the morphing of the embryo.

All organs are made during the morphing of the embryo. Thus, a *new* organ can only be made during the morphing of the embryo. That is why he cannot help his existing relatives.

And the only place the morphing of the embryo algorithm in DNA can be changed, to create the new pre-liver, is in the male DNA and female DNA of an existing species. Of course their DNA also has to be changed for the new gene complexes, etc., necessary to create the new types of cells, new biological structure, etc., of the new pre-liver.

A Problem for the Theory of Evolution

What has been said so far presents a major, major problem for the theory of evolution.

What all of this means is that for a proposed new species to have a better organ, for example, *massive changes must be made to the morphing of the embryo algorithm* of a *male and female* of their parent species!!

Thus, when "evolution" gets ready to create a new organ or new critical system, such as the semi-circular canals of a species which wants to convert from walking on four legs to walking on two legs, the *only way on the planet Earth* to create this new organ or new system *is to redesign the morphing of the embryo algorithm* in both a male and female. Only then can these systems show up in a new species.

Of course, other changes must be made to the DNA, such as genes, which are needed for the proteins, the rest of the gene complexes, etc., but the morphing of the embryo is where a massive amount of intelligence is needed to create the new organ.

The morphing of the embryo algorithm, which is what controls the morphing of the embryo, is the only possible place that the new organ can be created!! And the changes

must occur in the germ cells of a male and female of the parent species. If the changes occur in the non-germ cells, the changes will not appear in the new species.

Not only is the morphing of the embryo algorithms the most complex computer program on the planet earth, but it is the most vulnerable to the slightest errors. There is zero margin of error in the nucleotides which control the morphing of the embryo.

This concept alone totally obliterates the theory of evolution.

But let us get back to our scientist who is trying to build the pre-liver.

Back to the Scientist

This scientist not only has to design hundreds of new proteins for the new types of cells in the pre-liver, he must also design changes to the circulatory system, the nervous system, the brain programming, the lymph system, the biological structure (i.e. the way the physical parts of the body are linked together), etc.

And all of this must be built into the morphing of the embryo algorithm in the DNA of both the male and female.

This new organ will be designed to allow the *next generation* of his relatives to drink large volumes of alcohol, without worrying about getting cirrhoses of the liver. (Of course, a logical person would conclude it would be much simpler for him to convince his relatives to quit drinking.)

Obviously, this new organ must be a small chemical factory that will safely rid the body of dangerous mycotoxins before they get to the liver. Thus, this new organ will have to be placed in the body (during the morphing of the embryo) where it can filter out the toxins that are killing his relatives, *before* the toxins get to the liver. That is why it is called a “pre-liver;” it processes chemicals out of the bloodstream before they can get to the liver.

Furthermore, let us assume the “pre-liver” is to be placed right next to the liver in such a way that the toxins are filtered out just before they get to the liver.

Organs are composed of cells (some of which may be unique types of cells for that organ and that species) and the rest of the biological structure of the organ (which includes minerals and a lot of other things). Because all of this is designed by the DNA, and built during the morphing of the embryo, his first problem is redesigning human DNA.

He has to redesign the DNA to create hundreds of new proteins, needed by the pre-liver, new types of cells needed in the pre-liver, new biological structure, changes to the circulatory system, changes to the nervous system and brain to control the pre-liver and fix small damage to the pre-liver, etc. And above all, the morphing of the embryo algorithms must be able to integrate all of these changes to DNA at just the right time and in just the right places.

The changes must be made in both the male and female and they must mate.

Do you see the absurdity of scientists who claim that the morphing of the embryo algorithms are "simple" and only consist of a few nucleotides??!!

In fact, it is highly likely that much of the morphing of the embryo algorithms are in the gene complexes. For example, people with vastly different shaped noses have exactly the same DNA, except in their gene complexes. Thus, at least part of the morphing of the embryo algorithms must be in the gene complexes. This makes the gene complexes more sensitive to design flaws than people may think.

This means that parts of the morphing of the embryo algorithms are scattered throughout the DNA. This makes it difficult to track down all the nucleotides involved in the morphing of the embryo and it makes the accuracy of the DNA even more important (i.e. there is not as much "flexibility" in nucleotide sequences as some might think).

A thinking person would totally dismiss the theory of evolution simply based on the complexity of DNA and how critical pieces of DNA, which share a common function, are scattered throughout the DNA. DNA has to be designed by beings (or a Being) far, far more intelligent than we humans. Yet as this complexity is unraveled the theory of evolution always gets the credit.

Let's get back to the scientist.

So how would this scientist go about re-designing a person’s DNA so the new DNA will create not only the liver, but also the pre-liver?

Let's go into this in more detail.

More Details

First, he must figure out which proteins are needed to make the pre-liver so that the new types of cells in the new pre-liver can become miniature chemical factories. The new cells in the pre-liver must filter out the dangerous toxins. This scientist will quickly find out he needs to design many very complex three-dimensional proteins (which are not already made by the body) to perform the task of filtering out mycotoxins and other toxins before they get to the liver.

These very complex three-dimensional proteins must not only fold in such a way that they will fit together, but the right amino acids must be in the right places so the proteins will bind together to create the three-dimensional proteins.

Of course, a great amount of signaling will be needed to control the order and timing of when new proteins will be made from the DNA. This includes new types of signaling proteins which will be inside the new types of cells. These proteins in the new types of cells also need to be placed into the right location, at the right time, so the protein structures can be built.

Of course, if there are any new proteins needed by the pre-liver, there must be new genes placed in the DNA. He must design these genes so that each gene creates an average of 10 proteins and the gene knows exactly which of the proteins to make at just the right time (this means he will have to design highly sophisticated introns on the DNA). But the exons must be ordered so that *sequential subsets* of the exons can create the 10 new proteins (this is more complex than it sounds).

Also, new types of cells, not already in the body, must be designed which will capture the dangerous mycotoxins and other toxins and pull them into the new types of cells so the proteins and other chemicals inside the new types of cells can neutralize them. Thus, new types of receptors, and perhaps cell membrane ports, need to be designed.

Thus, let us say he must design 6 new types of cells with special carbohydrates and/or enzymes on their surface which will grab the various types of toxins and allow the cells to pull them in through protein ports built into the bilipid cell walls.

Plus other enzymes and carbohydrates must also be part of the biological structure so that cells can stick together to create biological structure with other organs.

This means changes to the external enzymes and carbohydrates *of other parts of the body* (such as the liver) must also be changed so the liver can bind to the new pre-liver. Thus he must change the design of many parts of the body which are not part of the pre-liver itself. In other words, an enormous amount of changes to cells *which are not part of the pre-liver* must be modified. All of these changes must be designed into the morphing of the embryo algorithm in the DNA.

During the morphing of the embryo, at some point, the first of each type of new cell must be a converted from an undifferentiated cell. The scientist has to figure out when the first new instance of each new type of cell will be created and how it will be created from an undifferentiated cell. He must also figure out how many of each new type of cell will need to be made, and where they are to be placed in the biological structure of the pre-liver.

He must figure out a way for nutrients and liquids to get inside of the new types of cells. Thus, he must change the morphing of the embryo so the circulatory system feeds the new types of cells. Certain chemicals must also get inside the new types of cells to neutralize the mycotoxins. They must come from the mother. All chemicals needed for the embryo must come from the mother.

Of course, once these various types of toxins are neutralized there must be a way to get the neutralized toxins out of the cell and then out of the body. There must be protein ports in the cells that allow the neutralized toxins to be placed into the veins and/or lymph system.

Let us suppose he decides that the new pre-liver will need 400 new kinds of proteins, not currently existing in the human body; to facilitate the mechanisms of the 6 new kinds of cells, currently found nowhere in the body.

What must he do next?

Suppose these new gene complexes (which will create the 400 new proteins) have an average length of 20,000 nucleotides (i.e. nucleotide pairs). Because there are 40 new genes (to create the 400 new proteins), he needs to design 800,000 additional nucleotide pairs in a human DNA. It will take him a long time to design these very complex gene complexes which are needed to create very complex 3-dimensional proteins that fit together, bind together and filter out mycotoxins.

These proteins need to have specific shapes and special amino acids in exact locations (as part of each protein) so the proteins can bind together. The binding of proteins to create protein structures is caused by specific types of amino acids, being in the right place in the structure (relative to the folding), so that the proteins will fit together and bind together to make a strong protein structure.

As if that weren't enough, the real problems now begin for this scientist.

Suppose he designs the 40 new gene complexes. Where is he going to place them on the human DNA? To understand this problem, suppose you had an encyclopedia of 5,000 pages and you want to add 40 new articles to this encyclopedia. It is easy for you to figure out where to put them in an encyclopedia, but it is not as easy to decide where to put 40 new gene complexes on DNA.

The human DNA is 3 billion nucleotide pairs long; where is he going to put the new gene complexes? Does it matter? Does the order of the gene complexes matter? No one knows, but most likely it will matter a great deal!!

How about redesigning key sections of non-gene nucleotides; the so-called "junk DNA?" Does that matter? It matters a great deal since there is no known section of DNA which is actually "junk."

But this is just the beginning of his problems. How is the DNA going to create the 6 new types of cells? As an embryo is forming, at what point are these new types of cells produced, and how are they produced? He will have to adjust the DNA (the morphing of the embryo algorithms) so that it knows how to make these 6 new types of cells and be able to create them at just the right time and be able to link them together and place them in just the right place in the body (i.e. the biological structure).

For example, if the morphing of the embryo algorithm was not designed correctly, then the formation of the embryo would not be just right, and the 6 new types of cells may end up being scattered among the fingers of the person, or the brain, or the toes of the person. In other words, the new cells would be worthless.

How is he going to make sure they are placed in exactly the right places, at the right times, so the pre-liver is fully functional and sitting next to the liver by the time the morphing of the embryo is finished?

How will he get chemicals from the mother's body into the morphing baby at just the right time and in just the right places? How will chemicals not in the body of the mother, but needed for the pre-liver, be created?

How will the DNA execute putting together the biological structure of the adjacent organs and other tissue during the morphing of the embryo? The cells not only have to be in the

right place at the right time, but they must be designed to form new biological structures with the pre-liver.

Remember that the arteries and veins must be redesigned to get blood to and from every cell of the new pre-liver and the other organs or systems which need to be modified. How is he going to manipulate the DNA so that arteries, veins, nerves, lymph fluid, etc. are correctly attached to the cells of the pre-liver such that all of the cells in the pre-liver are able to function? All this must be done in the DNA of the parents of the first child to have the pre-liver.

To accomplish these things, new arteries, new veins, new lymph channels, new nerves (which must be connected to the spinal cord and then up to the brain), etc. will all be required. These all have to be programmed into the DNA morphing algorithm.

Furthermore, the immune system must recognize these 6 new types of cells as friendly cells, so the immune system does not attack and kill the new types of cells. This, by itself, is a very complex process.

Also, he must reprogram the brain so that it knows the pre-liver is there, and he must reprogram the brain so that it can issue the correct nerve impulses in the correct sequence for the new pre-liver to operate and so the pre-liver structure can repair minor damage. The brain must also send the right signals to the nerves to get rid of the waste products left over after the pre-liver processes the toxins.

In addition, when the DNA is changed significantly, it should also be remembered that every cell in the body (almost) contains exactly the same DNA. Thus, every existing type of cell in the body will have the new DNA segments and must be able to adjust to "find" the right gene complexes and other segments of DNA that they need. This must be taken into account.

Solving all of these problems, and many others, with today's technology, would be thousands of times worse than having a first grade class try to build a space shuttle.

In fact, the morphing of the embryo algorithm is clearly his most difficult challenge. But, the reprogramming of the brain to accomplish the new and changed tasks of the brain is also an impossible task with today's technology.

The technology does not exist so that we humans can intelligently redesign a human DNA to create the pre-liver. It would involve designing new genes and new proteins, designing new types of cells, and above all redesigning the morphing of the embryo program, etc. to place the pre-liver in exactly the right position in the body, complete with arteries, veins, lymph, immune system, nervous system, new biological structure, etc. etc.

But that is not the end of his problems.

Understanding the Generations

Suppose this person did solve all of these problems. He would have to put this new DNA in both a woman and a man, so that their offspring could have this new organ. Remember, it is only during the morphing of the embryo that a new type of organ can be built.

Adding these 40 new gene complexes by modifying the DNA; would mean there was a new human genome, meaning a new human species. *The children and descendants of this man and woman could only mate with each other* (i.e. their own brothers and sisters at first). What if this couple only had one child? Or what if they had three children, but all of them were males?

If they had at least one male and one female these two people could mate and create a new child with the new pre-liver. What if these two people didn't like each other (brothers and sisters frequently don't get along even when they are adults)?

The descendants of the first two people to have the pre-liver could never breed (i.e. marry) with regular humans (that's the rest of us) due to the massive differences in their DNA. They could physically mate, but their children would likely be sterile. But even if they were not sterile they would be really messed up in terms of their DNA.

But suppose in 200 years there were thousands of this new species (i.e. a new species of humans), which are all pure descendents of the first two humans with a pre-liver.

Evolutionists would see a "benefit" to the pre-liver and would predict that eventually all human beings who did not have the pre-liver would become extinct.

However, there are many humans who would not need this new organ, the pre-liver. If a person doesn't drink alcohol, doesn't take antibiotics, doesn't eat contaminated grains, etc., they simply don't need the pre-liver. These people are equally as healthy as the new species of humans, the "pre-liver species" of humans. They are equally likely to survive as the pre-liver species. Evolution would not be able to "favor" the new species when considering that all humans would not need the new pre-liver to survive.

Furthermore, the "rest of us" would far outnumber the pre-liver species, thus it would not be wise for them to try to eliminate the rest of us.

Thus, the world would consist of two distinct species of human beings. We could call them *homo sapiens sapiens* and *homo sapiens preliver*. Before getting married the husband and wife would need to know if they are of the same species or they could not have offspring which could breed with anyone.

Summary

The point to this discussion is to explain how incomprehensibly complex the technology would need to be to create a single new organ by redesigning the DNA. Scientists today wouldn't have a clue where to begin.

But yet the evolution establishment claims that the many thousands of unique varieties of livers that have existed in different species of the past and present were easy to create by a series of pure accidents!! What utter and complete nonsense!!

And the various types of livers are just one problem for evolution to solve. Different types of hearts, for example, are zero-defect organs.

In the next chapter the discussion on the pre-liver will continue with a discussion of how evolution might create the pre-liver, or any other complex system.

Introduction to the Mathematics of Evolution

Chapter 12

The Pre-Liver Created By Evolution

Let Evolution Design the Pre-Liver

So let us consider how evolution would design the pre-liver to help alcoholics survive and breed. After all, it sounds so simple when you read the pro-evolution literature.

The process or redesigning human DNA to create a complete pre-liver is so complex it could not be done in one generation by evolution. It would take many generations of humans for evolution to make the cumulative improvements to the DNA in order to have a generation with a complete pre-liver.

In fact, this is exactly the way evolution is supposed to work. Science knows that it is statistically impossible for a male and female to coincidently have the same changes to their DNA, in one generation. For such a complex situation as a new pre-liver; evolution would predict it would take many generations of small random mutations to create the new pre-liver.

Thus, successive generations of humans would have to slowly accumulate the changes to their DNA until the complete pre-liver was made.

Furthermore, each generation of cumulative "small mutations" would require the male and female to be *born* with *the same exact "cumulative prior mutations"* and to have *the exact same "additional small mutations"* in their generation.

This is one of the reasons the evolutionists are willing to compromise their integrity and allow knowingly flawed radiometric dating techniques to be used. The flaws make the dates of fossils seem much, much higher than they really are. All of this is to accommodate the massive time needed for "gradual" evolution.

One of many problems with the theory of gradual evolution is that there would be no survival benefit to the new species until the entire process of changing the DNA was complete and all of the pieces discussed previously, and many more, were completely in place. In other words, the pre-liver would not function correctly, and would not be beneficial to alcoholics, until all the pieces mentioned in the prior chapter were in place.

The creation of the pre-liver would be an incredibly complex task (an "irreducible complex" task to use creation science terminology). Until all of the hundreds of thousands of changes to the DNA were complete (which would include not just the pre-liver, but the changes to the circulatory system, the brain, the morphing of the embryo

sections of the DNA, etc.), the pre-liver would not work and would not provide any survival benefit to alcoholics.

Let me repeat that last sentence because it is so important: Until all of the hundreds of thousands of changes to the DNA were complete (which would include not just the pre-liver, but the changes to the circulatory system, the brain, the morphing of the embryo sections of the DNA, etc.), the pre-liver would not work and would not provide any survival benefit to alcoholics.

The changes would take scores, if not hundreds, of generations of humans.

The Generations

Let's make it simple and assume it takes exactly 100 generations for evolution to create the pre-liver. Also, we will assume that exactly 1% of the total cumulative changes to the DNA were accomplished each generation, so that it took exactly 100 generations to redesign the DNA and make the pre-liver by evolution.

Problem number one is that in each generation the exact same changes must *randomly, blindly and without direction*, be made in both a male and a female, in their germ cells (i.e. their sperm or egg). And one of these males and one of the females, which coincidentally have the exact same mutations, must breed (i.e. mate) in that generation.

In fact, as will be seen, it is actually more complicated for evolution to create the new pre-liver in small steps than it would be for evolution to create it in one giant step. This is because the DNA must align, *male and female*, for 100 consecutive generations.

While the total changes to the DNA are the same, whether it is done in one giant step or 100 small steps, getting the right male and right female to mate at the right time, adds a lot of complexity.

This is complicated, so let us go though it generation by generation.

The Zero Couple (the "Original Couple") (Born With No Pre-Liver DNA Changes)

In the *zero generation*, or "zero couple," a man and a woman (who will be called the "original couple"), are born with none of the pre-liver changes to DNA. During their lifetimes, they must have the same *random* mutations (including the morphing of the embryo mutations) *in their germ cells*, in the same places in their DNA, and they must mate (i.e. they must marry in the case of humans).

At this point it doesn't matter if these two people are related to each other, but after this generation it will matter. The zero generation couple are normal human beings (i.e. they are born without any of the pre-liver DNA changes). However, during their lifetimes their DNA must mutate, *in their germ cells*, so that the 1% of the cumulative changes to DNA, which are necessary for the pre-liver, are made.

The First Couple
(Born With 1% of the Pre-Liver Changes)

In the *first generation*, or "first couple," are two of the children of the "original couple." Neither the male or female can be regular humans or else their DNA would not align. The male and female which mate in this generation must be brother and sister.

The "first couple" must mate. These are a new species, but they are only a transitional species. They are the first "people" to have pieces of the pre-liver at birth. However, they are born with only 1% of the necessary parts of the pre-liver.

In other words, the "original couple" must have at least a son and a daughter. And at least one son and at least one daughter, among their children, must mate. Any of their other children which mate (with non-siblings) will probably have sterile children or their children will not survive birth.

This key son and daughter are born with 1% of the pre-liver parts and pieces, which they inherited from their parents (the "original couple"). However, the DNA of the "first couple" must mutate (including the morphing of the embryo) so that their offspring have 2% of the cumulative pre-liver parts.

Remembering the discussion in prior chapters about the morphing of the embryo, it is insanely ludicrous to think that two children of the same couple would have just the right mutations to their DNA so that their offspring will have 2% of the parts of the pre-liver. It is even more ludicrous to think that 3 or 4 of their children will have exactly the same mutations!! Absurdity does have its limits.

Thus, it will be assumed that *in every generation, exactly two of the children (and not 3 or 4)* will have the necessary mutations to add another 1% to the pre-liver parts. In other words, the son who has these mutations will not have a choice (among his sisters) as to who to marry. The right son and the right daughter of the zero couple must marry. This is true in each generation.

However, there is no reason to suspect that the "right" male and "right" female will know who they are supposed to mate with. This adds another layer of complexity to multi-generation evolution.

Thus, the right brother and the right sister of the "original couple" must marry each other because they are the only two people on earth who were born with the first 1% of the pre-liver, *plus* they are the only ones among the children who had the necessary mutations to bring the cumulative percentage up to 2% for the next generation.

The Second Couple
(Born With 2% of the Pre-Liver Changes)

In the second generation, called the "second couple," a brother and a sister must mate. It must be a son and daughter of the "first couple" in order to be born with the complete 2% of the pre-liver parts and pieces.

Then, by totally random means they must have an identical 1% change to their DNA (in their germ cells) in order to achieve a 3% cumulative change for their children. Thus, the second couple must *be born with*, and *have exactly similar random mutations to their DNA* (including morphing of the embryo) in their germ cells.

In other words, the "right" brother and the "right" sister of the "first couple" must marry each other because they are the only two people on earth who were born with the first 2% of cumulative pre-liver changes and had the necessary mutations to bring the cumulative percentage up to 3% for the next generation.

By now the reader should see the pattern. This same process goes on in each generation until the pre-liver is complete.

(To keep this discussion simple, certain types of situations will not be discussed.)

The 100th Children
(Born With 100% of the Pre-Liver Changes)

In the one-hundredth generation, called the "one-hundredth children," all the parts of the pre-liver are in place and are fully functioning - *at birth*.

In other words, all of the children of the "ninety-ninth" couple, called the "one-hundredth children," are born with all the parts of the pre-liver. They are born with a fully functional pre-liver.

Note that at this point *any* of the brothers and sisters can intermarry (i.e. interbreed) because no more mutations are needed. However, the sons and daughters of the ninety-ninth couple must marry their siblings (i.e. their brothers or sisters), and have the last 1% of mutations, in order to have children who have the complete pre-liver (we have ignored some possibilities to keep it simple).

After this generation, first cousins, brothers and sisters can marry and drink all they want, *as long as they are pure descendants of the "100th couple."*

The Other Children

If we assume that each couple mentioned above (until the "100th Children") had 5 children, only 2 of which had the necessary mutations for the next generation, what happened to the other 3 children in each generation?

Starting with the children of the "first couple," the other 3 children were born with *partial mutations*, but they did not achieve the next level of mutations, thus their descendants could never be able to achieve a total pre-liver. Eventually they would marry someone with a different level of partial mutations (or no mutations at all), and they would not be able to have children which could have offspring with anyone (unless this other person just happened to have the right combination of partial mutations).

In other words, the 3 children in each generation would have no descendants after a few generations because they or their children would end up mating with people who did not have exactly the same cumulative percentage of mutations, thus they could not have children or their children could not have children.

For example, suppose someone with 97% of the pre-liver parts and pieces marries a person who was not a descendant of the original couple or only had 53% of the pre-liver mutations. Their children would never have a complete pre-liver and in fact they probably could not have children at all.

While this may explain the lack of transitional species found by paleontologists, the absurdity of the above sequence makes this a very poor explanation for the lack of transitional species. Remember, paleontologists only find bones.

A New Level of Absurdity

Can you imagine how absurd it is that any human with a complete pre-liver would exist via evolution?

It would take the "original couple" plus 99 more consecutive generations (though this is a simplification) of exact mutations of the "right" brother and the "right" sister (including the morphing of the embryo), in their germ cells. It is ludicrous to think this could happen in one generation, but to happen in 100 consecutive generations, just to get a new organ, is ridiculous beyond comprehension.

While this is a hypothetical situation, the mathematics are correct. The biggest problem in all of this is that a male and female must breed *who were born with exactly the same mutations* and have exactly the *same mutations*, in exactly the same places in their DNA, in the same generation. It is that ludicrous!!

It gets worse. Until the pre-liver was fully functional, after 100 consecutive generations, there would be no survival advantage to anyone in the previous generations (who only inherited partial mutations). In fact, even after 100 generations there would be no

survival advantage compared to most humans because most humans are not "lushes" (i.e. alcoholics).

Yet, the evolution establishment wouldn't hesitate to say such a complex process *has happened many, many millions of times on this earth*; all of them by pure accident and all of them taking many generations!!

Exactly where do the evolutionists draw the line of insane absurdity?

The whole concept of multi-generation changes to DNA, to achieve a desired result, is total nonsense.

It gets worse.

Inbreeding and Population Sizes

Evolutionists like to talk about populations. With huge populations the impossible events of evolution have a "higher" probability of happening. However, in the above example, *no matter what the population size of the species is*, a new species is in process and the "available population size" for new mutations, after the first generation, *is exactly two in each and every generation, and they must be brother and sister (or close cousins)*.

For example, even if the species has a billion members, only two of them can participate in the "next" generation of mutations in any generation after the "original couple."

Thus, for 99 consecutive generations the "population size" for evolution to work with is exactly two.

Large population sizes do not help the cause of the theory of evolution one iota when multi-generation DNA changes are involved.

Note that in this scenario, because only a very small percentage of the population has each of the different stages of the pre-liver; in order for the pre-liver to be completed, there is much breeding (i.e. marriage) among brothers and sisters or close cousins.

For 99 consecutive generations there is total and absolute "inbreeding" because evolution is following the descendants of a single family.

Inbreeding (the breeding of close relatives) is well known to make a species vulnerable to death from a single disease. Inbreeding causes a massive *loss* of genetic information!!

In other words, the reason all people in the world don't die of the same disease is that there is a great variety in our DNA because inbreeding is illegal in civilized countries. Take away that vast variety of DNA by inbreeding and you get very little variety and the entire species could be wiped out by a single virus or bacteria.

Many species on the earth today are vulnerable to extinction because as the species gets smaller and smaller in population size, inbreeding becomes more common and more genetic information is lost.

For example, if dinosaurs and other long-ago extinct species ever lived on this earth, it is likely most of them became extinct due to a combination of genetic entropy and inbreeding.

A new species will inherit all of the genetic defects of its parent species and it is not likely any species could survive for a million years simply because of genetic entropy and the inherited flaws in their DNA which they accumulated from *all of their ancestor species* (assuming the theory of evolution).

As the species dropped in population size due to genetic entropy, their survival problems would have been massively compounded by inbreeding. Inbreeding would have caused a massive loss in their genetic information.

Genetic entropy and inbreeding are a two-edged sword.

From a religious perspective, Adam and Eve's children had to marry each other. However, there is absolutely no doubt that God, who is the ultimate authority on DNA, made the DNA of Adam and the DNA of Eve vastly different. Thus, their children and grandchildren, etc. could have safely married among themselves for many generations.

The Pre-Liver Is An Example

While the pre-liver is a hypothetical organ, the above discussion applies to many of the supposed evolutionary improvements to animals.

For example, each species likely has a unique liver designed specifically for that species.

But let us take a different example.

Let us take the seemingly simple evolutionary change in primates so they could walk on two legs. It is assumed that walking on four legs preceded the walking on two legs (e.g. humans). So let us discuss what it takes for a species to "evolve" from walking on four legs to walking on two legs.

First, the bone structure of the animal must change. In fact, the main way paleontologists look for the transition from walking on four legs to walking on two legs has to do with the bone structure. There is a significant difference in the bone structure of primates that walk on four legs versus two legs.

But that is just the beginning. There must also be major changes in the muscle structure of the animal. The muscles involved in walking on four legs are very different than the muscles involved for an animal that walks on two legs.

When you change the bones and muscles you must also change the blood vessels (i.e. the arteries and veins). Many blood vessels would no longer be needed during the transition and many new vessels would be needed.

When you change the muscles you also have to change the nerves which control the muscles. Not only that but you also have to change the brain so that it can control the vastly different movements of walking on four legs to walking on two legs.

Also, there must be a sophisticated mechanism to allow the animal that walks on two legs to balance itself. In humans, this balancing mechanism is controlled in the inner ear by three small bones passing information to the semicircular canals.

The semicircular canals are three half-circular, interconnected tubes in the inner ear. They are each like miniature gyroscopes and have a complex angular relationship to each other (i.e. they are on different geometric planes).

Each canal is filled with endolymph (a fluid) and contains a motion sensor which has little hairs whose ends are attached to a gelatinous structure. The three half-circular tubes work together and are so sophisticated they can tell the difference between when we change the angle of our head versus we change the angle of our body.

The semi-circular canals send electrical impulses to our brain. Walking on two legs requires a more sophisticated mechanism than walking on four legs. Thus the brain must be reprogrammed to interpret the added signals received from the sensors of the semi-circular canals.

Four legged animals (quadrupeds) have a tail, which is actually very important in helping them balance. Humans don't need a tail to help them balance. Thus, the brain must be reprogrammed to quit receiving these signals.

Scientists admit that the highly sophisticated changes to a quadruped that led to a bipedal animal (one which walks on two legs) did not happen in one generation, or even ten generations.

So how can these sophisticated transitions occur over a period of many, many generations? That was the main point of the discussion on the pre-liver. There is no benefit to the generations and generations of creatures who don't have all the mechanisms in place to walk on two legs, especially the mechanisms needed to form the signals from the inner ear.

In fact, *there would be a huge, huge disadvantage* to generation after generation of species *which could not walk well on four legs or walk well on two legs*. This is because for the generations in transition (which are transitioning between walking on four legs versus walking on two legs), *they are very poor at walking on four legs or walking on two legs*. Thus, they could not escape predators or be able to obtain food.

According to the theory of evolution, things like the semicircular canal are built by "trial and error." Considering how sophisticated it is it would take many, many thousands of generations of "trial and error" to get the semicircular canal just right (e.g. at the right angles, etc.). During these generations the primates could not stand up very well, much less be able to run from predators or be able to hunt food.

"Natural selection" *would work against* these transitional species.

These many generations would have a very, very low survival rate. This supplies a very, very low number of animals which are available for the "next" step in the semicircular canal "trial and error" construction. Remember, you constantly have brother and sister breeding. Thus, if just one son or daughter does not survive, the cumulative affect is lost forever and the entire process may have to start over from scratch.

You would also have a great loss of genetic information during the transition.

The whole concept of evolution, which takes hundreds of generations to complete a single change, is scientific nonsense.

The Other Option

The reader might think that instead of taking 100 generations; that a change could only take 10 generations.

If you lower the number of generations, statistically you gain nothing because the end result must be the same.

However, if you lower the number of generations; you add the complexity of massive numbers of complex changes to DNA being made in each of these 10 generations.

Evolution Has No Direction

As if all the above were not bad enough, it must also be remembered that evolution is directionless.

In each of the above generations of creating the pre-liver, it is assumed that evolution knows exactly where it left off (in creating the pre-liver) and where it is going (in order to complete the pre-liver). It is also assumed the "right" brother and "right" sister know who to mate with. This is all nonsense.

In reality, evolution has no direction. For example, the 10th generation of creating the pre-liver has an equal chance of creating proteins for the brain of a horse or creating proteins for the heart of a crab as it does in creating the 10th generation of creating the human pre-liver. The probabilities are the same!!

For example, in the fifth generation above, or any other generation, there is absolutely no reason to think that the mutations in that generation would have anything to do with a human pre-liver.

To think that 100 consecutive generations of evolution would consecutively create 100 consecutive incremental improvements to a human pre-liver; is total nonsense. Evolution has *no* intelligence, *no idea where it is, and no idea where it is going.*

Thus, the whole concept of multi-generation mutations is nonsense. It implies an "intelligence" is keeping track of what stage the cumulative mutations are at, *and what the next stage should look like*, in both the male and female germ cells. This is nonsense beyond imagination.

Yet, this kind of thinking is at the heart of multi-generation cumulative mutations for major structural changes or new organs. It is like a multi-generation cumulative "wishful thinking."

Yet for evolution to be true there would have had to be *many millions of such multi-generational cumulative mutations* in order to account for all the complex functions of complex animals on this earth!!

It is all scientific nonsense.

Conclusion

Evolutionists say these unlikely successes have happened many millions of times and in many cases they worked on species with small populations. Of course, the size of the population is irrelevant after the first generation because a brother and sister must mate, yielding a population size for transitional species of only 2 for many consecutive generations. And the mutations have to be in the germ cells of the brother and sister.

Then it must be mentioned that evolution has no direction for any of the generations.

Is there anything as ludicrous as multi-generation random evolution? However it ranks in the absurdity column, it is definitely close to the top of the list. But surprisingly, it is not at the top, "genetic chaos" will take that prize, as will be seen later.

Introduction to the Mathematics of Evolution

Chapter 13

Basic Mathematics

> "If you want to make an apple pie from scratch, you must first create the Universe."
> Carl Sagan, astronomer

What is an Exponent?

An exponent is simply a way to represent a series of multiplications.

For example, suppose we wanted to multiply 10 by itself 12 times. We could represent this as:
10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10

This is cumbersome to write down, especially if we were to multiply 10 by itself a thousand times. Exponents are simply a shorthand way of expressing a number being multiplied by itself.

For example, 10, multiplied by itself 12 times, is represented as: 10^{12}.

$\underline{10}^{12}$ has a "base," the 10, which is the number being multiplied by itself.

$10^{\underline{12}}$ also has an "exponent," the 12, which is the number of times 10 is multiplied by itself.

Thus, listing the number 10, being multiplied by itself 12 times, is written 10^{12}.

The "base" does not have to be 10. For example, how would you write out 4^7?

The answer is: 4 x 4 x 4 x 4 x 4 x 4 x 4

Note that the number '7' is not in the above line. The '7' is the exponent in 4^7 and represents how many times 4 is multiplied by itself.

Remember, exponential notation is a way of writing a multiplication problem in a very short and simple way. Exponential notation was not designed to complicate things, but rather to simplify things.

Multiplying Exponents

When you multiply exponents, the numbers must have the same base!!

For example, this is legal: $10^5 \times 10^6 \times 10^8$

It is legal because all three exponents have the same base: 10

But this is illegal: $5^{10} \times 6^{10} \times 8^{10}$

It is illegal because the three bases are not the same number. 5, 6 and 8 are not the same number.

The rule of multiplying exponents is that when you multiply exponents, you add their exponents.

For example: $10^6 \times 10^7 = 10^{(6+7)} = 10^{13}$

Does this make sense? Let us do this longhand:
(10 x 10 x 10 x 10 x 10 x 10) x (10 x 10 x 10 x 10 x 10 x 10 x 10)
is equal to:
10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10 x 10

Thus, it does make sense to add exponents when multiplying numbers which have exponents.

It is always important to remember that when multiplying exponents the base must be the same!!

Dividing Exponents

When dividing exponents, the same rule applies: when dividing exponents the bases must be the same!!

When dividing exponents we subtract the exponents. The '/' symbol represents division.

Thus, $10^7 / 10^6$ is equal to $10^{(7-6)}$ equals 10^1 equals 10.

Is this logical? Consider the above problem written longhand:

(10 x 10 x 10 x 10 x 10 x 10 x 10) / (10 x 10 x 10 x 10 x 10 x 10)

Six of the 10s cancel each other out (the six 10s which cancel each other out are underlined in the next line):

(10 x 10 x 10 x 10 x 10 x 10 x 10) / (10 x 10 x 10 x 10 x 10 x 10)

Only one 10 is not underlined. Thus, the answer is:
$10^7 / 10^6 = 10^{(7-6)} = 10^1 = 10$.

Again, our method leads to a logical answer.

Also remember, the bases must be the same!!

Negative Exponents

What does a number like 10^{-5} mean? Actually, this is a way to write small numbers. While 10^5 is a big number, 10^{-5} is a small number.

Actually, 10^{-5} is equal to: $1 / 10^5$

10^5 equals 100,000, but 10^{-5} equals 1 / 100,000.

Another way to write 10^{-5} is: .00001

We can look this chart to better understand negative exponents:

$10^4 = 10 \times 10 \times 10 \times 10 = 10{,}000$
$10^3 = 10 \times 10 \times 10 = 1{,}000$
$10^2 = 10 \times 10 = 100$
$10^1 = 10$
$10^0 = 1$ (by definition any number to the zero power is 1)
$10^{-1} = .1$ (which is 1 / 10)
$10^{-2} = .01$ (which is 1 / 100)
$10^{-3} = .001$ (which is 1 / 1,000)
$10^{-4} = .0001$ (which is 1 / 10,000)
$10^{-5} = .00001$ (which is 1 / 100,000)

Thus, $10^5 / 10^8 = 10^{(5-8)} = 10^{-3} = 1 / 1{,}000 = .001$

What is a Probability?

Suppose you had a die or dice with 10 sides. What is the "probability;" if you rolled this dice; you would get a '1'?

The term "probability" means: "what is your chance?" Thus, "what is your chance;" or "what is the chance" you will roll a '1'?

There are 10 sides of the dice (e.g. with numbers: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10), and each side has the same chance of landing on top. The probability of rolling a '1' is 1 / 10 or 10^{-1}. In other words, the probability is 1 in 10 or 10%.

What is the probability you will roll a '1' two consecutive times?

In order to calculate this we need to multiply 10^{-1} x 10^{-1}. Remember, when we multiply two numbers with exponents we add their exponents, thus 10^{-1} x 10^{-1} equals $10^{(-1 + -1)}$ = 10^{-2}. In other words, 1 in a hundred or .01 or 1%.

Is this logical? Let us think about all the different orderings of rolling a ten-sided dice twice (there are 10^2 unique orderings):

The three dots (. . .) mean that some of the items are missing and the reader is expected to be able to figure out which pairs of numbers are missing.

1 & 1
1 & 2
1 & 3
1 & 4
. . .
2 & 1
. . .
3 & 1
. . .
10 & 1
10 & 2
. . .
10 & 10

There are 100 different possibilities of rolling a ten-sided dice twice. Rolling a '1' and '1' represents one of these 100 possibilities. This order of rolls has an equal chance as any other ordering of rolls. Thus the logical probability of rolling a '1' twice in a row is 1 in a hundred possibilities or 1 / 100 or .01 or 10^{-2}. So the answer is logical.

What is a Set?

A "set" in mathematics is a collection of objects. They can be physical objects, such as people; or abstract objects, such as numbers.

For example, the collection of all books in a library is a "set of books." A collection of marbles in a marble collection is a "set of marbles." The students in a particular school class are a "set of students."

Likewise, we could talk about more refined "sets." For example, the set of students who have brown hair, in Mrs. Smith's class; is a "set of students with brown hair in Mrs. Smith's class."

Sets can also relate to mathematics. For example, the set of even numbers (i.e. numbers divisible evenly by 2), less than 10, is a set. This set can be represented as:
{x | x is an even number less than 10}

The symbol "{x |" means the following: "x, such that." Thus, we could write the above set as this:
{x, such that x is an even number less than 10}

Or this set can be represented as:
{x | 0, 2, 4, 6, 8}

Or this set can simply be represented as:
{0, 2, 4, 6, 8}

The "members" of a set (e.g. 0, 2, 4, 6, and 8 in this case) are called the "elements" of the set. There are 5 elements: 0, 2, 4, 6, 8.

The key concept when discussing sets is that we can determine exactly what elements are in the set and which elements are not in the set.

For example, if we said "the girls in *the* 5th grade class," is *not* the same as: "all the girls in the 5th grade." The first statement would not be a set until we refined the definition of set membership so we could determine exactly which girls were in the set (e.g. which 5th grade class the set refers to).

If we said: "the girls in Mrs. Jones 5th grade class at Jefferson Grade School," then we could identify exactly which girls belonged to the set. And we could identify which girls were not in the set.

When we said above: "all the girls in the 5th grade," this is an accurate enough description of a set that we can determine the exact set membership (assuming we knew which school we were talking about).

Thus, a "set" is merely a well-defined set of objects, such that set membership can be exactly determined.

Sets can also be defined by abstract methods. For example, we could say: "the set of 4 letters of the alphabet, such that the first three letters are: ABC."

Before reading on, look away from this book and try to figure out how many elements there are in this set, and what those elements are.

The answer is there are 26 members or elements in this set. They are:
1) ABCA
2) ABCB
3) ABCC
4) ABCD
. . .
26) ABCZ

Note that we did not list all 26 elements; rather we listed a pattern of set membership which the reader is expected to fill in. For example, the first three members of the set which are not listed above are:
5) ABCE
6) ABCF
7) ABCG

Can you tell the last element of the set which is not listed above? The answer is:

25) ABCY

Many times all of the elements of the set are not listed, but only a pattern is given.

Sets are very important to understand when discussing key mathematical concepts because in many cases it is impractical or impossible to list all of the elements of a set.

Subsets

A "subset" of a set means "part of the set." In other words, you define the elements of a "parent set," then a "subset" is *some* of the elements of the set, but not all of them.

For example, suppose you defined a parent set (commonly called the Universal Set) to be the following names:
{fred, john, herman, mary, ann, marilyn}

This would be a subset of the parent set:
{fred, herman, marilyn}

This would also be a subset of the parent set:
{john}

However, a "subset" is sometimes defined so that all of the elements of the parent set are elements of the subset. For example, sometimes this would be a valid subset of the above parent set:
{fred, john, herman, mary, ann, marilyn}

In mathematics, frequently we are interested in all possible subsets of a set which follow a particular rule.

For example, suppose we defined the parent set to be all the letters of the alphabet: {a, b, c, . . ., x, y, z}

Here is a list of "subsets" of that set which contain 5 unique elements of the set:
{a, b, c, d, e}
{a, b, c, d, f}
{a, b, c, d, g}
{a, b, c, d, h}
. . .

The three dots (". . .") at the bottom of the listing indicates that we have not listed every possible subset, but only a pattern or a sample of the elements of the subset.

In fact, each element of the above set are themselves sets (i.e. sets of five letters of the alphabet). Thus, a set can have sets as members.

What is a Combination?

Let us consider the set, *Set 5U*, of all possible ways to pick 5 *unique* letters of the alphabet (duplicates are not allowed). Here are some examples as shown above:
{a, b, c, d, e}
{a, b, c, d, f}
{a, b, c, d, g}
{a, b, c, d, h}
. . .

Here are a few sets with 5 letters of the alphabet which are *not* elements of "Set 5U" because each set has duplicates:
{a, b, c, *e*, *e*}
{a, b, *c*, *c*, f}
{*a*, *a*, c, d, g}
{*a*, *a*, *a*, *a*, h}
. . .

The above sets of 5 elements are not valid elements of Set 5U because they do not follow the rules which defined the set.

There are two key rules when thinking about sets which are defined to be a "combination."

Rule #1 is that duplicates are not allowed.

Rule #2 is that the order of the elements in the set is *not* important.

Now let us think of Set 5U as a "combination." We have already forbidden using the same letter more than once in each set. But now we also have to exclude sets which contain the same 5 letters, but the letters are not in the same order. We have to exclude them because the order of the elements in each set are not important, and we don't want to repeat a set more than once.

For example, let us look at this proposed listing of elements of Set 5U:
{a, b, c, d, e}
{a, e, b, c, d}
{e, a, b, c, d}
{a, b, c, e, d}
. . .

Note that in all 5 of these potential elements or subsets there are five letters, but in each case the 5 letters are the same letters {a, b, c, d, e}; they are simply ordered differently.

Are all 5 of these potential elements members of the Set 5U, now that we have defined it to be a combination?

When talking about combinations, only one of these elements would be in the set. And which of the elements is chosen to be in the set is not important, because the order of the elements is not important. In other words, any of the elements could be in the set, but only one of them can be in Set 5U.

Remember, when defining a "combination" type of set, it doesn't matter which order the elements in a row are listed. It is the "combination" of 5 different elements which must be unique (i.e. duplicates are not allowed), not the order of the letters in the element.

What is a Permutation?

A "permutation" is the same thing as a "combination" except that a "permutation" is concerned about the "order" of the elements in each subset, plus duplicates are allowed.

Thus, a permutation does away with the two main rules of a combination.

Let us define Set 5A to be the same as Set 5U, but in this case Set 5A is a permutation set.

Each of these sets would be an element of Set 5A if Set 5A were defined to be a "permutation":
{a, b, c, d, e}
{e, d, c, b, a}
{a, c, b, d, e}
{d, d, d, e, a}
. . .

As noted in the last element above, duplication of letters is also allowed, thus these would also be elements of Set 5A:
{a, a, a, d, z}
{z, d, a, a, a}
{a, d, a, a, z}
{d, d, c, z, c}
. . .

Needless to say, Set 5A would be much, much larger than Set 5U because it has more relaxed rules!!

The set of 26 letters of the alphabet is also a "set," but it is not a member of Set 5A because each member or element or subset of Set 5A has exactly 5 elements.

In this book the focus will be on permutations because this book will be concerned with DNA, and the order of nucleotides on DNA is very important and duplicates are always allowed!!

The Number of Elements of a Set of Permutations

So how many different ways can we uniquely order 5 letters of the English alphabet? Make a wild guess before reading any further and write down your guess. Do not try to count them, you will see why in a moment.

First, let us clarify the rules.

Rule 1) The elements (i.e. elements of the listing); meaning the "subsets" in the listing; must each consist of 5 letters of the English alphabet.

Rule 2) The order of the letters (in each element subset) is important, meaning each element (i.e. each subset) must be unique (i.e. the ordering of 5 letters cannot be found anywhere else in the listing). Thus, aaaab and baaaa are two distinct and different elements of the listing. But if aaaab is the 50th element of the listing, it cannot also be the 1 millionth element in the listing because the same element would appear in the listing more than once.

Rule 3) Redundancy is allowed (i.e. the same letter can be used more than once in a single element). Thus, 'mmmmm' is an element of this set.

Rule 4) Every possible unique ordering of 5 letters, with redundancy, is required to be in the set.

With these four rules, the number of "elements" or "subsets" or "items" in the listing (i.e. the set of permutations) turns out to be 5^{26}. The exponent, 26, represents the number of letters in the English alphabet; and the base, 5, represents the number of letters in each element/subset in the listing.

This is equal to:
1,490,116,119,384,770,000 permutations (i.e. items in the listing)

This is more than 1 quintillion. Now you know why you shouldn't try to count them one at a time.

So, what is a "permutation?" Every one of the 5^{26} elements of the set we just talked about is a unique "permutation."

Here is a key statement you need to understand. Set 5A can be defined thusly: "*Set 5A is the set of all possible permutations of 5 letters of the alphabet*."

Thus every one of the 1,490,116,119,384,770,000 elements in the listing of Set 5A is a unique permutation.

A Simple Example

Since there is not enough paper in the world to list all the elements of Set 5A, let us look at a much smaller set so we can list every possible permutation.

Let us consider three people: Bob, Bill and Mary. How many different ways can we "order" these three names? This is exactly the same question as this: how many different permutations are there when listing the names of three people: Bob, Bill and Mary? They are the same question.

The original "set" is the names of three people: Bob, Bill and Mary.

There are in fact, 27 different permutations. Try to list these 27 different ways before reading any further.

(Each person is listed three times)
Bob, Bob, Bob
Bill, Bill, Bill
Mary, Mary, Mary

(Bob is listed twice)
Bob, Bob, Bill
Bob, Bill, Bob
Bill, Bob, Bob
Bob, Bob, Mary
Bob, Mary, Bob
Mary, Bob, Bob

(Bill is listed twice)
Left to the reader - should be 6 items or elements in list

(Mary is listed twice)
Left to the reader - should be 6 items or elements in list

(Each person is listed once)
Bob, Bill, Mary
Bob, Mary, Bill
Bill, Bob, Mary
Bill, Mary, Bob
Mary, Bob, Bill
Mary, Bill Bob

In total, there are 27 permutations. This is 3^3.

Each is a "permutation" of three names and each is a "unique ordering" of three names. The term "permutation" and the term "unique ordering" mean exactly the same thing.

Permutations and DNA

While the English alphabet has 26 letters, the DNA alphabet only has 4 letters: A, C, G, and T

How many different ways can we uniquely order (i.e. how many different permutations) four of these "letters:" A, C, G, T? These 4 letters represent the four different types of nucleotides, which are the key molecules which make up DNA. The answer, of course, is 4^4. Here are some examples:

ACCT
GGGG
TGTA
AACT
ACTG
GTCA

The study of permutations of nucleotides is at the heart and soul of the evolution debate.

Let us ask, how many permutations are there in a string of 150 nucleotides? There are 4^{150} permutations. This looks like a small number. Do you think you could list all of the different permutations? Just how big is this small-looking number?

A galaxy in our Universe consists of about 100 billion stars. Our sun, for example, is really a star. If you were several light-years away (a "light-year" is the distance the speed of light would travel in one year), and you looked at our sun from far away; our sun would look like any other star.

So how many galaxies are there in our Universe? About 100 billion galaxies, which have an average size of about 100 billion stars.

Comparing the size of our earth to the size of the average star would be like comparing the size of a tennis ball to the size of a Ferris wheel. Stars are huge in comparison to our little, puny earth.

Yet, there are 100 billion galaxies and 100 billion stars, on average, in each galaxy. This is a total of about 10,000,000,000,000,000,000,000 stars in our Universe. This is 10^{22} stars.

Now that we have talked about big things, let's talk about little things - atoms. Atoms are very small. They are so small it would take about 5 million million hydrogen atoms to fill an area the size of the head of a pin. This is 5×10^{12} or 5,000,000,000,000 atoms in an area the size of the head of a pin!!

Yet, in spite of these huge and small numbers, there are only about 10^{80} atoms in our entire Universe!!!

In other words, there are about:

100,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,000,000,000
atoms in our Universe.

The number we just talked about (4^{150}) is BIGGER than the number 10^{80}. In fact, 4^{150} is approximately equal to 10^{90}.

In other words, we could order 150 nucleotides in more unique ways than there are atoms in our Universe!!

Are you beginning to see the power of permutations? They look small, but in fact they are huge!!!

But human DNA does not contain 150 nucleotides, it includes:
3,000,000,000 pairs of nucleotides.

Comment

If you are lost at this point, you would be wise to seek out someone who can explain these things to you before going on because the use of exponents and an understanding of permutations will be very important in the rest of this book.

As a minimum read these same concepts from another source to make sure you understand them.

Introduction to the Mathematics of Evolution

Chapter 14

Understanding Big and Little Numbers

"Philosophy is a game with objectives and no rules. Mathematics is a game with rules and no objectives."
Ian Ellis

Understanding Really Big Numbers

One of the hardest things for human beings to do is comprehend the difference between a number like 900 versus a number like 10^{900}.

Both numbers have the symbols '900' in them. Thus, when someone sees a number like 10^{900} they naturally think of the number 900, and don't see much difference between 900 and 10^{900}.

The number 900 is just that, a number which any middle-school student can count to in a matter of a few minutes. If a person counted to 900, one number per second, they would count to 900 in 15 minutes.

If we paid $900 for a television set, we would see our bank account drop by $900.

But how long would it take us to count to 10^{900}?

First of all, let us look at the number 10^{900} written longhand.

The number 10^{900} is a '1' followed by 900 zeros. This is what it looks like:
1,000,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,000,000,000,000,
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000,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000

Each consecutive zero in this number represents a number which is 10 times larger than the number before it. For example, 100 is 10 times larger than 10. 1,000 is 10 times larger than 100. 10,000 is 10 times larger than 1,000. And so on. Thus, we are essentially multiplying 10, by itself, *900 times*.

If we were to write out a much, much smaller number (the number of atoms in the known Universe), we would write it out:
100,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,000,000,000

The number of atoms in 10 Universes (10^{81}) would be written out:
1,000,000,000,000,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,000,000,000

The number 10^{900} is the number of atoms in:
10,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,000,
000

As mentioned above, there are about 10^{80} atoms in our Universe. That is a '1' followed by 80 zeros.

How much smaller is 10^{-100} than 10^{-80}? The answer is $10^{(-100-80)}$ or 10^{-20}. Thus, picking the correct single atom from among 10^{100} atoms is much harder than picking the single correct atom in our Universe.

In fact, the probability of 10^{-100} is equivalent to picking *a single, correct atom*, from among all the atoms in 10^{20} or:
100,000,000,000,000,000,000 *different Universes*!! The atoms in our Universe would only constitute a very, very, very minute percentage of the 10^{100} atoms in this many Universes.

While as mentioned above, 10^{-100} is technically not an impossible probability, let us study some examples of just how big it really is.

Suppose there was a lottery in which a 10-sided dice was rolled 100 times. In order to win this lottery you had to roll a '1' for all 100 rolls. In other words, you had to roll a '1' for 100 consecutive rolls, including the first roll, the second roll, the third roll, the fourth roll, etc.

It sounds simple doesn't it? It turns out that rolling a '1' for 100 *consecutive times* is equivalent to picking the correct, *single atom* from among 10^{20} Universes, where each Universe has 10^{80} atoms!!

Each "ticket" in this lottery represents your attempt to roll the dice 100 consecutive times where the roll is a '1' in every attempt. If you rolled something other than a '1' your ticket immediately fails and you quit rolling the dice. Thus, if you roll a '5' on the first roll, there is no need to make any more rolls, your ticket has failed.

As another example, suppose for one "ticket" you rolled:
First roll: a '1'
Second roll: a '1'
Third roll: a '4'

You would stop after the third roll since the third roll was not a '1'. This "ticket" failed also.

In a computer simulation of rolling dice, *50 billion attempts* were made to roll 100 '1's in a row. Here are the results of this computer simulation:

Table: Maximum number of times a '1' was rolled at the beginning:

Note: The first item in the table means a '1' was not rolled in the first attempt. The second item in the table means a '1' was rolled on the first attempt, but not the second attempt. And so on.

```
Rolled a '1' [0] consecutive times:  Count = 44,999,935,077
Rolled a '1' [1] consecutive times:  Count = 4,500,063,675
Rolled a '1' [2] consecutive times:  Count = 449,993,542
Rolled a '1' [3] consecutive times:  Count = 45,006,419
Rolled a '1' [4] consecutive times:  Count = 4,500,592
Rolled a '1' [5] consecutive times:  Count = 450,545
Rolled a '1' [6] consecutive times:  Count = 44,967
Rolled a '1' [7] consecutive times:  Count = 4,682
Rolled a '1' [8] consecutive times:  Count = 454
Rolled a '1' [9] consecutive times:  Count = 43
Rolled a '1' [10] consecutive times: Count = 4  [max]
```

In other words, in ***50 billion attempts***, the closest to 100 consecutive '1's in a row was ***10 in a row***. And this only happened 4 times out of ***50 billion*** attempts.

Most people would think that it would be easy to roll 20 '1's in a row. But in 50 billion attempts, the most number of '1's in a row was 10.

Suppose you were given this offer: "If you invest your life's savings in this lottery (the lottery to roll 100 '1's in a row), you will be given 5,000 tickets (i.e. 5,000 attempts to win the lottery), for every second in a ***5 billion year period***."

In other words, we will assume this earth is 5 billion years old and you are given 5,000 tickets (i.e. attempts) every second; 24 hours a day, 365.25 days a year, for the entire time the earth has existed!!

Assuming your life's saving were $1,000,000, would you invest your life's savings in this lottery? Answer that question before reading on.

Let us see your odds of winning. We will assume you will be able to buy, ***at 5,000 tickets a second***:
1,000,000,000,000,000,000,000 tickets in 5 billion years (actually you would be able to buy slightly less than that). This is 10^{21}.

This is your last chance; would you spend your life's savings on these 10^{21} tickets?

To calculate your odds of winning, we do this simple calculation: $10^{(21-100)} = 10^{-79}$. In other words, your odds of winning this lottery, even with 10^{21} tickets, is only 1 chance in 10^{79}. This is about the same as picking the single correct atom from all the atoms in our Universe.

But let's suppose you didn't know the simple way to calculate your odds.

The next chart shows how to calculate your odds.

Chart A

Based on 1,000,000,000,000,000,000,000 Tickets (10^{21})

"0 ct" means the first roll was not a '1'
"1 ct" means the first roll was a '1', *but not the second roll*
"2 ct" means the first two rolls were a '1', *but not the third roll*, etc.
Only the "100 ct" line below is a winner.

Symbol	Probability	Predicted # of Times Rolled
0 ct	.9	9×10^{20}
1 ct	.09	9×10^{19}
2 ct	.009	9×10^{18}
3 ct	.0009	9×10^{17}
4 ct	.00009	9×10^{16}
5 ct	.000009	9×10^{15}
6 ct	.0000009	9×10^{14}
7 ct	.00000009	9×10^{13}
8 ct	.000000009	9×10^{12}
9 ct	.0000000009	9×10^{11}
10 ct	.00000000009	9×10^{10}
11 ct	.000000000009	9×10^{9}
12 ct	.0000000000009	9×10^{8}
13 ct	.00000000000009	9×10^{7}
14 ct	.000000000000009	9×10^{6}
15 ct	.0000000000000009	9×10^{5}
16 ct	.00000000000000009	9×10^{4}
17 ct	.000000000000000009	9×10^{3}
18 ct	.0000000000000000009	9×10^{2}
19 ct	.00000000000000000009	9×10^{1}
20 ct	.000000000000000000009	9×10^{0}
21 ct	.0000000000000000000009	9×10^{-1}
22 ct	.00000000000000000000009	9×10^{-2}
23 ct	.000000000000000000000009	9×10^{-3}
24 ct	.0000000000000000000000009	9×10^{-4}
25 ct	.00000000000000000000000009	9×10^{-5}
...		
98 ct		9×10^{-78}
99 ct		9×10^{-79}
100 ct (the only winner)		9×10^{-80} (approx 10^{-79})

Even though you own 10^{21} tickets, which is a huge number of tickets, your chance of winning is only 10^{-79}. As mentioned above, this just happens to be about the same probability as picking the correct, single atom, *from among all the atoms in our Universe*.

Thus, even though you get 5,000 tickets, every second, every day, every year for 5 billion years, your chance of winning this lottery is about the same as picking the single correct atom from among all the atoms in our Universe.

Would you spend you life's saving to enter this lottery? Well, would you spend your life's savings on picking the correct, single atom, from among all the atoms in our Universe? It is effectively the same question.

If you only bought *one* ticket, your chances would be the same as picking the single, correct atom, from among all the atoms in 10^{20} Universes!! Your chances would be 10^{-100}.

Hopefully you would not buy a single ticket in this lottery. You would save a lot of time and gasoline by simply flushing your dollar bills down the toilet.

The point to this exercise is that an event which has a probability of 10^{-100} is an event which is very, very unlikely to happen, *a single time*, in the age of our earth!! This is true even if there are 5,000 events (i.e. 5,000 tickets), every second, for the entire age of our earth.

The "First Living Cell"

Now let us assume the "first living cell" of evolution had 900,000 nucleotides. How many permutations of 900,000 nucleotides are there? The answer is $4^{900,000}$.

How much bigger is $4^{900,000}$ than 4^{150}, and remember that the number 4^{150} is bigger than the number of atoms in our Universe?

Try to calculate it before reading on.

If you said 6,000 times bigger, you would be wrong. The correct answer is $4^{899,850}$ times bigger!!!

Remember, when you are dividing exponents, which have a common base, you subtract their exponents, you do not divide their exponents. Thus, $4^{900,000}$ divided by 4^{150} is equal to $4^{(900,000-150)} = 4^{899,850}$.

And this is just the "first living cell." Human DNA has 3,000,000,000 pairs of nucleotides!! There are $4^{3,000,000,000}$ unique permutations of 3 billion nucleotides.

This is just an introduction to the subject of permutations of nucleotides.

Now let apply the "first living cell" permutations to our probability which is defined to be "impossible."

For example, suppose someone calculated the probability of the "first living cell" to be 10^{-100} (actually the probability of the "first living cell" is much, much lower than that). Furthermore, suppose scientists were able to create 5,000 attempted "first living cells" *every second, for 5 billion years*. Their chance of creating *a single* "first living cell" would be 10^{-79}.

Thus, even the chance of a "first living cell" (which is only the very, very beginning of evolution), is virtually impossible, even at 5,000 attempts every second, 24 hours a day,

for the age of our earth. And in the real world there would probably only be a few hundred attempts *every century* (and that is very generous to the theory of evolution).

The real probability of the "first living cell" is not 10^{-100}, but it is about $10^{-1,500}$, which is $10^{1,400}$ times *smaller* than the impossible probability of 10^{-100}!!

Without the "first living cell," there is no evolution.

The "impossible" probability of 10^{-100} effectively takes into account a large number of events which might be "winners," namely 5,000 possible events every second. But even with a large number of attempts to "win the lottery," a person is left with essentially an impossible probability.

Comment

The chapters on mathematics have covered a lot of concepts in a short amount of space. If you do not feel comfortable with these concepts, you would be advised to read these chapters again and even get some help from a friend or relative.

Introduction to the Mathematics of Evolution

Chapter 15

The Probability of Evolution

> *"A statistician is a person who stands in a bucket of ice water, sticks their head in an over and says: 'on average, I feel fine!'"*
> K. Dunnigan

Gene Complexes

In prior chapters we talked about genes and DNA, among other things. While a "gene" is a template to make a protein, a "gene complex" is a gene ***plus*** all of the other sections of DNA which are needed in order for this gene to be converted into a protein ***and*** for the protein to be placed into the proper position inside the cell, etc.

A gene would be useless without the rest of the gene complex.

No one really knows what the average number of nucleotide pairs (generally just referred to as "nucleotides") are in the average "gene complex." In the book: *Genetic Entropy & The Mystery of the Genome*, by Dr. Sanford, there is a clue (what he calls a "whole gene" is called a "gene complex" in this book):

> *"While only a small fraction of the [DNA] directly encodes for proteins, every protein-encoding sequence is embedded within other functional sequences that regulate the expression of such proteins. This includes promoters, enhancers, introns, leader sequences, training sequences, and sequences affecting regional folding and DNA architecture ... While a typical protein-coding sequence may only be 3,000 nucleotides long or less, the typical 'whole gene'[i.e. gene complex] that controls the expression of that protein can be in the range of 50,000 nucleotides long."*
> *Genetic Entropy & The Mystery of the Genome, page 38*

The numbers he quotes are for humans. In this chapter it will be assumed that the average "gene complex" for human beings, and for other very advanced animals, is 15,000 nucleotides. This number is just a guess since no one really has a clue what the exact number is.

Before getting into human evolution, let us apply the concept of "gene complex" to the "first living cell."

The Probability of the "First Living Cell"

Every gene of the "first living cell" had to form totally by random mutations of amino acids or nucleotides. There were no prior living cells (by definition) from which to serve as a pattern for the ordering of its amino acids or nucleotides.

To understand what the totally random formation of nucleotides is like, let us talk about Shakespeare. Suppose we put Shakespeare's King Henry VIII play into a computer and then scrambled the letters up randomly (we will also scramble up the spaces between words). Then, suppose we isolated 900 of these randomly generated letters and spaces. This is what the scrambled King Henry VIII might look like (note: a period ('.') is really a space in this list):

```
.gibmmeg.signrryd.uet..mrhbhcro..efeul.feoe.ewe.li.befubl.ne
k.ekenlhinat.oaet.hwde.trmtrlev..t.eluttl.r.hfdsepilrsafcltt
tv.esewes.y.holgo.nlialywlggtrd.a..r.lhcm..juldagute.imtkckh
.ooat..hrviesl.maablhe....asohf.a.e.i.r.nwnnnooolasia.atordw
yhviondseabdme.ntonlmnfor.ya.livyyceae..m.ii.o..aoaactliahtr
satythhrcwnrro.re.rca.anlitdntdtmihleosseiveammouweesrrtafli
peeittehfrnre..teyl..eiso.bytrk.dhcaemoigeieip.ut.oeymnm.nyu
sipseoo...othcttyeh..hbuaecsysesrus.rs.yaa..ly.tttrte.yihwra
m.cet.dolwdeen..keiehi.bannu.irwa.le.teotli.snot...dmluc.adf
iiocehdgdt.r.wo.aamr.w.aioisehh.r.ek.gtiigreaies..c.pohpnots
.ncyl...reauidhtesa.itthenldts.ioak.euwbieat.ionerk.otiftyr.
o.h.gtfhtnom..sesai....dgawutedie.on.dnechtua..pdertntar.ete
.noriehamehooevsedaiafsooi.mw.otlhistdm.s.e..aeh.ll.dkesuaa.
h.eosrdgye.dtesbctsoernlnsoacs.tanoyurhh..nwnhe.tdpako.tkyaa
aceehfcgt.hnmireds.ensi.dyinrwn.ohh.whofe.e.wcra.srt.yoktean
```

The gene complexes of the "first living cell" did not have viable patterns of nucleotides to serve as a pattern, thus the above attempt to replicate Shakespeare, from scratch, is a visual example of what the DNA of the "first living cell" would have looked like if we could "read" DNA as easily as we could read Shakespeare.

In other words, the first attempt to create a DNA strand for the "first living cell" would have been total gibberish because there was no prior pattern or ordering from which to pull nucleotides.

What if we randomly modified pure gibberish? I hope you understand that if you take gibberish, and randomly mutate it with more gibberish, you will still have gibberish.

So what mechanism converted pure gibberish into a viable DNA strand for the "first living cell?" There was no such mechanism because there was no life on this earth prior to the "first living cell."

The important thing to note is that there is no intelligence in the above Shakespeare rearrangement of its letters.

Actually, the above chart was generated by random numbers, but the random numbers were "weighted" by the exact proportion of letters in Shakespeare's play. For example, a letter of the alphabet that appeared very rarely in the play would appear very rarely in a "weighted" or "biased" randomly generated listing.

You won't get a better grade in literature class by reading thousands of pages of randomly generated letters of the alphabet, even when they are "weighted" by the actual proportion of each letter in the actual play.

Likewise, when we randomly scramble nucleotides, we would not expect to have a sequence of nucleotides which would provide any "information" or "intelligence" which would be useful to the "first living cell."

A scrambled; or randomly put together sequence of nucleotides; would not be expected to make a viable gene complex any more than a scrambled King Henry VIII play would tell us much about who King Henry VIII was and what his part was in the play. The play was named after him so you can assume he was one of the main characters (I suppose most people would consider him a villain, but others might consider him to be a role model).

In addition to randomness, there was no "survival of the fittest" in creating the "first living cell," meaning there were no intermediate semi-live cells which would provide a clue as to what the nucleotide sequences should look like.

Chemical Issues - Binding Sites

Proteins are nothing but a long string of amino acids. However, the amino acids need to be chemically bound together and then "folded" so that they form a shape so that they can be functional to the cell, even in the "first living cell."

Let us assume there was a "*protein structure*" in the "first living cell" which needed 50 different proteins (i.e. 50 different genes would be used to make 50 different proteins, and then the 50 different proteins were folded together make one very large *protein structure*).

Physically, the 50 different proteins must "fit together" much like you would build a toy robot using several different kinds of Lego® building blocks and fit the pieces together. For example, the toy robot may have 15 "subsystems," where each of the "subsystems" are made of several or many different blocks, and where the sum total of the 15 "subsystems" or "structures" makes the complete toy robot.

With this analogy, the "subsystems" are the *protein structures* and the individual building blocks are individual proteins.

But such a concept is only half the problem for the "first living cell."

Unlike building a toy robot, individual amino acids, from different proteins in the protein structure, must "stick" or "bind" to each other at certain locations so that the entire

protein structure is strong. This would be like gluing the Lego® building blocks together at certain points so it could be carried to another room.

But with living structures, some sections of the proteins in a protein structure in a cell must repel each other. There are no building blocks that do that.

What this means is that not only must the 50 different proteins (that form one protein structure) have shapes that fit together "like a complex glove," certain amino acids (in different proteins in the protein structure) must have very specific amino acids, *in exactly the right place*, so that some of the 50 protein parts "stick" to each other or repel each other, etc.

Thus, proteins not only must have the right amino acids in the right places in order for the proteins to fold in the right places, there must also be just the right amino acids in just the right places so the proteins with bind together, will repel each other, will repel water, will attract water, and so on. Designing complex protein structures is an insanely complex process.

The focus of the book: The Edge of Evolution, by Dr. Michael J. Behe, totally disproves the theory of evolution by talking about "binding sites." His claim is that it is impossible that random mutations of nucleotides could produce enough binding sites to create a single complex protein structure. He is right, it is a superb book. However, like his other book, his "Edge" book is not very popular among the evolutionists.

Probability and the First Living Cell

Let us assume the "first living cell" had 300 gene complexes, with an average length of 3,000 nucleotides (or nucleotide pairs). Human gene complexes are far more complicated, and longer, than the gene complexes of the "first living cell" (if such a cell ever existed).

Now let us assume the probability of a *random permutation* of 3,000 nucleotides, being able to create a gene complex for the "first living cell," was 10^{-5}. This number is ridiculously generous to the theory of evolution (i.e. the real probability is much, much less than that).

Thus, we have a probability that an RNA or DNA strand for the "first living cell" would have a viable permutation of nucleotides is: $10^{(-5x300)}$ which is equal to $10^{-1,500}$. The "-5" is the probability of a single new gene complex forming from a randomly generated permutation of 3,000 nucleotides; and the 300 is the number of gene complexes which must be made.

Using the above example, 50 of the 300 gene complexes would be used to create one protein structure.

But even the above probability of $10^{-1,500}$ ignores a lot of things, such as the viability of different *combinations of proteins* (remember, proteins must fit together, thus just having a bunch of proteins doesn't help at all, they must be a "set" of proteins which have very

specific shapes and have specific amino acids in just the right places), but we will use the above numbers.

Remember, 10^{-100} is an impossible probability. A probability of 10^{-500} is an insane probability because it is 10^{400} times *smaller* than an impossible probability.

Now we are talking about a number which is $10^{1,000}$ times *smaller than an insane probability* (i.e. $10^{(1,500-500)}$ equals $10^{1,000}$).

Randomly Creating a "First Living Cell" in a Lab

Now let us assume a group of scientists claimed that they used *a randomly generated DNA or RNA strand of 900,000 nucleotides*, and ended up creating life from non-life. The "life" would include at least 300 very complex gene complexes (i.e. the proteins made from the gene complexes are mainly used to create protein structures). 50 of them are assumed to create one of the key protein structures inside the "first living cell."

Would you believe the scientists? Note that in the above paragraph is the phrase: "randomly generated DNA or RNA."

If they *carefully designed the order of the nucleotides for the DNA* of a "first living cell;" good for them, they should win the Nobel Prize (and no doubt they would).

But in this case the scientists are claiming that they used a *totally random sequence of nucleotides* to simulate true evolution to order the amino acids and proteins necessary to create life from non-life. They claimed they were simulating the pre-biotic world.

Should you believe these scientists? No, you should not believe them. They are trying to deceive you. It is *not* the accumulation of 900,000 amino acids which is the problem (though this is actually a very severe problem because amino acids do not chemically bind to each other); rather *it is the permutation of nucleotides* which is the problem.

Even though there would be many successful permutations of nucleotides which would create a living cell; even taking this into account, if these scientists had had a thousand failures, the chances of a success would still be $10^{-1,497}$. Simply put, *such a claim would be a clear case of fraud and deceit*.

The point is that in nature, the same statistics apply. Not only would you not believe the scientists if they said they randomly created a "first living cell," you would also not believe them if they said nature randomly created a "first living cell" by using random mutations.

Building a New Species Randomly

Let us, for the sake of argument, assume that the average gene complex, for very advanced animals and plants, including humans, consists of 15,000 nucleotides (i.e. "nucleotide pairs"). Dr. Sanford says they can be as large as 50,000 nucleotides (i.e. "nucleotide pairs").

By the way, Dr. Sanford's book is one of the best sources for understanding genetic entropy. Genetic entropy is, by itself, an absolutely superb evidence that the theory of evolution cannot be true as will be seen later.

But let us assume that in the "evolution" from the first complex animal (an "animal" which had circulating blood or some other circulating fluid) to human DNA, that the ***average*** size of a gene complex was only 5,000 genes. This is an average for a lot of different species, some of which were much simpler than human DNA.

There are exactly $4^{5,000}$ different ways that a sequence of 5,000 nucleotides can be ordered (remember, each way they can be uniquely ordered is called a "permutation"). Converting from base 4 to base 10, this number is approximately $10^{3,000}$. This number is about $10^{2,920}$ times larger than the number of atoms in our Universe and it represents the number of permutations in ***just one gene complex***.

Once the "first living cell" was alive; its DNA needed to be mutated to make new species of single-celled animals.

Eventually, ***simple*** complex animals needed to be formed. Considering the "evolution" from the first complex animal to human DNA, do you think the probability of "evolution" got easier or harder as time passed, speaking from a probability standpoint?

Well, it got harder, much harder. From the first complex animal (which was an ancestor of humans according to the theory of evolution), many, many species were needed before humans could "evolve" into existence.

In this book it will be assumed there were 3,000 different species, meaning "ancestor species" of humans, meaning different species of animals which were ancestors of humans and were complex species (i.e. some fluid circulated).

First, we need to analyze how a single new species could "evolve" from an existing species.

Random mutations (in this context where viable DNA already existed) are events that occur ***to an existing species*** (starting with the "first living cell," but actually we will start with the first complex animal which is an ancestor of humans - meaning one of our "ancestor species").

Remember, an "ancestor species" is a species from which we are descended on our phylogenetic tree or evolutionary tree (assuming the theory of evolution is true for a moment).

To create a single new species, from an existing species, we will take the DNA of an existing species, and
1) Randomly copy one or more DNA strands from an existing species and place this copy somewhere else on the DNA (other options will be discussed in later chapters);
2) Randomly mutate some of the nucleotides (i.e. randomly change one nucleotide into another nucleotide, randomly add nucleotides or randomly delete nucleotides) which were copied from the DNA of the existing species; and

3) Randomly mutate (add, change or delete) some of the nucleotides of the DNA of the existing species which were not part of the copied DNA segments (e.g. for the nucleotides involved in the morphing of the embryo algorithms); and

A single gene complex of a new species would likely consist of about 5,000 *randomly chosen nucleotides*, as mentioned above. A "gene complex" is very specialized *for a specific type of animal or plant.* All mutations must be effective for the specific type of animal or plant they occur inside of.

We must remember that each animal or plant has a very sophisticated set of highly coordinated functions. In other words, you cannot take a rat liver and put it in a horse. The horse liver must be compatible with the other organs in a horse.

All the computers in the world, in a trillion years, could not calculate the probability of accidentally creating a single viable gene complex for a specific type of animal.

So we have to use some common sense (or use sampling). It will be assumed the probability of randomly mutating (i.e. copying, changing, deleting and adding nucleotides), which will result in the formation of a new gene complex for a new species, is 10^{-10} (1 in 10 billion), though in reality it is probably worse than 10^{-40} (which is why it is impossible to calculate without taking samples or using common sense).

This probability is lower than for the "first living cell" because the gene complexes for advanced animals are longer and more complicated.

The number 10^{-10} is very, very generous to the theory of evolution.

How Many Unique Gene Complexes Per Unique Species?

The next assumption we must make is to calculate how many unique gene complexes are in a typical unique species.

Human DNA has 30,000 gene complexes. The "first living cell" would have had about 300 gene complexes. Thus, we have an increase of 29,700 gene complexes going from the DNA of the "first living cell" to human DNA (obviously assuming evolution, which is what we are trying to calculate the probability of).

However, the gene complexes of human DNA are huge compared to the gene complexes of the "first living cell" or even the first complex animal which was an ancestor species of humans (assuming evolution), plus human DNA would have to be far, far more complex. So we can ignore the "first living cell" DNA or the DNA of the first complex ancestor of humans. Thus, for all practical purposes, we need to build 30,000 gene complexes from scratch, even if we start with the first complex animal.

Assuming there are 3,000 unique species between the DNA of the first complex animal (which is an ancestor of humans), and human DNA, the average "*ancestor species*" (i.e. a *species* which is on our evolutionary tree) would have 10 unique gene complexes (30,000 divided by 3,000).

In summary, we will make these assumptions in our next calculation:

1) The average "gene complex" of a complex species is 5,000 nucleotides.
2) The probability of a randomly generated sequence of 5,000 nucleotides being able to form a single, viable gene complex for a specific species: 10^{-10}
3) Each unique species, of our ancestor species, has an average of 10 unique gene complexes.

With these generous assumptions, the probability of a new species "evolving" by random mutations of nucleotides (which is the only way that the theory of evolution can work) is: $10^{(-10x10)} = 10^{-100}$

This probability is for ***one new species*** using randomly generated and modified nucleotides from an existing species.

This probability applies to ***every one*** of the unique species which have lived, and do live, on this earth. In other words, for every complex species which has ever lived on this earth (including extinct species), there is a probability of 10^{-100} that this species was derived by random mutations of nucleotides (actually this is an average).

And even this probability is very, very generous to the theory of evolution.

There are actually other factors which have been ignored which would be very damaging to the theory of evolution if they had been included.

For example, consider the male and female issue. When there is a new species, which has a male and female, the DNA (*after the random mutations in each of their germ cells*) must be identical; meaning their DNA must "align," meaning all the functional sections of the DNA must be in the same order, in the germ cells of both the male and female, in every generation, in order for them to have viable offspring.

What this means is that the probability that a male and female will have the same random mutations in the same generation in the same location of earth is impossible. The 10^{-100} probability does not even begin to take this absurdity into account.

Another example is the morphing of the embryo algorithm (i.e. computer program) in the DNA of each and every complex species which converts a single egg into a living animal. Every time there is a physical structural change in the species, the highly complex morphing of the embryo algorithm must change in a very precise way in the male and female. This, by itself, is an insane probability.

Multi-generational issues are also ignored. Multi-species issues are also ignored.

In any case, the 10^{-100} applies to 3,000 ancestor species of humans. This means that the probability of human evolution is about: $10^{(-100x\ 3000)}$ or $10^{-300,000}$.

A Consecutive Lottery

It is critical that the reader does not think of evolution as a single event with a probability of $10^{-300,000}$.

For example, if there are 3,000 species, between the first complex animal and human DNA, then each of these ancestor species *had to be consecutive*, meaning one after the other, because they are all our ancestor species.

Just like our grandfather (our father's father) and our father cannot both be born in the same year, our 3,000th ancestor species (starting with our oldest ancestor species with complex DNA) must have existed prior to our 2,999th ancestor species. Our 2,999th ancestor species had to exist prior to our 2,998th ancestor species. And so on.

Thus, human evolution, from the DNA of our oldest complex ancestor species to the DNA of human beings, would be like winning "3,000 *consecutive* or *sequential* (i.e. *one after the other*) lotteries," where the probability of each was 10^{-100}!!!

In other words, the probability of going from our 3,000th ancestor species to our 2,999th ancestor species was 10^{-100}. The probability of going from our 2,999th ancestor species to our 2,998th ancestor species was 10^{-100}. And note that our 2,999th ancestor had to completely exist before the process of creating our 2,998th ancestor could even begin, as one example!!

In other words, we could not start to create our 2,998th ancestor species until after our 2,999th ancestor species already existed, so essentially we have to start the lottery over again to create our 2,998th ancestor species. Thus, after our 2,999th ancestor species existed we could start a new lottery, with a probability of 10^{-100}, of creating our 2,998th ancestor species.

And so on.

Thus, the theory of evolution consists of 3,000 true "consecutive or sequential lotteries," each with a probability of 10^{-100}.

There is no word in the English language to describe just how ludicrous the theory of evolution is!!

The $10^{300,000}$ number is the number of atoms in $10^{299,980}$ Universes. Thus, the probability of the theory of evolution, even when making very generous assumptions, is the same probability as picking the single, correct atom from among $10^{299,980}$ Universes!!

But even the $10^{-300,000}$ probability for the theory of evolution is ludicrously generous because evolution must have "won" about 3,000 consecutive or sequential "lotteries," each with a probability of 10^{-100}!!

The problem of consecutive lotteries for the theory of evolution is "time." Not only is the probability of evolution ludicrous for a Universe which is a trillion trillion years old, on the

planet Earth evolution had to occur (from the first complex animal) in about 600,000,000 to 660,000,000 years.

Would you bet your life on winning a lottery which requires winning 3,000 consecutive lotteries, each with a probability of 10^{-100}, in a period of 660,000,000 years? Do the math.

Remember, never has new genetic information or new genetic intelligence ever been observed being created from random mutations of nucleotides. Now you know why.

How Many Species?

Let us define a "species" as having a unique *DNA structure*, meaning a species has a unique set of gene complexes, in the same order on their DNA, the same morphing of the embryo algorithms, etc.

How many unique species have existed on this earth? Scientists know of many millions of species which have lived on this earth (counting plants and animals). However, in these counts there are many examples of "microevolution," meaning variation in a single "species," as defined above.

The key question is how many unique species have lived, and do live, on this earth?

The answer will be assumed to be about 10 million unique species. This includes living plants and animals (including fish and other species in the deep ocean) and extinct plants and animals (including extinct fish and other species in the deep ocean).

This means that in the 5 billion years evolutionists claim this earth has existed (most of this time there was no life on earth, except single-celled organisms, according to science); an insane probability of 10^{-100} had to have happened *10 million times*!!!

Actually, all of this had to happen in less than a billion years because we are starting with animals with complex DNA (i.e. a "complex species" means there are multiple types of cells which perform some coordinated function necessary for life, specifically a circulating fluid).

But it gets worse.

Each species, whether living or extinct, would have needed unique ancestor species back to the point they have a mutual ancestor species with humans or other animals. We see in this case the need for literally *hundreds of thousands* of situations where 5 or 10 or 50 *consecutive lotteries* must be won, which have nothing to do with human DNA. And this is being very careful to avoid any duplication of ancestor species (i.e. no species is counted more than once).

Are you *beginning* to see the inane absurdity of the theory of evolution?

A Murder Mystery #1

To comprehend why the theory of evolution is scientific nonsense, let us consider a murder mystery.

Suppose a person was murdered in a small town, a 4 hour drive from Paris, France, at exactly 1 A.M. Central Standard Time, U.S.A., on a Thursday morning.

Suppose for some reason the French government wanted to frame me (i.e. Webster Kehr) for the murder.

Thus, they gathered hundreds of pieces of evidence which implicated me in the murder.

Suppose that I did not know the person who was murdered, in fact I did not know a single person in the city where he lived. Nor do I speak French. Yet, supposedly, there was a ton of contrived "evidence" that I was guilty.

How could I prove my innocence?

Suppose on the week this person was killed, I was working 8 hours a day (from 7:30 AM to 4:30 PM, which includes a lunch break) in Ft. Leavenworth, Kansas. Suppose my activities at work were very, very well documented and there were lots of witnesses to my being at work on those days and during those hours.

To prove my innocence, I would prove that I was at work, as scheduled, every day in the week the person was murdered.

Let us assume the following facts:

1) It would take me 30 minutes to drive to the nearest large airport, the Kansas City International airport (KCI).
2) I would have to be at the airport at least 1 hour before the plane left, since it was an international flight.
3) I would have to change planes (there are no non-stop flights from Kansas City to Paris), which would take another 1 hour.
4) The total flying time to Paris would take 12 hours.
5) It would have taken me 4 hours to drive from the Paris airport to the city where the murdered man lived.

Thus, to get from Ft. Leavenworth to the city where the person was murdered, would have taken me at least 18 ½ hours. It would have taken a similar amount of time to get back to work.

Thus, it would have taken me 37 hours to complete the trip to the city in France, murder the man, and come back home.

How much time did I have? The answer is 15 hours. From 4:30 P.M. to 7:30 A.M. is 15 hours.

I could not have killed the person. I was innocent.

A Murder Mystery #2

Now let us take all the above facts, but in this case the person was murdered on a distant planet, 5 light years away.

How long would it take for me to travel 5 light years, at 100,000 miles per hour?

It would take about *67,000 years* to go to the star and back.

How could I travel for 67,000 years in 15 hours? Again, I was innocent.

Conclusions

The problem with the theory of evolution is time. The scientific establishment has tried to make it appear that the theory of evolution has had 600 million years to 1 billion years, since the first complex animal.

That is not enough time. Even 600 trillion trillion trillion trillion years is not enough time. The theory of evolution is more like Murder Mystery #2 than Murder Mystery #1. There simply hasn't been enough time on this earth for the theory of evolution to have occurred.

Could you win 3,000 "consecutive lotteries" in 660 million years, where the probability of each lottery was 10^{-100}? Such a belief would be mathematical and scientific nonsense. It is virtually impossible you could win 3 "consecutive lotteries" in 660 million years.

But even the problem of winning 3,000 "consecutive lotteries" is just a small tip of the iceberg for the theory of evolution.

Winning 3,000 "consecutive lotteries" is just for human DNA. How about the DNA of millions of other unique species and the "consecutive lotteries" each of them needed to have "won," which did not include any duplication of ancestor species.

You also have problems with the male and female issue. Both the male and female have to have DNA which aligns with each other in order to have offspring. Thus, each must have the same impossible mutations *in their germ cells*, and the male and female must live in the same geographical area and same time period. This alone generates insane probabilities.

Those who support the theory of evolution might say that the same "external" events caused the same mutations in the DNA of the male and female. This theory is totally absurd for many, many reasons, but this book will not take the time to discuss these issues.

The point is that six-hundred million years is not enough time for evolution to have worked.
Even *600 billion years* would not be enough.
Even $10^{100,000}$ years would not be near enough time for evolution to have occurred by random mutations of DNA. Not even close.

Do the math. You will find out that adding a few numbers to an exponent do not help the overall problem the theory of evolution faces.

Evolution never happened, not on this earth or on any other earth, or on any other galaxy or on any other Universe.

This Universe, the planets, and life on this earth were created by intelligent beings, all under the watchful eye of God Himself or life was created by God Himself. There is no other explanation for the DNA of millions of different species of animals and plants.

Introduction to the Mathematics of Evolution

Chapter 16

Copy Genes and Evolution Genes

Mathematical Note

It was noted in the prior chapter on mathematics that 1 / 100 or 10^{-2} was equal to .01. .01 can also be written as 1%. In other words, if we have a percentage, such as 14.65%, we can move the decimal over two places to the ***left*** and write it as .1465.

Likewise, if we have a number such as .0045, we can convert this to a percentage by moving the decimal point two places to the ***right***. Thus, .0045 is equal to: .45%.

In this chapter, sometimes a small number will be represented as a decimal (such as: .000004616) and sometimes this same exact number will be represented as a percentage (i.e. .0004616%). They are the same thing.

The Different Kinds of Mutations

There are actually several different kinds of mutations.

For example, there are mutations where entire genes are copied more than once; which is called: duplication. There are also mutations where entire chromosomes are copied more than once. And so on.

When a gene is copied, the copy of the gene has no function. It is felt that if one of these extra copies of a gene are bombarded with point mutations; that a new gene (actually a new gene complex is needed) may be able to be created by random mutations of nucleotides.

In other words, you start with a worthless, extra copy of a gene, mutate its nucleotides many times and end up with a new gene for a new species.

This is important to the theory of evolution because creating a gene from scratch is a very slow process and is riddled with statistical problems.

But let us consider the problems created by starting with a copy of a gene complex and trying to modify it; using numerous point mutations; to become a new functional gene complex for a new species.

In fact, this very thing had to have happened about ***200 million times*** for the theory of evolution to be true (assuming each of the 10 million unique species has 20 unique gene

complexes on average). With 200 million unique gene complexes formed by evolution, it should be easy to convert a copy of a gene into a new gene with a new biological function.

For example, suppose a complex animal, such as a female chimpanzee, had an extra copy of a gene in one of her germ cells, as the result of a mutation. Suppose the female chimpanzee mates. We will ignore male and female issues.

Is it possible this second, useless copy of a gene can mutate to the point that it is a new, fully functional gene, which leads to a new species (a new species requires at least one new gene complex, but generally has dozens of unique gene complexes)?

Suppose we consider the potential evolution (via point mutations) of the extra copy of this chimpanzee gene.

Suppose, for example, that 50% of the nucleotides of this extra copy were identical to a gene which does not exist in chimpanzees, but which does exist in a more advanced primate. Could the extra copy of a chimpanzee have been the source of a new gene complex for a more advanced primate?

Let us consider that "Gene A" is an extra copy of an existing gene, meaning it is a "copy gene" of a valid gene complex.

Let us say that the claim is made that "Gene A," in the old species, via random point mutations, becomes "Gene B" in the new species.

Remember, in this discussion 50% of the nucleotides of "Gene A" start out to be identical to the nucleotides in "Gene B," which does not yet exist. "Gene A" is believed to "evolve" by random point mutations to become "Gene B."

Let us consider a nucleotide in a position of Gene A (say a 'T' is in nucleotide position 2,576). Suppose a 'T' is also in position 2,576 of Gene B since B is a copy of A. We will call this 2,576th nucleotide in Gene A a "right" nucleotide since it does not need to be changed to equal the 2,576th nucleotide in Gene B.

If a nucleotide in another position of Gene A is not equal to the same position of Gene B, we will call it a "wrong" nucleotide.

Thus, using this terminology, in our example 50% of the nucleotides in Gene A start out as "right" nucleotides and 50% of the nucleotides in Gene A start out as "wrong" nucleotides.

Let us study point mutations as they occur to Gene A.

How Point Mutations Affect "Wrong" and "Right" Nucleotides

First of all, any point mutations to this extra copy of the gene could affect any of the nucleotides, not just the "wrong" nucleotides. Thus, a mutation would be just as likely to affect a "right" nucleotide as it would a "wrong" nucleotide.

Thus, you would have a never-ending battle trying to preserve the "right" nucleotides from mutating into "wrong" nucleotides while you are simultaneously trying to "fix" wrong nucleotides.

Furthermore, even when there is a mutation to a "wrong" nucleotide, there is still a 67% chance that the new mutation will still be a "wrong" nucleotide. To understand this, suppose there is a nucleotide in position 3,000 which is an 'A' (which is a "wrong" nucleotide). Let us assume the "right" nucleotide is a 'G'.

There are three possible mutations of this 'A' nucleotide. It can mutate into a 'C' a 'G' or a 'T'. Note that two of these three mutations are still "wrong" (i.e. the 'C' and 'T' are still wrong). Thus, 2 out of the 3 possible mutations (i.e. 67%) are still "wrong" even if there is a mutation to a "wrong" nucleotide.

There are thus three categories of mutations:

First, if the mutation changes a "wrong" nucleotide into a "right" nucleotide, we will call it a "good" mutation.

If the mutation simply changes one "wrong" nucleotide into a different "wrong" nucleotide, we will call it a "neutral" mutation (because it does not change the overall number of "right" nucleotides).

If the mutation changes a "right" nucleotide into a "wrong" nucleotide, we will call it a "bad" mutation.

Law #1: When there is a mutation to a "wrong" nucleotide, there is only a 33% chance the mutation will lead to a "right" nucleotide.

Law #2: When there is a mutation to a "right" nucleotide, there is a 100% chance it is replaced by a "wrong" nucleotide because any nucleotide other than the "right" nucleotide will be a "wrong" nucleotide (Note: a "mutation" implies the nucleotide is changed).

Since 50% of the nucleotides in the "copy gene" are correct, and because 50% of the nucleotides in the "copy gene" are wrong; there is a 50% chance a "wrong" nucleotide is changed. But only 33% of these changes create a "right" nucleotide. Thus, only 16.67% of the early point mutations (i.e. 50% times 33%) will convert a "wrong" nucleotide into a "right" nucleotide.

The other 33.33% of the early mutations of a "wrong" nucleotide will convert a "wrong" nucleotide into a different "wrong" nucleotide. This is the "neutral" mutation.

Thus, only 16.67% of the early mutations will be beneficial.

On the other hand, 50% of the early mutations will convert a "right" nucleotide into a "wrong" nucleotide. Every time you change a "right" nucleotide, it will become a "wrong" nucleotide.

Thus, 50% of the early mutations will be detrimental.

Do you see what is happening? 16.67% of the early mutations are "good" mutations. 33.33% of the early mutations are "neutral" mutations and do not affect the total number of "right" nucleotides, thus they can be ignored. But 50% of the early mutations are "bad" mutations.

Thus, *computer simulations would show a deterioration of the nucleotide sequence* (i.e. a deterioration of the percentage of "right" nucleotides) as time passed. No matter what percentage of "right" nucleotides you start with; a stable 25% "good" mutation level (i.e. only 25% of the nucleotides would be "right" nucleotides) will eventually result.

Let us analyze why the DNA will deteriorate until 25% of the nucleotides are "right" nucleotides.

Assuming 25% of the nucleotides are correct, all of the "right" nucleotides (25%) in this sequence, if they are changed by a mutation, will represent a "bad" mutation. Thus, 25% of the mutations are "bad" mutations, which convert a "right" nucleotide into a "wrong" nucleotide.

25% of the "wrong" nucleotides (75% "wrong" nucleotides times a 33.33% chance the new nucleotide is a "right" nucleotide) are "good" mutations.

50% of the "wrong" nucleotides (75% "wrong" nucleotides times a 66.67% chance the new nucleotide is also a "wrong" nucleotide) are "neutral" mutations.

Thus the 25% "right" nucleotides will be a very stable percentage of "right" nucleotides once it is achieved.

You would eventually end up with 25% "right" nucleotides whether Gene A started out with 95% of its nucleotides identical to Gene B or if Gene A started out with 10% of its nucleotides identical to Gene B.

The bottom line is that regardless of the beginning percentage of "right" nucleotides, as more and more nucleotides were randomly mutated, the percentage of "right" nucleotides would slowly adjust up or down to 25%.

Of course, a gene complex which is only 25% "right," will perform no function and will be useless.

Even if you started out with no nucleotides, and simply added nucleotides, the 25% "right" nucleotides will be a very consistent percentage right from the beginning.

Let us understand why all of this is true by looking at computer simulations.

Understanding Point Mutations to Gene Copies

Let us suppose that Gene A is a medium-sized gene complex with 20,000 nucleotides. Let us further suppose that when this gene complex is copied, an extra copy of the gene complex is created. This extra copy has no function.

Let us further suppose that 95% of the nucleotides of the extra copy of Gene A are identical to Gene B, which does not exist yet, but is the goal of evolution (i.e. via random point mutations).

We will call the extra copy of Gene A the "copy gene," and we will call the goal of mutations by evolution the "evolution gene." The "copy gene" starts out, in this example, with 95% "right" nucleotides. The goal is for the "copy gene" to become the "evolution gene" by random point mutations, which has 100% "right" nucleotides by definition.

First of all, only 5% of the nucleotides (meaning 1,000 of them) start out to be "wrong" nucleotides. This means that only 5% of the "first mutation" (i.e. the very first point mutation we are considering) will affect a "bad" mutation. 5% of 20,000 nucleotides is 1,000 nucleotides (this is the number of nucleotides which start out as "wrong" nucleotides, which is 5% of 20,000).

However, as mentioned above, 66.67% of any "first mutation" on a "wrong" nucleotide would also be a "wrong" nucleotide. This would be a "neutral" mutation.

This means only 33.33% of the mutations, on the 5% of "wrong" nucleotides, would yield an improvement in the total number of "right" nucleotides.

Multiplying .05 times .33333... yields a .01666... probability; meaning a 1.666...% probability, that the "first mutation" will convert a "wrong" nucleotide into a "right" nucleotide.

In other words, since we started out with 1,000 "wrong" nucleotides (i.e. 5% of 20,000 nucleotides), there is only a 1.666...% probability that the first mutation will increase the total number of "right" nucleotides to 19,001.

On the other hand, we know immediately that there is a 95% probability that the first mutation will be a "bad" mutation because 95% of the initial nucleotides are "right" nucleotides, and if one of these is mutated, it will automatically be a "bad" mutation.

We can summarize these probabilities thusly:
1st mutation is a "bad" mutation: 95%
(i.e. a "right" nucleotide is changed into a "wrong" nucleotide)
1st mutation is a "neutral" mutation: 3.333...%
(i.e. a "wrong" nucleotide is affected, but it is still a "wrong" nucleotide)
1st mutation is a "good" mutation: 1.666...%
(i.e. a "wrong" nucleotide is changed into a "right" nucleotide)

First Simulated Point Mutation

Let us consider 500,000 computer simulations. A "computer simulation" is a situation where a computer randomly picks a number and applies this number to the beginning condition (i.e. the simulation starts with 19,000 out of 20,000 nucleotides are "right" nucleotides).

Out of 500,000 cases where a "copy gene" is attempting to become an "evolution gene (i.e. 500,000 simulations) where a Gene A started out as 95% equal to Gene B, we would only expect 8,333 cases (i.e. 500,000 times .01666...%) where there were 19,001 "right" nucleotides after the first mutation (i.e. there was one additional "right" nucleotide added to the initial 19,000 "right" nucleotides).

Here is the calculation of how many "good" mutations we could expect in the very first mutation:

1) 1,000 "wrong" nucleotides at beginning of simulation

2) 1,000 / 20,000 = .05 or 5% of the initial nucleotides start as "wrong" nucleotides (these are the nucleotides we are hoping to change into "right" nucleotides)

3) However, even when a "wrong" nucleotide is affected, in only 33.333...% of the cases is a "wrong" nucleotide actually converted into a "right" nucleotide.

4) Thus in .05 times .3333... = 1.666...% of the initial mutations is a "wrong" nucleotide changed into a "right" nucleotide

5) Thus, in 500,000 simulations of the first point mutation, we would expect:
500,000 times .01666... = 8,333.33 instances where the number of "right" nucleotides increased.

Thus, 8,333 of the 500,000 simulations would be expected to be "good" mutations. In other words, after 1 point mutation, in 8,333 of the 500,000 simulations there will be 19,001 "right" nucleotides.

The Second Simulated Point Mutation

What is the probability that *both the first and second mutations* will be "good" mutations and there will be 19,002 "right" nucleotides after the second point mutation?

Here is the calculation:

1) We assume the first point mutation was a "good" mutation (i.e. one of the 1,000 initial "wrong" nucleotides was converted into a "right" nucleotide), leaving 999 "wrong" nucleotides after the first mutation (i.e. before the second mutation).

2) 999 / 20,000 = .04995 (probability one of the 999 "wrong" nucleotide is affected by a point mutation)

3) .04995 times .3333... (probability "wrong" is converted to "right) = .01665

4) Now we need to multiply the probability of the 1st "good" mutation with the probability of a 2nd "good' mutation:
.01666... times .016665 = .0002775

5) 500,000 times .0002775 = *139 cases* out of 500,000 will have two consecutive "good" mutations in the first two attempts.

Thus, out of 500,000 cases where a Gene A started out as 95% equal to Gene B, we would only expect 139 of the 500,000 cases to create 19,002 "right" nucleotides after 2 mutations.

The Third Simulated Point Mutation

What is the probability that the first 3 mutations would all be "good" mutations? Try to figure this out for yourself before looking at the answer.

For the third mutation, there are 19,002 "right" nucleotides and 998 "wrong" nucleotides to start with (i.e. after the second mutation).

Here is the calculation:

1) 998 "wrong" nucleotides at beginning (i.e. before the third mutation)

2) 998 / 20,000 = .0499 (probability a "wrong" nucleotide is affected)

3) .0499 times .3333... = .0166333... there is a "good" mutation applied to a "wrong" nucleotide

4) Now we need to multiply the probability of the 1st two "good" mutations with the probability of the 3nd consecutive "good' mutation:
.0166333... times .0166500 times .0166666... = .000004616

500,000 times .0000046156 = 2

In summary, out of 500,000 computer simulations of the first 3 point mutations, we would only expect 2 of them to have the first three consecutive mutations be "good" mutations, ending up with 19,003 "right" nucleotides.

Conclusions of First 3 Simulations

Thus we have these statistics for the first 3 mutations for 500,000 simulations:
1) Expected number with one "good" mutation: 8,333 (.01666...)
2) Expected number with two consecutive "good" mutations: 139 (.0002775)
3) Expected number with three consecutive "good" mutations: 2 (.000004616)

Do you see a trend? The probability of getting consecutive "good" mutations drops very quickly and will continue to drop.

But even if there were three "good" mutations in the first three attempts, there would still be only 19,003 "right" nucleotides and 997 "wrong" nucleotides. It would be ludicrous to think that the first 1,000 mutations would all be good mutations because the probability drops so quickly.

However, there are many different way to get to 19,003 "good" mutations. Consider this scenario:
Start out with 19,000 "good" mutations,
First Mutation: a "neutral" mutation (still 19,000 "right" nucleotides)
Second Mutation: a "good" mutation (19,001 "right" nucleotides)
Third Mutation: a "bad" mutation (19,000 "right" nucleotides)
Fourth Mutation: a "good" mutation (19,001 "right" nucleotides)
Fifth Mutation: a "neutral" mutation (19,001 "right" nucleotides)
Sixth Mutation: a "good" mutation (19,002 "right" nucleotides)
Seventh Mutation: a "good" mutation (19,003 "right" nucleotides)

In this case it took seven mutations to get to the goal of 19,003 "good" mutations. However, there are still 997 "bad" mutations to fix before getting to where evolution wants to get.

Rather than consider all of the possible paths to 20,000 "good" mutations, and the probability of each path, there is a much easier way to grasp the problems with converting a "copy gene" (i.e. a copy of an existing gene) into an "evolution gene" (i.e. a gene which has a nucleotide sequence which is the goal of evolution, meaning the goal of random mutations).

This far better method is called computer simulations. Computer simulations have a great deal of advantages to highly complex statistical analysis in a situation like this one.

A Single Simulation

Let us consider the two kinds of genes we have been talking about (which will be simulated in a computer program):
"copy gene" is an accidental mutation copy of an entire "old gene,"
"evolution gene" is the gene which the "copy gene" is attempting to mutate into.

One theory of evolution is that new genetic material comes from mutations affecting copies of existing genes. The "evolution gene" represents this new genetic material and is, by definition, a new "gene complex" of one of the new genes in a new species. The goal of evolution in this example is for the "copy gene" to mutation, one nucleotide at a time, into the "evolution gene."

Let us assume the "copy gene" and "evolution gene" are each 20,000 nucleotide pairs long.

Let us further assume the "copy gene" starts out being 95% identical to the "evolution gene." The 95% represents the 19,000 nucleotide pairs of the "copy gene" which are identical to the same nucleotides, in the same positions, in the "evolution gene."

This means that evolution must fix the other 5% of the nucleotide pairs to create a new, fully functional gene complex.

In other words, evolution only has to fix 1,000 nucleotides (i.e. 5%) on the copy gene to equal the evolution gene. Sounds easy, doesn't it. Let's see if it is easy.

It is the job of evolution to "fix" the 1,000 "wrong" nucleotide pairs. Evolution does this by mutating one nucleotide pair at a time. Actually we don't worry about "pairs" of nucleotides; we only care about one side of the "pair" because the other side automatically follows the main side (e.g. if an 'A' is on one side a 'T' is automatically on the other side). Thus, we are only concerned about the main side of the DNA in the gene complex.

The computer simulation starts out with a "copy gene" with 20,000 nucleotides on one side of the DNA. Of course this gene complex only exists in a computer.

The simulation randomly mutates one of the "nucleotides" (i.e. nucleotide positions) at a time.

Given the speed of computers, even home computers, a computer can simulate tens of thousands of random, sequential mutations fairly quickly.

After each random mutation, we can assess how many "right" nucleotides there are in the "copy gene."

For example, using just one randomly chosen computer simulation of 75,000 sequential point mutations (we are only dealing with one DNA strand and applying 75,000 consecutive point mutations to this one "copy gene").

These are the results of the first ten mutations:

Column 1 is the mutation number (i.e. 1 equals the first mutation)
Column 2 is the number of "right" nucleotides after the latest mutation
Column 3 is the percentage of "right" nucleotides after the latest mutation
Column 4 is the type of mutation

Results of a Single Computer Simulation, Where 10 Randomly Selected Mutations Were Sequentially Applied to the Copy Gene:

1	19001	95.005%	"good" mutation
2	19000	95%	"bad" mutation
3	18999	94.995%	"bad" mutation
4	18998	94.99%	"bad" mutation
5	18997	94.985%	"bad" mutation
6	18996	94.98%	"bad" mutation
7	18995	94.975%	"bad" mutation
8	18994	94.97%	"bad" mutation
9	18993	94.965%	"bad" mutation
10	18992	94.96%	"bad" mutation

Here are some other selected mutation points of this simulation so the reader can see the overall trend. The first column is the mutation number (i.e. 1000 means the 1,000th consecutive point mutation as applied to this "copy gene"). The second column is the number of "right" nucleotides. The third column is the percentage of "right" nucleotides.

Results of a Single Computer Simulation, Where 100,000 Randomly Selected Mutations Were Sequentially Applied to the Copy Gene:

Column #1: Simulation # (only the first 10,000 are shown)
Column #2: # of "right" nucleotides after the number of simulations)

```
1000        18082       90.41%
2000        17229       86.145%
3000        16438       82.19%
4000        15701       78.505%
5000        14998       74.99%
6000        14347       71.735%
7000        13741       68.705%
8000        13181       65.905%
9000        12666       63.33%
10000       12154       60.77%
```

Note the overall downward trend. This is because most of the nucleotides start out as "right" nucleotides, thus most of the early mutations turn a "right" nucleotide into a "wrong" nucleotide.

Continuing on after 10,000 simulations, somewhere between the 15,000th mutation and the 16,000th mutation, the percent of "right" nucleotides dropped below 50%.

```
15000       10043       50.215
16000       9736        48.68
```

Somewhere between the 37,000th and 38,000th mutation the percentage of "right" nucleotides dropped below 30%.

```
37000       6073        30.365
38000       5953        29.765
```

As predicted, eventually the percentage of "good" mutations stabilized around 25%.

Multiple Simulations

A single simulation may tell us the trend of degeneration, but it doesn't really prove anything. But the power of the computer again comes to our aid. My home computer can do 50,000 simulations, similar to the one above, in less than four hours.

However, each simulation only runs to the point that the percentage of "good" mutations drops below 85% (which is 10% less than the starting percentage). At this point it is considered "impossible" that future mutations will ever raise the "good" mutations above the initial level of 19,000 "good" mutations. The reader will understand why in a moment.

On average, the number of "right" nucleotides dropped below 85% on the 2,313th mutation (i.e. simulation).

Note that 10% of the total number of nucleotides is 2,000 and 15% of the nucleotides is 3,000. Thus, within an average of only 2,313 mutations, the total number of "right" nucleotides had dropped by 2,000 to a total of 3,000 wrong nucleotides. This should give the reader an idea of how quickly the number of "right" nucleotides drops when starting out with 95% "right" nucleotides.

To insure I was getting consistent data, I actually ran the 500,000 simulations in 10 sets of 50,000 simulations. It is actually best to do it this way to make sure your patterns are consistent. These ten groups of 50,000 simulations tell us a lot about mutating a "copy gene" into an "evolution gene."

Let us consider the results of the computer simulations.

First, let us consider only the first mutation of these 500,000 simulations:

1st mutation was a "bad" mutation:	475,123	95.02%
1st mutation was a "neutral" mutation:	16,470	3.29%
1st mutation was a "good" mutation:	8,407	1.68%

These are very consistent with our predicted results above:	
1st mutation predicted to be a "bad" mutation:	95%
1st mutation predicted to be a "neutral" mutation:	3.33%
1st mutation predicted to be a "good" mutation:	1.67%

Now let us look at the "maximum" percentage of "good" mutations achieved for each simulation. To gather this information, for each simulation, and after each and every mutation, the "maximum" percentage of "good" mutations was kept track of. The "highest" "maximum" percentage, for each simulation, was recorded.

Out of the 500,000 simulations, the maximum percentage of "good" mutations that was ever achieved was 95.015%. This was 19,003 "right" nucleotides. In other words, among the 500,000 simulations, *none of these simulations* ever achieved 19,004 "right" nucleotides!!

And the 19,003 level of "right" nucleotides was achieved in only 4 of the 500,000 simulations.

Here is the complete table of the maximum achieved percentage of "right" nucleotides among the 500,000 different simulations:

Above 95.015% (above 19,003)	0	0%
# Achieved 95.015% (19,003)	4	0.0008%
# Achieved 95.01% (19,002)	167	0.03%
# Achieved 95.005% (19,001)	8,648	1.7%
# Achieved 95% (19,000)	24,496	4.9%
# Achieved 94.995% (18,999)	466,685	93.3%

In the above discussion, we predicted that only 2 simulations, out of 500,000, would have the first 3 consecutive mutations all be "good" mutations. There were actually 4 simulations which achieved 19,003 "right" nucleotides. This is not surprising because

there are multiple ways to reach 19,003 "right" nucleotides other than just the first 3 mutations being correct.

Nevertheless, achieving 19,003 "right nucleotides" would be an "outlier," meaning it would be a very rare event, and the number of outliers is always hard to predict.

In order for the "copy gene" to randomly mutate into an "evolution gene," it would be necessary to achieve 20,000 "right" nucleotides. Yet, not even 19,004 "right" nucleotides (starting with 19,000 "right" nucleotides!!) were achieved in 500,000 attempts (i.e. 500,000 simulations).

Another interesting result of the 500,000 simulations was how quickly the total number of "right" nucleotides dropped below 19,000, never to rise to the 19,000 level again.

This is critical to understand: by the time the 11th mutation was calculated, in all 500,000 simulations, the total number of "right" nucleotides was below 19,000, and never achieved 19,000 "good" mutations again.

In other words, after the 11th mutation, every one of the 500,000 simulations was below 19,000 "right" nucleotides, and never achieved 19,000 "right" nucleotides after the 11th mutation.

Only once in 500,000 simulations was the 10th mutation at 19,000 "right" nucleotides. Here is the progress of that one simulation.

Simulation number 29,058 in the seventh set (of ten sets) of 50,000 simulations:

```
1st mutation (good)   95.005%    19,001 "right" nucleotides
2nd mutation (bad)    95%        19,000 "right" nucleotides
3rd mutation (good)   95.005%    19,001 "right" nucleotides
4th mutation (bad)    95%        19,000 "right" nucleotides
5th mutation (bad)    94.995%    18,999 "right" nucleotides
6th mutation (bad)    94.99%     18,998 "right" nucleotides
7th mutation (bad)    94.985     18,997 "right" nucleotides
8th mutation (good)   94.99      18,998 "right" nucleotides
9th mutation (good)   94.995     18,999 "right" nucleotides
10th mutation (good)  95%        19,000 "right" nucleotides
```

Even though this simulation "kept its head above water" longer than any other simulation, it only achieved 19,001 "right" nucleotides.

This shows just how quickly the overwhelming problems created by the vast number of "right" nucleotides (which always mutate into a "wrong" nucleotide) prevented a significant net accumulation of "right" nucleotides.

While there is some flexibility in the exact sequence of an "evolution gene," these numbers make it very, very clear that even taking into account a reasonable amount of flexibility, converting a "copy gene" into an "evolution gene" is impossible, even starting at 95% identical nucleotides.

Starting At Even Higher Percentages

If we had started at 97% "right" nucleotides, instead of 95% "right" nucleotides, an even higher percentage of the first mutations would be "bad" mutations. This is because there is a higher percentage of "right" nucleotides to mutate into "wrong" nucleotides.

There is actually a paradox involved. Study this next sentence very, very carefully because it will become important in future discussions:

The higher the percentage of "right" initial nucleotides, the lower the probability that the first few mutations will result in a net gain in the number of "right" nucleotides.

Let us consider some comparison statistics.

Simulations Where "Plus Two" or Above Was Achieved

"Plus two" means the simulation achieved 2 nucleotides higher than were it started. For example, if it started at 19,000, "plus two" means a simulation achieved 19,002 "right" nucleotides or above.

At 95% (initial percentage of "right" nucleotides), 19,000 nucleotides started as "right" nucleotides. Among 500,000 simulations, 167 simulations achieved "plus two" nucleotides or above (i.e. 19,002). Also, 4 simulations achieved "plus three" nucleotides (i.e. 19,003).

At 97%, 19,400 nucleotides started as "right" nucleotides. Among 500,000 simulations, *only 51 simulations* achieved "plus two" (as opposed to 167) nucleotides (i.e. 19,402). Also, only 1 simulation achieved "plus three" (as opposed to 4) nucleotides (i.e. 19,403).

At 99%, 19,800 nucleotides started as "right" nucleotides. Among 500,000 simulations, *only 4 simulations* achieved "plus two" nucleotides (i.e. 19,802). Also, none of the simulations achieved "plus three" nucleotides (i.e. 19,803).

Clearly, as the initial percentage of nucleotides start out as "right" nucleotides, it is harder to achieve a "plus two" and "plus three" condition.

How Quickly Simulations Dropped Below Initial

The next question to answer is how many mutations did it take for the simulation to drop below the initial "right" nucleotide level, never to rise above it again.

At 95%, by the 11th mutation, every simulation was below the initial number of "right" nucleotides, never to achieve the initial number of "right" nucleotides again.

At 97%, by the 9th mutation, every simulation was below the initial number of "right" nucleotides, never to achieve the initial number of "right" nucleotides again.

At 99%, by the 6th mutation, every simulation was below the initial number, never to achieve the initial level of "right" nucleotides.

We conclude from this set of data that the higher percentage of initial "right" nucleotides, the faster the DNA will deteriorate.

How Many Simulations Never Achieved the Initial Condition

In each simulation there was a "first mutation." In most cases this first mutation was a "bad" mutation. The question becomes, in what percentage of the simulations was the first mutation a "bad" mutation, ***and*** the simulation was never able to achieve the initial condition of "right" nucleotides. For example, at 95%, what percent of the time was the first mutation a "bad" mutation ***and*** subsequent mutations never achieved the initial 19,000 "right" nucleotide level?

At 95%, 93.3% of the simulations never achieved the initial number of "right" nucleotides.

At 97%, 96.0% of the simulations never achieved the initial number of "right" nucleotides.

At 99%, 98.7% of the simulations never achieved the initial number of "right" nucleotides.

How Quickly Did Simulations Reach an Unrecoverable Condition

When the deterioration of the DNA dropped 10% below the initial level of "right" nucleotides, it was considered impossible for the simulation to ever recover enough to reach the initial level. The simulation was terminated at this point.

At 95%, by the 2,313th mutation, the percentage of "right" mutations had, on average, dropped by 10% (i.e. from 95% to below 85% or from 19,000 "right" nucleotides to below 17,000 "right" nucleotides).

Note that a drop of 10% amounted to the total number of "right" nucleotides deteriorating by 2,000. Thus, within 2,313 mutations, the number of "right" nucleotides had dropped by 2,000!!

At 97%, by 2,244 mutations, the number of "right" nucleotides had deteriorated by 2,000.

At 99%, by 2,179 mutations, the number of "right" nucleotides had deteriorated by 2,000.

We can clearly see that the higher the initial number of "right" nucleotides, the faster the DNA will deteriorate by 10%.

All of this results in a paradox for evolution:

Kehr's Paradox: The higher the percentage of initial correct nucleotides, the more quickly the DNA will deteriorate because of random mutations.

While this paradox may seem obvious after our discussion, it actually is far more significant to the evolution debate than appears on the surface.

Looking At This Another Way

The above numbers reveal very, very critical concepts. The overall concept is that the higher the initial percentage of "right nucleotides," the faster the DNA will deteriorate. Eventually, the DNA will deteriorate to 25%, no matter what percentage of "right" nucleotides it starts with.

But what if we don't know the actual percentage of "right" nucleotides? How can we get an idea of the initial percentage of "right" nucleotides?

Ponder that last question before reading on because the answer should be obvious from Kehr's Paradox.

The answer is by studying the ratio (i.e. percentage) of "good" mutations to "bad" mutations.

What the above data tells us is that if, for a particular species, the percentage of "good" mutations is very, very rare; then we can logically conclude that this DNA has a very, very high percentage of "right" nucleotides.

In other words, if we know the percentage of initial "right" nucleotides, we can take a good guess at calculating the probability that early mutations will be "good" or "bad."

However, if we don't know the initial percentage of "right" nucleotides, we can look at the percentage of "good" mutations versus "bad" mutations and take a good guess at how many "right" nucleotides there are at any given time. In the next chapter, this concept will be discussed in more detail.

Conclusion

The theory of evolution depends heavily on new genetic material. Without new genetic material there are no new species and there is no evolution. Period. Random, pointless, directionless mutations are at the heart and soul of neo-Darwinism.

With the discovery of DNA the debate between the theory of evolution and creation science should have made a major turn. Suddenly, fossil morphology should have taken a "back seat" to the analysis of DNA in terms of studying mutations to determine the probability of evolution.

However, that didn't happen. The reason is that a study of DNA mutations is a massive, massive embarrassment to the theory of evolution for several reasons.

When science sees something that is not favorable to the theory of evolution, the discovery gets buried.

Thus, instead of DNA and probability analysis, which is embarrassing to the theory of evolution, nineteenth century morphology is still the main tool of evolutionists.

The next chapter will further explain why science has avoided any mathematical discussion of how new genetic material is created.

Introduction to the Mathematics of Evolution

Chapter 17

Ramifications of the Computer Simulations

Randomness is Predictable

Most people think that randomness is not predictable. While predicting the value of a single random value is not possible; picking the overall results of thousands or millions of random values is very predictable. This was demonstrated in the prior chapter.

"Outliers," meaning rare events (such as hitting the 19,003 "right" nucleotide level starting at 95%), cannot be predicted as to when they will happen, or how often they will happen; but predicting the vast majority of the normal data is quite easy. There is always very little variation except for the outliers.

For example, in the 500,000 simulations at 95%, the range of "first mutations" (i.e. only looking at the very first mutation in each simulation) which were "bad" mutations, in each group of 50,000 simulations, only ranged from 47,399 to 47,602.

In this same set of simulations, the range of simulations which never even achieved 1,000 "right" nucleotides, ranged from 46,594 to 46,772.

Also, in these 10 groups of 50,000 simulations, the maximum number of "right" nucleotides achieved, among all the simulations in each group, was either 19,002 or 19,003. In other words, from 500,000 simulations; 19,004 "right" nucleotides was never achieved.

Large volumes of random data will follow the pattern predicted by statistics. In fact, that is one way to verify your formulas are correct or to deal with situations where it is not practical to derive a formula because there are so many different scenarios.

However, we also saw from the simulations, that when a single event has a probability of .000004644 or less, it is not going to happen very often; even though it is impossible to predict exactly when it will happen or exactly how often it will happen. But we do know the event will be very rare.

Thus, even though we cannot predict the exact number of outliers, or when they will occur, we know they will be very rare.

Only "Good" Mutations are Allowed

In order to challenge the very damaging evidence from statistics, some scientists have speculated that only the "wrong" nucleotides are mutated. In other words, they claim that an original "right" nucleotide; or a "right" nucleotide which resulted from a mutation; is somehow protected and will not mutate into a "wrong" nucleotide.

With this theory, "right" nucleotides are never converted to "wrong" nucleotides. Thus, the number of "right" nucleotides never goes down, it only goes up.

While such a theory may help the mathematical problems of the theory of evolution, *the theory is scientific nonsense* and has absolutely no basis in fact.

There is no secret mechanism in the body; of a developing new species; which knows which nucleotides to preserve or protect, meaning there is no mechanism that knows which are the "right" nucleotides or which are the "wrong" nucleotides.

To put it another way, there is no secret, unseen, abstract, non-existent pattern of DNA which knows what the goal of evolution is for a new gene complex; which has never existed before in Nature.

Thus, there no mechanism which can prevent a "right" nucleotide from mutating into a "wrong" nucleotide. Nor is there any mechanism which can selectively fix only "wrong" nucleotides.

It is nothing but an absurd tactic, without any scientific basis, to try and overcome the statistical problems of the theory of evolution.

Even if "natural selection" selected a gene complex which barely worked, there is still no mechanism to selectively "fix" the "wrong" nucleotides. At no time is there ever anything but totally random, totally mindless, and totally without direction mutations of nucleotides. This is the entire basis of neo-Darwinism. Neo-Darwinism has no goal in mind.

While there is in fact a mechanism related to DNA which can fix certain kinds of errors in an existing DNA strand, this mechanism does not know what nucleotide should be in a particular position. The mechanism only knows which kind of nucleotide should be *paired* with an existing nucleotide (i.e. it knows an 'A' should be paired with a 'T"). It may do this by examining the hydrogen bond to see if it is the right kind of bond.

Creating New Genes From Scratch

Let us consider an "evolution gene" of 20,000 nucleotides (technically a moderate sized gene complex).

We already know that if we instantly created a random DNA strand of 20,000 nucleotides, the probability this random DNA strand would equal our "evolution gene"

would be $4^{-20,000}$. Even taking into account a reasonable amount of "flexibility" in the nucleotides (i.e. a reasonable number of permutations which would "work"), the probability a new gene complex could be created form scratch is still obscenely ridiculous.

There are some who would say that there are so many viable permutations of nucleotides that the probability of evolution is reasonable, given several billion years. In other words, they claim there is a high level of "flexibility" in sequences of nucleotides.

This is known to be false. The vast majority of human DNA is not coded for proteins; rather, it consists of "instructions" or "computer programs." There is very little "flexibility" in these sections of our DNA. But even nucleotides which code for proteins have very little variability.

At the single nucleotide level there may be some flexibility, but when you start changing dozens of individual nucleotides, which are part of the same function, you could end up with a disaster.

The term "allele" (i.e. allelomorph) has to do with variety of nucleotides in specific locations on DNA. It is beyond the scope of this book to discuss alleles on human DNA, but I can assure the reader that a study of human DNA alleles would confirm my comments; namely that human DNA is not as flexible as thought by the average person, meaning I am being very generous to the theory of evolution with my probabilities.

But there is another reason neo-Darwinism is incorrect, even with regards to nucleotides which code for proteins. When an animal of a new species needs a new gene it needs a highly specialized new gene.

For example, if a camel needs a new type of heart protein, in order for a new species to arise with a superior heart; it needs a highly, highly specialized heart protein made specifically for a camel.

If a camel needed a new heart protein (for example, so the camel can function better in the extreme heat of the desert); but instead it got a new lever protein for a mouse; the new liver protein for a mouse would not provide the camel any survival benefit.

It would literally be like taking a bolt from the engine of a 50 year old automobile and trying to find a place to put it in a new jet engine.

In general, when an animal needs a new protein or new enzyme, it needs a highly specialized protein or enzyme because the protein needs to fit in with, or help create, new complex protein structures which include several or many proteins. Thus, there is very little "flexibility" even when considering nucleotides which code for specialized proteins.

Thus, to assume there is a lot of flexibility in DNA is simply not true. The flexibility is usually in microevolution, but even then there is little margin for error.

So what if the new gene complex, created from scratch, was not right, could it over time mutate into being the right sequence of nucleotides? In this case, we have the same situation as in the prior chapter. Even if the new, from scratch, gene complex was 95%

right on the first attempt; within about 11 mutations the percentage of "right" nucleotides would deteriorate below 95%, just as in the prior chapter.

Thus, the very first attempt at making a new gene complex would have to be virtually perfect, perhaps 99.999% accurate. Essentially, the gene complex would have to work the first time because almost all new mutations will make it worse.

But if the copy of the gene complex worked the first time, there would be *no new genetic information*!!

The problem comes in creating new genetic information. It is the mutations which attempt to create new genetic information which causes the deterioration of the DNA.

The Claims of "Modern" Science

Frequently, two genes, or other sequences of DNA, are claimed to be identical in two or more species. That is interesting, but a person never knows exactly what scientists who make such claims are really talking about.

Many times scientists will see some similarities in a single sequence of nucleotides in two different animals; and will claim that entire genes (actually it would have to be the entire gene complex, which they never talk about) are identical in two different animals. Scientists are somehow very vague when talking about these kinds of things.

For example, you sometimes see claims that the DNA of a certain kind of primate is 96% "identical" to human DNA. This is nonsense. They may be talking about a single, small section of DNA. I am never quite sure what they are talking about because they always speak in broad generalities.

But even if it were true, this would simply be a proof that human intelligence comes from our spirit intelligence, not from our physical brain. Any religion which believes in "life after death" believes in "intelligence after death" and thus believes that our human intelligence comes mainly from our spirit body, not our physical body.

Thus, it would be fine with me if some primate had 96% identical DNA to human DNA, but it is simply not true.

Look at this claim that the DNA of a worm functions nearly identically to human DNA:

> *"The main difference between worm DNA and human DNA lies in the amount [of DNA]; a human genome has about 30 times as much DNA as a worm genome."*
> YourGenome.org

In other words, worm DNA is *30 times shorter than human DNA*, yet the "main difference" between worm DNA and human DNA is in the length of the DNA. Ugh.

I suspect that the laws governing DNA are identical in all species, so I don't exactly know the intent of the above quote. Perhaps that was their point because certainly human DNA is far more sophisticated than worm DNA.

The point is that no matter what scientists discover, they somehow "spin" it into a claim for the theory of evolution. That is how you get published.

Human DNA

There are two ways to look at the data in the prior chapter.

A person can say that the higher the ratio or percentage of *initial* "copy gene" nucleotides to "evolution gene" nucleotides, the quicker the total number of "right" nucleotides will drop forever below the initial level and even will more quickly drop below the 10% "lower than initial" level (Kehr's Paradox).

But there is another way to look at this same data. The second way is to say that the "more perfect" human DNA is:
1) The more common it will be that a mutation will be negative (or neutral), and
2) The rarer it will be that a mutation will be positive.

If DNA was "perfect," meaning 100% "right" nucleotides, the first mutation will be a "bad" mutation 100% of the time.

But even as we saw in the prior chapter, when the "copy gene" was 99% equal to the "evolution gene," "good" mutations were rare in the early stages of mutations.

Thus, we can conclude that if we analyze the percentage or ratio of "good" mutations to "bad" mutations, in an existing species, we can tell how perfect the DNA of an animal or plant is.

Ponder that prior sentence carefully.

Applying this mathematical fact to human DNA; the more perfect human DNA is; the fewer "wrong" nucleotides there are to convert to "right" nucleotides and the more rare "good" mutations will be.

The reality is the vast, vast majority of mutations in human DNA are either neutral (i.e. they have no effect) or they are harmful.

Unfortunately many point mutations are "neutral." This does not mean, however, that they are really neutral.

For example, as could be surmised from Dr. Sanford's book on genetic entropy, many of the "neutral" mutations may be small detrimental mutations or small positive mutations which cannot be measured due to other factors (i.e. "background noise").

For example, a mutation may be positive or negative, but it may have such a small effect compared to other factors, the effect is essentially "drown out," meaning the effect of the mutation cannot be detected.

As Dr. Sanford explained, this scenario can be compared to laying on top of a stack of 15 mattresses. If you put a small rock under the bottom mattress (to represent a point mutation) you won't be able to feel it because the stack of 15 mattresses you are laying on buffers or "drowns out" the negative effects of the small rock. Thus it is counted as a "neutral" point mutation, even though it is negative.

Such is the genius and fault tolerance of human DNA!!!!

As another example, a football player, on the offensive line, may miss a block, but the overall play may still result in a touchdown for his team. His missed block may be lost to the crowd because of the overall exuberation which results from the touchdown.

However, it would be logical to say that the "neutral" mutations follow roughly the same pattern as those mutations which can be measured. This would mean that virtually all "neutral" mutations are in fact negative, but we simply cannot detect the damage because so many other things (such as fault tolerance) get in the way of measuring the damage or the damage is so small.

The Ratio in the Real World

So what is the actual ratio of "favorable" point mutations to "unfavorable" point mutations? Here is a quote from Dr. Sanford:

> *"I have seen estimates of the ratio of deleterious-to-beneficial mutations which range from one thousand to one, up to one million to one."*
> Genetic Entropy & The Mystery of the Genome, page 24

Actually, as Dr. Sanford points out in his book, even this ratio is misleading. Most so-called "beneficial" mutations actually *decrease the information* in DNA. It just so happens that certain types of decreasing of DNA information turn out to have some relatively favorable results.

One example of this is the Chihuahua dog. In extreme heat, as Dr. Sanford mentions on page 17, reduction of size and loss of hair may be beneficial, but *this benefit is the result of a loss of genetic information*, not an increase in genetic information.

(By the way, it is almost a requirement to read Dr. Sanford's book at some point - it is an absolute eye-opener and is actually a requirement to read in order to grasp some of the concepts in this book!! It is essential that a person fully understand the concept of "genetic entropy" because it is at the core of understanding several key concepts in this book. This book cannot go into the depth of Dr. Sanford's book on this topic.)

So even when there are beneficial mutations, relative to a given situation, it always involves either a *loss of genetic information* or a change to normal genetic information. It *never* involves an increase in genetic information!!

The key question is this - *has science actually ever seen new genetic information result from random genetic mutations; especially new genetic information which includes a new gene complex?*

The prior chapter proves the answer to this question is 'no'!! A future chapter will go into this in even more detail.

Let us again quote Dr. Sanford, a world-famous plant geneticist:

> *"When it was discovered that certain forms of radiation and certain chemicals were powerful mutagenic agents [i.e. they caused mutations], millions and millions of plants were [intentionally] mutagenized and screened for possible improvements. Assuming the Primary Axiom [of neo-Darwinism], it would seem obvious that this would result in rapid "evolution" of our crops. For several decades this was the main thrust of crop improvement research. Vast numbers of mutants were produced and screened, collectively representing many billions of mutation events. A huge number of small, sterile, sick, deformed, aberrant plants were produced. However, from all this effort, almost no meaningful crop improvement resulted. The effort was for the most part an enormous failure, and was almost entirely abandoned."*
> Genetic Entropy, page 25

In all these experiments, he mentioned one notable case where there was a benefit. However, this benefit actually resulted from the *net loss* in genetic information.

Thus, the whole concept of "beneficial mutations" is misleading. The "beneficial mutations" that scientists see are the result of a *loss of genetic information* or a variation in normal DNA sequences.

They have never seen new genetic information result from random mutations, especially if a person is speaking of enough new genetic information to create a new gene complex.

When thinking about the computer simulations in the prior chapter, and the above quote and comments, *it is very, very, very clear that human DNA; and the DNA of all species on the planet earth; are virtually perfect!!!*

This is obvious because *almost every noticeable mutation is detrimental and even the "beneficial" mutations really result from a loss of genetic information*.

That prior paragraph is so critical to understand I am going to repeat it:

This is obvious because *almost every noticeable mutation is detrimental and even the "beneficial" mutations really result from a loss of genetic information*.

This observation is proof that human DNA is not 99% or 99.9% or 99.99% perfect, but is virtually 100% perfect. In fact, considering genetic entropy, meaning our DNA is continuously deteriorating, *it hasn't been long ago since human DNA was perfect*.

Let's do some math. Assuming human DNA was 99% perfect; a random mutation would affect a "wrong" nucleotide only 1% of the time. However, only 33.33% percent of these mutations would end up creating a "right" nucleotide. This amounts to .01 times .3333...: giving an answer of .00333...

Thus, out of 100,000 mutations, there would be about 333 "good" mutations.

However, a realistic rate of the ratio of unfavorable to favorable mutations is that for every 100,000 mutations, only 1 of them is a "good" mutation. *Thus, human DNA could be said to be 333 times better than if our DNA was 99% perfect!!*

And even that rare favorable mutation probably was the result of a loss of genetic information.

To put it another way, if human DNA were 99% perfect; beneficial mutations, with no negative side-effects, would be fairly common (333 times more common that today).

We can conclude: *human DNA, and the DNA of all other creatures on earth, is virtually perfect!!!*

This is very important to understand and it is the result of understanding the prior chapter!!

Genetic Diseases

With our DNA so perfect, it is likely to expect that genetic disease would be rare.

In fact, there are many different kinds of genetic diseases, but when considering the total population of humans; severe genetic diseases are very rare.

When there is a genetic disease, the disease will be passed on to some or all of the children of the person with the disease (assuming the person lives to be old enough to have children).

Scientists can, in fact, look at the percentage of the population which has a particular type of genetic disease, and make a fairly good guess as to which century the common ancestor (I am not talking about common ancestor species) of these people first got the mutation in their DNA.

By tracking how genetic mutations are passed from one generation to another, it turns out that genetic diseases should spread fairly quickly.

Think about a huge tree of human genealogy, including every person who has ever lived on this earth, beginning with Adam and Eve, who lived about 6,000 years ago. The closer to Adam and Eve a genetic mutation occurs, the more people downstream (i.e. today) would be affected.

Most genetic problems with humans are not diagnosed because they are so mild. In some cases, multiple genes affect one condition or multiple genes affect multiple

conditions. That is why genetic epidemiology is so complex. But generally genetic-caused conditions are mild.

But no genetic disease affects such a high percentage of humans that it can be traced back more than a few hundred years.

Of course, some genetic diseases create such a severe health condition that the person does not live to be old enough to have children.

But enough "mild" genetic diseases exist that no "mild" genetic disease can be traced back more than a few hundred years.

This is an evidence that as we move back in time closer to Adam and Eve, that human DNA was even more perfect than it is today.

The key concept is that "good" mutations are so rare that there is huge evidence human DNA is incredibly perfect.

Even though DNA mutations must be in germ cells to be passed on to the next generation, genetic diseases are still good evidence as to the perfection of human DNA several thousand years ago.

Adam and Eve

If our DNA is nearly perfect, the DNA of Adam and Eve must have been totally perfect. DNA does not improve over time, rather DNA deteriorates over time.

So how did human DNA start out so perfect? The only logical answer turns out to be that human DNA was designed by an Intelligence much higher than our own and that human DNA started out to be perfect.

In fact, it is scientifically consistent with real data to say that Adam and Eve had perfect DNA. The reason I say this is that our DNA today is almost perfect, and our current DNA has deteriorated slowly since the days of Adam and Eve. *Their DNA had to be better than ours and ours is almost perfect*.

There is no way that a person can say that the DNA of Adam and Eve was inferior to ours. That would be nonsense. DNA deteriorates, and the more perfect it is, the faster it deteriorates because all nucleotides are "right" nucleotides in perfect DNA, thus all mutations are "bad" mutations when starting with perfect DNA. But even when DNA starts out imperfect (there is no evidence this has ever happened in a new species), but close to perfect, it still deteriorates.

Thus, the fact that our DNA is nearly perfect is an indication that Adam and Eve's DNA was significantly more perfect than ours.

It is also an indication that the Biblical account of Adam living to be more than 900 years old is not only true, but is an indication of the potential of our DNA.

George and Mary

Now let us talk evolution's alternative to Adam and Eve.

According to science, the first two *homo sapiens sapiens* lived about 100,000 years ago. The exact time claimed by science changes from year to year, but in this book we will assume 100,000 years is an average of all the numbers that have been put forth so far.

In order to perpetuate the human race, there had to be two first *homo sapiens sapiens*, namely a male and a female.

These two early humans, a man and a woman, *who have the exact same type of DNA as our modern DNA*, will be named George and Mary. What Adam and Eve are to creationists; George and Mary are to orthodox science.

Adam and Eve would have lived about 6,000 years ago, according to Biblical accounts, and George and Mary would have lived about 100,000 years ago, according to various fossils which have been discovered.

Someone might assume that the DNA of George and Mary was perfect 100,000 years ago. Had their DNA been perfect, our DNA today would be much more imperfect than it is today. Remember, no genetic diseases can be traced back more than a few hundred years. DNA deteriorates fairly quickly (when we think about millennia, not years), thus, there is no way our current DNA would be as perfect as it is if our ancestors were alive 100,000 years ago.

However, if the theory of evolution is true, the DNA of George and Mary would have been *very imperfect*.

There are many reasons the DNA of George and Mary would have been very imperfect.

First, genetic mutations are not only passed from one individual to another, but *genetic mutations are passed from one species to another*, if the theory of evolution were true. The parents of George and Mary would have inherited very imperfect DNA from their ancestor species and so on.

Second, George and Mary had both a father and a mother. To think that their DNA was perfect and that each of them had exactly the same random mutations to their DNA, so that George and Mary could have been born with perfect DNA, is totally ludicrous.

Not only did the parents of George and Mary have imperfect DNA, but the mutations to their gene cells would not have been exactly the same, thus the DNA of George and Mary would have been worse than the DNA of their parents.

Thus, it is obvious the DNA of George and Mary would have been very flawed.

But DNA does not improve with the generations. If George and Mary had imperfect DNA; our DNA today would be so severely damaged that few of us could survive and all of us would have serious genetic diseases.

In other words, if George and Mary had had a severe genetic flaw, all humans today would have that same genetic flaw.

But most people don't have any serious genetic flaw.

More will be said about genetic entropy affecting multiple species in a future chapter.

All of this creates a paradox for the theory of evolution.

If science wants flexibility in DNA (to try to overcome the statistical problems of the theory of evolution); then George and Mary would have had very imperfect DNA. Had that been the case, the DNA of *homo sapiens sapiens* today would be a complete disaster. Humans today would be like the mutants monsters in the movies.

Actually, a much more likely scenario is that humans would have been extinct many thousands of years ago due to damage to the morphing of the embryo algorithms, among other DNA problems.

While it is true that individuals born with serious genetic damage generally die before they can have children, or at least they cannot have children; many "moderate" genetic defects exist that do not cause this severity of damage. The inescapable reality is that if we were descendants of a couple who lived a hundred thousand years ago our DNA would be severely damaged *and "good" mutations would be common.*

That is the point. The perfection of our human DNA is so good that point mutations are almost always bad or neutral.

For example, suppose one of the descendants of George and Mary, who lived 80,000 years ago, had a moderate genetic defect. This moderate defect would be noticeable in all human beings today because any descendant of George and Mary of 80,000 years ago would be an ancestor of all humans today (do your genealogy)!!

The other side of the paradox is that if science claims no flexibility, and claims the DNA of George and Mary were perfect, then they have to subject their claims to a much higher statistical tolerance. This would make the theory of evolution even more ludicrous than when a great deal of "flexibility" is allowed.

Either way the theory of evolution fails to explain the real scientific data.

But the irrefutable fact is that had the DNA of George and Mary been perfect, by combining their DNA with 100,000 years of DNA entropy (i.e. deterioration), there is no question our human DNA today would be much worse than it really is.

But even more important, if human DNA was 100,000 years old, genetic diseases would be spread over a much larger percentage of the population today than they really are.

But the reality is that no genetic flaw causes a disease except in a very small percentage of the human population. Thus, all non-fatal and non-reproducing mutations (i.e. mutations which prevent reproduction) which currently inflict the human race are of very, very recent origin.

Certainly, by now favorable mutations would be very common due to the vast number of "wrong" nucleotides after 100,000 years of genetic entropy. But we don't see favorable mutations.

Thus we see enormous scientific evidence, real scientific evidence, that human beings are not only a very recent species (i.e. our DNA is still very, very perfect); but that our DNA was initially perfect.

Defective point mutations which occurred during the generations of human beings; between the time of Adam and our own time; may be the very nucleotides which, if changed back to their original Adamic nucleotide; can lead to the very rare positive mutations, which have no negative side-effects, that are occasionally seen. But don't hold your breath waiting for one these net favorable mutations to happen in someone's germ cell.

The reality is that humanity will never achieve, by random mutations, the perfect DNA of Adam and Eve. Human DNA is continuing to slowly deteriorate. But don't worry; God knows all of this and like everything else, it is all part of His plan. There is no doubt He designed DNA to be significantly fault-tolerant, which it is.

Introduction to the Mathematics of Evolution

Chapter 18

Patterns of Intelligence

"He who joyfully marches to music in rank and file has already earned my contempt. He has been given a large brain by mistake, since for him the spinal cord would fully suffice."
Albert Einstein, Nobel Prize, 1921 in Physics

Introduction

The key claim, meaning the prime assumption, of neo-Darwinism is that random mutations of nucleotides created *new genetic information and intelligence*. This had to have happened before natural selection came into play because natural selection can only act on existing species, not on species under construction. The term "selection" is used in "natural selection" because it "selects" among *existing* species.

Because randomness had to create the patterns of DNA or RNA for the "first living cell," and because randomness had to create the patterns of mutations which led to new species (these are the first two keys of Neo-Darwinism), essentially the prime assumption of evolution is that *patterns of randomness* can create highly sophisticated *patterns of intelligence and information*; because DNA has both highly sophisticated intelligence and information coded among its nucleotides.

This chapter will ask the question: "Can patterns of randomness create patterns of massively sophisticated information and intelligence?"

The answer turns out to be 'no', as will now be seen.

This chapter first describes this issue descriptively, then it describes it visually and finally it describes it statistically.

A Computer Program

First, let us look at a computer program. This is a program I wrote so I could have an alarm clock on my computer. While I wrote the program, actually most of the program was written by Microsoft Corporation programmers. They essentially wrote a lot of subroutines which did various things; then I came along and organized their library of subroutines into an alarm clock program.

The program was actually "compiled" as bits of information, meaning a long string of '0's and '1's. Analyzing '0's and '1's is kind of boring so I grouped each 8 consecutive '0's and '1's into a "byte" and analyzed the program as a set of "bytes."

A "byte" is really nothing but eight consecutive '0's and '1's. For example, these are "bytes" (i.e. permutations of 8 bits):

```
00000000
01010100
11011110
10101011
00001100
11111101
```
and so on.

After breaking down the program (which was a long string of '0's and '1's whereby I took each 8 consecutive bits and converted the 8 bits into one byte), I then took each byte and counted how many times this byte occurred in the listing of the program. In other words, I took the compiled binary (i.e. 0s and 1s) listing of the program; then took each 8 consecutive bits and counted how many times each permutation of 8 bits (i.e. each byte) occurred. This counting process generates what is called a "histogram."

A "histogram" simply "counts" how many times a particular permutation occurs, in this instance.

The intent was to count how many times each byte (i.e. permutation of 8 'bits') occurred and then analyze these counts.

In this table is a listing of how many times each byte occurred in the compiled binary listing of the alarm clock program.

Alarm Clock Program Histogram
Table 1:

```
 0 [.] = 42114 (i.e. consecutive bits: 00000000)
 1 [ ] = 2208  (i.e. consecutive bits: 00000001)
 2 [ ] = 2442  (i.e. consecutive bits: 00000010)
 3 [.] = 322   (i.e. consecutive bits: 00000011)
 4 [.] = 1848  (i.e. consecutive bits: 00000100)
 5 [ ] = 377    and so on.
 6 [ ] = 634
 7 [ ] = 486
 8 [ ] = 539
 9 [.] = 174
 10 [.] = 2045
 11 [.] = 409
 12 [.] = 295
 13 [.] = 170
 14 [.] = 243
 15 [ ] = 113
 16 [ ] = 200
```

17 [ ] = 416
18 [ ] = 263
19 [ ] = 338
20 [ ] = 171
21 [ ] = 179
22 [ ] = 491
23 [ ] = 336
24 [ ] = 246
25 [ ] = 244
26 [ ] = 183
27 [ ] = 158
28 [ ] = 172
29 [ ] = 171
30 [-] = 232
31 [] = 500
32 [ ] = 1296
33 [!] = 59
34 ["] = 163
35 [#] = 52
36 [$] = 93
37 [%] = 185
38 [&] = 175
39 ['] = 69
40 [(] = 509
41 [)] = 79
42 [*] = 280
43 [+] = 128
44 [,] = 648
45 [-] = 88
46 [.] = 1407
47 [/] = 41
48 [0] = 1354
49 [1] = 570
50 [2] = 159
51 [3] = 321
52 [4] = 303
53 [5] = 672
54 [6] = 267
55 [7] = 411
56 [8] = 304
57 [9] = 412
58 [:] = 118
59 [;] = 65
60 [<] = 118
61 [=] = 600
62 [>] = 78
63 [?] = 41
64 [@] = 121
65 [A] = 512
66 [B] = 189
67 [C] = 524
68 [D] = 476

69 [E] = 117
70 [F] = 105
71 [G] = 83
72 [H] = 138
73 [I] = 130
74 [J] = 27
75 [K] = 223
76 [L] = 339
77 [M] = 481
78 [N] = 74
79 [O] = 142
80 [P] = 462
81 [Q] = 53
82 [R] = 166
83 [S] = 695
84 [T] = 340
85 [U] = 40
86 [V] = 287
87 [W] = 59
88 [X] = 89
89 [Y] = 72
90 [Z] = 72
91 [[] = 42
92 [\] = 46
93 []] = 36
94 [^] = 31
95 [_] = 592
96 [`] = 49
97 [a] = 1537
98 [b] = 981
99 [c] = 750
100 [d] = 743
101 [e] = 4301
102 [f] = 390
103 [g] = 224
104 [h] = 130
105 [i] = 1407
106 [j] = 57
107 [k] = 391
108 [l] = 1606
109 [m] = 1252
110 [n] = 1280
111 [o] = 2938
112 [p] = 550
113 [q] = 36
114 [r] = 2035
115 [s] = 1768
116 [t] = 2749
117 [u] = 1617
118 [v] = 352
119 [w] = 156
120 [x] = 347

121 [y] = 797
122 [z] = 64
123 [{] = 1240
124 [|] = 49
125 [}] = 226
126 [~] = 19
127 [ ] = 26
128 [ ] = 153
129 [ ] = 50
130 [,] = 13
131 [ƒ] = 20
132 [„] = 34
133 […] = 17
134 [†] = 67
135 [‡] = 22
136 [ˆ] = 54
137 [‰] = 15
138 [Š] = 15
139 [‹] = 18
140 [Œ] = 36
141 [ ] = 35
142 [ ] = 36
143 [ ] = 31
144 [ ] = 50
145 [‘] = 22
146 [’] = 17
147 [“] = 31
148 [”] = 27
149 [•] = 19
150 [–] = 31
151 [—] = 21
152 [˜] = 36
153 [™] = 20
154 [š] = 55
155 [›] = 17
156 [œ] = 19
157 [ ] = 10
158 [ ] = 24
159 [Ÿ] = 10
160 [ ] = 34
161 [¡] = 40
162 [¢] = 44
163 [£] = 9
164 [¤] = 24
165 [¥] = 9
166 [¦] = 21
167 [§] = 7
168 [¨] = 30
169 [©] = 16
170 [ª] = 13
171 [«] = 7

172 [¬] = 8
173 [-] = 15
174 [®] = 8
175 [¯] = 9
176 [°] = 27
177 [±] = 14
178 [²] = 8
179 [³] = 10
180 [´] = 13
181 [µ] = 9
182 [¶] = 14
183 [·] = 7
184 [¸] = 26
185 [¹] = 7
186 [º] = 13
187 [»] = 9
188 [¼] = 21
189 [½] = 10
190 [¾] = 11
191 [¿] = 14
192 [À] = 43
193 [Á] = 12
194 [Â] = 8
195 [Ã] = 9
196 [Ä] = 18
197 [Å] = 21
198 [Æ] = 27
199 [Ç] = 6
200 [È] = 15
201 [É] = 9
202 [Ê] = 24
203 [Ë] = 10
204 [Ì] = 37
205 [Í] = 13
206 [Î] = 12
207 [Ï] = 10
208 [Ð] = 9
209 [Ñ] = 61
210 [Ò] = 17
211 [Ó] = 14
212 [Ô] = 12
213 [Õ] = 7
214 [Ö] = 14
215 [×] = 14
216 [Ø] = 20
217 [Ù] = 13
218 [Ú] = 9
219 [Û] = 13
220 [Ü] = 28
221 [Ý] = 12
222 [Þ] = 30
223 [ß] = 10

```
224 [à] = 20
225 [á] = 13
226 [â] = 14
227 [ã] = 9
228 [ä] = 17
229 [å] = 5
230 [æ] = 14
231 [ç] = 8
232 [è] = 29
233 [é] = 28
234 [ê] = 5
235 [ë] = 28
236 [ì] = 12
237 [í] = 10
238 [î] = 14
239 [ï] = 11
240 [ð] = 32
241 [ñ] = 15
242 [ò] = 12
243 [ó] = 2
244 [ô] = 29
245 [õ] = 6
246 [ö] = 9
247 [÷] = 19
248 [ø] = 19
249 [ù] = 5
250 [ú] = 8
251 [û] = 10
252 [ü] = 11
253 [ý] = 14
254 [þ] = 58
255 [ÿ] = 1403
```

Total = 110592 bytes

Note in the above chart that the minimum number of times a single byte was found was 2. This happened once for byte 243.

The maximum number of times a byte was found was 42,114, for byte 0. The second highest was 4,301, for byte 101.

Note also the large number of times that bytes 97 through 128 were found!! Compare this to the number of times bytes 163 through 254 were found (with a few exceptions).

The above chart is a "histogram," meaning a chart which shows the frequency of how many times a particular pattern of 8 'bits' exists in the program.

The computer program, in total, had 110,592 bytes.

Using A Random Number Generator

I then used the random number generator to generate 110,592 random "bytes." The next chart is this histogram:

Alarm Clock Histogram Generated By Random Number Generator Table 2:

```
0 [.] = 451
1 [ ] = 407
2 [ ] = 402
3 [.] = 442
4 [.] = 428
5 [ ] = 426
6 [ ] = 440
7 [ ] = 444
8 [ ] = 458
9 [.] = 434
10 [.] = 452
11 [.] = 437
12 [.] = 429
13 [.] = 469
14 [.] = 415
15 [ ] = 466
16 [ ] = 430
17 [ ] = 469
18 [ ] = 431
19 [ ] = 460
20 [ ] = 394
21 [ ] = 437
22 [ ] = 427
23 [ ] = 453
24 [ ] = 428
25 [ ] = 426
26 [ ] = 473
27 [ ] = 403
28 [ ] = 414
29 [ ] = 413
30 [-] = 445
31 [] = 460
32 [ ] = 419
33 [!] = 450
34 ["] = 438
35 [#] = 449
36 [$] = 434
37 [%] = 395
38 [&] = 440
39 ['] = 404
40 [(] = 462
```

41 [)] = 461
42 [*] = 429
43 [+] = 405
44 [,] = 445
45 [-] = 480
46 [.] = 473
47 [/] = 443
48 [0] = 444
49 [1] = 410
50 [2] = 457
51 [3] = 452
52 [4] = 432
53 [5] = 458
54 [6] = 470
55 [7] = 438
56 [8] = 432
57 [9] = 424
58 [:] = 442
59 [;] = 403
60 [<] = 449
61 [=] = 420
62 [>] = 447
63 [?] = 459
64 [@] = 486
65 [A] = 481
66 [B] = 413
67 [C] = 413
68 [D] = 417
69 [E] = 450
70 [F] = 412
71 [G] = 427
72 [H] = 406
73 [I] = 402
74 [J] = 460
75 [K] = 431
76 [L] = 435
77 [M] = 416
78 [N] = 439
79 [O] = 484
80 [P] = 432
81 [Q] = 407
82 [R] = 402
83 [S] = 416
84 [T] = 435
85 [U] = 411
86 [V] = 440
87 [W] = 404
88 [X] = 421
89 [Y] = 402
90 [Z] = 433
91 [[] = 394
92 [\] = 428

93 []] = 432
94 [^] = 447
95 [_] = 448
96 [`] = 444
97 [a] = 430
98 [b] = 415
99 [c] = 413
100 [d] = 467
101 [e] = 458
102 [f] = 419
103 [g] = 409
104 [h] = 449
105 [i] = 413
106 [j] = 422
107 [k] = 462
108 [l] = 439
109 [m] = 428
110 [n] = 420
111 [o] = 413
112 [p] = 437
113 [q] = 418
114 [r] = 436
115 [s] = 464
116 [t] = 448
117 [u] = 430
118 [v] = 415
119 [w] = 406
120 [x] = 409
121 [y] = 427
122 [z] = 423
123 [{] = 442
124 [|] = 443
125 [}] = 372
126 [~] = 406
127 [ ] = 423
128 [ ] = 443
129 [ ] = 409
130 [‚] = 403
131 [ƒ] = 387
132 [„] = 440
133 […] = 403
134 [†] = 438
135 [‡] = 454
136 [ˆ] = 423
137 [‰] = 423
138 [Š] = 441
139 [‹] = 440
140 [Œ] = 426
141 [ ] = 429
142 [ ] = 483
143 [ ] = 411

144 [ ] = 452
145 [‘] = 412
146 [’] = 469
147 [“] = 415
148 [”] = 437
149 [•] = 397
150 [–] = 438
151 [—] = 439
152 [˜] = 438
153 [™] = 417
154 [š] = 476
155 [›] = 403
156 [œ] = 417
157 [ ] = 416
158 [ ] = 441
159 [Ÿ] = 441
160 [ ] = 458
161 [¡] = 463
162 [¢] = 452
163 [£] = 450
164 [¤] = 450
165 [¥] = 418
166 [¦] = 451
167 [§] = 432
168 [¨] = 427
169 [©] = 422
170 [ª] = 418
171 [«] = 403
172 [¬] = 444
173 [-] = 466
174 [®] = 382
175 [¯] = 404
176 [°] = 429
177 [±] = 393
178 [²] = 449
179 [³] = 437
180 [´] = 436
181 [µ] = 425
182 [¶] = 441
183 [·] = 459
184 [¸] = 387
185 [¹] = 440
186 [º] = 481
187 [»] = 436
188 [¼] = 439
189 [½] = 430
190 [¾] = 434
191 [¿] = 421
192 [À] = 450
193 [Á] = 430
194 [Â] = 401

195 [Ã] = 430
196 [Ä] = 445
197 [Å] = 437
198 [Æ] = 406
199 [Ç] = 423
200 [È] = 458
201 [É] = 435
202 [Ê] = 423
203 [Ë] = 453
204 [Ì] = 420
205 [Í] = 407
206 [Î] = 417
207 [Ï] = 443
208 [Ð] = 426
209 [Ñ] = 451
210 [Ò] = 434
211 [Ó] = 404
212 [Ô] = 423
213 [Õ] = 432
214 [Ö] = 432
215 [×] = 441
216 [Ø] = 421
217 [Ù] = 446
218 [Ú] = 459
219 [Û] = 440
220 [Ü] = 445
221 [Ý] = 446
222 [Þ] = 443
223 [ß] = 454
224 [à] = 444
225 [á] = 408
226 [â] = 420
227 [ã] = 406
228 [ä] = 417
229 [å] = 433
230 [æ] = 424
231 [ç] = 417
232 [è] = 421
233 [é] = 434
234 [ê] = 418
235 [ë] = 461
236 [ì] = 424
237 [í] = 403
238 [î] = 409
239 [ï] = 428
240 [ð] = 462
241 [ñ] = 463
242 [ò] = 419
243 [ó] = 442
244 [ô] = 389
245 [õ] = 405
246 [ö] = 453

```
247 [÷] = 413
248 [ø] = 425
249 [ù] = 437
250 [ú] = 411
251 [û] = 413
252 [ü] = 421
253 [ý] = 430
254 [þ] = 456
255 [ÿ] = 422

Total = 110592
```

Whereas the histogram range for an actual intelligently designed computer program ranged from 2 to 42,114 (or "to 4,301" if you don't count 0), the range for the randomly generated histogram was 372 (for byte 125) to 486 (for byte 64).

The "range" or "gap" for an intelligently designed computer program was at least 4,299 (i.e. 4,301 - 2), whereas the "gap" for a randomly designed computer program (which obviously would not have done anything useful) was 114 (i.e. 486 - 372). The size of the "gap" of the randomly generated program was only 2.65% of the range or "gap" of the intelligently generated program!!

Random number generators; which are essentially what random mutations of nucleotides are represented by; do not have nearly the variety of counts as a truly intelligent set of bits. The wide variety of bits of an intelligent program is a side-effect of intelligence.

The point is that in order to create intelligence you need a wide range in values in the histogram, but a random number generator cannot create that wide range of values.

There is no randomness in intelligence and there is no intelligence in randomness!!

We could have done the same thing with a book. A book written in the English language would have very few 'z' or 'q' or 'j' characters. Yet, if we randomly generated the letters in the book, one out of 26 of the letters would be a 'z' or a 'q' or a 'j'.

If we "weighted" or "biased" the selection of letters, to the same proportion as in a real book; we would get the right weighting, *but not the right distribution of groups of letters*. It would be gibberish, as has already been seen in a prior chapter.

The point to this exercise is this question: "Could we ever randomly generate the alarm clock program using a random number generator?" The answer is 'no', at least not in the time frame of a trillion years.

Intelligence has patterns which are vastly different than the patterns of randomness. You don't get intelligence from randomness.

Randomness creates very consistent patterns, which is exactly the wrong thing to do if you are trying to generate intelligence or information.

But intelligence creates a high variety of patterns. If you plotted the above numbers for intelligence on a graph; the intelligence would create a very active chart which would have a wide range of highs and lows.

On the other hand, you would see a very flat and boring pattern generated by the random numbers. From a distance the pattern would look like a straight line.

The Photograph

Just for fun, I did a similar thing with a photograph used commonly by Microsoft. This doesn't really have any intelligence to it, but it certainly was not a photograph generated by a random number generator.

Using the "bliss.bmp" file, and checking out its "intelligence," I got a minimum value of 324 and a maximum value of 26,792. That is a range or gap of 26,468.

The random number generator generated a minimum of 5,379 and a maximum of 5,848. The bliss.bmp file is 1,440,054 bytes long so more random numbers had to be generated. It generated a gap of 469. The ratio of the two gaps, randomness to intelligence (i.e. non-random), was: 1.77%.

Again, we see a vast difference in the patterns. Could a random number generator ever generate the "bliss.bmp" file? No.

In fact, I wrote a computer program to generate random images. Never, at any time did any small section of any of the images ever resemble an identifiable object. Not even a small object in a small section of the screen could be identified.

What About DNA?

Analyzing DNA should yield the same kind of results. In fact, I took a portion of chromosome 5 and analyzed it.

Chromosome 5 has about 1,643 genes in it, which is about 5.1% of all the genes in the entire DNA. It also has about 198 million base pairs, which is about 6.1% of the entire human genome (including the X and Y chromosomes).

I analyzed a section of 41,199,371 consecutive nucleotides, which is about 21% of the nucleotides in chromosome 5.

If you want to see this sequence, do the following:
http://www.ncbi.nlm.nih.org
On left side click: Genomic Biology
In middle of page click: Homo sapiens (human)
Then click: chromosome number: 5
On right side of page click: "Download/View Sequence/Evidence"
Select the item nearest 41.2 million nucleotides.

Here is their breakdown of the actual nucleotides in this segment.

Total = 41,199,371

```
A     = 12,664,928
C     =  7,942,096
G     =  7,927,395
T     = 12,664,952
```

In order to examine "bytes," I took each four consecutive nucleotides and compressed them into one byte. This meant the number of "bytes" I examined was 1/4th the number of nucleotides because each four consecutive nucleotides (i.e. A, C, G, T) were compressed into one byte.

To make this conversion I used the following chart:

```
A converted to bits: 00, by definition
C converted to bits: 01, by definition
G converted to bits: 10, by definition
T converted to bits: 11, by defintion
```

Here is an example of how four consecutive nucleotides were converted into a single byte. Let us take the sequence AGTC.

```
The A would convert to 00 (i.e. the first two bits in the byte),
The G would convert to 10 (i.e. the second two bits in the byte),
The T would convert to 11 (i.e. the third two bits in the byte),
```
The C would convert to 01 (i.e. the fourth two bits in the byte).

Thus, the four nucleotides would convert to: 00 10 11 01.

```
The 00101101 is a “binary number,” meaning a “base 2” number.
Starting with the far left digit, converting binary to decimal
uses this conversion:
Far left bit is multiplied by 128 (x 0)
Next bit is multiplied by 64 (x 0)
Next bit is multiplied by 32 (x 1)
Next bit is multiplied by 16 (x 0)
Next bit is multiplied by 8  (x 1)
Next bit is multiplied by 4  (x 1)
Next bit is multiplied by 2  (x 0)
Far right bit is multiplied by 1 (x 1)
```

This is how it is done:
(00-10-11-01 base 2 equals 45 in base 10):

The first two bits came from the ‘A’
0 x 128 = 0 (the far left bit)
0 x 64 = 0 (the second bit from the left)

The second pair of bits came from the ‘G’
1 x 32 = *32* (the third bit)

0 x 16 = 0 (the fourth bit)

The third pair of bits came from the ‘T’
1 x 8 = *8* (the fifth bit)
1 x 4 = *4* (the sixth bit)

The fourth pair of bits came from the ‘C’
0 x 2 = 0 (the seventh bit)
1 x 1 = *1* (the eighth bit)

Thus, 00-10-11-01 binary is equal to:
0 + 0 + 32 + 0 + 8 + 4 + 0 + 1 = 45 base 10, meaning decimal.

Thus, the sequence AGTC would convert to “byte 45.”

Here is the histogram of the actual "bytes" of the chromosome 5 sequence of nucleotides; where each "byte" represents 4 consecutive nucleotides of real human DNA compressed into one "byte":

Histogram of Actual Human DNA (chromosome 5)
Table 3:

Column (A) Byte #
Column (B) Byte Equal To These Four Nucleotides
Column (C) Frequency of this Sequence of Four Nucleotides (i.e. frequency of each byte)

(A)	(B)	(C)
0	[AAAA]	171795
1	[AAAC]	61526
2	[AAAG]	79756
3	[AAAT]	116638
4	[AACA]	67711
5	[AACC]	32325
6	[AACG]	5389
7	[AACT]	51658
8	[AAGA]	74007
9	[AAGC]	37807
10	[AAGG]	46434
11	[AAGT]	53799
12	[AATA]	87920
13	[AATC]	44581
14	[AATG]	66135
15	[AATT]	86968
16	[ACAA]	61864
17	[ACAC]	39693
18	[ACAG]	52031
19	[ACAT]	59606
20	[ACCA]	43027
21	[ACCC]	26463

22	[ACCG]	3909
23	[ACCT]	38724
24	[ACGA]	4852
25	[ACGC]	4302
26	[ACGG]	4807
27	[ACGT]	6860
28	[ACTA]	37209
29	[ACTC]	34159
30	[ACTG]	45136
31	[ACTT]	53514
32	[AGAA]	86015
33	[AGAC]	37158
34	[AGAG]	55425
35	[AGAT]	52914
36	[AGCA]	49296
37	[AGCC]	35622
38	[AGCG]	4511
39	[AGCT]	43890
40	[AGGA]	54327
41	[AGGC]	38471
42	[AGGG]	35063
43	[AGGT]	38208
44	[AGTA]	42704
45	[AGTC]	30407
46	[AGTG]	45253
47	[AGTT]	52034
48	[ATAA]	78825
49	[ATAC]	38726
50	[ATAG]	41093
51	[ATAT]	84098
52	[ATCA]	51202
53	[ATCC]	32900
54	[ATCG]	4464
55	[ATCT]	52936
56	[ATGA]	57129
57	[ATGC]	35173
58	[ATGG]	44685
59	[ATGT]	59339
60	[ATTA]	69003
61	[ATTC]	51404
62	[ATTG]	47417
63	[ATTT]	117256
64	[CAAA]	79363
65	[CAAC]	32127
66	[CAAG]	42815
67	[CAAT]	47654
68	[CACA]	55620
69	[CACC]	33151
70	[CACG]	7179
71	[CACT]	45928
72	[CAGA]	56564
73	[CAGC]	41329

74	[CAGG]	48062
75	[CAGT]	45195
76	[CATA]	46917
77	[CATC]	35989
78	[CATG]	48113
79	[CATT]	65381
80	[CCAA]	45500
81	[CCAC]	35934
82	[CCAG]	48737
83	[CCAT]	44965
84	[CCCA]	46621
85	[CCCC]	25223
86	[CCCG]	6354
87	[CCCT]	35270
88	[CCGA]	4555
89	[CCGC]	4965
90	[CCGG]	5318
91	[CCGT]	4858
92	[CCTA]	30469
93	[CCTC]	41512
94	[CCTG]	48098
95	[CCTT]	47006
96	[CGAA]	4840
97	[CGAC]	2618
98	[CGAG]	6200
99	[CGAT]	4553
100	[CGCA]	4452
101	[CGCC]	6407
102	[CGCG]	1565
103	[CGCT]	4517
104	[CGGA]	4428
105	[CGGC]	4852
106	[CGGG]	6324
107	[CGGT]	3933
108	[CGTA]	4245
109	[CGTC]	4037
110	[CGTG]	7351
111	[CGTT]	5433
112	[CTAA]	43131
113	[CTAC]	27535
114	[CTAG]	29209
115	[CTAT]	41542
116	[CTCA]	52774
117	[CTCC]	42889
118	[CTCG]	6080
119	[CTCT]	55831
120	[CTGA]	50215
121	[CTGC]	39849
122	[CTGG]	48277
123	[CTGT]	52140
124	[CTTA]	41672
125	[CTTC]	47446

126	[CTTG]	42909
127	[CTTT]	79790
128	[GAAA]	82388
129	[GAAC]	30267
130	[GAAG]	47142
131	[GAAT]	51502
132	[GACA]	37677
133	[GACC]	19607
134	[GACG]	3864
135	[GACT]	30747
136	[GAGA]	54787
137	[GAGC]	26835
138	[GAGG]	41002
139	[GAGT]	33589
140	[GATA]	36672
141	[GATC]	24331
142	[GATG]	35921
143	[GATT]	44264
144	[GCAA]	39578
145	[GCAC]	25373
146	[GCAG]	39433
147	[GCAT]	34728
148	[GCCA]	36945
149	[GCCC]	22184
150	[GCCG]	4720
151	[GCCT]	38291
152	[GCGA]	3996
153	[GCGC]	4097
154	[GCGG]	4920
155	[GCGT]	4322
156	[GCTA]	27903
157	[GCTC]	26921
158	[GCTG]	41554
159	[GCTT]	37492
160	[GGAA]	51638
161	[GGAC]	20083
162	[GGAG]	42961
163	[GGAT]	33060
164	[GGCA]	37084
165	[GGCC]	23339
166	[GGCG]	6415
167	[GGCT]	35520
168	[GGGA]	38931
169	[GGGC]	22252
170	[GGGG]	25116
171	[GGGT]	26461
172	[GGTA]	26299
173	[GGTC]	19789
174	[GGTG]	33347
175	[GGTT]	32735
176	[GTAA]	39612
177	[GTAC]	19306

178	[GTAG]	28035
179	[GTAT]	38647
180	[GTCA]	31986
181	[GTCC]	20194
182	[GTCG]	2612
183	[GTCT]	37235
184	[GTGA]	41003
185	[GTGC]	25002
186	[GTGG]	36220
187	[GTGT]	39178
188	[GTTA]	33122
189	[GTTC]	30685
190	[GTTG]	32094
191	[GTTT]	61630
192	[TAAA]	96295
193	[TAAC]	32788
194	[TAAG]	41940
195	[TAAT]	68926
196	[TACA]	52499
197	[TACC]	26011
198	[TACG]	4285
199	[TACT]	42863
200	[TAGA]	46015
201	[TAGC]	27648
202	[TAGG]	30346
203	[TAGT]	37514
204	[TATA]	71110
205	[TATC]	36991
206	[TATG]	46579
207	[TATT]	88109
208	[TCAA]	55867
209	[TCAC]	40668
210	[TCAG]	50537
211	[TCAT]	56858
212	[TCCA]	49110
213	[TCCC]	39054
214	[TCCG]	4520
215	[TCCT]	54738
216	[TCGA]	4493
217	[TCGC]	4023
218	[TCGG]	4621
219	[TCGT]	5058
220	[TCTA]	46049
221	[TCTC]	55454
222	[TCTG]	56439
223	[TCTT]	74027
224	[TGAA]	68470
225	[TGAC]	31575
226	[TGAG]	52522
227	[TGAT]	50570
228	[TGCA]	48917
229	[TGCC]	37185

```
230   [TGCG]       4415
231   [TGCT]      49589
232   [TGGA]      48758
233   [TGGC]      36807
234   [TGGG]      46031
235   [TGGT]      42586
236   [TGTA]      52586
237   [TGTC]      37682
238   [TGTG]      55631
239   [TGTT]      67303
240   [TTAA]      78181
241   [TTAC]      39932
242   [TTAG]      42944
243   [TTAT]      78553
244   [TTCA]      69125
245   [TTCC]      51528
246   [TTCG]       4914
247   [TTCT]      85861
248   [TTGA]      55806
249   [TTGC]      39335
250   [TTGG]      45168
251   [TTGT]      61447
252   [TTTA]      95607
253   [TTTC]      82318
254   [TTTG]      80201
255   [TTTT]     170849

Total = 10,299,843
```

Note that the number of bytes is about 1/4th the number of nucleotides.

Note that the minimum was 1,565 in byte 102. The maximum was 171,795 in byte 0. Byte 0 represented four consecutive 'A' nucleotides. You might remember that byte 0 also had the highest byte count in the computer program. The sequence TTTT (i.e. 255) had a 170,840 count, not far behind AAAA.

The counts for AAAA, CCCC, GGGG and TTTT are somewhat consistent with the overall proportion of these nucleotides. Remember from above:

```
A     = 12,664,928 (30.74%)
C     =  7,942,096 (19.28%)
G     =  7,927,395 (19.24%)
T     = 12,664,952 (30.74%)
```

Now look at the histogram for these sequences:

```
AAAA    =    171,795 (43.72%)
CCCC    =     25,223 ( 6.42%)
GGGG    =     25,116 ( 6.39%)
TTTT    =    170,840 (43.47%)
```

The important number for our purposes was the gap 170,230
(i.e. 171,795 - 1,565).

Now let us look at the randomly generated bytes of the same total count:

Randomly Generated DNA
Table 4:

```
 0 [.] = 40123
 1 [_] = 40154
 2 [_] = 39966
 3 [.] = 40361
 4 [.] = 40451
 5 [_] = 40384
 6 [_] = 39995
 7 [_] = 40119
 8 [_] = 40125
 9 [.] = 40242
 10 [.] = 39867
 11 [.] = 40166
 12 [.] = 40094
 13 [.] = 40073
 14 [_] = 40120
 15 [_] = 40387
 16 [_] = 39842
 17 [_] = 40323
 18 [_] = 40185
 19 [_] = 40159
 20 [_] = 40473
 21 [_] = 40144
 22 [_] = 40219
 23 [_] = 40145
 24 [_] = 40188
 25 [_] = 39993
 26 [_] = 40405
 27 [_] = 40106
 28 [_] = 40093
 29 [_] = 40161
 30 [_] = 40317
 31 [_] = 40233
 32 [ ] = 40291
 33 [!] = 40280
 34 ["] = 40134
 35 [#] = 40542
```

```
36 [$] = 39953
37 [%] = 40225
38 [&] = 40130
39 ['] = 40541
40 [(] = 40223
41 [)] = 40330
42 [*] = 40167
43 [+] = 40230
44 [,] = 40010
45 [-] = 40606
46 [.] = 39825
47 [/] = 40352
48 [0] = 40245
49 [1] = 40273
50 [2] = 40356
51 [3] = 40421
52 [4] = 39912
53 [5] = 39984
54 [6] = 40422
55 [7] = 40379
56 [8] = 40307
57 [9] = 40599
58 [:] = 40217
59 [;] = 40045
60 [<] = 40501
61 [=] = 40429
62 [>] = 40168
63 [?] = 39992
64 [@] = 40358
65 [A] = 40195
66 [B] = 39787
67 [C] = 40144
68 [D] = 40014
69 [E] = 40233
70 [F] = 40230
71 [G] = 40187
72 [H] = 40336
73 [I] = 40254
74 [J] = 40490
75 [K] = 40239
76 [L] = 39982
77 [M] = 40272
78 [N] = 40018
79 [O] = 39685
80 [P] = 40343
81 [Q] = 40471
82 [R] = 40088
83 [S] = 40558
84 [T] = 40156
85 [U] = 40144
86 [V] = 40004
87 [W] = 39890
```

88 [X] = 40209
89 [Y] = 40301
90 [Z] = 40067
91 [[] = 40401
92 [\] = 40542
93 []] = 39999
94 [^] = 40292
95 [_] = 40191
96 [`] = 40326
97 [a] = 40081
98 [b] = 40022
99 [c] = 40225
100 [d] = 40322
101 [e] = 40150
102 [f] = 40360
103 [g] = 40451
104 [h] = 40121
105 [i] = 40449
106 [j] = 40385
107 [k] = 40113
108 [l] = 40241
109 [m] = 40185
110 [n] = 40288
111 [o] = 40168
112 [p] = 40067
113 [q] = 40549
114 [r] = 40677
115 [s] = 40597
116 [t] = 40081
117 [u] = 40317
118 [v] = 40479
119 [w] = 40329
120 [x] = 40065
121 [y] = 40320
122 [z] = 39912
123 [{] = 39967
124 [|] = 40444
125 [}] = 40201
126 [~] = 40322
127 [ ] = 40217
128 [ ] = 40196
129 [ ] = 40138
130 [,] = 40209
131 [ƒ] = 40162
132 [„] = 40097
133 […] = 40568
134 [†] = 39991
135 [‡] = 40402
136 [ˆ] = 40202
137 [‰] = 40143
138 [Š] = 40257

139 [‹] = 39959
140 [Œ] = 40361
141 [ ] = 40741
142 [ ] = 39965
143 [ ] = 40298
144 [ ] = 40129
145 [‘] = 40093
146 [’] = 40299
147 [“] = 40254
148 [”] = 40293
149 [•] = 40018
150 [–] = 40651
151 [—] = 40180
152 [˜] = 40083
153 [™] = 40354
154 [š] = 40066
155 [›] = 40098
156 [œ] = 40239
157 [ ] = 39784
158 [ ] = 40291
159 [Ÿ] = 40254
160 [ ] = 40118
161 [¡] = 40207
162 [¢] = 40374
163 [£] = 40228
164 [¤] = 40411
165 [¥] = 40150
166 [¦] = 40581
167 [§] = 40078
168 [¨] = 39835
169 [©] = 40038
170 [ª] = 40773
171 [«] = 40151
172 [¬] = 40355
173 [¬] = 40172
174 [®] = 40184
175 [¯] = 40409
176 [°] = 40195
177 [±] = 40335
178 [²] = 40103
179 [³] = 39992
180 [´] = 39874
181 [µ] = 40238
182 [¶] = 40434
183 [•] = 40428
184 [¸] = 40095
185 [¹] = 40254
186 [º] = 40406
187 [»] = 39842
188 [¼] = 40473
189 [½] = 40260

190 [¾] = 40013
191 [¿] = 40211
192 [À] = 40312
193 [Á] = 40260
194 [Â] = 40131
195 [Ã] = 40022
196 [Ä] = 40370
197 [Å] = 40410
198 [Æ] = 40597
199 [Ç] = 40066
200 [È] = 40340
201 [É] = 40474
202 [Ê] = 40109
203 [Ë] = 40417
204 [Ì] = 40284
205 [Í] = 40535
206 [Î] = 40252
207 [Ï] = 40244
208 [Ð] = 40124
209 [Ñ] = 40152
210 [Ò] = 40151
211 [Ó] = 40427
212 [Ô] = 40352
213 [Õ] = 40163
214 [Ö] = 40401
215 [×] = 40457
216 [Ø] = 40232
217 [Ù] = 40375
218 [Ú] = 40282
219 [Û] = 40409
220 [Ü] = 40515
221 [Ý] = 40001
222 [Þ] = 39875
223 [ß] = 40305
224 [à] = 40014
225 [á] = 39961
226 [â] = 40488
227 [ã] = 40326
228 [ä] = 40543
229 [å] = 40128
230 [æ] = 40146
231 [ç] = 40369
232 [è] = 40378
233 [é] = 40330
234 [ê] = 40218
235 [ë] = 40171
236 [ì] = 40315
237 [í] = 40254
238 [î] = 40264
239 [ï] = 40024
240 [ð] = 40331
241 [ñ] = 40223

```
242 [ò] = 39898
243 [ó] = 40435
244 [ô] = 40161
245 [õ] = 40523
246 [ö] = 40195
247 [÷] = 40465
248 [ø] = 40042
249 [ù] = 40114
250 [ú] = 40312
251 [û] = 40628
252 [ü] = 40302
253 [ý] = 40549
254 [þ] = 40245
255 [ÿ] = 40242

Total = 10299843
```

In this chart, the minimum was 39,685 in byte 79 and the maximum was 40,773 in byte 170. The gap was 1,088.

The ratio of gaps was 1,088 / 170,230 and it equaled 0.64%; *which is less than 1%!!*

I ordered all of the different byte counts in the actual DNA histogram. ONLY 4 of the 256 byte counts fell in the range of the minimum and maximum byte counts generated by the random number generator. Here they are:

```
17  [_] = 39693
121 [y] = 39849
241 [ñ] = 39932
209 [Ñ] = 40668
```

The other 252 counts were outside the range of the random distribution!!

Again, we see the patterns for an intelligently designed DNA strand are vastly different than the flat patterns of a randomly generated DNA.

There is simply no way that randomly generated nucleotides could generate the type of intelligence and information in a real DNA strand!!

Using Predicted Values (i.e. Bias)

Let us review how many of the four different nucleotides were found in this segment of real human DNA:

```
A     = 12,664,928 (30.74%)
C     =  7,942,096 (19.28%)
G     =  7,927,395 (19.24%)
T     = 12,664,952 (30.74%)
```

Total = 41,199,371

We can predict how many times a particular sequence of 4 nucleotides (i.e. a "byte") occurs by using the above ratios or bias. For example, we could design a random number generator to make sure an 'A' is chosen 30.74% of the time and a 'C' is chosen 19.28% of the time, and so on.

This would be called a "biased random number generator" because it doesn't just randomly pick a nucleotide string; it picks nucleotide strings based on the percentage of times they occur in a real DNA sequence.

If we do this, we can compare the actual number of times a sequence or byte occurs and compare it to how many times we would predict it would occur, using our biased random number generator.

Here is what the chart would look like for the REAL HUMAN DNA (i.e. this chart does NOT use a random number generator, it uses real human DNA):

Real Human DNA Histogram Compared to Predicted Histogram
Table 5:

Column (A) is the byte number
Column (B) is the sequence of 4 nucleotides
Column (C) is the ACTUAL times the sequence/byte occurred
Column (D) is Column (F) minus Column (C), if positive
Column (E) is Column (C) minus Column (F), if positive
Column (F) is the number of predicted occurrences

(A)	(B)	(C)	(D)	(E)	(F)
0	[AAAA] =	171795	0	79818	*91977*
1	[AAAC] =	61526	0	3848	*57678*
2	[AAAG] =	79756	0	22185	*57571*
3	[AAAT] =	116638	0	24661	*91977*
4	[AACA] =	67711	0	10033	*57678*
5	[AACC] =	32325	3845	0	*36170*
6	[AACG] =	5389	30714	0	*36103*
7	[AACT] =	51658	6020	0	*57678*
8	[AAGA] =	74007	0	16436	*57571*
9	[AAGC] =	37807	0	1704	*36103*
10	[AAGG] =	46434	0	10398	*36036*
11	[AAGT] =	53799	3773	0	*57572*
12	[AATA] =	87920	4057	0	*91977*
13	[AATC] =	44581	13097	0	*57678*
14	[AATG] =	66135	0	8563	*57572*
15	[AATT] =	86968	5009	0	*91977*
16	[ACAA] =	61864	0	4186	*57678*
17	[ACAC] =	39693	0	3523	*36170*
18	[ACAG] =	52031	0	15928	*36103*
19	[ACAT] =	59606	0	1928	*57678*
20	[ACCA] =	43027	0	6857	*36170*
21	[ACCC] =	26463	0	3781	*22682*

```
22  [ACCG] =   3909  18731      0  *22640*
23  [ACCT] =  38724      0   2554  *36170*
24  [ACGA] =   4852  31251      0  *36103*
25  [ACGC] =   4302  18338      0  *22640*
26  [ACGG] =   4807  17791      0  *22598*
27  [ACGT] =   6860  29243      0  *36103*
28  [ACTA] =  37209  20469      0  *57678*
29  [ACTC] =  34159   2011      0  *36170*
30  [ACTG] =  45136      0   9033  *36103*
31  [ACTT] =  53514   4164      0  *57678*
32  [AGAA] =  86015      0  28444  *57571*
33  [AGAC] =  37158      0   1055  *36103*
34  [AGAG] =  55425      0  19389  *36036*
35  [AGAT] =  52914   4658      0  *57572*
36  [AGCA] =  49296      0  13193  *36103*
37  [AGCC] =  35622      0  12982  *22640*
38  [AGCG] =   4511  18087      0  *22598*
39  [AGCT] =  43890      0   7787  *36103*
40  [AGGA] =  54327      0  18291  *36036*
41  [AGGC] =  38471      0  15873  *22598*
42  [AGGG] =  35063      0  12507  *22556*
43  [AGGT] =  38208      0   2172  *36036*
44  [AGTA] =  42704  14868      0  *57572*
45  [AGTC] =  30407   5696      0  *36103*
46  [AGTG] =  45253      0   9217  *36036*
47  [AGTT] =  52034   5538      0  *57572*
48  [ATAA] =  78825  13152      0  *91977*
49  [ATAC] =  38726  18952      0  *57678*
50  [ATAG] =  41093  16479      0  *57572*
51  [ATAT] =  84098   7879      0  *91977*
52  [ATCA] =  51202   6476      0  *57678*
53  [ATCC] =  32900   3270      0  *36170*
54  [ATCG] =   4464  31639      0  *36103*
55  [ATCT] =  52936   4742      0  *57678*
56  [ATGA] =  57129    443      0  *57572*
57  [ATGC] =  35173    930      0  *36103*
58  [ATGG] =  44685      0   8649  *36036*
59  [ATGT] =  59339      0   1767  *57572*
60  [ATTA] =  69003  22974      0  *91977*
61  [ATTC] =  51404   6274      0  *57678*
62  [ATTG] =  47417  10155      0  *57572*
63  [ATTT] = 117256      0  25278  *91978*
64  [CAAA] =  79363      0  21685  *57678*
65  [CAAC] =  32127   4043      0  *36170*
66  [CAAG] =  42815      0   6712  *36103*
67  [CAAT] =  47654  10024      0  *57678*
68  [CACA] =  55620      0  19450  *36170*
69  [CACC] =  33151      0  10469  *22682*
70  [CACG] =   7179  15461      0  *22640*
71  [CACT] =  45928      0   9758  *36170*
72  [CAGA] =  56564      0  20461  *36103*
73  [CAGC] =  41329      0  18689  *22640*
```

```
74  [CAGG] =  48062      0  25464  *22598*
75  [CAGT] =  45195      0   9092  *36103*
76  [CATA] =  46917  10761      0  *57678*
77  [CATC] =  35989    181      0  *36170*
78  [CATG] =  48113      0  12010  *36103*
79  [CATT] =  65381      0   7703  *57678*
80  [CCAA] =  45500      0   9330  *36170*
81  [CCAC] =  35934      0  13252  *22682*
82  [CCAG] =  48737      0  26097  *22640*
83  [CCAT] =  44965      0   8795  *36170*
84  [CCCA] =  46621      0  23939  *22682*
85  [CCCC] =  25223      0  10999  *14224*
86  [CCCG] =   6354   7843      0  *14197*
87  [CCCT] =  35270      0  12588  *22682*
88  [CCGA] =   4555  18085      0  *22640*
89  [CCGC] =   4965   9232      0  *14197*
90  [CCGG] =   5318   8853      0  *14171*
91  [CCGT] =   4858  17782      0  *22640*
92  [CCTA] =  30469   5701      0  *36170*
93  [CCTC] =  41512      0  18830  *22682*
94  [CCTG] =  48098      0  25458  *22640*
95  [CCTT] =  47006      0  10836  *36170*
96  [CGAA] =   4840  31263      0  *36103*
97  [CGAC] =   2618  20022      0  *22640*
98  [CGAG] =   6200  16398      0  *22598*
99  [CGAT] =   4553  31550      0  *36103*
100 [CGCA] =   4452  18188      0  *22640*
101 [CGCC] =   6407   7790      0  *14197*
102 [CGCG] =   1565  12606      0  *14171*
103 [CGCT] =   4517  18123      0  *22640*
104 [CGGA] =   4428  18170      0  *22598*
105 [CGGC] =   4852   9319      0  *14171*
106 [CGGG] =   6324   7821      0  *14145*
107 [CGGT] =   3933  18665      0  *22598*
108 [CGTA] =   4245  31858      0  *36103*
109 [CGTC] =   4037  18603      0  *22640*
110 [CGTG] =   7351  15247      0  *22598*
111 [CGTT] =   5433  30670      0  *36103*
112 [CTAA] =  43131  14547      0  *57678*
113 [CTAC] =  27535   8635      0  *36170*
114 [CTAG] =  29209   6894      0  *36103*
115 [CTAT] =  41542  16136      0  *57678*
116 [CTCA] =  52774      0  16604  *36170*
117 [CTCC] =  42889      0  20207  *22682*
118 [CTCG] =   6080  16560      0  *22640*
119 [CTCT] =  55831      0  19661  *36170*
120 [CTGA] =  50215      0  14112  *36103*
121 [CTGC] =  39849      0  17209  *22640*
122 [CTGG] =  48277      0  25679  *22598*
123 [CTGT] =  52140      0  16037  *36103*
124 [CTTA] =  41672  16006      0  *57678*
125 [CTTC] =  47446      0  11276  *36170*
```

```
126 [CTTG] =  42909      0   6806  *36103*
127 [CTTT] =  79790      0  22111  *57679*
128 [GAAA] =  82388      0  24817  *57571*
129 [GAAC] =  30267   5836      0  *36103*
130 [GAAG] =  47142      0  11106  *36036*
131 [GAAT] =  51502   6070      0  *57572*
132 [GACA] =  37677      0  1574  *36103*
133 [GACC] =  19607   3033      0  *22640*
134 [GACG] =   3864  18734      0  *22598*
135 [GACT] =  30747   5356      0  *36103*
136 [GAGA] =  54787      0  18751  *36036*
137 [GAGC] =  26835      0   4237  *22598*
138 [GAGG] =  41002      0  18446  *22556*
139 [GAGT] =  33589   2447      0  *36036*
140 [GATA] =  36672  20900      0  *57572*
141 [GATC] =  24331  11772      0  *36103*
142 [GATG] =  35921    115      0  *36036*
143 [GATT] =  44264  13308      0  *57572*
144 [GCAA] =  39578      0   3475  *36103*
145 [GCAC] =  25373      0   2733  *22640*
146 [GCAG] =  39433      0  16835  *22598*
147 [GCAT] =  34728   1375      0  *36103*
148 [GCCA] =  36945      0  14305  *22640*
149 [GCCC] =  22184      0   7987  *14197*
150 [GCCG] =   4720   9451      0  *14171*
151 [GCCT] =  38291      0  15651  *22640*
152 [GCGA] =   3996  18602      0  *22598*
153 [GCGC] =   4097  10074      0  *14171*
154 [GCGG] =   4920   9225      0  *14145*
155 [GCGT] =   4322  18276      0  *22598*
156 [GCTA] =  27903   8200      0  *36103*
157 [GCTC] =  26921      0   4281  *22640*
158 [GCTG] =  41554      0  18956  *22598*
159 [GCTT] =  37492      0   1389  *36103*
160 [GGAA] =  51638      0  15602  *36036*
161 [GGAC] =  20083   2515      0  *22598*
162 [GGAG] =  42961      0  20405  *22556*
163 [GGAT] =  33060   2976      0  *36036*
164 [GGCA] =  37084      0  14486  *22598*
165 [GGCC] =  23339      0   9168  *14171*
166 [GGCG] =   6415   7730      0  *14145*
167 [GGCT] =  35520      0  12922  *22598*
168 [GGGA] =  38931      0  16375  *22556*
169 [GGGC] =  22252      0   8107  *14145*
170 [GGGG] =  25116      0  10997  *14119*
171 [GGGT] =  26461      0   3905  *22556*
172 [GGTA] =  26299   9737      0  *36036*
173 [GGTC] =  19789   2809      0  *22598*
174 [GGTG] =  33347      0  10791  *22556*
175 [GGTT] =  32735   3301      0  *36036*
176 [GTAA] =  39612  17960      0  *57572*
177 [GTAC] =  19306  16797      0  *36103*
```

```
178 [GTAG] =  28035   8001      0  *36036*
179 [GTAT] =  38647  18925      0  *57572*
180 [GTCA] =  31986   4117      0  *36103*
181 [GTCC] =  20194   2446      0  *22640*
182 [GTCG] =   2612  19986      0  *22598*
183 [GTCT] =  37235      0   1132  *36103*
184 [GTGA] =  41003      0   4967  *36036*
185 [GTGC] =  25002      0   2404  *22598*
186 [GTGG] =  36220      0  13664  *22556*
187 [GTGT] =  39178      0   3142  *36036*
188 [GTTA] =  33122  24450      0  *57572*
189 [GTTC] =  30685   5418      0  *36103*
190 [GTTG] =  32094   3942      0  *36036*
191 [GTTT] =  61630      0   4058  *57572*
192 [TAAA] =  96295      0   4318  *91977*
193 [TAAC] =  32788  24890      0  *57678*
194 [TAAG] =  41940  15632      0  *57572*
195 [TAAT] =  68926  23051      0  *91977*
196 [TACA] =  52499   5179      0  *57678*
197 [TACC] =  26011  10159      0  *36170*
198 [TACG] =   4285  31818      0  *36103*
199 [TACT] =  42863  14815      0  *57678*
200 [TAGA] =  46015  11557      0  *57572*
201 [TAGC] =  27648   8455      0  *36103*
202 [TAGG] =  30346   5690      0  *36036*
203 [TAGT] =  37514  20058      0  *57572*
204 [TATA] =  71110  20867      0  *91977*
205 [TATC] =  36991  20687      0  *57678*
206 [TATG] =  46579  10993      0  *57572*
207 [TATT] =  88109   3869      0  *91978*
208 [TCAA] =  55867   1811      0  *57678*
209 [TCAC] =  40668      0   4498  *36170*
210 [TCAG] =  50537      0  14434  *36103*
211 [TCAT] =  56858    820      0  *57678*
212 [TCCA] =  49110      0  12940  *36170*
213 [TCCC] =  39054      0  16372  *22682*
214 [TCCG] =   4520  18120      0  *22640*
215 [TCCT] =  54738      0  18568  *36170*
216 [TCGA] =   4493  31610      0  *36103*
217 [TCGC] =   4023  18617      0  *22640*
218 [TCGG] =   4621  17977      0  *22598*
219 [TCGT] =   5058  31045      0  *36103*
220 [TCTA] =  46049  11629      0  *57678*
221 [TCTC] =  55454      0  19284  *36170*
222 [TCTG] =  56439      0  20336  *36103*
223 [TCTT] =  74027      0  16348  *57679*
224 [TGAA] =  68470      0  10898  *57572*
225 [TGAC] =  31575   4528      0  *36103*
226 [TGAG] =  52522      0  16486  *36036*
227 [TGAT] =  50570   7002      0  *57572*
228 [TGCA] =  48917      0  12814  *36103*
229 [TGCC] =  37185      0  14545  *22640*
```

```
230 [TGCG] =   4415  18183      0  *22598*
231 [TGCT] =  49589      0  13486  *36103*
232 [TGGA] =  48758      0  12722  *36036*
233 [TGGC] =  36807      0  14209  *22598*
234 [TGGG] =  46031      0  23475  *22556*
235 [TGGT] =  42586      0   6550  *36036*
236 [TGTA] =  52586   4986      0  *57572*
237 [TGTC] =  37682      0   1579  *36103*
238 [TGTG] =  55631      0  19595  *36036*
239 [TGTT] =  67303      0   9731  *57572*
240 [TTAA] =  78181  13796      0  *91977*
241 [TTAC] =  39932  17746      0  *57678*
242 [TTAG] =  42944  14628      0  *57572*
243 [TTAT] =  78553  13425      0  *91978*
244 [TTCA] =  69125      0  11447  *57678*
245 [TTCC] =  51528      0  15358  *36170*
246 [TTCG] =   4914  31189      0  *36103*
247 [TTCT] =  85861      0  28182  *57679*
248 [TTGA] =  55806   1766      0  *57572*
249 [TTGC] =  39335      0   3232  *36103*
250 [TTGG] =  45168      0   9132  *36036*
251 [TTGT] =  61447      0   3875  *57572*
252 [TTTA] =  95607      0   3629  *91978*
253 [TTTC] =  82318      0  24639  *57679*
254 [TTTG] =  80201      0  22629  *57572*
255 [TTTT] = 170849      0  78871  *91978*

  Total Nucleotides = 10299843
  Max Value Below Predicted = 31858
  Max Value Above Predicted = 79818
```

Before commenting on these numbers, let us look at some computer simulations so we have something to compare them to.

Computer Simulations of Nucleotides

Because of the massive drain on computer power caused by floating point operations, I could only run 70,000 simulations.

The 70,000 simulations were not run at one time. For example, 25,000 of the 70,000 simulations were run at one time. In each of the 25,000 simulations (one of the blocks to make up the 70,000 simulations) represented in the below chart, a sequence of operations was performed:
1) In each simulation 10,299,843 nucleotides were chosen, with bias (i.e. taking into account the real distribution of nucleotides).
2) A histogram for each simulation was made for the 256 different possible permutations of 4 nucleotides (e.g. AAAA, AAAC, AAAG, etc.).
3) Thus, there were 25,000 different histograms of 4 different permutations of nucleotides.

4) The program went through those 25,000 histograms and found the minimum and maximum values for each permutation in each simulation.

Let us look at the chart of 25,000 simulations:

25,000 Simulations of DNA, With Bias
Table 6:

Column (A) is the sequence of 4 nucleotides
Column (B) is the MINIMUM times the sequence occurred *among 25,000 simulations*
Column (C) is the MAXIMUM times the sequence occurred *among 25,000 simulations*
Column (D) is Column (C) minus Column (B)
Column (E) is the number of predicted occurrences

(A)	(B)	(C)	(D) GAP	(E)	
[AAAA] =	90882	93244	2362	*91977*	
[AAAC] =	56733	58597	1864	*57678*	
[AAAG] =	56524	58483	1959	*57571*	
[AAAT] =	90841	93193	2352	*91977*	
[AACA] =	56758	58683	1925	*57678*	
[AACC] =	35356	36979	1623	*36170*	
[AACG] =	35363	36827	1464	*36103*	
[AACT] =	56795	58875	2080	*57678*	
[AAGA] =	56595	58640	2045	*57571*	
[AAGC] =	35353	36831	1478	*36103*	
[AAGG] =	35172	36800	1628	*36036*	
[AAGT] =	56591	58470	1879	*57572*	
[AATA] =	90629	93216	2587	*91977*	
[AATC] =	56723	58763	2040	*57678*	
[AATG] =	56534	58562	2028	*57572*	
[AATT] =	90661	93543	2882	*91977*	**
[ACAA] =	56617	58561	1944	*57678*	
[ACAC] =	35464	36979	1515	*36170*	
[ACAG] =	35312	36817	1505	*36103*	
[ACAT] =	56621	58690	2069	*57678*	
[ACCA] =	35458	36979	1521	*36170*	
[ACCC] =	22095	23307	1212	*22682*	
[ACCG] =	22046	23193	1147	*22640*	
[ACCT] =	35406	36963	1557	*36170*	
[ACGA] =	35414	36948	1534	*36103*	
[ACGC] =	22060	23297	1237	*22640*	
[ACGG] =	21982	23232	1250	*22598*	
[ACGT] =	35332	36835	1503	*36103*	
[ACTA] =	56672	58640	1968	*57678*	
[ACTC] =	35420	36929	1509	*36170*	
[ACTG] =	35368	36846	1478	*36103*	
[ACTT] =	56660	58576	1916	*57678*	
[AGAA] =	56627	58573	1946	*57571*	
[AGAC] =	35401	36904	1503	*36103*	
[AGAG] =	35301	36735	1434	*36036*	

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[AGAT] = 56590   58492   1902   *57572*
[AGCA] = 35415   36845   1430   *36103*
[AGCC] = 22023   23302   1279   *22640*
[AGCG] = 22061   23177   1116   *22598*
[AGCT] = 35235   36887   1652   *36103*
[AGGA] = 35313   36958   1645   *36036*
[AGGC] = 21978   23174   1196   *22598*
[AGGG] = 21942   23117   1175   *22556*
[AGGT] = 35235   36782   1547   *36036*
[AGTA] = 56472   58606   2134   *57572*
[AGTC] = 35319   37018   1699   *36103*
[AGTG] = 35313   36811   1498   *36036*
[AGTT] = 56630   58588   1958   *57572*
[ATAA] = 90732   93060   2328   *91977*
[ATAC] = 56785   58660   1875   *57678*
[ATAG] = 56524   58505   1981   *57572*
[ATAT] = 90786   93343   2557   *91977*
[ATCA] = 56759   58618   1859   *57678*
[ATCC] = 35327   36995   1668   *36170*
[ATCG] = 35356   36899   1543   *36103*
[ATCT] = 56651   58700   2049   *57678*
[ATGA] = 56630   58504   1874   *57572*
[ATGC] = 35364   36796   1432   *36103*
[ATGG] = 35233   36862   1629   *36036*
[ATGT] = 56641   58501   1860   *57572*
[ATTA] = 90900   93061   2161   *91977*
[ATTC] = 56549   58543   1994   *57678*
[ATTG] = 56618   58525   1907   *57572*
[ATTT] = 90784   93180   2396   *91978*
[CAAA] = 56659   58650   1991   *57678*
[CAAC] = 35345   36958   1613   *36170*
[CAAG] = 35342   36927   1585   *36103*
[CAAT] = 56777   58562   1785   *57678*
[CACA] = 35421   36908   1487   *36170*
[CACC] = 21967   23302   1335   *22682*
[CACG] = 21956   23264   1308   *22640*
[CACT] = 35453   36908   1455   *36170*
[CAGA] = 35351   36801   1450   *36103*
[CAGC] = 22066   23191   1125   *22640*
[CAGG] = 22014   23182   1168   *22598*
[CAGT] = 35425   36965   1540   *36103*
[CATA] = 56729   58636   1907   *57678*
[CATC] = 35346   37096   1750   *36170*
[CATG] = 35317   36816   1499   *36103*
[CATT] = 56725   58674   1949   *57678*
[CCAA] = 35408   37015   1607   *36170*
[CCAC] = 22086   23301   1215   *22682*
[CCAG] = 22060   23298   1238   *22640*
[CCAT] = 35402   36953   1551   *36170*
[CCCA] = 21956   23295   1339   *22682*
[CCCC] = 13774   14745    971   *14224*
[CCCG] = 13699   14721   1022   *14197*
```

[CCCT] = 22060   23260   1200   *22682*
[CCGA] = 21999   23270   1271   *22640*
[CCGC] = 13695   14673   978   *14197*
[CCGG] = 13705   14713   1008   *14171*
[CCGT] = 22052   23186   1134   *22640*
[CCTA] = 35361   36944   1583   *36170*
[CCTC] = 22097   23245   1148   *22682*
[CCTG] = 22061   23268   1207   *22640*
[CCTT] = 35416   36912   1496   *36170*
[CGAA] = 35334   36904   1570   *36103*
[CGAC] = 22089   23227   1138   *22640*
[CGAG] = 22015   23178   1163   *22598*
[CGAT] = 35352   36828   1476   *36103*
[CGCA] = 22053   23291   1238   *22640*
[CGCC] = 13728   14680   952   *14197*
[CGCG] = 13678   14626   948   *14171*
[CGCT] = 21960   23234   1274   *22640*
[CGGA] = 21853   23228   1375   *22598*
[CGGC] = 13666   14712   1046   *14171*
[CGGG] = 13688   14664   976   *14145*
[CGGT] = 21909   23196   1287   *22598*
[CGTA] = 35216   36901   1685   *36103*
[CGTC] = 22094   23246   1152   *22640*
[CGTG] = 22033   23138   1105   *22598*
[CGTT] = 35323   36820   1497   *36103*
[CTAA] = 56682   58637   1955   *57678*
[CTAC] = 35370   36981   1611   *36170*
[CTAG] = 35331   36940   1609   *36103*
[CTAT] = 56717   58771   2054   *57678*
[CTCA] = 35371   36981   1610   *36170*
[CTCC] = 22063   23225   1162   *22682*
[CTCG] = 22058   23224   1166   *22640*
[CTCT] = 35377   36988   1611   *36170*
[CTGA] = 35215   36966   1751   *36103*
[CTGC] = 22048   23182   1134   *22640*
[CTGG] = 21985   23148   1163   *22598*
[CTGT] = 35403   36795   1392   *36103*
[CTTA] = 56584   58651   2067   *57678*
[CTTC] = 35308   37031   1723   *36170*
[CTTG] = 35339   36855   1516   *36103*
[CTTT] = 56702   58623   1921   *57679*
[GAAA] = 56513   58675   2162   *57571*
[GAAC] = 35421   36883   1462   *36103*
[GAAG] = 35246   36742   1496   *36036*
[GAAT] = 56645   58593   1948   *57572*
[GACA] = 35326   36981   1655   *36103*
[GACC] = 22043   23336   1293   *22640*
[GACG] = 21998   23200   1202   *22598*
[GACT] = 35432   36861   1429   *36103*
[GAGA] = 35209   36794   1585   *36036*
[GAGC] = 22032   23202   1170   *22598*
[GAGG] = 21941   23182   1241   *22556*

[GAGT] = 35362   36785   1423   *36036*
[GATA] = 56598   58521   1923   *57572*
[GATC] = 35358   36912   1554   *36103*
[GATG] = 35303   36797   1494   *36036*
[GATT] = 56626   58529   1903   *57572*
[GCAA] = 35429   36884   1455   *36103*
[GCAC] = 22074   23219   1145   *22640*
[GCAG] = 21991   23223   1232   *22598*
[GCAT] = 35306   36882   1576   *36103*
[GCCA] = 21971   23210   1239   *22640*
[GCCC] = 13691   14683   992   *14197*
[GCCG] = 13681   14647   966   *14171*
[GCCT] = 22022   23197   1175   *22640*
[GCGA] = 22023   23189   1166   *22598*
[GCGC] = 13691   14643   952   *14171*
[GCGG] = 13638   14595   957   *14145*
[GCGT] = 21986   23173   1187   *22598*
[GCTA] = 35313   36863   1550   *36103*
[GCTC] = 21991   23247   1256   *22640*
[GCTG] = 22028   23191   1163   *22598*
[GCTT] = 35366   36852   1486   *36103*
[GGAA] = 35308   36820   1512   *36036*
[GGAC] = 21920   23222   1302   *22598*
[GGAG] = 21927   23154   1227   *22556*
[GGAT] = 35273   36840   1567   *36036*
[GGCA] = 21982   23230   1248   *22598*
[GGCC] = 13670   14612   942   *14171*
[GGCG] = 13640   14591   951   *14145*
[GGCT] = 21965   23204   1239   *22598*
[GGGA] = 21925   23260   1335   *22556*
[GGGC] = 13615   14604   989   *14145*
[GGGG] = 13637   14622   985   *14119*
[GGGT] = 21923   23146   1223   *22556*
[GGTA] = 35280   36875   1595   *36036*
[GGTC] = 22027   23206   1179   *22598*
[GGTG] = 21965   23141   1176   *22556*
[GGTT] = 35342   36817   1475   *36036*
[GTAA] = 56733   58699   1966   *57572*
[GTAC] = 35364   36830   1466   *36103*
[GTAG] = 35262   36773   1511   *36036*
[GTAT] = 56657   58586   1929   *57572*
[GTCA] = 35381   36920   1539   *36103*
[GTCC] = 21996   23236   1240   *22640*
[GTCG] = 21965   23257   1292   *22598*
[GTCT] = 35419   36917   1498   *36103*
[GTGA] = 35258   36853   1595   *36036*
[GTGC] = 22006   23238   1232   *22598*
[GTGG] = 21984   23185   1201   *22556*
[GTGT] = 35280   36787   1507   *36036*
[GTTA] = 56631   58535   1904   *57572*
[GTTC] = 35349   36789   1440   *36103*
[GTTG] = 35292   36830   1538   *36036*

[GTTT] = 56640   58584   1944   *57572*
[TAAA] = 90841   93173   2332   *91977*
[TAAC] = 56567   58617   2050   *57678*
[TAAG] = 56663   58504   1841   *57572*
[TAAT] = 90695   93174   2479   *91977*
[TACA] = 56680   58615   1935   *57678*
[TACC] = 35351   36949   1598   *36170*
[TACG] = 35308   36830   1522   *36103*
[TACT] = 56782   58635   1853   *57678*
[TAGA] = 56623   58494   1871   *57572*
[TAGC] = 35371   36881   1510   *36103*
[TAGG] = 35324   36776   1452   *36036*
[TAGT] = 56627   58563   1936   *57572*
[TATA] = 90660   93176   2516   *91977*
[TATC] = 56635   58652   2017   *57678*
[TATG] = 56606   58555   1949   *57572*
[TATT] = 90824   93273   2449   *91978*
[TCAA] = 56756   58714   1958   *57678*
[TCAC] = 35439   36980   1541   *36170*
[TCAG] = 35261   36983   1722   *36103*
[TCAT] = 56756   58598   1842   *57678*
[TCCA] = 35436   37002   1566   *36170*
[TCCC] = 22116   23304   1188   *22682*
[TCCG] = 22050   23229   1179   *22640*
[TCCT] = 35413   36881   1468   *36170*
[TCGA] = 35362   36857   1495   *36103*
[TCGC] = 21980   23297   1317   *22640*
[TCGG] = 22028   23247   1219   *22598*
[TCGT] = 35292   36789   1497   *36103*
[TCTA] = 56725   58643   1918   *57678*
[TCTC] = 35350   36885   1535   *36170*
[TCTG] = 35248   37083   1835   *36103*
[TCTT] = 56703   58616   1913   *57679*
[TGAA] = 56648   58450   1802   *57572*
[TGAC] = 35286   36957   1671   *36103*
[TGAG] = 35307   36800   1493   *36036*
[TGAT] = 56672   58606   1934   *57572*
[TGCA] = 35252   36865   1613   *36103*
[TGCC] = 22072   23262   1190   *22640*
[TGCG] = 21925   23197   1272   *22598*
[TGCT] = 35343   36860   1517   *36103*
[TGGA] = 35217   36782   1565   *36036*
[TGGC] = 22035   23199   1164   *22598*
[TGGG] = 21865   23108   1243   *22556*
[TGGT] = 35230   36807   1577   *36036*
[TGTA] = 56611   58431   1820   *57572*
[TGTC] = 35169   36864   1695   *36103*
[TGTG] = 35274   36801   1527   *36036*
[TGTT] = 56617   58480   1863   *57572*
[TTAA] = 90805   93185   2380   *91977*
[TTAC] = 56841   58612   1771   *57678*
[TTAG] = 56632   58566   1934   *57572*

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[TTAT] = 90703   93136   2433   *91978*
[TTCA] = 56809   58647   1838   *57678*
[TTCC] = 35422   36921   1499   *36170*
[TTCG] = 35353   36899   1546   *36103*
[TTCT] = 56772   58553   1781   *57679*
[TTGA] = 56626   58474   1848   *57572*
[TTGC] = 35320   36993   1673   *36103*
[TTGG] = 35334   36812   1478   *36036*
[TTGT] = 56665   58599   1934   *57572*
[TTTA] = 90838   93193   2355   *91978*
[TTTC] = 56656   58648   1992   *57679*
[TTTG] = 56558   58632   2074   *57572*
[TTTT] = 90761   93362   2601   *91978*

Maximum Gap (MAX minus MIN) = 2882 (AATT)
Maximum Gap Below Pred. = 1566 (Calc Not Shown)
Maximum Gap Above Pred. = 1348 (Calc Not Shown)
```

The predicted value was always between the minimum value and the maximum value for each permutation (i.e. each row).

While the maximum difference between the low and high simulation, for all permutations, was 2,882; the maximum gap below the predicted value was 1,566 and the maximum gap above the predicted value was 1,348.

Let us compare these two numbers with what we saw in the real DNA segment:

Using real DNA, the maximum below predicted, considering all permutations, was 31,858. The simulations generated a maximum below predicted of 1,566, meaning only 4.92% of the real DNA. This, in spite of the fact that 70,000 simulations were run and the chart above was for the group of 25,000 simulations which had the highest gaps.

Using real DNA, the maximum above predicted, considering all permutations, was 79,818. The simulations generated a maximum of 1,348, or only 1.69% of the difference using real DNA.

We see again that randomness cannot even come close to creating intelligence or information. This is because when using strings of nucleotides, randomness sticks far too close to predicted values, even when considering bias.

The fact remains that random numbers generate such a small range of values for each permutation histogram, *compared to predicted values*, a person can safely conclude that it is impossible for randomly generated nucleotides (in nature, per neo-Darwinism) to generate any type of information or intelligence.

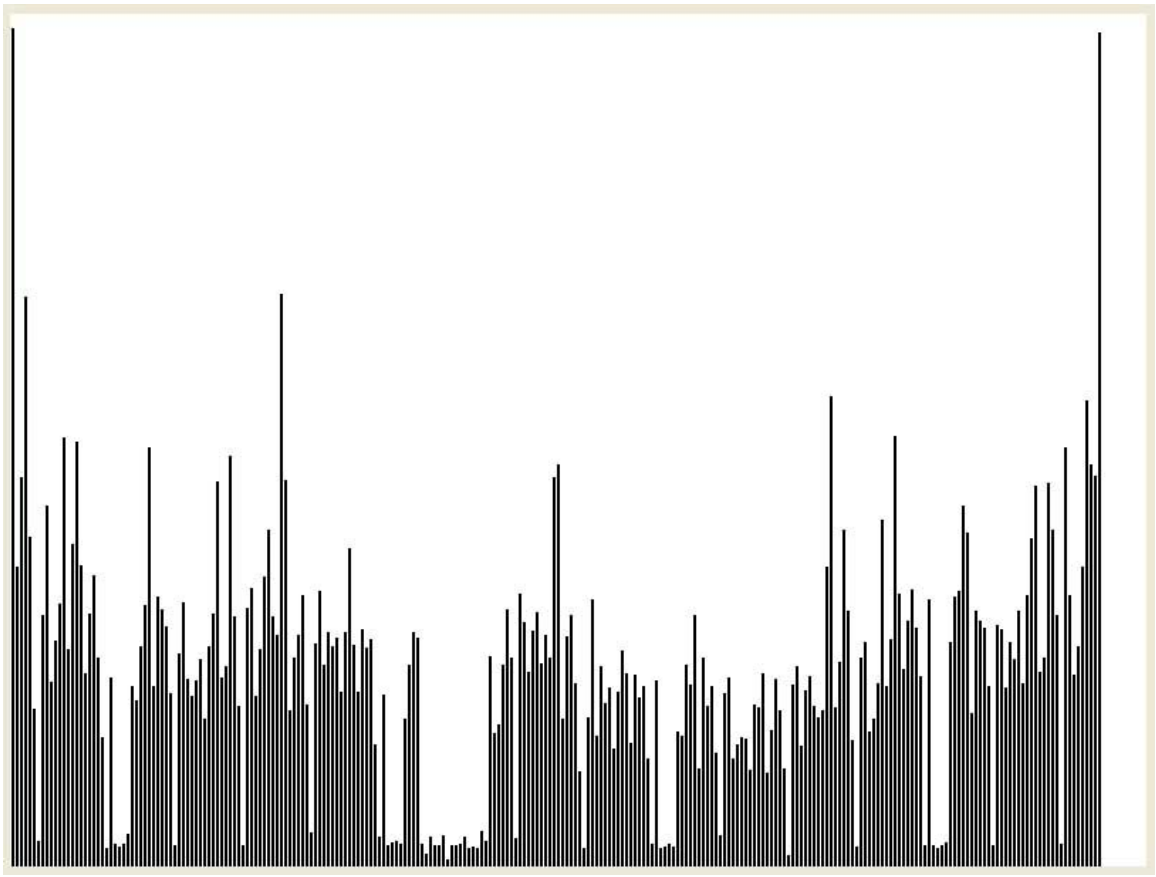
In fact, this is what has happened in the real world. Billions of attempts to create new genetic information, via random mutations, have been attempted in the real world. No one has ever proven that any new genetic information was generated by these randomly generated mutations. (see the Sanford book)

The rare beneficial mutations mentioned in the Sanford book were examples of a loss of genetic information which only coincidentally led to some environmental benefit.

You cannot create intelligence even if you use bias in your selection of nucleotides!!

A Higher Viewpoint

Sometimes a picture is worth a thousand words. Let us look at the histogram of real human DNA, which was mathematically described above:



As can be seen, there are many very small numbers, such as those bars which are very short and can barely be seen at the bottom of the chart. There are also some very tall bars and many medium-length bars. What this graph shows is a lot of variety from the small numbers, to the medium numbers, to the very tall numbers. Some sequences of nucleotides are rarely seen and others are frequently seen. The histogram represents a "pattern of intelligence."

Now let us look at a representative histogram of a randomly generated DNA, using unbiased data. This is not the same randomly generated DNA mathematically described above, but all randomly generated unbiased DNA look basically the same:

Where is the variety in this second picture?? There is none. Randomness is very predictable when looking at large volumes of data.

Can the patterns of randomness, shown in this second graph, ever accidentally generate the patterns of intelligence in the first graph, which represented real human DNA? No.

Statistics

The concept of "standard deviation" is a mathematical or statistical way to represent variety in a bar chart. For example, the "standard deviation" in the real DNA chart above would be expected to be much, much higher than in a random chart because its bars have a much greater variety.

In fact, the histogram data of real DNA is as follows:
Minimum = 1,565
Maximum = 171,795
Standard Deviation = 25,505

This value of the standard deviation, more than 25,000, represents a very wide variety of values in the histogram. This is what we see visually in the above histogram of real DNA.

By comparison, I ran 10,000 computer simulations of randomly generated nucleotides of the same size as the real human DNA from chromosome 5. In each simulation I kept track of the standard deviation. Here is a summary of these 10,000 standard deviations:

Minimum Standard Deviation = 169.46
Maximum Standard Deviation = 236.15

Neither of these numbers are above 1% of the standard deviation (i.e. variety) of the real human DNA, meaning none of the 10,000 computer simulations had a standard deviation of 1% or more of the standard deviation using real human DNA.

I also ran a standard deviation of the 10,000 standard deviations just mentioned, to see how much variety there was among the standard deviations. Here is that number:

Standard Deviation of Standard Deviations = 8.94

This, actually, is to be expected given the minimum and maximum above. All of this indicates that if we had run millions of randomly generated DNA strands that our variety of standard deviations would never get anywhere near the standard deviation of real human DNA of over 25,000!!

This means it is impossible to randomly generate real human DNA (or the real DNA of any living species) by using random mutations of nucleotides. *This demonstrates that patterns of randomness will ever yield patterns of intelligence.*

Yet, evolution claimed that patterns of randomness created patterns of intelligence millions of times within the short timeframe of a billion years. It is nonsense.

Adding Bias

What if we add bias when choosing nucleotides? If we add bias we will definitely get very high standard deviations.

But in this case the standard deviation doesn't mean anything because it we plotted the "predicted" values we would also get a high standard deviation.

What you need to do is plot the *difference* between the biased histogram and the biased predicted values. The difference between these two numbers will yield very small standard deviations. In other words, the biased data is really nothing more than a slight deviation from the predicted value.

But real human DNA does not follow the predicted values. In short, adding bias will not add intelligence even though the pure standard deviation will be higher.

Summary

The point to this chapter is simple: patterns of randomness can never generate patterns of intelligence or information. Never, never, never, never. There is no field in science which would dispute this fact, not even high speed computer simulations would challenge this fact.

For example, if the theory of evolution were true, and randomness could create intelligence, all corporations could fire their computer programmers and replace them with randomly generated computer programs which "evolve," step-by-step, with selection, into very large, highly intricate and sophisticated computer programs.

Actually, "selection" would never come into play because none of the randomly generated computer programs would ever do anything useful, thus there would be nothing to "select" (i.e. nothing was "alive," using evolution terminology).

Computers are many, many trillions of times faster than evolution would be in the real world, so new highly sophisticated computer programs could be written fairly quickly by computerizing the model of evolution. But no corporation would do such a foolish thing because randomness cannot create intelligence.

The conclusion is that it is impossible to generate information and intelligence from randomly generated nucleotides. Neo-Darwinism is a scientifically false concept. *There will never, never be a new gene complex generated by random mutations of nucleotides. It is impossible!!* Yet about 200 million gene complexes randomly formed in about 1 billion years according to the theory of evolution. This is mathematical nonsense.

In this chapter we are actually explaining *why* the impossible probabilities; incurred by the concept of permutations of nucleotides; are so impossible. We are now saying that because of the way random numbers or random permutations are chosen, it is impossible for a set of randomly generated nucleotides to generate information and the massive, massive intelligence of human DNA!!

The concept of "permutations of nucleotides" and the concept of "randomly generated numbers" tell the same story - the theory of neo-Darwinism is mathematically impossible. Now you know why!!

When these concepts are coupled with the scientific fact of genetic entropy, and the many other problems the theory of evolution faces, the reader can understand why the theory of evolution is scientific nonsense.

Introduction to the Mathematics of Evolution

Chapter 19

Genetic Entropy and Genetic Debris

Favorable Mutations

In prior chapters, a "favorable" mutation was assumed to occur 25% of the time because there are only four types of nucleotides. But in the real world of genetics, "favorable" mutations only occur "one in a million" times, according to Dr. Sanford's book on genetic entropy. And Dr. Sanford was quoting other sources when he gave that statistic!

> *"I have seen estimates of the ratio of deleterious-to-beneficial mutations which range from one thousand to one, up to one-million to one. The best estimates seem to be one-million to one (Gerrish and Lenski, 1998). The actual rate of beneficial mutations is so extremely low as to thwart any actual measurement (Bataillon, 2000, Elena et al, 1998). ... In conclusion, mutations appear to be overwhelmingly deleterious, and even when one may be classified as beneficial in some specific sense, it is still usually part of an over-all breakdown and erosion of [the] information [in the DNA]."*
> *Genetic Entropy & The Mystery of the Genome, page 24 & 27*

Dr. Sanford was talking mainly about "point mutations," meaning the removal, add or change of a single nucleotide on DNA. There are, of course, several other types of mutations.

If there are only four different types of nucleotides, why are point mutations beneficial only "one in a million" times?

Actually, the "one in a million" number itself is deceptive. Even in the case of "favorable" mutations, there is a *loss* of genetic information, as Dr. Sanford mentions. It is environmental reasons which cause the "benefit," *not new genetic information*.

The reason beneficial mutations are so rare is because the body does not look at DNA as individual nucleotides. The body looks at DNA as groups of nucleotides.

To understand this concept, suppose we looked at the works of Shakespeare. What if we randomly changed a single letter in one word in one of his plays? Would this give us a one-in-26 chance of intellectually benefiting from one of his plays?

The answer is 'no' because the probability that the overall concepts in that play would be noticeably improved, by that one change of one letter in one word, is virtually zero.

When we look at a play, we see the "big picture" of what the play is telling us. We also see the smaller picture of what the current scene is telling us and we even see what one dialog is telling us and even what one word is telling us.

When we get down to the level of a specific dialog we are concentrating on every word that is said and visualizing that word *in the context of the entire play and scene*. To randomly change one letter of one word, when we are thinking about the "big picture" of the play, is not likely to give us added intellectual benefit.

In fact, if we analyzed every letter in every word of a play by Shakespeare, it is unlikely we could find more than a few single letters in the play which could be changed such that there would be an overall improvement in the value of a scene or the entire play.

A similar thing can be said about DNA, except that DNA is millions of times more complex and more intertwined than any of Shakespeare's plays!!

Similar to the way we look at Shakespeare's plays, the body uses DNA in a "Big Picture" way. DNA has many layers of sophistication and it has many different groups of complex instructions. That is why random mutations have never been observed to create new genetic information and/or new genetic intelligence.

This is also why scientists are having such a hard time decoding what DNA is really doing.

It is also why it is so difficult for humans to intelligently create new DNA from scratch (such as designing the DNA of an extinct egg-laying dinosaur, both male and female).

While one point mutation can be bad, it would be very, very rare when one point mutation would yield new, useful genetic information when considering the "Big Picture" of human DNA. It would take large numbers of nucleotides to create new genetic information, but we have already seen the statistical absurdity of that happening.

This is why "beneficial" mutations are always the result of a loss of genetic information. This loss of genetic information (such as making short hair instead of long hair) may coincidentally have an environmental benefit because the animal lives in a very hot climate.

This can also be seen in medicine. When a bacteria or other microbe develops a resistance to a drug, this resistance is not developed because of any intelligence on the part of the microbe or any additional genetic information; rather the benefit is caused by a loss of genetic information which just coincidentally creates a resistance to a drug. The book: The Edge of Evolution--The Search for the Limits of Darwinism, by Dr. Michael J. Behe, goes into this subject in great detail.

In animals and plants, a single mutation does not provide additional information to the cell or additional benefit (such as an improved and more intelligent "supervisor protein"), it only provides benefit in the context of coincidental environmental issues.

If a favorable point mutation is ever observed, it will most likely be *a former detrimental point mutation* which was coincidently reversed to its original state by a new mutation.

Evolutionists believe a new species has a significantly higher level of *new genetic information* than the "old" species from which it "evolved." But new genetic information has never been observed to form from mutations.

The entire basis of neo-Darwinism is that new genetic information is formed by mutations. This has never been observed in the real world. What has been observed is the loss of genetic information or more likely, neutral mutations have been observed which have no noticeable affect.

Multiple Mutations

Let us again think of a play by Shakespeare. If we made a random change to a single letter, *in thousands of different words*, it is impossible that the overall play would be made more satisfying. It is far more likely that a single letter change in a single word would create a favorable outcome than if one change was made to each of thousands of different words.

So it is with DNA. If only one in a million mutations is favorable, then the more mutations you have, the less likely it is that there will be an overall favorable outcome!!

In other words, if you randomly made a million mutations in a DNA strand, it is far less likely you will have a favorable outcome than if you made one mutation because detrimental mutations will massively overwhelm any very, very rare favorable mutation.

But one mutation will never create a new species or a new gene complex. This is actually a paradox for evolution. The more changes you make, the less likely there will be an overall favorable outcome, but many changes are necessary to create a new species.

The only possible way for evolution to work is for an entire gene to be copied (or some other bulk mutation is made) and then the copy is mutated with point mutations. These point mutations, and even additional nucleotides, would be necessary so the new gene complex (of a new species) provided some new feature (i.e. new genetic information and/or intelligence) for the new species.

But we have already seen this is impossible because the more perfect the copy of the gene is to begin with, the quicker the segment deteriorates due to random mutations (i.e. Kehr's Paradox).

A person might think that evolution would work by modifying existing gene complexes. The problem with this theory is that if you have a failed attempt to convert an existing gene complex into a new and improved gene complex; then you have destroyed an existing, and important, gene complex in the germ cell!!

Also, in ways no human fully understands, pivotal genetic sequences, which are involved in one action, are the result of non-contiguous segments of DNA (e.g. introns). The DNA needs all the information contained in the non-contiguous sections, thus it must know where the scattered pieces are located and what they do.

Thus, creating a new species will likely involve making changes to many different locations on the DNA, which, in itself, creates massive problems for the theory of evolution.

But things get worse for evolution, because like it or not, the DNA of all species is arbitrarily deteriorating at random points on the DNA. This is universally called: genetic entropy.

Genetic Entropy and Evolution

Genetic entropy means that the DNA of all species on earth is deteriorating due to various types of mutations. It is a scientific fact which is known by all geneticists.

Let us try to conceive what genetic entropy really means when considering hundreds of millions of years of speculated evolution.

Let us start with the "first living cell." To think that the "first living cell" had perfect DNA would be ludicrous. If there was a "first living cell," most likely it could barely survive. Most likely it had very poor DNA, but was just able to survive.

What about the second "living cell?"

The second living cell would also have had very poor DNA. In fact, it is unlikely the "first living cell" could have replicated.

But in any case, as more and more cells came into existence, all made from the mold of the "first living cell," which had poor DNA, all of the descendants of the "first living cell" would also have had poor DNA.

But genetic entropy would have made their DNA even worse.

Actually, the mechanism of copying nucleotides in the "first living cell" would have been far less perfect than the sophisticated mechanism which copies nucleotides in today's species. Thus, genetic entropy would have been far worse in the early days of life than it is now. But even now mutations are dangerously common.

This copying mechanism, by the way, is made of proteins, which is a paradox because it means a protein had to exist to copy the RNA or DNA before the first protein was made.

Even if there had been a "first living cell," it is unlikely life on this planet could have survived for very long. Not only would the "first living cell" have had poor DNA, but genetic defects; which would have accumulated from one generation of the "first living cell" species to the next generation; would have quickly wiped out the first and only species on this planet.

But let us move forward and talk about the first multi-celled creature which had circulating blood (or some other fluid that was circulating).

How could such a creature have ever come into existence? If you start with poor DNA from the "first living cell," and then you have generation after generation of abnormally high genetic entropy, meaning the deterioration of the DNA because of various types of errors in copying DNA segments, how could a complex species ever have come into existence?

Moving Backwards in Time

With this introduction, let us now start to look at DNA from the perspective of the first *homo sapiens sapiens*, who, according to evolution, lived more than 100,000 years ago.

Let us trace the ancestry of the first *homo sapiens sapiens* (who would have been brother and sister for reasons previously mentioned) back to the first complex cell with a circulatory system of some sort.

First of all, we would go through many generations of their "ancestor species." An "ancestor species," as we have seen, is a species on the evolutionary tree or phylogenetic tree of the species.

We will define the first *homo sapiens sapiens* to be "Species 1." We humans are Species 1 according to evolution.

So let us say that the species on the phylogenetic tree represented by the parent species of "Species 1" is called: "Species 2." In other words, on ***our*** phylogenetic tree, Species 2 was the species just before Species 1, which is *homo sapiens sapiens*.

How many generations of "Species 2" existed (moving backwards in time) to go back to "Species 3," the parent species of "Species 2?"

We obviously don't know (since evolution doesn't exist), but let us assume it was 22,000 generations.

Then let us assume there were 22,000 generations of Species 3 (we are moving backwards in time) to get to Species 4.

Then let us assume there were 22,000 generations of Species 4 before we get to Species 5.

And so on.

Let us assume, for the sake of argument, that the earliest "ancestor species" of humans which had a circulatory system (again, assuming the theory of evolution were true) was Species 3,000 and that in each case there were 22,000 generations between each of the 3,000 species. (Technically it would have been species 3,001, but let's keep things simple.)

Note that as we get further from humans; that the time between birth and breeding (or dividing) gets shorter and shorter. While humans may reproduce at an average age of

25 years, Species 3,000 on our evolutionary tree probably bred or divided within days of "birth." We will assume an average breeding age of 10 years.

Thus we have:
Species 3,000 (our *earliest* and first ancestor species with a circulatory system, which lived 660,000,000 years ago)
22,000 generations of Species 3,000
Species 2,999, created by evolution from Species 3,000
22,000 generations of Species 2,999
Species 2,998, created by evolution from Species 2,999
22,000 generations of Species 2,998

... (these three dots represent hundreds of millions of years)

Species 3 (grandparent species of *homo sapiens sapiens*)
22,000 generations of Species 3
Species 2 (parent species of *homo sapiens sapiens*)
22,000 generations of Species 2
Species 1 (*homo sapiens sapiens*)
5,000 generations of Species 1 to get to you and me (at an average age of 20 when our ancestors had children according to the theory of evolution)

Altogether we have 3,000 different species (from the first species with a circulating system) and *66 million generations* (22,000 times 3,000) and roughly 660 million years (at 10 years per generation).

Keeping in mind that the DNA of Species 3,000 was not very good, and keeping in mind that genetic entropy would have been in force for 66 million consecutive generations (i.e. 660 million years), and most importantly, keeping in mind that there is no mechanism to "fix" most types of DNA damage or remove unneeded nucleotides from DNA; *all genetic mutations would have accumulated on the DNA* of animals from generation to generation and from species to species.

In other words, in this process the worthless and defective nucleotides (created by genetic entropy) would have remained on the DNA, and been passed from one generation to another, and from one species to another, forever because there is no mechanism to remove them from defective DNA.

There would have been a continuously *accumulating* number of genetic defects at birth among our ancestor species!!

Every one of the 66 million generations which led to humans would have had some genetic entropy. *Thus, human DNA today (that is the DNA of you and me), and the DNA of our earliest ancestors, would have the cumulative genetic defects of 66 million generations of animals!!*

In other words, genetic defects would have not only very seriously damaged the DNA of each species, but the genetic defects would have remained and accumulated on the DNA, from generation to generation and from species to species.

So how bad would the DNA of the first homo sapiens sapiens have been after 660 million years of increasingly accumulated genetic defects?

Suppose, for example, there was a single mutation every year, due to genetic entropy. Humans would have 660,000,000 mutations on our human DNA!! *We could never have existed!!*

It would be impossible for a species to exist after 660 million years of accumulated genetic defects. It is ludicrous. And remember than Species 3,000 had poor DNA to begin with and the copy mechanism back then would have been far less perfect than it is today.

Every generation of a species would have had genetic defects passed on to the next generation. Furthermore, when there was a new species, *the genetic defects of the prior species would have been passed on to the new species*.

DNA deteriorates over time, it doesn't get better. If the theory of evolution were true, every human, you and me, would have 660 million years of accumulated genetic defects. We could not exist.

The Facts

What is the scientific fact? *The scientific fact is that human DNA is virtually perfect*. If it were not perfect, genetic diseases, and deaths at birth from genetic defects, would be millions of times worse than they really are.

Ponder this carefully: evolution claims to start with a "first living cell," which had a very short RNA or DNA which could barely allow it to survive, and then after many hundreds of millions of years of accumulated genetic defects/entropy, from generation to generation and from species to species; humans (*homo sapiens sapiens*) come on the scene with virtually perfect DNA; plus they have incomprehensively complex DNA containing 3 billion pairs of nucleotides!! This is nonsense; hundreds of millions of years of constantly deteriorating DNA does yield virtually perfect DNA of a much, much greater length and an almost infinitely higher level of sophistication.

It is claimed that natural selection created this massive, massive increase in DNA length and DNA sophistication. But natural selection only works on existing living, walking and breathings species. Natural selection does not create species, it only "selects" from among existing species. Natural selection only affects the mix of species, not the creation of species.

Every minute step of evolution had to be driven by totally blind, random mutations of DNA and all of these random mutations (which started with simple and poor DNA) were constantly being degraded by genetic entropy!!

You can rest assured that genetic entropy works *much, much faster* than favorable random mutations of nucleotides. In fact, we can compare genetic entropy to a jet airplane, and compare favorable mutations to a child with a pair of "roller skates."

The jet airplane of genetic entropy has been flying at jet speeds for 660 million years and the roller skates of favorable mutations (which actually don't exist) has tried to catch up and surpass the jet airplane. But every year the child on roller skates gets further and further behind.

Evolution essentially claims that favorable mutations can create new species at the same time as the deterioration of the species is moving at jet speeds. It is scientific nonsense.

Genetic Debris

If the theory of evolution were true, any human could trace their ancestry back to the "first living cell."

While we have discussed genetic entropy, genetic entropy does not count failed attempts to create new genetic information. In addition to genetic entropy, we also have what I call "genetic debris," meaning failed attempts by evolution to create a new and improved species.

Remember, new species are created by evolution by "bulk mutations," followed by point mutations. Of course this is simplistic, but it is the only way evolution could have happened.

Genetic debris means there is a *failed* attempt by evolution to create a new species (e.g. new genetic information). *The attempt does create the bulk mutations, but the point mutations fail to create new genetic information. Thus, the mutated bulk mutations stay on the DNA without adding any new genetic information.*

For each new species there would have been many thousands or many millions of failed attempts to create the new species, especially if several new gene complexes were needed for the new species.

There is no mechanism on DNA to remove these failed attempts to expand and improve DNA. The copies of DNA which failed to create any benefit to the new species will just sit there on the DNA forever.

Someone might think that genetic debris is not an issue because any attempt to create a new species, which included failed attempts to create new genes (which would normally include a large amount of copied genetic material via a mutation) would simple lead to the death of the attempted new species.

However, most new species would need 10 or 20 or more new gene complexes. It is statistically impossible that 20 or more new gene complexes could be created, *each in a single attempt*. It is absurd to think otherwise.

Thus, because it is insane to think that all new gene complexes for a new species were created in the first attempt for a new species; the first male and female of each and every new species would of necessity have had many failed attempts to create all of the required new gene complexes. These failed attempts would stick to their DNA forever.

Humans would thus have the left-over failures (i.e. failures to create new gene complexes) of every one of our 3,000 ancestor species, permanently stuck on our DNA. The number of nucleotides stuck on our DNA would number in the many, many billions.

(Note: Evolutionists may claim that it was *existing* gene complexes which were modified by evolution; and that it was not *copies* of existing gene complexes that were modified. As already mentioned, this theory generates its own problems for evolution. The reason is that if you modify an existing gene complex, and the attempt fails to create new genetic material; then you have *destroyed existing genetic material* and the offspring of the animal will likely die off as a result rather than form a new species.)

The point is that the failures of "genetic debris" would have been "on top" of the failures caused by genetic entropy. Genetic entropy can be thought of as point mutations, whereas genetic debris can be thought of as large amounts of DNA being copied, in preparation for a new species. But the copies did not turn out to be useful.

This means that in addition to genetic entropy, many additional clumps of genetic defects, in each new ancestor species, would have been added to our DNA in the attempts of our ancestor species to create new genetic information (i.e. genetic debris).

So what are the facts? Human DNA is between 50% and 99+% necessary and useful. Regardless of what the percentage is, our human DNA is virtually perfect and genetic defects are very rare.

How do you start with simplistic garbage (the DNA of the "first living cell") and end up with incomprehensibly complex human DNA which has very, very, very few defects? You don't end up with perfect DNA by using randomness; that is for sure. Yet, randomness is *the one and only* heart and soul of neo-Darwinism.

What all of this means is this:
1) Because humans have virtually perfect DNA, our first ancestors would have had perfect DNA,
2) Because of genetic entropy our first ancestor with perfect DNA could not have lived more than several thousand years ago (or our DNA would be very imperfect by now).

But this is not all. *All complex living species today are in exactly the same situation as humans; meaning they have virtually perfect DNA, meaning their earliest ancestor could only have lived a few thousand years ago!!*

The theory of evolution is scientific nonsense. The teaching of Adam and Eve and the Garden of Eden is the only doctrine which matches *real scientific data*.

But things get even worse for evolution as we will see in the next chapter.

Introduction to the Mathematics of Evolution

Chapter 20

Genetic Chaos

Introduction to Genetic Chaos

Let us now look at evolution from the perspective of the creation of a single new gene complex, which, by the way, is not likely to be contiguous on the DNA.

We must remember that this new gene complex does not live in a vacuum; it lives in an incomprehensively complex environment. Thus, to generate a new species is to modify an incomprehensively complex DNA and come up with numerous sophisticated modifications to create a new incomprehensively complex species.

In other words, the changes to the DNA need to be made in many different places, especially if there is a significant change in the function of any organ, bone structure, physical function, etc.

For example, if you change the bone structure you also have to change the muscle structure, the circulatory system, the lymph system, the programming in the brain, etc. These are likely to require making *changes* in the DNA in many different locations; plus making *additions* to the DNA in many different locations, in order to create new genetic information and new species function. Even some deletions of nucleotides may be needed (but this will be ignored in this chapter).

But we will be simple for now.

Let us start with the DNA of an animal which has 2 billion pairs of nucleotides. We will randomly create an extra "copy" of one of sections of the DNA, a gene complex, which has 5,000 nucleotides.

We will place this copy, of a contiguous section of DNA, in a new location on the DNA in the attempt to begin to create a new species. The DNA now has 2,000,005,000 nucleotides.

In order to create a new gene complex let us assume we need to do two things to the copied gene complex (i.e. just creating an extra copy of a gene complex won't give us a new species because it does not add any new genetic information to the DNA).

First, let us assume, to create a new species, we need to *modify* 1,000 of the 5,000 nucleotides of the new gene complex.

Second, let us assume we need to *add* 1,000 more nucleotides to the new gene complex. To simplify things, we will assume these additional nucleotides need to be inside the copied gene complex area.

Thus, our initial 2 billion nucleotide (pair) DNA is first increased to 2,000,005,000 nucleotide pairs by copying a gene complex. Next, 1,000 of the 5,000 copied nucleotides will be modified by point mutations, and simultaneously 1,000 new nucleotides will be added to the new gene complex area. This will give us a new gene complex, new genetic information and a new species.

Of course, the order in which mutations or adding new nucleotides is done is not important, only the end result is important.

We expect to end up with a DNA of 2,000,006,000 nucleotides which will have new genetic information inside of a new gene complex and the new DNA will constitute a new species.

Of course, in the real world, a new species would require a lot more changes than in this example. But let us start small.

The Key Issue

Before going on, we need to have a little discussion. If we have a single point mutation, where will it be on the DNA of the new species? Will the single point mutation be within the 5,000 nucleotides which were accidentally copied from an "old" gene complex? Or will the point mutation occur somewhere else on the DNA outside the copy of the "old" gene complex?

In other words, if we randomly mutate a nucleotide somewhere *on the entire DNA*, what is the probability that this mutation will be in the range or area of the 5,000 contiguous nucleotides where we want the mutation to be?

The probability is 5,000 divided by 2,000,005,000 or 1 in 400,001.

What this means is that if we randomly mutate *this DNA strand* 400,001 times, only *one* of these mutations will likely occur in the desired new segment of 5,000 nucleotides.

There are two problems when doing this. First, we are not sure the one mutation (inside the segment of 5,000) changes a nucleotide which needs to be mutated within that segment. Second, we are not sure, even if a desired nucleotide is mutated, that it will mutate to the correct nucleotide we want.

But there is a third and even bigger problem: there will be 400,000 mutations in sections of the DNA where *we definitely don't want to mutate the DNA*!!

In other words, in order to make a single nucleotide change where we want the change to take place (i.e. mutating a single nucleotide in a section where we want mutations), we will accidentally mutate the DNA strand in 400,000 places where we *don't want* any mutations.

What kind of damage is going to be done by random mutations in 400,000 places where we don't want any mutations? The damage would obviously be fatal.

And this is just the first mutation of a single nucleotide in the desired section!!

The second mutation inside the extra gene copy will result in another 400,000 mutations in places where we don't want to mutate the DNA.

And on and on and on.

In fact, by the time we have created 1,000 mutations to the extra gene copy, which is the requirement, we have made approximately *400,000,000 undesirable mutations* (that is *400 million* undesirable mutations!!) on the former "good part" of the DNA (i.e. outside the area where we want mutations).

Likewise, when we try to add 1,000 new nucleotides to the new gene complex area, we will have to *add* roughly 400,000,000 *additional* nucleotides to the entire DNA, in places we don't want to add nucleotides, in order to add 1,000 nucleotides to the new gene complex area.

If you do the math that is 800,000,000 damaging mutations just to get one new gene complex. However, while doing this will create 1,000 different nucleotides to the new gene complex, and 1,000 new nucleotides inside the new gene complex area, there is no guarantee that these 2,000 mutations are the 2,000 mutations we want!! It is at this point that the prior chapters on this subject come into play because the chances these 2,000 mutations (including 1,000 new nucleotides) create a new gene complex is virtually zero.

Thus, not only is the probability of creating a new gene complex virtually zero, we have damaged the DNA of the new species by 800,000,000 undesirable mutations or new nucleotides in undesirable locations.

Our resulting DNA strand will have roughly 2,400,006,000 nucleotides, of which there are 400,000,000 mutations in sections we don't want mutations and 400,000,000 new nucleotides are in places where we don't want added nucleotides!!

Literally one-third of the DNA (800,000,000 divided by 2,400,006,000) of this species will be damaged while trying to create a single new gene complex from an old gene complex!!! Do you think a species can survive if one-third of its DNA is *randomly damaged* by undesirable mutations just to take a chance on creating one new gene complex?? Obviously not.

I call this "genetic chaos."

What if we took a computer program; and remember human DNA is more complex and more functional than any computer program on earth; and randomly changed 1/6th of its "bits" and randomly add 1/6th (of the original size) additional random bits. Do you think the computer program would still work? Obviously not!! Do you think the computer program will be more productive? This is absurd!!

However, we have only talked about one new gene complex. A new species will likely need to have 20 new gene complexes and massive changes to hundreds of other sections of the DNA which remain as part of the new species, but need to be modified (e.g. modifications to the DNA which controls the creation of the circulatory system)!!

Trying to add 3 new gene complexes to an existing DNA will wipe out (i.e. randomize) the entire DNA with mutations, but the average new species probably needs 20 new gene complexes.

400,000,000 additional nucleotides will be added in the attempt to create a single new gene, as mentioned above. *But for 20 new genes there will be 8,000,000,000 additional nucleotides, making a total length of about 10,000,000,000 nucleotides on the DNA, all of which were either randomly added or were randomly mutated several times over!!!*

And this is just for one new species!!

In prior chapters our mutations were always conveniently put inside the copy genes were we wanted the mutations to occur. But in the real world, all mutations are random. This means the *location* of each and every mutation can happen *anywhere* on the DNA, not just the section we want the mutation to occur!!

Comments on Genetic Chaos

What just happened in this discussion is that in the attempt to create a new species and create new gene complexes, new morphing of the embryo algorithms, etc.; *which is a requirement of the theory of evolution*, we killed the new species long before its new DNA was modified (though even at this point the modifications are not guaranteed to be functional, all we have done at this point is count the mutations in the area where we want them).

So many mutations and undesirable new nucleotides were added to this species, in the attempt to add a single new gene complex, that we killed the species. No species could survive with this many random mutations or even 1% of this many mutations in undesirable locations.

But as just mentioned, the average new species, considering complex species, probably needs at least 20 new gene complexes, plus massive numbers of changes to the morphing of the embryo algorithms, the reprogramming of the brain, etc. etc.

And don't forget that the new species needs both a male and female, *whose DNA must align (this applies to genetic debris as well)*. Thus, if these billions of detrimental mutations happened to a male, then a female (especially considering the added nucleotides) would need to have billions of added nucleotides in the *same places* on her DNA so their DNA would align. But all of the mutations in the male and female would be totally random and *independent* of each other!!

The point is that randomness is randomness. Randomness can hit any part of DNA at any time; not just the highly specific places we want to change.

So when an evolutionist says that a copy of a gene (they should talk about the entire gene complex, not just the gene) is modified to create a new gene (complex), the reality is that the mutations needed to change the old gene into a new gene can occur *anywhere* on the DNA strand, not just where we want them to occur!!

Thus, in the attempt to create a new gene, "genetic chaos" (or we could call it "genetic randomization") occurs randomly all over the DNA and is guaranteed to kill the new species long, long, long before any benefit is realized from the mutations.

Even if we were not dealing with a copy of a gene complex, but were dealing with modifying an original gene complex, the numbers are almost identical.

"Nothing Is Statistically Impossible"

The theory of evolution claims that "nothing is statistically impossible." When they are shown the statistical insanity of a new species arising by random mutations, they simply say "nothing is statistically impossible."

But their comments are based on the assumption that the *location* of mutations is exact. But genetic chaos takes into account the fact that the *location* of mutations *is itself random*.

Thus, the location of the mutation and the mutation itself are both random.

While "nothing is statistically impossible" (when assuming every mutation occurs in the exact location where you want it to occur), genetic chaos doesn't follow the assumptions of evolution. The insane probability of evolution has just become inane.

In other words, genetic chaos goes beyond probability. Probability has to do with the actual mutations in places where they are needed. But genetic chaos says that in the *process* of converting and adding specific nucleotides in specific places, something unexpected happens: billions of unwanted mutations and billions of new nucleotides occur in areas they are not supposed to occur. *Statistics cannot fix this problem.*

The results of the *process* are not statistical, but factual. And the *process* is fatal in every case once complexity is introduced to the DNA because there is no way to avoid killing the new species due to the complexity of its DNA.

There is no mechanism on the DNA of any species to "fix" these genetic errors, whether they are mutations where we don't want them, or additional nucleotides where we don't want them. As far as scientists know, all mutations become "baggage" forever, meaning the baggage is passed on to all descendants.

Between genetic entropy, genetic debris and genetic chaos (the latter two of these three phenomenon do not occur in nature, but would occur if the theory of evolution were true), *our human DNA would be many, many billions of defective nucleotides long*. This length alone would kill us by the amount of energy our DNA would consume. But even if the energy did not kill us, the genetic damage would kill us.

Peppering DNA With Random Mutations

Suppose we took a perfectly good DNA strand and started randomly changing nucleotides and randomly adding nucleotides one at a time. I call this "genetic peppering" of DNA, though technically it is called "genetic entropy."

Doing this would be like taking a digital picture and randomly changing the values of the Red, Green and Blue (or whatever color scheme is used) pixel values.

If we "pepper" a digital picture often enough it will eventually become total noise. Likewise, if we pepper DNA often enough it will eventually become total garbage.

But DNA is functional and pictures are not functional, they are only aesthetic.

As mentioned before, you can change one nucleotide in a fertilized germ cell and kill the forming baby or create massive damage to the new baby. Imagine making ten thousand random changes to the morphing of the embryo algorithm of a recently fertilized egg!!

In short, if you pepper the morphing of the embryo algorithm you could have *instant death to the new species*.

Human DNA is not very resistant to peppering because it is so sophisticated. As another example, inside every human gene are introns and exons. If you mess with either of these types of nucleotides, you are going to get damaged genes and thus damaged proteins.

But if you have a damaged protein, the entire protein structure, to which this protein belongs, may not bind where it needs to bind or it may not repel where it needs to repel or it may not be water-resistant where it needs to be water-resistant, etc. In other words, one or more incorrect amino acids which are inserted into the protein structure may neutralize the function of the protein structure.

Also, at the end-points of each gene on the DNA are special nucleotide sequences which tell other proteins where the gene begins and where it ends. If you mess with one of these nucleotides, two genes could run together to make one very long protein. This would effectively destroy the usefulness of the proteins made by both genes. This in itself may destroy an entire protein structure inside the cell.

The point is that genetic chaos will destroy the DNA *much faster than the reader may think*. Considering that only the DNA in the germ cells are passed to the next generation, and that these same germ cells use the critical morphing of the embryo algorithms, and considering that all evolution must occur exclusively in the germ cells, it is clear that genetic chaos does not need the millions of randomly mutated nucleotides or millions of randomly added nucleotides to destroy a new species. *It may only take one misplaced nucleotide or one misplaced additional nucleotide.*

There are many reasons genetic chaos is proof that the theory of evolution is scientific nonsense.

So What is the Truth?

If the theory of evolution were true, there would be so much baggage accumulated on our DNA, from our ancestors and ancestor species, that only a puny fraction of a billionth of 1% of our DNA would be functional. But this is not what is observed.

If evolution was true, we humans would not only accumulate genetic entropy and genetic debris from our ancestors and ancestor species, we would also accumulate genetic chaos. But the genetic chaos created by the change or addition of *one single nucleotide* would result in the death of the new species. And a new species typically needs about 20 new *gene complexes*.

Some people might speculate that there is some unseen template that protects correct nucleotides from being mutated. If this were true mutations would only affect unimportant sections of the DNA. This possible response is nonsense; there is no hidden or secret template that protects correct nucleotides from being mutated, *especially for a new species which doesn't exist yet*. Even evolutionists admit that evolution is "blind" and has no direction when it is creating new species.

Furthermore, no one can point to a section of human DNA and prove it is worthless. Scientists used to think that large sections of human DNA were so worthless they called them "junk DNA." As Dr. Sanford stated, the concept of "junk DNA" is disappearing as scientists learn what these DNA sections are used for. For example, scientists still don't have a clue where all of the morphing of the embryo algorithms are scattered on human DNA.

Also, some might speculate that when an extra copy of a gene is made, even though the extra copy is useless to the plant or animal; they may theorize that mutations will be more likely to happen to the extra copy of the gene than to the rest of the gene.

While the endpoints of the copy of a gene may be abnormally vulnerable to mutations because they may be weak bindings, these represent only a handful of nucleotides. The vast majority of the copy of the gene is no more or less prone to mutations than is any other part of the DNA.

Time

As always, there is also the issue of time. As mentioned above, in order to get one nucleotide "inside" the area of the DNA where a new gene complex is supposedly being built, it took 400,000 damaging mutations in sections of DNA where you did not want mutations.

How long (in terms of time) do you suppose it takes a DNA strand of 2 billion nucleotides to experience 400,001 mutations (and 400,000 additional nucleotides), in the attempt to get one mutation and one new nucleotide inside a key area?

This creates a paradox for evolutionists. If they say mutations happen fast, to accommodate evolution; then they are admitting that genetic entropy would have killed off every one of our very distant ancestor species due to accumulated genetic entropy.

On the other hand, if they say mutations are slow, then there is not enough time, meaning the first animal or plant of a new species would die of old age long before the first ***nucleotide*** of the first new gene complex lands in an area where it is needed.

In fact, taking a middle ground leads to the conclusion the new animal or plant would die of old age long, long before a single new ***gene complex*** could form.

If evolution were true, genetic chaos would be true and we would not exist. Because we exist, therefore evolution is false.

Introduction to the Mathematics of Evolution

Chapter 21

The Claims of Evolution

"God grant me the courage not to give up what I think is right, even though I think it is hopeless."
Admiral Chester W. Nimitz

Introduction

This chapter will discuss some of the "evidence" of the scientific establishment that the theory of evolution is a valid scientific theory. Not only are their theories nonsense, their techniques to convince people to believe in evolution are also nonsense.

Claim #1: Macroevolution Has Been Observed

Those who claim that macroevolution has been observed *are being totally deceptive*.

In order to observe "macroevolution," someone must observe and prove that *new genetic information* has been formed by totally random processes. *This new genetic information must include at least one new gene complex; by totally random means*. This has never happened and never will happen!!

Macroevolution has *NEVER* been observed and will *NEVER* be observed. It completely violates the laws of mathematics.

Their false claims are based on:
1) Microevolution, or
2) Point mutations which reduce the amount of genetic information but coincidentally create some benefit, or
3) The use of inconsistent definitions.

Let us talk about the use of inconsistent definitions

In this book the term "species" is defined by the *DNA structure* of the animal.

In this book the term "microevolution" is defined by the *DNA structure* of the animal.

In this book the term "macroevolution" (i.e. true evolution) is defined by the *DNA structure* of the animal.

These three definitions are consistent because all three of them are based on "DNA structure."

Now consider these four definitions:

The term "species" is defined based on the *ability of two animals to physically mate*.

The term "microevolution" is defined based on the *ability of two animals to physically mate*.

The term "macroevolution" (i.e. evolution), *as used by some scientists*, is based on the *ability of two animals to physically mate*.

The term "macroevolution" (i.e. evolution), *as used by the general public*, is based on the *DNA structure* of the two animals.

What is wrong with these four definitions? What is wrong is that three of the definitions are *based on the physical ability to mate*; and one of them, *the one used by the general public*, is based on DNA structure.

In recent years science has claimed that evolution occurred by random mutations of DNA. Thus, *in recent years the general public has been converted into thinking about true evolution solely in terms of DNA structure*.

Among scientists, many of them still use the term "evolution" to mean two animals cannot physically mate with each other.

This intentionally deceptive tactic can be explained as follows:

Suppose scientists follow many generations of a type of animal which has a high degree of microevolution (i.e. high variation in physical features in spite of the fact they all have *the same DNA structure*).

Eventually, after many generations, the variation in this species becomes so great that two of the variations cannot physically mate with each other.

The scientists then claim that this is "proof of evolution." What is wrong with this claim? Nothing, so far.

In the minds of these scientists, the term "evolution" is used when two variations *of the same animal* cannot physically mate. In other words, t*hey use the term "evolution" in their claim that they have observed two variations of the same animal (the two variations have the same DNA structure) and these variations cannot physically mate!!*

Now comes the problem.

When these scientists go public with their claims, because they use the term "evolution," the general public thinks that the two animals *have a different DNA structure*. But they do not have different DNA structure; they have the same DNA structure. They are "cousins," but they cannot mate because of physical differences caused by microevolution.

For example, there are breeds of dogs, which have the same DNA structure, which cannot mate because of a massive difference in their physical size. For example, try to breed a Great Dane and a miniature Poodle.

The same is true of some breeds of horses.

Thus, because of the clever terminology used by scientists, *the general public thinks there is new genetic information and new genes because the term "evolution" was used*. But there are *NO* new genes and *NO* new genetic information because *the two variations have exactly the same DNA structure.*

Microevolution can be so powerful that two animals *with an identical DNA structure cannot mate due to physical differences*.

But this is not "macroevolution," it is the result of "microevolution." Be warned that scientists may call this phenomenon "evolution." But it is not "evolution," it is microevolution.

In fact, when dogs, or any other animal, are bred for a specific physical feature, the end result is the *loss of genetic information*. It is not the loss of nucleotides; rather it is the loss of variation in their genes.

Because patterns of randomness can never create patterns of intelligence, such as a new gene complex, m*acroevolution has NEVER, NEVER, NEVER been observed*; nor will it ever be observed. Let me repeat that again: *macroevolution has NEVER, NEVER, NEVER been observed*, nor will it ever be observed.

Never forget that. When such a ludicrous claim is made, ask to see the new genetic material and how the "new" species DNA compares to the "old" species DNA.

Claim #2: Wishful Thinking is a Source of New Genetic Information

How many times have you watched a television show on evolution and heard a statement such as this one: "this species developed the ability to stand on two legs so that it could reach fruits which were higher up in the tree."

This is "wishful thinking," meaning an animal "wished" it had a different physical feature so it could reach fruit higher up the tree; then over many generations, even over many centuries, the species developed the new features necessary to reach the fruit which was higher in the tree.

To the credit of some evolutionary biologists, they abhor such nonsensical "wishful thinking" claims; but the popular media and popular textbooks are full of such claims. However, on many occasions evolutionary biologists have inadvertently used "wishful thinking," such as when they look at a fossil and claim: "This dinosaur wanted to fly."

There are three major problems with using "wishful thinking" to prove evolution.

First, new physical features require massive, complex changes to DNA. For example, if you change the leg bone, most likely you will also have to change the circulatory system, the muscles, the brain (to control the muscles), etc. All of this requires highly sophisticated changes to DNA, including morphing of the embryo algorithms.

Second, no animal on earth knows what DNA is - except humans, thus no animal knows how to change their DNA. Even humans have only known about DNA *for just over 50 years*. Thus, no animal on earth, *including humans*, knows how to redesign its DNA so that it could have some new physical feature (note the pre-liver chapters).

For example, any new physical feature in humans would have to include major changes to the morphing of the embryo algorithms in our DNA. Scientist don't have a clue where the morphing of the embryo algorithms are in human DNA, much less how to redesign them.

Third, even if an animal did know how to change its DNA (which, of course, is a ludicrous theory for all animals except humans), how could it physically change its DNA? What mechanism exists, for example, in a chimpanzee, such that a chimpanzee would physically change the DNA in their germ cells?

In short, the entire concept of "wishful thinking" is *total and absolute nonsense*.

Amazingly, the concept is also applied to single-celled microbes, such as viruses.

When the scientific community states that "microbes developed a resistance to a new drug," they are implying three things:

First, they imply that a group of viruses held a series of scientific meetings to discuss how they could mutate their DNA to become resistant to a new drug.

Second, these viruses had the "scientific brains" to figure out which nucleotide(s) to change in their own DNA in order to develop a resistance to the new drug.

Third, these viruses had the ability to physically change their own exact nucleotide(s), with pinpoint precision, using point mutations; so that their offspring (which, by the way, are identical copies of themselves) are able to develop a resistance to the new drug.

All three steps are nonsense.

The Dr. Michael Behe book: The Edge of Evolution, discusses single-celled microbes and drugs in great detail.

In fact, much of the theory of evolution is "wishful thinking." Just like viruses, and other microbes, cannot custom design and custom change their DNA; no animal which has ever lived (including humans) has had the intelligence, and the ability, to know where to change their DNA; and has had the ability to physically change their DNA.

The whole concept of "wishful thinking" is just so much nonsense.

What this means is that every mutation of DNA, in the history of the world, must have been totally mindless, totally random, totally accidental, totally without direction, etc.

This includes highly complex changes in DNA, such as the change from walking on four legs to walking on two legs, which would have required massive changes to DNA (such as the creation of semi-circular canals in the ears, which are a long way from the leg bones and are incredibly, incredibly complex).

A good example of "wishful thinking" was given by one of the most famous evolutionists. He claimed that roses may have developed thorns to keep from being eaten. There are many flaws with this logic, such as:
1) The only roses which know about being eaten are already in the belly of some animal, and by then it is too late to mutate their DNA.
2) How does a rose which is in the belly of an animal communicate to its fellow roses to warn them to build thorns to avoid getting eaten?
3) Why hasn't wheat developed thorns strong enough to puncture the tires of farm tractors?

But above all of these things; the addition of thorns to a rose bush, which has never had thorns, requires massive changes to their DNA. To claim that "wishful thinking" of roses was able to create massive, intelligent changes to the DNA of a rose is more ludicrous than thinking a first grade class can build a space shuttle by themselves.

Any change in a species which requires a change to DNA cannot be the result of "wishful thinking." Evolution can only be the result of totally mindless, totally accidental, totally without direction, mutations of DNA.

Claim #3: Multi-Species Evolution Has Been Proven

Multi-species evolution is the claim that it took evolution multiple different species to fully effect a major change to a bodily structure, such as a new and improved eye. For example, it may be claimed that the steps needed to convert the eye from a light sensor only, to being able to fly an F-22 Raptor, was so complex that it took multiple species to totally effect the massive change.

Aside from the absurdity of multi-generation evolution, *multi-species evolution* is even more absurd. There is no evidence that multi-species evolution ever occurred.

For example, it is claimed that the human eye "evolved" from very simple "eyes," which could only detect light (but not see anything) to more sophisticated light detection, to "pinhole" eyes, etc., from species to species, all the way to human eyes.

There is no evidence for this theory. There is nothing in the fossil record to verify this theory. *The species which are used as "evidence" for this theory are not ancestors of humans*.

The appearance on the earth of new species for the first time is "punctuated." Perhaps the Cambrian Explosion is the best example of this. Suddenly, without ancestors, numerous new complex species were formed on this earth.

Simon Conway Morris is the world's foremost expert on the Burgess Shale fossils (they are in the Canadian Rockies), which were part of the Cambrian Explosion.

Many of the creatures found in Canada are very, very odd and are nothing like any animal currently on earth. Simon Conway Morris said this about his research on the wide and strange variety of animals he studied:

> *"It is almost as if you've gone to another planet, you've been given a fishing boat and a net and you've been allowed to throw that net over into the deep ocean and you have no idea what was going to come up."*
> PBS Video: Evolution Series: "Great Transformations"

The vast array of weird and strange species in the Burgess Shale site; and in other Cambrian Explosion sites; do not have any ancestors, nor did they have any descendants. Thus, all of their features just suddenly appeared on this earth without ancestors and just as suddenly disappeared.

So how about the human eye?

> *". . . there is no evidence whatsoever of how a single-celled organism might have converted into multicelled organisms. The metazoa just abruptly appear in the fossil record with every organ and structure complete. Some of the most complex structures are present in the Cambrian [Explosion] organisms, such as the eye of the squid, which is very similar to the human eye."*
> Luther D. Sunderland, Darwin's Enigma, Revised Edition, p. 52

For all practical purposes, the eye of the squid that Mr. Sunderland was talking about is equally complex as the modern human eye. Yet the squid has no ancestors in the fossil record.

In short, there is no evidence that the human eye evolved from species to species.

Claim #4: Natural Selection Solves the Improbability Issues

This is one of the arguments designed to justify the theory of evolution in spite of its statistical problems.

The problem with this theory is that natural selection does not affect the mutations of genes.

Natural selection occurs *AFTER* the new species exists. In other words, natural selection occurs *AFTER* totally random mutations of DNA have created a new species (assuming the theory of evolution is true). The only thing natural selection can do is decide which *of the already existing species* will survive. Natural selection has absolutely nothing to do with the creation of the species or the design of its DNA.

Natural selection, which is non-differentiating as mentioned before, does not come into play until all of the mutations are finished and the species is ready to start surviving. Why do you think it is also called "survival of the fittest?" The term "fittest" means the species is already alive.

Claim #5: Evolution Occurred at the Gene Level

This is yet another theory designed to "solve" the statistical problems of the theory of evolution.

Some evolutionists have claimed that evolution occurred at the level of the gene.

A prior chapter talked about protein synthesis.

Let us remember that a "gene" is nothing but a "cookie cutter," meaning a template. A gene is a sequence of nucleotides on the vast sequence of nucleotides of an entire DNA strand. It is nothing but a sequence of nucleotides (i.e. a pattern) used by the cell to create one or more proteins.

But that is just the beginning. More nucleotides are needed to convert the gene from a cookie-cutter to being placed in the cell as a complex, folded protein, than the actual number of nucleotides of the gene itself.

Thus, when changing a gene, the entire gene complex must be changed.

In order for evolution to occur at the level of the gene, several things must happen.

First, the gene (which is nothing but a "template" or "cookie-cutter" for a protein, meaning a sequence of nucleotides) must be alive and trace the progress of its "offspring" from being a gene, to an mRNA strand, then to being a polypeptide (created by ribose), then to a folded amino acid string (i.e. a folded polypeptide), and then the placement of the protein into the cell.

Second, the gene must also observe the survival skills of the entire animal (not just the cell in which the gene and DNA live). The cookie-cutter must evaluate the relative survival skill of the animal in which it lives, compared to other animals.

Third, the gene must decide that it needs to be modified based on what it observes of the animal (not just the cell) in which it lives and the surrounding species.

Fourth, it must theoretically redesign itself and its gene complex in order to provide the entire animal better survival skills.

Fifth, it must have control over some mechanism which can *physically reorder* the nucleotide sequences which make up itself (the gene) and the entire gene complex. This reordering of nucleotides is based on the theoretical evaluation of the weaknesses in the current order of nucleotides.

(Note: As noted above, a microbe does not have the "intelligence" to know where to change its DNA or how to change its DNA. But some scientists claim that a strand of nucleotides is smarter than a microbe and can improve the DNA of a complex animal; which is a far more complex task than just developing an immunity to a drug.)

If the needed changes to the species involved multiple genes (complex changes to a species involve changes to many genes). These genes must also be notified that they need to be changed, along with instructions on what changes need to be made.

All of this must be orchestrated by a cookie-cutter, a segment of a static DNA string.

Oh, by the way, I almost forgot to mention, this cookie-cutter (i.e. gene) must also figure out how to change the morphing of the embryo algorithm if any new types of cells or new morphology changes are involved.

Now, is it possible that a cookie-cutter can monitor its offspring, all the way to the macro animal level and environment, and redesign itself and the entire gene complex and redesign and change the morphing of the embryo algorithm, and many other things?

The absurdity of thinking that evolution occurred at the gene level or the nucleotide level is totally ludicrous. Cookie-cutters do not have intelligence.

Introduction to the Mathematics of Evolution

Chapter 22

Debate Tactics

Assumptions Used as Proof of Evolution

What is the "evidence" for the theory of evolution, knowing that from a scientific standpoint the theory of evolution is total nonsense?

In other words, they have zero evidence that life can be created from non-life. They have zero evidence that any new information or intelligence has been created by random mutations of nucleotides. And so on.

So what do they use for their "evidence?"

Their primary evidence is to *assume* the theory of evolution is true and to claim that each new discovery in biology or genetic research is the result of evolution.

The scenario goes something like this:
1) Scientists assume the theory of evolution is true,
2) Then they look at the "data" and spin whatever kind of story they can come up with to "prove" the theory of evolution is true,
3) They then claim they have "evidence" for the theory of evolution.

Nowhere is this tactic more obvious than in the fossil record. Let us consider an example of how this works.

The Natural History Museum

Suppose there is a huge building, a natural history museum, which houses all of the fossils found in the world which became extinct during a specific range of time. Suppose this collection includes the bones of many tens of thousands of extinct species which have lived on this earth.

An *evolutionist*, who is also a paleontologist, would look at these bones very differently than someone familiar with DNA who is a *creationist*.

A paleontologist, who is also an evolutionist, would look for ways to explain why the data supports evolution. They would look at the bones with a strong assumption that the theory of evolution is true. They would build their phylogenetic tree based on morphology. They would date some of the fossils based on where they fit on the phylogenetic tree.

If a person assumes evolution is true, the person will look at the huge numbers of similar physical features of the different species, and the ever present phylogenetic trees, and say: "evolution is true." If a person assumes evolution is true, then the bones are “proof” to him or her that evolution is true.

While this is perfectly logical for someone who assumes the theory of evolution is true and is looking for "evidence"; let us suppose a second person, in this same building, who is a creationist, ponders what the DNA of each of these species might have looked like. This person would contemplate the huge volume of favorable random mutations which would have been needed to generate all of the features of these species.

The mutations would have been massive in number and would have had to have occurred in a relatively short amount of time.

Multi-generation evolution would be considered. Male and female issues would also be considered. Changes to the circulatory system, changes to the nervous system, etc. would also be pondered. New physical features would be considered. The reprogramming of the brain would be pondered.

The vast array of complex physical features combined with the necessary vast array of unique gene complexes, new types of cells, and incredibly complex morphing of the embryo algorithm changes would be visualized.

This second person would conclude the vast variety of bones, and the requisite totally random mutations to DNA necessary to create all of this variety in a relatively short amount of time, was proof that the theory of evolution was ***false***.

Also, the theory of evolution would be rejected because of the lack of transitional species. Too many of the species would not have any transitional species preceding them; nor would some of them seem to have any ancestors at all.

Any huge jumps (i.e. jumps without transitional species) would need huge and sophisticated changes to their DNA which would be impossible due to the complexity of the morphing of the embryo algorithms and vast number of new gene complexes, new types of cells, male and female issues, multi-generation issues, etc.

Huge changes to DNA, from one species to another, where there is no clear transitional species, are not statistically consistent with the theory of evolution for many reasons.

The answer of evolutionists, of course, would be the same are Darwin's - the fossil record is not complete. But the creationist could answer back by talking about living species, such as the giraffe, and many other living species, and ask: where are their ancestor species; which are or were only "slightly different" than they are?

Second, the creationist would reject the theory of evolution, as applied to all of these bones, because the many necessary favorable random permutations of nucleotides could not mathematically have happened in only a few hundred million years among such a relatively small population base. Population size is limited to the surface area of this planet and is usually limited to a small geographic area.

No one faults paleontologists for searching for bones and for reporting on their findings. That is not the problem. True scientific data is never the problem and never will be the problem. The problem is in the interpretation of the vast data.

With the bones of many, many millions of different examples at their disposal; scientists can spin any number of different "theories" about evolution. It is like owning a gigantic bucket of every different type of Lego® building block ever made. You can make anything you want to make with them.

If you make the right assumptions, and avoid the mathematical and DNA issues, you can avoid the most troublesome issues which face the theory of evolution.

Thus, the person who assumes evolution is true; will conclude that the probability of evolution is 100% because of the way they interpret the data and because they only consider morphology and its child the phylogenetic tree.

The person who assumes creation science is true would conclude the theory of evolution is scientific nonsense because of the complexity of the necessary changes to DNA, especially as applied to the male and female issue, just to name one issue.

Science is supposed to be about data - analyzed with an open mind and taking all issues into account. Scientific conclusions should not be based on huge, totally unproven assumptions.

To make things worse, modern textbooks on biology are so anxious to be published and sold that they are consistently full of clever definitions, doctored photographs, bad logic, theories stated as facts, huge unproven assumptions, bogus data and in many cases the perpetuation of well-known fraudulent "discoveries."

The book: Icons of Evolution, by Jonathan Wells, goes into all of these things in great detail and is highly recommended to the reader. But even his book is only the tip of the iceberg.

An even more detailed book is Evolution Exposed - Your Evolution Answer Book for the Classroom, by Roger Patterson, in which the author actually went through several major biology textbooks in great detail. *It took an entire book to document all of the errors and unjustified bias favorable to the theory of evolution in these highly popular books*.

It must never be forgotten by the reader that every discovery in biology or genetics is automatically claimed to be the result of evolution. Yet there is absolutely zero scientific evidence that random mutations of DNA caused any of their claims!!

Thus, one side would claim a 100% probability for the theory of evolution and the other side would claim a 0% probability for the theory of evolution.

The Debate Tactics of Modern Science

Assuming the theory of evolution is true is a tactic that can only go so far. If someone assumes the theory of evolution is true and tries to convince someone familiar with the

permutation of nucleotides mathematical issues, and other major problems such as genetic entropy, their assumption won't work.

So another tactic used by science is to limit the discussion of evolution to areas in which they can get away with assuming the theory of evolution is true. In other words, they carefully avoid areas of discussion where they cannot control the discussion using unproven assumptions.

In other words, they only use highly subjective subject matter to spin their tales. Highly subjective issues, such as fossils, can be twisted and turned without the reader ever realizing what is happening.

Back in the days of Darwin, the only tool Darwin had to discuss the theory of evolution was morphology, meaning the study of the shapes of animals; and more specifically the shapes of bones. Darwin had no clue DNA existed. Scientists in the nineteenth century thought cells were globs of goo and were very simple.

The nineteenth-century technology of morphology, combined with the theory of evolution, led Darwin to believe in gradualism and to believe that many more transitional species would be found by paleontologists.

Today, scientists have the late twentieth century and early twenty-first century technology of DNA analysis.

So why do scientists today refuse to talk about the twenty-first century technology issues such as permutations of nucleotides, the morphing of the embryo algorithms (which will probably be a twenty-second century technology), male and female issues related to DNA, multi-generational issues related to DNA, genetic entropy issues, genetic chaos issues, why modern human DNA is so perfect, the complexity of cells, etc. etc.

Why are scientists still using nineteenth-century morphology, and its child the phylogenetic tree, which is designed based on the assumption the theory of evolution is true, as their main "evidence" for the theory of evolution?

The reason is that morphology, which is really a distraction and diversion from true scientific evidence, and *is a technology totally subjective and totally subject to wishful thinking and vivid imaginations*, is still their only "evidence" for evolution.

They want to talk about morphology, yet they don't want to talk about intelligent design, which is another observational technology.

While morphology is stuck in the mud of nineteenth century observation technology; intelligent design is based on a modern day understanding of the complexity of cells and the complexity of DNA.

In other words, even though morphology and intelligent design are both observational technologies, morphology uses very old bones and very old technology; whereas intelligent design uses state-of-the-art cellular analysis, DNA analysis, the study of how proteins fit together and bind to each other, etc.

Yet, morphology, even though it is *totally unscientific* and is totally subjective, is considered "scientific." Intelligent design, which is based on state-of-the-art technologies, is considered "unscientific."

In reality, the theory of evolution has failed to exist on the basis of true science for over 50 years. In 1953, the theory of evolution should have been instantly rejected based on the complexity and size of DNA.

Yet, somehow, DNA, and all of the discoveries since 1953; have been assigned to the theory of evolution.

The vast majority of people who believe in the theory of evolution do so because they have been deceived by monopolistic information and are therefore vulnerable to the arguments of subjective data. All the average person has ever heard in their life is that the theory of evolution is a proven fact of science. They have heard it so often and for so long they have concluded the theory of evolution is true.

We can summarize the tactics of science in the following way:

First, they totally control what everyone hears about evolution;

Second, they give credit to all new discoveries in science to the theory of evolution, thus the theory of evolution is itself evolving;

Third, their scientific "evidence" for the theory of evolution is to assume the theory of evolution is true;

Fourth, their best public "evidence" is nineteenth century, totally subjective, morphology (who is to say that God did not create all of those species?);

Fifth, they intentionally misrepresent the evidence for creation science when they can't suppress it;

Sixth, they carefully suppress any area of discussion where a true creation scientist might have their evidences discussed.

But why? Let us remember the key quote from Phillip E. Johnson:

> *"Science is committed to philosophical naturalism and therefore science must assume that no Creator, and no purposeful intelligence, is behind our existence ... All that science can address is the question of: 'granted that we are here as a result of purposeless material mechanisms, what's the most plausible purposeless material mechanism that we can imagine?'"*
> *Phillip E. Johnson, author, attorney; quoted on UCTV*

It is all about their desire to be considered the most intelligent beings in the Universe (i.e. philosophical naturalism).

Using Microevolution As Evidence

Most of the "evidence" for evolution (and some of their "evidence" is nothing but the use tricky definitions) comes from microevolution or point mutations. For example, Darwin never observed evolution, he only observed microevolution. As another example, the peppered moth, which is in almost every biology book, is an example of microevolution. It is no different than two people having different colored hair.

Neither microevolution, nor point mutations (e.g. a bacteria developing a resistance to a drug) have anything to do with creating new genetic information, including new genes. Creating new genetic information, including new gene complexes, is a requirement for true evolution (this is true macroevolution) and has never been observed in the lab or in nature - only by assumption (i.e. if you assume it is true, you cannot claim you have proven it is true) or wishful thinking (which is total nonsense). Logic should travel from truth down to assumptions, not from assumptions up to truth.

Non-Differentiating Issues

The logic of the scientific establishment is that everything is a disproof of intelligent design (i.e. God). Two examples are natural selection (i.e. survival of the fittest), and the concept of using DNA to prove common descent. Both of these examples are fatally flawed because they are both non-differentiating, meaning they apply equally well to the theory of evolution and to creation science, but for different reasons. Microevolution is another non-differentiating event which is claimed to be a "proof" of evolution. Microevolution is sometimes used, along with tricky and defective definitions, to "claim" macroevolution has been observed.

Summary

The total control of the media allows the scientific establishment the luxury of developing and incorporating a wide array of deceptive tactics to pretend the theory of evolution has some scientific validity to it.

One tactic is to ignore the evidence, such as the permutation of nucleotides issues, the male and female issues, the morphing of the embryo issues, and so on.

By using a wide array of tactics to hide the truth, cover up the embarrassing issues, bury the mathematical issues, mock the creation scientists, use "straw man" tactics at every opportunity, etc., they have totally convinced many people that a totally bogus theory is a scientific fact.

Never forget that the main purpose of brainwashing is to create a society which has a "uniform pattern of public utterance." Once this is achieved, "evidence" becomes irrelevant, especially if you can bury it.

Introduction to the Mathematics of Evolution

Chapter 23

Seven Scientific Reasons the Theory of Evolution Cannot Be True

"A new scientific truth does not triumph by convincing its opponents and making them see the light, but rather because its opponents eventually die and a new generation grows up that is familiar with it."
Max Planck, Nobel Prize, 1918 in Physics

Introduction

This chapter is an important summary of several of the prior chapters because it allows the reader to see the "big picture" of the problems with the theory of evolution.

The first seven sections are concepts which prove the theory of evolution cannot be true on this planet or on any other planet. The reader might note that all seven of these items have to do with DNA.

Prior to the discovery of DNA the only thing evolutionists and creation scientists had to debate about were the morphology of fossils, bones and living species. Because the fossil record was overwhelmingly against the theory of evolution; such as the fact that the predicted gradualism was never observed and intermediate species were rarely found; the theory of evolution was dying a slow death.

When DNA was discovered in 1953, the theory of evolution should have died on the spot because now creation scientists had a new tool to disprove the theory of evolution. That tool was probability. But the theory of evolution did not die even after the Wistar Symposium in 1966.

What has happened is that the scientific establishment's total and absolute control of the media has completely buried the mathematical and genetic problems with the theory of evolution.

The blacklisting of the problems with the theory of evolution is so complete that many people today do not even know that there are scores of anti-evolution books which are very critical of the theory of evolution.

But in the process of burying the creation scientists, *the scientific establishment had a lot of outside help!!* Various "charities," ultra wealthy families, and other organizations (such as the American Civil Liberties Union), spent many, many, many millions of dollars exercising their massive influence over the media, the universities (via grant money) and

the courts to the extent that these outside groups came to the rescue of the scientific establishment.

In fact, for reasons left to conspiracy historians, the theory of evolution started to flourish and today it is a very, very dominant scientific theory even though the scientific establishment still cannot address even the simplest criticisms of the theory of evolution.

Seven reasons why it is impossible that the theory of evolution could ever have happened anywhere in the Universe will now be discussed in summary form. After these seven sections, some additional criticisms will be discussed.

Reason #1) Genetic Entropy

"Genetic entropy" is a scientific fact which is admitted by all prominent geneticists. Genetic entropy is the natural deterioration of DNA via mutations which are caused by various types of errors; such as errors in copying a chromosome. Dr. Sanford, for example, stated that DNA is deteriorating at an alarming rate.

If evolution were true, our human DNA, and the DNA of all other living species on this earth, could trace their genealogy back to the "first living cell" and thus all DNA on earth would contain *660 million years of accumulated genetic defects because there would have been 660 million years of accumulating and continuous genetic entropy.*

Why would we see these mutations on our DNA? The reason is that there is no mechanism on any DNA to fix most type of genetic errors.

The genetic defects would have accumulated from generation to generation and from species to species. It is ludicrous that any animal could survive 1 million years of continuous genetic entropy, but to survive for 660 million years of continuous genetic entropy is simply far beyond ludicrous.

Human DNA is too perfect to have been exposed to 660 million years of genetic entropy. If George and Mary (evolution's equivalent to Adam and Eve) existed 100,000 years ago, they would have had 660 million years of accumulated genetic defects (e.g. genetic entropy).

Furthermore, if George and Mary had lived 100,000 years ago, our human DNA would have an additional 100,000 years of genetic entropy, on top of the 660 million years of George and Mary's genetic entropy.

If the theory of evolution were true, and all of our ancestors and ancestor species only had 1 mutation every year on average, we humans would have 660,100,000 *random* defective mutations on our DNA due to genetic entropy. No species could survive with this massive amount of defects in their DNA.

If evolution were true, 22% of our DNA would be defective. This means 22% of our gene complexes, 22% of our morphing of the embryo algorithms, etc. would be defective. But there is very little tolerance in many aspects of our DNA, so humans could not exist even if our DNA was 0.1% randomly defective.

But in reality our ancestors would have had far more than 1 mutation per year on average and the 22% would be far, far above 100%.

Furthermore, if a significant set of additional genetic defects would have occurred in a descendant of George and Mary, say 90,000 years ago, this defect would be seen in a very, very high percentage of humans today. But no such broad genetic defect has been observed.

Science claims that DNA has improved by random mutations of nucleotides. This theory is in direct opposition to discoveries in genetics. DNA deteriorates, not progresses, over time. This is a scientific fact. Given the mathematical problems of the theory of evolution, detrimental mutations caused by genetic entropy would have occurred ***millions of times faster*** than favorable mutations. It would be like trying to swim upstream of a 5,000 foot tall waterfall.

The vast majority of mutations are neutral or detrimental in all species. Yet the entire theory of neo-Darwinism is that DNA improves over time; that new genetic information is constantly being formed; and that more complex DNA is constantly being developed by random mutations of DNA. There is no scientific evidence for any of these claims.

But the main point of this section is that because genetic entropy is a scientific fact, and if evolution were true, we humans could not exist because our DNA would have the accumulated mutations of 660 million years of genetic entropy.

But the fact is that no complex species can exist for more than a million years due to genetic entropy.

Bottom Line: If evolution were true; because of genetic entropy; humans could not exist. Furthermore, our DNA is far too perfect to contain 660 million years of accumulated genetic defects.

See Chapter 19 for more information on genetic entropy.

Reason #2) Genetic Chaos

"Genetic chaos" is not a scientific fact because evolution is not a scientific fact. But if evolution were true, genetic chaos would be far more significant than genetic entropy!!

There is an assumption in the theory of evolution that when an extra copy of a gene or chromosome is accidentally made, that the mutations needed to complete the transition to a new species all occur in exactly the right locations on the DNA. This is nonsense.

"Genetic chaos" is the concept that all mutations on DNA can occur *anywhere on the DNA*, not just in the locations evolutionists want the mutations to occur.

For example, suppose you have a 2,000,000,000 nucleotide pair long DNA. Suppose you make a copy of a gene complex which is 5,000 contiguous nucleotides long and

place it somewhere on the DNA (or suppose you want to change an existing gene complex, the math is about the same). The DNA is now 2,000,005,000 nucleotides long.

Now suppose you have 400,001 random point mutations. How many of these random point mutations will occur inside the area of the copy of the gene, given that all mutations are randomly distributed over the ***entire DNA***, which consists of 2,000,005,000 nucleotides?

The percent of the DNA where the desired mutations are located is:
5,000 divided by 2,000,005,000, which equals 0.00025%.

Thus the target area for the mutations is 0.00025% of the entire DNA.

400,000 mutations times .00025% is 1, meaning 1 mutation will be in the target area.

In other words, of the 400,001 mutations, only a ***single mutation*** (i.e. 1 out of 400,001 mutations) will be inside the desired target area of the gene complex because every nucleotide on a DNA strand has an equal probability of mutating.

Thus, to get a single mutation inside the area of the copy gene where you desire mutations, you will have 400,000 random mutations of DNA ***outside*** of the area where you want the mutations to be; meaning they will be ***in areas where you don't want any mutations***.

No species on earth could tolerate 400,000 random mutations to their DNA in locations where the mutations are not wanted!!

Thus, in the attempt to get a ***single nucleotide*** inside the desired area for the mutations (in order to create new genetic information) the mutations in wrong places would literally ***destroy*** the "new species" due to genetic damage.

But a typical new species would need thousands of favorable mutations to create one new gene complex (i.e. modify an existing gene complex or modify a copy of a gene complex) and would usually need 10 to 20 or more new gene complexes to create a new species!!

Furthermore, not only would existing nucleotides need to be modified (after genes are copied), but ***new*** nucleotides would need to be ***added*** to the DNA to increase the sophisticated genetic information and intelligence on the DNA.

If you multiply 10 new gene complexes, by 3,000 desired mutations per gene complex, you have 30,000 desired mutations. In addition, you would likely need 30,000 ***additional*** nucleotides to the DNA for more sophisticated information and intelligence on the DNA.

But in the process of getting 30,000 mutations in the desired areas to create a new species, you will create ***12,000,000,000 mutations in undesirable locations (i.e. 30,000 times 400,000)***!!! This would wipe out the entire DNA several times over!!!

If you also add 30,000 ***new*** nucleotides to get even more new genetic information, you will have 12,000,000,000 ***additional*** nucleotides (i.e. which would be a second form of

mutations) in undesirable locations (i.e. they are added outside of the desired target area). The DNA of humans out be 14 billion nucleotides long!!

In summary, to create a single new species from an existing species, *would add 12 billion undesirable additional nucleotides to the DNA, plus there would be 12 billion undesirable mutations scattered among the 14 billion nucleotides.*

Virtually 100% of the original DNA would have been randomly mutated.

By the way, there is no guarantee that the 30,000 mutations that are inside the desired area; and the 30,000 additional nucleotides in the desired area; are the correct nucleotides in the correct locations!!

And all of this is for a single new ancestor species. This book estimates humans have 3,000 ancestor species. If evolution were true, our human DNA would be more than a *trillion* nucleotides long, and far more than 99.999% of our DNA would be totally random nucleotides.

Welcome to genetic chaos.

Literally, the undesirable mutations which miss the "target area" (i.e. miss the area of the copied genes) would totally destroy (i.e. totally randomize) *the entire DNA* of the new species *many times* in the attempt to put new genetic material on the DNA for the new species.

The new species would be peppered or littered with unexpected mutations which would destroy the new species long, long before any benefits from the mutations could be obtained.

Bottom Line: No new species could ever exist via evolution because in the attempt to create new genetic information, the species would die long, long before the new genetic information could be created. Nor is there any evidence on human DNA of massive numbers of undesirable mutations or undesirable added nucleotides.

See Chapter 20 for more information on genetic chaos.

Reason #3) Genetic Debris

"Genetic debris" is not a scientific fact because evolution is not a scientific fact. But if evolution were true, genetic debris would manifest itself on our human DNA; meaning our human DNA would be vastly different than it is today if evolution were true!!

Genetic debris is similar to genetic entropy, but it works at a different level.

The theory of evolution postulates that new genetic material can be caused by "bulk mutations," such as creating an extra copy of a chromosome or an extra copy of a section of DNA, and after the bulk mutation, point mutations (which would include new individual nucleotides) fine tune these bulk mutations into new gene complexes, new morphing of the embryo algorithms, etc.

Genetic debris has to do with the ***failed*** attempts by evolution to create new species. The attempt does create the bulk mutations, but the point mutations fail to create new genetic information. ***Thus, the mutated bulk mutations stay on the DNA without adding any new genetic information.***

Let us start by looking at the big picture of evolution.

After the "first living cell," evolution had to create much more genetic material than it had to create for the "first living cell." Not only was there more genetic material, but it had to be massively more complex.

For example, the average gene on the "first living cell" would have only created one protein. Modern day human genes can create an average of 10 proteins, and each one of these proteins is much longer and massively more complex than any gene on the "first living cell" would have been.

Not only that, but human genes have "introns" in between the "exons" and the introns are not part of the final mRNA. In fact, typically, not even all of the exons are part of the final mRNA. This means that the instructions for making proteins are no longer in contiguous sections of the DNA, which adds a lot of complexity to DNA.

When complex life started to exist (assuming the theory of evolution); gene complexes, the morphing of the embryo algorithms, etc. became so complex that the percentage of viable random permutations (given the growing length and complexity of DNA for the increasingly complex species) became increasingly and astonishingly small.

As things got more complex, and the percentage of viable permutations plummeted, the seemingly infinite number of failed attempts to create a new gene complex (either from an existing gene complex or a copy of an existing gene complex) or make a change in the morphing of the embryo algorithm, etc. would massively outnumber the successful attempts.

There are two problems for evolution at this point.

If you start to modify an existing gene complex, but the attempt fails to create a functional new gene complex, you have very likely destroyed an existing and important gene complex and it will never again function properly in the descendants of the animal!! This also means the offspring of this animal may not survive.

On the other hand, if you start to modify a copy of an existing gene complex, but the point mutations fail to create a new gene complex, then you have a large amount of worthless genetic material on the DNA.

Neither of these options are good. But if evolution were true, both of these options would have happened many millions of times during the creation of human DNA due to the statistical problems of the theory of evolution. Vastly, vastly more failures would occur than successes.

These failed attempts would extend the length of the DNA, by worthless nucleotides, plus would have extended the length of time needed to create humans, even under the most ideal conditions, to a virtually infinite amount of time.

These failures would have massively extended the length of DNA because there is no mechanism to remove unwanted debris.

A person might think that if there was a failed attempt in creating a new gene complex; that the new species simply would not survive, thus the genetic debris issue would not be a factor.

It is not that simple because most new species would have needed 10 or 20 or even more new gene complexes. The probability of creating 20 new gene complexes, ***each on the first attempt***, on a new DNA strand (i.e. in the same attempt to create a new species) is insanely absurd and would not happen a single time in a quintillion quintillion quintillion years!!

Thus, it would be impossible that the creation of a new species would ***not*** include massive amounts of "baggage or debris" from failed attempts to create viable gene complexes from copies of existing gene complexes.

In fact, starting with the first complex species (i.e. a species which had a circulating fluid), every new species would have had residuals of bulk mutations which did not end up being viable genetic material.

There is no mechanism on DNA to get rid of these mutations; partly because these are new species, by definition, and the final design of the DNA is unknown until the species is complete and functioning.

Since humans have roughly 3,000 ancestor species (i.e. different species on our evolutionary or phylogenetic tree), on 3,000 different occasions there would have been a significant amount of new genetic debris added to our DNA.

Scientists do not see any residual bulk mutations, which have no function, on human DNA. While there are sections of DNA which are not understood yet, there is no section of DNA which has been shown to be unnecessary.

But genetic debris would have created many trillions of unused nucleotides during the creation of the 3,000 ancestor species of humans due to the impossible odds of creating a new gene complex by random mutations, on the first attempt, and the fact that many new ancestor species would have needed 10 or 20 new gene complexes.

Bottom Line: If evolution were true, massive, massive numbers of non-functional nucleotides would be left on our DNA due to the concept of "genetic debris." Such nucleotides are not observed.

See Chapter 19 for more information on genetic debris.

Reason #4) Consecutive Impossible Probabilities

We have assumed that the number of ancestor species, between the first complex species (which was our ancestor species) and human beings, was 3,000.

In a prior chapter it was calculated that the probability of creating a new species from an existing species is 10^{-100}. Thus, a person might conclude that the probability of human beings being created, after the first complex animal, was $10^{-300,000}$.

Evolutionists would look at this probability and say "this is no big deal." This is how they "brush off" their obscene statistical problems.

Well, they can't brush off this probability for two reasons. First, this probability is equivalent to picking the single, correct atom from among $10^{299,920}$ Universes, because it is estimated that there are 10^{80} atoms in our Universe. Try to pick the single correct atom (in a game of "hide and seek") from among $10^{299,920}$ Universes in a billion years!!

But there is a second reason which makes the theory of evolution even more absurd. That concept is "consecutive or sequential lotteries."

Creating each new species from an existing species is like winning a lottery with a probability of 10^{-100}.

The concept of "consecutive or sequential lotteries" is that you have to win one lottery before you can even "buy tickets" in the next lottery.

If there are 3,000 species, between the first complex animal and human DNA, then each of these ancestor species had to be created consecutively, meaning one after the other, because they are all our ancestor species, assuming the theory of evolution.

Just like our grandfather (our father's father) and our father cannot both be born in the same year, our 3,000th ancestor species (starting with our oldest ancestor species with complex DNA) must have existed prior to our 2,999th ancestor species. And our 2,999th ancestor species had to exist prior to our 2,998th ancestor species. And so on.

Thus, human evolution, from the DNA of our oldest complex ancestor species to the DNA of human beings, would be like winning "3,000 consecutive or sequential (i.e. one after the other) lotteries," where the probability of winning each lottery was 10^{-100}!!!

This creates an issue of time for the theory of evolution.

For example, suppose you could buy 1,000 tickets in a lottery every second, 24 hours a day, in a lottery with a probability of winning of 10^{-100}. How long would it take you to buy half of the lottery tickets to give you a 50% chance of winning this lottery?

You could buy less than a trillion lottery tickets a year, which is 10^{9}, but we will assume you could buy a trillion lottery tickets a year (this book is always generous to the theory of evolution).

It would take 5 times 10^{99} (this is the number of tickets you must buy) divided by 10^{9} (which is the number of tickets you could buy every year) to have a 50% chance of winning this lottery. This would be more than 10^{90} years!!

Thus, it would take more than:
1,000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000,
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000,000,000,000,000,000,000,000,000,000,
000,000,000,000,000,000,000,000,000,000 years to have a 50-50 chance of winning *one lottery*!!

But you must win 3,000 of these lotteries, one after the other!! In other words, you cannot buy a "ticket" in the second lottery until after you win the first lottery. You cannot buy a "ticket" in the third lottery until after you have won the first lottery, then the second lottery.

To apply this to evolution, suppose you take an existing animal, which is an ancestor species of humans, and you make 1,000 attempts to create the next ancestor species of humans, every second, 24 hours a day, for 10 billion years. It is almost impossible you could create the next ancestor species of humans in double the estimated age of our earth.

But that is not the problem.

Each of our 3,000 ancestor species must be created consecutively or sequentially, meaning one after the other.

For example, we could not begin to create our 2,999th ancestor species until after our 3,000th ancestor species already existed (i.e. we had already won that lottery).

Likewise, we could not begin to create our 2,998th ancestor species until after our 2,999th ancestor species already existed (i.e. we had already won two consecutive lotteries).

And so on.

Thus, the theory of evolution consists of 3,000 true "consecutive or sequential lotteries," each with a probability of 10^{-100}.

While evolutionists might brush off a probability of $10^{-300,000}$, they cannot just brush off a probability of winning 3,000 consecutive or sequential lotteries, each with a probability of 10^{-100}. They have to win 3,000 impossible lotteries, one after the other (i.e. one lottery cannot start until after the prior lottery is won), in a time period of about a billion years.

There is no word in the English language to describe just how ludicrous the theory of evolution is!!

Bottom Line: Evolution could not have occurred in a billion years or even a trillion years or even a quintillion quintillion years. The reason is that human DNA would have required "winning" 3,000 consecutive or sequential evolution lotteries, each with an impossible probability of 10^{-100}.

See chapter 15 for more information

Reason #5) The Multi-Generation Issues

Many of the claimed jumps in evolution had to have occurred over the time frame of many generations.

For example, the claimed evolutionary change of animals which walked on four legs evolving into animals which walked on two legs. This complex change had to occur over the period of many years and many generations.

For example, let us assume that a million mutations to the DNA of the four-legged species had to be made to generate a species which walked on two legs (this includes the creation of the semi-circular canal, redesigning the bones, redesigning the circulatory system, etc.).

To simplify things let us assume that it took 100 generations to make the changes, and that each generation had an average of 10,000 new mutations (to total 1 million mutations spread over 100 generations).

There are many problems with multi-generation evolution. The first problem is population size.

Because of probability issues, those who support evolution contend that there were large populations on which evolution occurred.

The large population concept works just fine for the first generation of a multi-generation evolutionary process, but after that the population size drops to two and they have to be brother and sister and they must mate and must have at least one male and one female offspring.

To understand this, suppose there is a species with 2,000,000 animals which walked on four legs. From this population, evolution wants to create a new physical feature, such as walking on two legs so the animals can reach higher in the trees. This will take 100 generations to complete.

From this population size, it is unlikely, but possible, to find a male and female which have the same 10,000 partial mutations (remember it takes many generations of mutations to make a large physical change), meaning the first 1% of the total mutations needed for evolution.

However, for the second round of mutations, the population size can only be two, and they must be brother and sister (i.e. male and female of the same parents), meaning they must be animals which were ***born*** with the first 1% of the mutations.

Why do they have to be brother and sister? The reason is that their parents had the first 1% of the mutations and their offspring (i.e. which are all brothers and sisters) are the only animals on the planet earth which were born with the first 1% of the mutations. To get to 2%, you have to start with 1% of the mutations in both the male and female. If you skip that first 1%, you have to start all over again.

While all of the offspring of the original parents were born with 1% of the mutations, it is highly unlikely two of them would coincidentally have the same additional 1% of new mutations (to equal 2% of the desired mutations), but to think that three of them had the same mutations is absurd. So we will assume exactly two of the offspring had the correct additional 1% of the next generation of mutations.

In other words, to get to 2% cumulative mutations, only those animals ***which were born with*** the 1% cumulative mutations could mate to extend the cumulative mutations to 2%. This means they must be brother and sister because they must be born with 1% of the mutations.

Then, by sheer coincidence, one male and one female offspring had to have an additional 1% of mutations, such that both of them had 2% of the mutations. Then they have to mate with each other, not some other animal.

For the third round of mutations, a male and female, which are born with the same two cumulative partial mutations (i.e. the 1% then 2% partial mutations) must have offspring. By coincidence, a male and female of this generation must have an additional 1% of new mutations for the next "step" of the multi-generation evolution. This makes 3%, but only two animals on earth have the 1%, then 2% then 3% mutations.

While we have been assuming brother and sister mated, technically it could have been first cousins or even second cousins. But even this is of no help to the statistical problems of evolution so this possibility is ignored (i.e. a population difference between 2 and 100 does not help evolution, evolution needs millions of attempts in each generation).

What this means is that in 99 consecutive generations the "population size" for evolution to work with consisted of the offspring of a single male and female. And in each case their offspring had to include both a male and female which by sheer accident had an additional 1% of new mutations in addition to the mutations they were born with. Plus they must mate with each other and have a male and female offspring.

When all is said and done, to get to 100% of the mutations, a long sequence of males must have the set of mutations: 1%, then 2% then 3%, etc. and these males must mate with a long sequence of females which also have the same set of mutations: 1%, then 2%, then 3%, etc.

To show how absurd this is, consider that a male with the set of: 1%, then 2%, then 3%, then 4%, then 5% mutations; mates with a female with the set of: 1%, then 2%, then 3%,

then 4%, then 6% mutations. Their descendants can never walk on two legs. It is also unlikely they could have any offspring because their DNA won't align.

In other words, multi-generation evolution breaks down completely, and becomes increasingly more absurd, after the first generation, because for generation after generation a male and female, which must be brother and sister (or close cousins), which have exactly the same sets of prior mutations, must have the same mutations in their generation and then they must mate and have at least one son and one daughter.

Bottom Line: Multi-generation evolution is pure and absolute nonsense, even if it takes only 3 or 4 generations. Yet many "jumps" in evolution would have required multi-generation evolution.

See Chapters 11 and 12 for more information.

Reason #6) The Male / Female Issues

The male and female issues have to do with the alignment of DNA in the germ cells of a male and female when they mate.

When there is a new species which has both a male and female, evolution must create a massive amount of new genetic material. Bulk mutations must be made, then point mutations must follow behind to fine tune the bulk mutations into new genetic material.

This is hard enough to do when the species does not have a male and female, but when there is a male and female, things get a lot more complex.

When mating, the male and female DNA must have the same gene complexes, *in the same locations on the DNA*, plus the same morphing of the embryo algorithms in the same locations, etc. etc.

With evolution there is a severe problem with this when there is a male and female. The same bulk mutations and point mutations must occur *totally coincidentally in the same locations on the DNA of both a male and female*, in the same generation, in the same geographical area, and they must mate.

In other words, the same totally random mutations must independently happen to both the DNA of the male and the DNA of the female in the same locations on their DNA.

While there is some minor tolerance in this issue, there is not even remotely enough tolerance to salvage the theory of evolution.

Here is a story to help explain this concept. Suppose a man and a woman, who do not know each other, were sent a "soft copy" (i.e. an electronic copy) of an encyclopedia. Each person was told to randomly make 10,000 changes to the data in the volumes of the encyclopedia. This included adding, deleting and changing individual letters. What are the odds 98% of their changes would be in the same volumes, same pages, same sentences and affect the same letters? The probability is purely insane.

Likewise, it is insane to think that new genetic material could form on a germ cell of a single male of an existing species; and to think that coincidentally the same impossible new genetic material could also coincidentally be created on the germ cell of a female, *in the same locations on the DNA*, and in the same generation and in the same geographical area, and these two animals would mate. It is far beyond insanity.

Now let us combine the male-female issues with multi-generation evolution. In the above example, not only did a male and female have to have the same 1% new mutations in each generation (with a population size of 2 in each of the last 99 generations); but when considering the alignment issues between a male and female, the 1% random mutations in each generation *had to align almost perfectly, between the male and female, for 100 consecutive generations!!*

This is far, far beyond nonsense.

Bottom Line: The theory of evolution became impossible when species included both a male and female. No more evolution could have occurred, especially when multi-generation evolution was involved.

See Chapters 11, 12, 15, et. al. for more information.

Reason #7) Patterns of Intelligence

Computers are very good at creating random numbers. I have personally run many billions of computer simulations to test various aspects of the theory of evolution.

But 10,000 of these simulations may be the most important. These are the simulations in which I made 10,000 attempts to create 40 million real human nucleotides.

It was not an attempt to duplicate these 40 million nucleotide pairs; that would not have been a fair test; rather it was an attempt to achieve the statistical "standard deviation" of these 40 million nucleotide pairs.

The concept of "standard deviation" is a concept which mathematically measures how much variety there is in a sample or population.

For example, if a histogram looks like a mountain range then it will have a high standard deviation.

On the other hand, if a different chart looks like a slightly squiggly, horizontal line, then it will have a very small standard deviation.

As was mathematically shown in Chapter 18; patterns of randomness always create a slightly squiggly line and thus create a very small standard deviation. In the case of the 10,000 computer simulations, their standard deviations ranged from a low of 169 to a high of 236.

On the other hand, the patterns of intelligence, taken from real human DNA, resulted in a standard deviation of 25,505. As can be easily calculated, all 10,000 of the patterns of

randomness standard deviations were less than 1% of the standard deviation of patterns of intelligence (i.e. real DNA).

The data in the charts was actually a histogram of patterns of 4 consecutive nucleotides, either real nucleotides or randomly generated nucleotides, depending on the chart.

Mathematically, it was shown that intelligence, in just a 40 million nucleotide range of DNA, was impossible to replicate using patterns of randomness.

This subject is far too complex to discuss in detail in a summary chapter. If interested, the reader is directed to chapter 18 for mathematical, graphic and statistical information.

Bottom Line: Patterns of randomness cannot create the highly sophisticated patterns of information and intelligence, such as exist on real DNA.

See chapter 18 for more information.

Other Things to Consider

The seven concepts above are clear and absolute proofs that the theory of evolution is scientific nonsense and could not have happened on this planet or on any other planet.

Here are a few more things to consider when looking at the theory of evolution. These represent significant reasons the theory of evolution cannot be true, but they are not as strong as the above items.

1) The First Living Cell

The "first living cell" was not descended from existing life, by definition. Thus, its RNA or DNA had to consist of totally and absolutely random permutations of nucleotides.

While "evolutionists" claim that existing DNA was easy to modify into new genetic material and new species, they have no basis for such a claim for the "first living cell."

The probability that a purely random permutation of nucleotides will create life, even if it is carefully put inside of a cell membrane, was calculated in an earlier chapter to be $10^{-1,500}$ (see chapter 15). This is an insane probability. It is like picking the correct, single atom from among $10^{1,480}$ Universes!!

And even this probability ignores a lot of things, such as having the correct combination of genes, the chemical binding problems of amino acids, various paradoxes, the formation of the cell membrane of the "first living cell," etc.

If any scientist claims they have created life from non-life, using a randomly generated permutation of nucleotides, you know they have committed pure fraud. If billions of attempts were made; every second for a hundred billion years; it is still a case of fraud.

But scientists still have not created life from non-life using the luxury of carefully designing DNA (i.e. stealing ideas from DNA created by God) for a "first living cell."

2) The Morphing of the Embryo Algorithms

Scientists know virtually nothing about the morphing of the embryo algorithms on human DNA. This is because the algorithms are so complex, humans cannot comprehend them.

The morphing of the embryo algorithms, which are really incomprehensively complex computer programs which are coded on DNA, are so accurate and so intolerant of mutations, that no complex species (i.e. a male and female), or its descendent species, could survive for 1 million years due to just genetic entropy of these algorithms, much less genetic chaos.

In other words, the morphing of the embryo algorithm is so sensitive to errors that it would be quickly destroyed by the smallest amount of mutations caused by genetic entropy and/or genetic chaos.

While some aspects of DNA may have a little tolerance for error, the morphing of the embryo is not one of them.

No one knows how many nucleotides are involved in the morphing of the embryo algorithms in an advanced species, but it surely numbers in the millions of nucleotides. One or two defects in this mechanism, via genetic entropy, genetic debris or genetic chaos (obviously in the germ cells) and there will not be any surviving offspring or new species.

The issue this algorithm creates for evolution is that it makes any type of mutation to be far more damaging, far more quickly, than a person might thing.

There is no mechanism to protect these nucleotides from mutation, since they are obviously scattered throughout the DNA.

3) Fossil Evidence

If evolution did occur by random mutations of DNA, the laws of large numbers of random mutations would mandate that an "increasing gradualism" would be observed in the fossil record (i.e. the *number of new species* would appear on the earth for the first time evenly spaced over time, but the number of new species would gradually increase over time due to a gradually increasing number of species).

This is because creating a new species is so difficult that you simply won't see clusters of new species (i.e. a "punctuated" number of new species appear on the earth at the same time).

When you deal with large numbers, "outliers" (i.e. rare exceptions) are so small in number that it is impossible evolution could have created any significant "punctuated pattern" of new species appearing on the earth for the first time.

However, there is no evidence in the fossil record for an "increasing gradualism."

In addition, the Cambrian Explosion is a total violation of the laws of the mathematics of random mutations of DNA (i.e. the laws of random numbers) because many, many new and odd species suddenly came on the scene.

Science uses paleontology (fossils don't have DNA), and huge imaginations, to "prove" evolution. This is in spite of the lack of transitional species and the lack of "increasing gradualism" in the fossil record.

Every fossil paleontologists find is "proof" of evolution according to science. No, they are not a proof of evolution; they are a proof of *their commitment* to the theory of evolution. There is no "proof" by the use of the nineteenth century technology of morphology. The evolution establishment refuses to talk about real issues, such as how mutations of nucleotides could have generated the morphology, and instead talks about totally subjective (i.e. visual) issues.

4) The Failure of Evidence

Scientists have *never observed* the random creation of new genetic information, including at least one new functional gene complex. All evidence of genetics indicates that *this will not happen a single time in the next billion years*. Yet, it had to happen *hundreds of millions* of times for all the species on the earth to be explained.

Every time a new species is discovered (alive or extinct); the theory of evolution becomes more ludicrous because it just means there is more unique genetic information to explain by random mutations (i.e. more impossible probabilities to explain).

Thus, not only have scientists totally failed to create life from non-life, but they have also never seen new genetic material form.

Nor are scientists, even with the DNA of millions of species to study and steal ideas from; ready to design the DNA of extinct dinosaurs which had both a male and female.

While scientists constantly claim they have witnessed "evolution," this is nonsense. The test for true evolution is the creation of new genetic material, *including at least one new gene complex*.

In *every case* where science claims they have witnessed evolution, one of three things has happened:
1) It was a case of microevolution,
2) It was a case of microevolution coupled with tricky definitions,
3) It was a case of point mutations which resulted in a *loss* of genetic information, but due to environmental reasons, there was a survival benefit.

They have never witnessed, and will never witness, a new gene complex being created by evolution. Never!!

So on what basis do they claim the theory of evolution is a proven fact of science? It is nothing but wishful thinking.

5) Genetic Leftovers

Virtually every gene, on every DNA, of every ancestor species of humans, from number 3,000 to 1,000, is no longer needed in humans because these old genes were needed for functions which do not apply to humans. Thus, there was no need for evolution to modify these genes.

So where are the sets of genes for at least 2,000 of our ancestor species than humans do not need?

Because there is no mechanism to remove the no longer needed gene complexes from our ancestor species (remember these gene complexes are not in any way needed by humans), they must still be *stuck on our DNA* because these species are our ancestors. But they cannot be found on our DNA!!

If evolution were true, human DNA would include many billions of previously used, *but no longer needed*, nucleotide pairs from a variety of our ancestor species.

For example, human DNA would include the entire DNA of the "first living cell" and the unique DNA of all of our ancestor species (which apply to functions which humans do not have), because there is no mechanism to identify and remove useless, failed and old DNA sequences.

Our DNA would include many billions of unused nucleotides if evolution were true. But in reality no more than 1.5 billion nucleotides are unaccounted for. But remember that scientists still haven't unraveled many mysteries of DNA, so most of these unaccounted for nucleotides will some day be known to be needed.

Again, human DNA is a proof that the theory of evolution never happened.

6) Hormones

Hormones are the very complex molecules which lure a male and female of a species to mate and thus allow that species to perpetuate.

Isn't it interesting that when a new species is made by evolution that *new hormones*, unique to that species, and different between a male and a female, just happen to be created?

Are hormones also accidents, like all other actions of evolution?

Actually, like many other things, it is ludicrous to think that these unique, highly complex and highly specialized molecules would be made every time there is a new species and that a different hormone is made for the males than for the females.

Furthermore, in many species, the hormones don't "kick-in" until the male and female are of age to mate. Another coincidence?

This is yet more evidence as to the absurdity of evolution.

7) The Perfection of Human DNA

Time after time the results of evolution would create massive defects in DNA of species after species.

But human DNA today is so perfect it is obvious (given evolution's claims of 660 million years of genetic entropy, genetic chaos, genetic debris, etc.) that evolution is scientific nonsense.

In fact, our human DNA is so perfect it is obvious that our earliest *homo sapiens sapiens* ancestors had *perfect* DNA.

Furthermore, due to the lack of global-wide genetic defects of the same type, it is clear that genetic defects on human DNA can only be traced back *three or four thousand* years, not *tens of thousands* of years or *hundreds of millions* of years!!

The Biblical account of Adam and Eve fits real scientific data *perfectly*. But real scientific data, meaning the perfection of our DNA, doesn't fit the theory of evolution at all!!

Comments

The evolution establishment claims: "The theory of evolution is a proven fact of science."

The theory of evolution is not a fact. In reality, it is not even a theory. The theory of evolution is scientific nonsense - or as one person put it, is nothing but a "fairy tale."

The two most basic pieces of the theory of evolution are the "first living cell" and the theory that randomly mutating very highly precise DNA strings will create new and improved genetic information and intelligence and it will create new and improved superior species.

However, there is *absolutely zero scientific evidence* for either of these things.

In fact, every piece of true scientific and mathematical evidence is overwhelmingly against the theory of evolution.

The theory of evolution does not exist in science; it only exists in the minds of those who *assume the theory of evolution is true and ignore all scientific evidence, such as genetic entropy, the theory behind genetic chaos, etc. etc.*

Indeed, almost all "evidence" for the theory of evolution (e.g. the phylogenic tree) is based on assuming the theory of evolution is true then using someone's assumptions and imaginations to generate "evidence" to "prove" the theory of evolution is true.

Without any scientific evidence, the scientific establishment continues to attribute all discoveries in paleontology, genetics and biology to the theory of evolution. There is absolutely zero scientific justification for this allocation of credit.

If the two most basic components of the theory of evolution are both nonsense, how can they say that evolution is a "proven fact of science?"

They can't, but yet they do because they want people to embrace philosophical naturalism. Their claim that evolution is "true" is nothing but a highly disguised statement: "if you ignore God, the theory of evolution is our 'best guess' as to how human DNA came to be because we want to believe in philosophical naturalism and we want to be considered the highest form of intelligence in the Universe." Creation scientist Phillip E. Johnson got it right.

As was said before, the battle over the theory of evolution is about the *vastly superior science of creation science* versus the *vastly superior control of the media, universities, journals and courts by the evolution establishment*.

It is a battle between truth and the control of information. As far as the general public is concerned, the control of information will always win.

What science should say is this: "Our absolute control of the media, courts, universities and science journals is a proven fact." Then they would be telling the truth.

Their control over these things is so complete that they have created a fantasyland of totally fictitious science which is now believed by virtually all people on the planet earth.

It is all a fabrication to justify their philosophies and their egos. They want to be considered the highest form of intelligence in the Universe. Evolution is all about ego, status and prestige; it is certainly not about science.

Introduction to the Mathematics of Evolution

Chapter 24

Final Comments

The Evolution Debate

When my children were growing up, I used to play mind-games with them. One person would try to mentally "kill" the other person. However, the person could not directly "kill" the other person in the imaginary story, they could only put the other person in a situation from which it was impossible to escape alive.

For example, the conversation might go like this:

Me:	The bad news is that you fell out of an airplane at 30,000 feet.
Son:	The good news is that I had a parachute.
Me:	The bad news is that your parachute didn't open.
Son:	The good news is that I was headed for a haystack.
Me:	The bad news is that there was a pitchfork in the haystack.
Son:	The good news is that I missed the pitchfork.
Me:	The bad news is that you missed the haystack.
Son:	The good news is that I landed on a pile of manure.
Me:	The bad news is that the manure was frozen solid.
Son:	The good news is that my suit of armor was very hot and melted the frozen manure instantly.

and so on.

This is a good demonstration of the evolution debate. It doesn't matter how ludicrous the scientific evidence for the theory of evolution is, or how bad the probability is, evolutionists will simply come up with some new spin to justify the theory of evolution.

I will give you a simple counterexample to the concept of "survival of the fittest." Have you ever seen a liter of kittens just about the time they are able to leave the mother and go out into the dangerous world by themselves? Who goes out first? The strongest and most ambitious kitten goes out first. Is this kitten ready to take on the world? Absolutely not.

In fact, the strongest and most ambitious kittens are frequently killed because they are so ambitious they are most likely to leave the protection of their mother long before they are strong enough to defend themselves.

Of course, the evolutionists would disagree because they will always disagree with anything a creation scientist says. And that is the point. It doesn't matter what you say.

The battle between the theory of evolution and creation science will not end until the end of the world. That is the fact. There are so many people who ***want*** the theory of evolution to be true, for a multitude of different reasons; they will never give up their cherished theory.

If an unbiased "jury" were to look at the true scientific evidence from both sides of the debate, the theory of evolution would be rejected as scientific nonsense.

The problem is there is no such thing as an unbiased jury. Nor is there such a thing as an unbiased judge.

But even if there was, the media would never give any publicity to any debate the theory of evolution lost. So what would be the point of the debate?

In 1966, at the Wistar symposium, the theory of evolution lost badly. Several world-famous evolutionists were at the symposium and had no answers for the criticisms of the theory of evolution generated by computer simulations and mathematics. At that time scientists knew a little about DNA, but they had absolutely no clue how sophisticated DNA was. And the theory of evolution still got hammered!!

It didn't matter. After the symposium the evolutionists simply brushed themselves off, and continued to write new evolution books and preach the theory of evolution. They were not interested in finding the truth; they were interested in supporting their egos.

The battle will go on and on and on.

Final Comments About the Theory of Evolution

It has been said that the lottery is a tax on people who are bad at math. Actually, the lottery is a tax on people who are bad at understanding the power of permutations.

In fact, a belief in the theory of evolution is a "tax" on people who are bad at understanding the power of permutations!!

For example, I wrote an encryption program which is "uncrackable." Most people don't think an uncrackable encryption algorithm can be written. Actually, many people can write such an algorithm. All you have to do is have a really big "key" and include some mathematical techniques which cannot be traced backwards from the answer to the raw numbers in the formula or the raw numbers used in the mathematical function.

The general public is under the impression that no matter what encryption algorithms are developed in other countries, our "intelligence community" will be able to crack the code. This is nonsense. Many people around the world know how to write uncrackable encryption algorithms.

The laws forbidding the export of powerful encryption algorithms are designed to pacify the general public into an artificial state of security. Almost all civilized nations have people who can write impossible to crack encryption algorithms.

The federal laws regulating encryption really exist so the "intelligence community" can spy on their own citizens by not allowing them to use "strong encryption." The fourth amendment has been removed from the constitution under the doctrine that every citizen is considered a "suspected terrorist."

Let me talk about my encryption algorithm (and key size). If the entire planet earth were converted into a huge microprocessor, and if the speed of electricity were increased a trillion-fold, my encryption keys could not be cracked in a trillion trillion trillion trillion years. Why? Because I understand the power of permutations.

The "intelligence community" doesn't like permutation-based encryption algorithms because they are impossible to break (if they are done right) because they involve huge, huge permutation exponents. They only allow mathematical-based algorithms because they are easy to break or they allow algorithms which have small keys which can be cracked by brute force with their huge computers.

My algorithm is impossible to break, yet the "key" used in my algorithm is 9,000 times *shorter* that a key would be if it were the size of human DNA. If we converted human DNA into base 10, the number of permutations needed to analyze DNA would be about $10^{1,800,000}$. The number of permutations of my key would be a little over $10^{200,000}$. Remember, there are 10^{100} atoms in 10^{20} Universes. There are $10^{200,000}$ atoms in $10^{199,920}$ Universes. That is why my key cannot be cracked by using "brute force."

I could give the "intelligence community" the source code to my program and they still couldn't crack my keys.

Most people would look at the above permutations of human DNA ($10^{1,800,000}$) and the number of permutations in my key ($10^{200,000}$) and say that a key the size of human DNA would be 9,000 times more difficult to crack than a key the size of my key (1,800,000,000 / 200,000).

That is the problem.

People don't understand how to work with permutations. A key the size of human DNA would be $10^{1,600,000,000}$ *times more difficult to crack* than my key. That is: $10^{(1,800,000-200,000)}$ equals $10^{1,600,000,000}$. People don't understand the power of permutations because they don't understand the mathematics behind it.

If my key is impossible to crack, in a trillion trillion trillion trillion years, using a microprocessor the size of this earth, which is a trillion times faster than electricity; then the theory of evolution is mathematical nonsense. If someone couldn't break my key using a computer the size of this planet, then evolution could not have created a human being, *plus the DNA of 10 million other species*, by random, mindless and directionless mutations, in one billion years or even a quintillion years. It is insane, purely insane to think otherwise.

Even allowing for $10^{200,000}$ permutations of human DNA which could create a unique and viable human being (as always I use numbers which are generous to the theory of evolution); a random permutation of human DNA would only have a probability of leading to a viable human being of $10^{-1,600,000,000}$. This is far, far beyond an insane probability. How about the probability of the other 10 million species on this earth, or which have been on this earth, which have multiple unique gene complexes?

What about consecutive species, meaning the consecutive "lotteries" involved in their random creation?

So what do all the bones of all the species tell us? They tell us God has a very vivid imagination. They also tell us that scientists have very vivid imaginations and that they don't want any competition from God.

Some people think that evolution occurred on some other planet or on some other galaxy or some other Universe and was transported to this earth. Are the laws of permutations different on other planets? Are the laws of chemistry different on other planets? I think not.

The fact is that if evolution didn't happen here, it didn't happen anywhere in any Universe.

Scientists, with their limited intelligence, cannot even begin to comprehend the Universe, thus in their minds they wish to create their own Universe, with themselves at the head.

So what is the truth?

Go outside on some dark, cloudless evening. Look at the stars. Or better yet get a large telescope and look at other galaxies. For every star our ancestors of a thousand years ago could see, we can now see trillions of stars. What you are looking at in the sky *is the handiwork of God*.

When you study a DNA strand, you are looking through a microscope *at the handiwork of God*. No human, and certainly no random series of accidents, could have created human DNA or a single prokaryotic or eukaryotic cell.

When you hold the tiny fingers of a newborn baby, you are holding *the handiwork of God*.

These things are the truth. Scientists are not the center of the Universe.

Most religions consider humans to be the literal children of God. That is true. Perhaps, when the theory of evolution is done away with, we will start to move forward and find out we really are important.

But we are not important because we have made ourselves important by living in a scientific fantasyland; we are important because we know our spirits are the literal children of God and thus God has made us important because we are His children.

That is why we are important!!

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Appendix

Recommended Books and Videos

A Required Movie

It is required to watch this movie: Expelled - No Intelligence Allowed, by Ben Stein. This movie generally gets poor reviews by movie critics because most movie critics are evolutionists or they have no clue what science is all about. Evolutionists don't like this movie!!

But it is an absolutely *superb, superb movie!!!* Ben Stein interviews evolutionists and creation scientists and asks the key question: "Why doesn't the scientific establishment want to consider God." He also asks why college professors got fired for supporting creation science (which is what the title of the movie is based on).

The Top Two Books

There have been many books written in defense of creation science. However, two of these books are head-and-shoulders above the rest from a technical viewpoint. These should be considered required reading for any true student of creation science:

#1) Genetic Entropy & The Mystery of the Genome
by. Dr. J. D. Sanford (Elim Publishing)

While an understanding of the genome is still in its infancy, this world-famous plant biologist, who is not afraid to be on the side of creation science, sets the record straight about how quickly DNA is deteriorating across the board. Because the entire premise of the theory of evolution is to pretend that DNA can dramatically improve via random mutations; this book totally annihilates this proposition using real data from a large number of real geneticists.

Another valuable aspect of this book is in the way it explains why such a high percentage of human DNA is required for life and why the genes need so many other nucleotides in order for proteins to be formed and implemented.

#2) The Edge of Evolution - The Search for the Limits of Darwinism
by Michael J. Behe (Free Press)

Dr. Behe is famous for being the father of "intelligent design," but his new book goes far beyond intelligent design. He discusses point mutations in single-celled microbes and in complex animals. He proves that evolution could never have advanced beyond single-

celled microbes. He also discusses the bacterial flagellum, and other complex designs, from a more advanced viewpoint than his Darwin's Black Box book.

The title of the book refers to the random generation of binding sites on proteins and he mathematically proves that it was impossible for complex structures inside of cells to have "evolved" by random mutations because of the polypeptide folding issue, and more importantly, the "binding site" issues.

Other Excellent Creation Science Books

1) Evolution: A Theory in Crisis
by Dr. Michael Denton

This well-known creationist covers everything from the fossil record and morphology to advanced genetic information.

2) Darwin's Black Box - The Biochemical Challenge to Evolution
by Michael J. Behe

This is the classic book on intelligent design. While the scientific establishment discounts intelligent design, it is not because they have an answer to intelligent design; it is because they do *not* have an answer to intelligent design. Behe's newer book, mentioned above, takes intelligent design a step further.

3) Of Pandas and People - The Central Question of Biological Origins
by Percival Davis and Dean H. Kenyon

Dr. Kenyon was the co-author of Biochemical Predestination (by Dean H. Kenyon and Gary Steinman). Biological Predestination was the classic college textbook on chemical evolution (i.e. the formation of the "first living cell") for about twenty years. The problem was that about five years after co-authoring the biochemical book *he switched from being an evolutionist to a creationist*.

Of Pandas and People is an excellent summary of why creation science is superior to evolution. However, there is one very disappointing aspect of this book: he does not vigorously pursue the issue of amino acid bindings, which is the primary reason he switched to creation science in the first place.

This book has been the center of controversy because it was originally written talking about "creation science", but references to this term were changed to being references of "intelligent design" after the Supreme Court made the term "creation science" illegal to use in schools. This terminology conversion was insignificant from a technical viewpoint, but it gave the evolution establishment a way to divert people's attention away from the excellent content of the book.

4) Darwin on Trial
by Phillip E. Johnson

If you like logic, this is the book for you. Mr. Johnson, an attorney, is frequently at the lead of the creation science side of the evolution debate. His books are full of piercing logic.

5) Icons of Evolution - Science or Myth?
by Jonathan Wells

This is an excellent book on exposing the myths of the arguments of evolution. He goes through the main "icons" (i.e. main arguments) of the theory of evolution one by one and dissects each one with the facts. This is a highly recommended book.

6) Evolution Exposed - Your Evolution Answer Book for the Classroom
by Roger Patterson

This book examines the most popular biology textbooks used in the public schools and exposes error after error in their claims. Most parents have little clue what their children are exposed to in the public classrooms. Highly recommended for people helping youth understand the evolution debate!!

7) Darwin's Enigma, Revised Edition
by Luther D. Sunderland (late)

This is an older book on the evolution debate, but its discussion on the fossil record, and particularly the politics of the fossil record, is excellent. It also includes mention of the Wistar seminar on the mathematics of evolution, which seminar was very, very disturbing to those who supported evolution. However, as might be expected, the way to deal with disturbing facts is to ignore them, and this seminar is never mentioned by the media-controlled evolution establishment.

There are many, many other excellent books on creation science.

DVDs

1) Unlocking the Mystery of Life (DVD)
Illustra Media (www.illustramedia.com)

This movie recounts a seminar involving several of the premier creation scientists (e.g. Denton, Behe, Johnson, etc.). While it was not written to be technically convincing, it is an excellent broad overview of the power of the arguments of creation science and has some excellent graphics on protein synthesis.

2) Incredible Creatures That Defy Evolution I (DVD)
with Dr. Jobe Martin
Exploration Films (www.explorationfilms.com)

This DVD might be termed "super intelligent design." This excellent movie details the complexity of many different species which are so unique they could not have developed these characteristics piecemeal by random mutations. In other words, *these animals are so unique they don't have ancestors*.

3) The Privileged Planet (DVD)
Illustra Media (www.illustramedia.com)

This excellent movie is about the vast number of conditions which must all simultaneously occur in order for a planet to support complex life. It is kind of like "intelligent design," but instead of being at the level of animals, it is at the level of the solar system, and the galaxy. This is a highly recommended movie for those interested in why life exists at all on this planet. We are part of a very, very rare set of conditions, which could only have been very carefully designed by a Creator. One of the co-authors lost his job at a university because of his involvement in the book on which this DVD was based.